Supplemental Table S3. List of proteins identified in the conditioned medium of SCC4 cells.

Protein name	Accession No.	Gene name	Molecular weight (kDa)	Protein probability (%)	No. of unique peptides	No. of unique spectra	Spectral counts	% sequence coverage	Peptide sequence	Best Peptide probability (%)	Mascot score		Calculated MH+	No. of identified spertra				No. of tryptic termini	Peptide index	
											Best ion score	Best identity score		+1	+2	+3	+4		Start No.	Stop No.
1,4-alpha-glucan-branching enzyme	GLGB_HUMAN	GBE1	80.44	100.0	5	6	11	6.55	QFSQILK	95.0	36.4	25.0	863.50	0	1	0	0	2	51	57
									SGEILYR	95.0	29.8	25.0	837.45	0	2	0	0	2	150	156
									QFHLTDDDLLR	95.0	32.0	25.0	1372.69	0	0	2	0	2	566	576
									IIAFER	95.0	34.1	25.0	748.44	0	2	0	0	2	613	618
									IVLDSDAAEYGGHQR	95.0	####	25.0	1630.78	0	2	2	0	2	648	662
116 kDa U5 small nuclear ribonucleoprotein component	U5S1_HUMAN	EFTUD2	109.42	100.0	4	5	11	5.56	TLDELGIHLTK	95.0	54.5	25.0	1239.69	0	2	0	0	2	395	405
									GNEEAQIFRPLK	95.0	38.3	25.0	1401.75	0	2	2	0	2	570	581
									IAVEPVNPSELPK	95.0	67.6	25.0	1392.77	0	3	0	0	2	590	602
									LGEFFQTK	95.0	48.8	25.0	969.50	0	2	0	0	2	714	721
									GGGQIIPTAR	95.0	44.4	25.0	969.55	0	22	0	0	2	804	813
14-3-3 protein beta/alpha	1433B_HUMAN	YWHAB	28.07	100.0	4	5	102	49.20	LAEQAER	95.0	45.7	25.0	816.42	0	8	0	0	2	14	20
									YDDMAAAMK	95.0	62.0	25.0	1047.41	0	7	0	0	2	21	29
									AVTEQGHELSNEER	95.0	####	25.0	1598.74	0	33	14	0	2	30	43
									NLLSVAYK	95.0	50.3	25.0	907.52	0	78	0	0	2	44	51
									NLLSVAYKNVVGAR	95.0	74.1	25.0	1503.86	0	4	2	0	2	44	57
									VISSIEQK	95.0	67.5	25.0	903.51	0	47	0	0	2	63	70
									YLIPNATQPESK	95.0	73.4	25.0	1360.71	0	18	0	0	2	106	117
									MKGDYFR	95.0	33.5	25.0	932.43	0	4	0	0	2	123	129
									YLSEVASGDNK	95.0	68.7	25.0	1182.56	0	35	0	0	2	130	140
									QTTVSNSQQAYQEAFEISK	95.0	####	25.0	2159.03	0	2	0	0	2	141	159
									KEMQPTHPIR	95.0	47.4	25.0	1252.65	0	0	6	0	2	160	169
									EMQPTHPIR	95.0	51.5	25.0	1124.55	0	38	8	0	2	161	169
									DSTLIMQLLR	95.0	73.9	25.0	1205.66	0	85	0	0	2	215	224
14-3-3 protein epsilon	1433E_HUMAN	YWHAE	29.16	100.0	17	21	338	55.70	DDREDLVYQAK	95.0	32.3	25.0	1351.65	0	2	0	0	1	2	12
									LAEQAER	95.0	45.7	25.0	816.42	0	8	0	0	2	13	19
									YDEMVESMK	95.0	40.7	25.0	1163.46	0	8	0	0	2	20	28
									KVAGMDVELTVEER	95.0	71.0	25.0	1591.80	0	4	1	0	2	29	42
									VAGMDVELTVEER	95.0	####	25.0	1463.70	0	8	0	0	2	30	42
									NLLSVAYK	95.0	50.3	25.0	907.52	0	78	0	0	2	43	50
									IISSIEQK	95.0	62.5	25.0	917.53	0	13	0	0	2	62	69
									IISSIEQKEENK	95.0	67.7	25.0	1417.75	0	24	0	0	2	62	73
									QMVETELK	95.0	46.7	25.0	993.49	0	21	0	0	2	87	94
									HLIPAANTGESK	95.0	55.0	25.0	1237.65	0	20	2	0	2	107	118
									YLAEFATGNDR	95.0	60.7	25.0	1256.59	0	11	0	0	2	131	141
									YLAEFATGNDRK	95.0	54.5	25.0	1384.69	0	8	5	0	2	131	142
									KEAAENSLVAYK	95.0	56.6	25.0	1322.70	0	5	0	0	2	142	153
									EAAENSLVAYK	95.0	58.4	25.0	1194.60	0	8	0	0	2	143	153
									AASDIAMTELPPTHPIR	95.0	72.1	25.0	1835.93	0	9	14	0	2	154	170
									DSTLIMQLLR	95.0	73.9	25.0	1205.66	0	85	0	0	2	216	225
									EALQDVEDENQ	95.0	65.6	25.0	1289.55	0	4	0	0	2	245	255
14-3-3 protein eta	1433F_HUMAN	YWHAH	28.20	100.0	6	6	15	38.60	LAEQAER	95.0	45.7	25.0	816.42	0	8	0	0	2	13	19
									YDDMASAMK	95.0	33.2	25.0	1063.41	0	4	0	0	2	20	28
									AVTELNEPLSNEDR	95.0	92.9	25.0	1586.77	0	3	0	0	2	29	42
									NLLSVAYK	95.0	50.3	25.0	907.52	0	78	0	0	2	43	50
									NLLSVAYKNVVGAR	95.0	74.1	25.0	1503.86	0	4	2	0	2	43	56
									VISSIEQK	95.0	67.5	25.0	903.51	0	47	0	0	2	62	69

									YLAEVASGEK	95.0	45.6	25.0	1066.54	0	4	0	0	2	133	142
									KNSVVEASEAAYK	95.0	70.9	25.0	1395.71	0	2	0	0	2	143	155
									NSVVEASEAAYK	95.0	44.0	25.0	1267.62	0	1	0	0	2	144	155
									EQMQPTHPIR	95.0	29.2	25.0	1252.61	0	1	0	0	2	163	172
									DSTLIMQLLR	95.0	73.9	25.0	1205.66	0	85	0	0	2	218	227
14-3-3 protein gamma	1433G_HUMAN	YWHAG	28.29	100.0	7	9	89	44.90	LAEQAER	95.0	45.7	25.0	816.42	0	8	0	0	2	13	19
									YDDMAAAMK	95.0	62.0	25.0	1047.41	0	7	0	0	2	20	28
									NVTELNEPLSNEER	95.0	97.2	25.0	1643.79	0	30	0	0	2	29	42
									NLLSVAYK	95.0	50.3	25.0	907.52	0	78	0	0	2	43	50
									NLLSVAYKNVVGAR	95.0	74.1	25.0	1503.86	0	4	2	0	2	43	56
									VISSIEQK	95.0	67.5	25.0	903.51	0	47	0	0	2	62	69
									NCSETQYESK	95.0	34.2	25.0	1245.51	0	1	0	0	2	111	120
									YLAEVATGEK	95.0	69.5	25.0	1080.56	0	23	0	0	2	133	142
									ATVVESSEK	95.0	27.1	25.0	949.48	0	1	0	0	2	144	152
									AYSEAHEISK	95.0	72.8	25.0	1134.54	0	23	1	0	2	153	162
									EHMQPTHPIR	95.0	34.6	25.0	1261.61	0	1	2	0	2	163	172
									DSTLIMQLLR	95.0	73.9	25.0	1205.66	0	85	0	0	2	218	227
14-3-3 protein sigma	1433S_HUMAN	SFN	27.76	100.0	9	10	150	38.70	LAEQAER	95.0	45.7	25.0	816.42	0	8	0	0	2	12	18
									LAEQAERYEDMAAFMK	95.0	30.8	25.0	1934.86	0	0	2	0	2	12	27
									YEDMAAFMK	95.0	28.9	25.0	1137.46	0	2	0	0	2	19	27
									NLLSVAYK	95.0	50.3	25.0	907.52	0	78	0	0	2	42	49
									NLLSVAYKNVVGGQR	95.0	57.1	25.0	1617.91	0	2	0	0	2	42	56
									VLSSIEQK	95.0	67.5	25.0	903.51	0	47	0	0	2	61	68
									SNEEGSEEKGPEVR	95.0	####	25.0	1546.70	0	51	38	0	2	69	82
									YLAEVATGDDK	95.0	82.2	25.0	1181.57	0	17	0	0	2	130	140
									YLAEVATGDDKK	95.0	49.2	25.0	1309.66	0	8	0	0	2	130	141
									SAYQEAMDISK	95.0	61.1	25.0	1258.56	0	19	0	0	2	149	159
									SAYQEAMDISKK	95.0	51.8	25.0	1386.66	0	5	0	0	2	149	160
									EMPPTNPIR	95.0	38.5	25.0	1070.53	0	6	0	0	2	161	169
									DSTLIMQLLR	95.0	73.9	25.0	1205.66	0	85	0	0	2	215	224
14-3-3 protein theta	1433T_HUMAN	YWHAQ	27.75	100.0	11	12	190	46.90	TELIQK	95.0	34.8	25.0	731.43	0	2	0	0	2	4	9
									LAEQAER	95.0	45.7	25.0	816.42	0	8	0	0	2	12	18
									AVTEQGAELSNEER	95.0	####	25.0	1532.72	0	45	0	0	2	28	41
									NLLSVAYK	95.0	50.3	25.0	907.52	0	78	0	0	2	42	49
									NLLSVAYKNVVGGR	95.0	55.5	25.0	1489.85	0	2	0	0	2	42	55
									VISSIEQK	95.0	67.5	25.0	903.51	0	47	0	0	2	61	68
									EKVESELR	95.0	38.6	25.0	989.53	0	8	0	0	2	84	91
									YLIANATNPESK	95.0	73.2	25.0	1320.68	0	27	0	0	2	104	115
									MKGDYFR	95.0	33.5	25.0	932.43	0	4	0	0	2	121	127
									KQTIDNSQGAYQEAFDISK	95.0	####	25.0	2143.03	0	2	0	0	2	139	157
									QTIDNSQGAYQEAFDISKK	95.0	49.4	25.0	2143.03	0	0	1	0	2	140	158
									KEMQPTHPIR	95.0	47.4	25.0	1252.65	0	0	6	0	2	158	167
									EMQPTHPIR	95.0	51.5	25.0	1124.55	0	38	8	0	2	159	167
									DSTLIMQLLR	95.0	73.9	25.0	1205.66	0	85	0	0	2	213	222
14-3-3 protein zeta/delta	1433Z_HUMAN	YWHAZ	27.73	100.0	9	11	253	42.40	LAEQAER	95.0	45.7	25.0	816.42	0	8	0	0	2	12	18
									YDDMAACMK	95.0	34.4	25.0	1136.41	0	1	0	0	2	19	27
									SVTEQGAELSNEER	95.0	####	25.0	1548.71	0	82	0	0	2	28	41
									NLLSVAYK	95.0	50.3	25.0	907.52	0	78	0	0	2	42	49
									NLLSVAYKNVVGAR	95.0	74.1	25.0	1503.86	0	4	2	0	2	42	55
									VVSSIEQK	95.0	70.0	25.0	889.50	0	17	0	0	2	61	68
									EKIETELR	95.0	41.5	25.0	1017.56	0	13	0	0	2	84	91

									IETELR	95.0	34.0	25.0	760.42	0	5	0	0	2	86	91
									FLIPNASQAESK	95.0	62.2	25.0	1304.68	0	25	0	0	2	104	115
									YLAEVAAGDDK	95.0	63.5	25.0	1151.56	0	1	0	0	2	128	138
									YLAEVAAGDDKK	95.0	72.3	25.0	1279.65	0	73	30	0	2	128	139
									KEMQPTHPIR	95.0	47.4	25.0	1252.65	0	0	6	0	2	158	167
									EMQPTHPIR	95.0	51.5	25.0	1124.55	0	38	8	0	2	159	167
									DSTLIMQLLR	95.0	73.9	25.0	1205.66	0	85	0	0	2	213	222
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3	PLCB3_HUMAN	PLCB3	138.78	100.0	4	4	19	3.48	EVLGFGGPDAR	95.0	59.3	25.0	1117.56	0	8	0	0	2	88	98
									YEPNQQFLER	95.0	42.0	25.0	1323.63	0	6	0	0	2	279	288
									SPMEFVEYNK	95.0	37.8	25.0	1259.56	0	3	0	0	2	632	641
									EVVLDANTTQFK	95.0	59.8	25.0	1364.71	0	2	0	0	2	1070	1081
26S protease regulatory subunit 6A	PRS6A_HUMAN	PSMC3	49.19	100.0	3	3	15	9.57	AMEVDERPTEQYSDIGGLDK	95.0	48.3	25.0	2269.03	0	0	2	0	2	174	193
									GVLMYGPPGTGK	95.0	39.2	25.0	1192.60	0	2	0	0	2	222	233
									VDILDPALLR	95.0	61.0	25.0	1124.67	0	11	0	0	2	335	344
26S protease regulatory subunit 7	PRS7_HUMAN	PSMC2	48.62	100.0	10	10	25	21.70	ALDEGDIALLK	95.0	48.4	25.0	1157.64	0	2	0	0	2	24	34
									IINADSEDPK	95.0	38.8	25.0	1101.54	0	1	0	0	2	101	110
									YQIHIPLPPK	95.0	20.3	25.0	1205.70	0	0	1	0	2	147	156
									FVNLGIEPPK	95.0	57.9	25.0	1113.63	0	5	0	0	2	201	210
									GVLLFGPPGTGK	95.0	57.8	25.0	1142.66	0	9	0	0	2	211	222
									VIGSELVQK	95.0	30.8	25.0	972.57	0	1	0	0	2	240	248
									FDDGAGGDNEVQR	95.0	68.5	25.0	1379.58	0	2	0	0	2	285	297
									FELLAR	95.0	31.5	25.0	748.44	0	2	0	0	2	370	375
									IATEKDFLEAVNK	95.0	56.6	25.0	1477.79	0	1	0	0	2	403	415
									DFLEAVNK	95.0	41.1	25.0	935.48	0	1	0	0	2	408	415
26S protease regulatory subunit 8	PRS8_HUMAN	PSMC5	45.61	100.0	9	10	21	27.60	IEELQLIVNDK	95.0	84.1	25.0	1313.73	0	2	0	0	2	28	38
									VDPLVSLMMVEK	95.0	62.9	25.0	1392.71	0	2	0	0	2	131	142
									VPDSTYEMIGGLDK	95.0	97.6	25.0	1540.72	0	2	0	0	2	143	156
									HPELFEALGIAQPK	95.0	47.5	25.0	1549.84	0	2	2	0	2	171	184
									ELFVMAR	95.0	29.0	25.0	881.46	0	2	0	0	2	233	239
									LEGGSGGDSEVQR	95.0	35.2	25.0	1290.59	0	3	0	0	2	259	271
									IDILDSALLRPGR	95.0	28.2	25.0	1438.84	0	2	0	0	2	298	310
									IAELMPGASGAEVK	95.0	50.9	25.0	1388.71	0	2	0	0	2	347	360
									VHVTQEDFEMAVAK	95.0	50.8	25.0	1619.77	0	2	0	0	2	376	389
26S protease regulatory subunit S10B	PRS10_HUMAN	PSMC6	44.16	100.0	3	3	9	8.48	ALQSVGQIVGEVLK	95.0	65.0	25.0	1440.84	0	5	0	0	2	49	62
									VALDMTTLTIMR	95.0	89.2	25.0	1396.72	0	2	0	0	2	98	109
									VGIIPPK	95.0	33.5	25.0	723.48	0	2	0	0	2	162	168
26S proteasome non-ATPase regulatory subunit 1	PSMD1_HUMAN	PSMD1	105.82	100.0	5	5	9	5.25	QFAALVASK	95.0	46.7	25.0	934.54	0	2	0	0	2	58	66
									NNNTDLMILK	95.0	26.8	25.0	1191.60	0	1	0	0	2	345	354
									EALQLMATYLPK	95.0	33.5	25.0	1393.74	0	1	0	0	2	418	429
									QDVYDLLK	95.0	47.5	25.0	993.53	0	3	0	0	2	491	498
									VSTAVLSITAK	95.0	79.3	25.0	1089.65	0	2	0	0	2	828	838
26S proteasome non-ATPase regulatory subunit 11	PSD11_HUMAN	PSMD11	47.45	100.0	8	9	19	22.50	EASIDILHSIVK	95.0	75.3	25.0	1324.75	0	4	0	0	2	21	32
									TGQAAELGGLLK	95.0	63.6	25.0	1157.65	0	2	0	0	2	60	71
									YVRPFLNSISK	95.0	21.8	25.0	1323.74	0	0	1	0	2	72	82
									LVSLYFDTK	95.0	51.2	25.0	1085.59	0	2	0	0	2	133	141
									YQEALHLGSQLLR	95.0	68.5	25.0	1527.83	0	2	4	0	2	143	155
									IMLNTPEDVQALVSGK	95.0	46.9	25.0	1730.90	0	2	0	0	2	259	274
									TYEAALETIQNMSK	95.0	83.4	25.0	1614.77	0	1	0	0	2	396	409
									VVDSLYNK	95.0	31.0	25.0	937.50	0	1	0	0	2	410	417
26S proteasome non-ATPase regulatory subunit	PSD12_HUMAN	PSMD12	52.89	100.0	4	4	13	7.68	IYVEIER	95.0	35.2	25.0	921.50	0	1	0	0	2	136	142
									VEFILEQMR	95.0	75.0	25.0	1180.60	0	4	0	0	2	183	191

12									LFTTMELMR	95.0	52.3	25.0	1173.56	0	4	0	0	2	308	316
									LNSLMSLVNK	95.0	48.4	25.0	1134.62	0	4	0	0	2	432	441
26S proteasome non-ATPase regulatory subunit 13	PSD13_HUMAN	PSMD13	42.90	100.0	5	5	14	14.40	QMTDPNVALTFLEK	95.0	68.8	25.0	1622.81	0	3	0	0	2	86	99
									LNIGDLQVTK	95.0	53.9	25.0	1100.63	0	2	0	0	2	123	132
									QLTFEEIAK	95.0	34.9	25.0	1078.58	0	1	0	0	2	290	298
									ITVNEVELLVMK	95.0	87.3	25.0	1403.78	0	6	0	0	2	302	313
									GSIDEVDKR	95.0	37.2	25.0	1018.52	0	2	0	0	2	322	330
26S proteasome non-ATPase regulatory subunit 2	PSMD2_HUMAN	PSMD2	100.18	100.0	15	16	50	20.60	APVQPQQSPAAAPGGTDEKPSGK	95.0	44.7	25.0	2218.11	0	0	4	0	2	9	31
									DTSLYRPALEELR	95.0	33.6	25.0	1562.82	0	2	0	0	2	67	79
									DTSLYRPALEELRR	95.0	33.4	25.0	1718.92	0	0	1	0	2	67	80
									EWQELDDAEK	95.0	44.0	25.0	1262.55	0	2	0	0	2	169	178
									FGGSGSQVDSAR	95.0	84.4	25.0	1167.54	0	6	0	0	2	358	369
									YLYSSEDYIK	95.0	32.2	25.0	1280.60	0	2	0	0	2	432	441
									SGALLACGIVNSGVR	95.0	88.5	25.0	1473.78	0	2	0	0	2	442	456
									EDVLTLLLPVMGDSK	95.0	39.2	25.0	1645.87	0	1	0	0	2	495	509
									SETELKDTYAR	95.0	49.9	25.0	1312.64	0	4	0	0	2	546	556
									LNILDTLSK	95.0	37.8	25.0	1016.60	0	3	0	0	2	704	712
									DPNNLFMVR	95.0	60.5	25.0	1121.54	0	8	0	0	2	755	763
									LAQGLTHLGK	95.0	40.4	25.0	1037.61	0	1	0	0	2	764	773
									SHYVLYGLVAAMQPR	95.0	31.9	25.0	1720.88	0	0	2	0	2	814	828
									VGQAVDVVGQAGKPK	95.0	77.7	25.0	1452.82	0	6	2	0	2	846	860
									TITGFQTHTTPVLLAHGER	95.0	53.1	25.0	2079.10	0	0	4	0	2	861	879
26S proteasome non-ATPase regulatory subunit 3	PSMD3_HUMAN	PSMD3	60.96	100.0	5	5	14	9.93	ELDTVTLEDIK	95.0	59.6	25.0	1275.67	0	2	0	0	2	66	76
									AVQGFFTSNNATR	95.0	80.3	25.0	1412.69	0	4	0	0	2	116	128
									FNQVLDQFGEK	95.0	63.4	25.0	1324.65	0	2	0	0	2	375	385
									ISLADIAQK	95.0	47.2	25.0	958.56	0	5	0	0	2	417	425
									EQQDLEFAK	95.0	41.6	25.0	1107.53	0	1	0	0	2	515	523
26S proteasome non-ATPase regulatory subunit 5	PSMD5_HUMAN	PSMD5	56.18	100.0	7	7	13	14.50	LEAPLEELR	95.0	57.1	25.0	1069.59	0	2	0	0	2	15	23
									ALHSVLQAVPLNELR	95.0	51.9	25.0	1659.95	0	2	0	0	2	24	38
									LGPLFSLLNENHR	95.0	37.7	25.0	1509.82	0	3	0	0	2	46	58
									LLQAMEPVHVAR	95.0	58.8	25.0	1379.75	0	1	0	0	2	71	82
									GLIHPDDSVK	95.0	30.0	25.0	1080.57	0	1	0	0	2	91	100
									YPIFVEK	95.0	34.4	25.0	895.49	0	2	0	0	2	293	299
									DPLELFR	95.0	28.5	25.0	889.48	0	2	0	0	2	394	400
26S proteasome non-ATPase regulatory subunit 6	PSMD6_HUMAN	PSMD6	45.52	100.0	4	4	7	7.20	FLLSLPEHR	95.0	33.7	25.0	1111.63	0	2	0	0	2	24	32
									RLDEELEDAEK	95.0	42.8	25.0	1346.64	0	1	0	0	2	83	93
									LDEELEDAEK	95.0	54.8	25.0	1190.54	0	2	0	0	2	84	93
									KGDLLLNR	95.0	38.0	25.0	928.56	0	2	0	0	2	372	379
26S proteasome non-ATPase regulatory subunit 7	PSD7_HUMAN	PSMD7	37.01	100.0	3	3	6	10.80	NDIAINELMK	95.0	42.8	25.0	1176.59	0	2	0	0	2	104	113
									DIKDTTVGTLSQR	95.0	52.1	25.0	1433.76	0	2	0	0	2	178	190
									SVVALHNLINNK	95.0	24.5	25.0	1321.76	0	0	2	0	2	268	279
2-oxoglutarate dehydrogenase, mitochondrial	ODO1_HUMAN	OGDH	115.92	100.0	3	3	10	2.35	FEEFLQR	95.0	38.7	25.0	968.48	0	4	0	0	2	264	270
									LSGQDVER	95.0	43.2	25.0	903.45	0	2	0	0	2	673	680
									KPLIIFTPK	95.0	48.9	25.0	1056.68	0	4	0	0	2	852	860
3'(2'),5'-bisphosphate nucleotidase 1	BPNT1_HUMAN	BPNT1	33.37	100.0	4	5	16	14.60	VIAEGDLGIVEK	95.0	56.6	25.0	1242.69	0	4	0	0	2	29	40
									IIQLIEGK	95.0	50.3	25.0	913.57	0	4	0	0	2	225	232
									LTDIHGNVLQYHK	95.0	63.3	25.0	1537.81	0	2	2	0	2	262	274
									HMNSAGVLATLR	95.0	57.4	25.0	1285.67	0	4	0	0	2	278	289
3,2-trans-enoyl-CoA isomerase, mitochondrial	D3D2_HUMAN	DCI	32.80	100.0	4	4	14	14.20	VLVEPDAGAGVAVMK	95.0	86.5	25.0	1471.78	0	4	0	0	2	47	61
									ILADNPR	95.0	29.1	25.0	798.45	0	4	0	0	2	165	171
									DADVQNFVSFISK	95.0	69.6	25.0	1469.73	0	1	0	0	2	271	283

									SLQMYLER	95.0	43.3	25.0	1055.52	0	5	0	0	2	289	296
3-hydroxyisobutyrate dehydrogenase, mitochondrial	3HIDH_HUMAN	HIBADH	35.31	100.0	6	6	24	25.00	TPVGFIGLGNMGNPMAK	95.0	55.7	25.0	1735.85	0	3	0	0	2	40	56
									EFQDAGEQVVSSPADVAEK	95.0	91.2	25.0	2005.94	0	4	0	0	2	77	95
									KGSLLIDSSTIDPAVSK	95.0	73.0	25.0	1730.95	0	2	0	0	2	125	141
									GSLLIDSSTIDPAVSK	95.0	####	25.0	1602.86	0	5	0	0	2	126	141
									MGAVFMDAPVSGGVGAAR	95.0	88.2	25.0	1724.81	0	4	0	0	2	150	167
									DLGLAQDSATSTK	95.0	64.6	25.0	1306.65	0	6	0	0	2	285	297
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	HIBCH_HUMAN	HIBCH	43.47	100.0	3	3	7	8.81	IAPVFFR	95.0	30.1	25.0	849.50	0	3	0	0	2	113	119
									LAMLEEDLLALK	95.0	60.6	25.0	1374.76	0	2	0	0	2	222	233
									ENIASVLENYHTESK	95.0	68.7	25.0	1733.83	0	2	0	0	2	238	252
40S ribosomal protein S11	RS11_HUMAN	RPS11	18.41	100.0	6	6	12	21.50	VLLGETGK	95.0	32.1	25.0	816.48	0	1	0	0	2	23	30
									NIGLGFK	95.0	32.0	25.0	748.44	0	3	0	0	2	39	45
									EAIEGTYIDK	95.0	38.4	25.0	1138.56	0	3	0	0	2	49	58
									EAIEGTYIDKK	95.0	28.4	25.0	1266.66	0	1	0	0	2	49	59
									RDYLHYIR	95.0	31.7	25.0	1135.60	0	0	2	0	2	90	97
									DYLHYIR	95.0	27.9	25.0	979.50	0	2	0	0	2	91	97
40S ribosomal protein S13	RS13_HUMAN	RPS13	17.21	100.0	3	3	9	15.20	GLSQSALPYR	95.0	49.9	25.0	1091.58	0	2	0	0	2	10	19
									KGLTPSQIGVILR	95.0	45.9	25.0	1381.85	0	2	0	0	2	43	55
									GLTPSQIGVILR	95.0	53.8	25.0	1253.76	0	5	0	0	2	44	55
40S ribosomal protein S14	RS14_HUMAN	RPS14	16.25	100.0	3	4	21	22.50	ELGITALHIK	95.0	52.1	25.0	1094.66	0	5	1	0	2	87	96
									TPGPGAQSALR	95.0	68.5	25.0	1054.56	0	13	0	0	2	107	117
									IEDVTPIPSDSTR	95.0	63.3	25.0	1429.72	0	2	0	0	2	129	141
40S ribosomal protein S15a	RS15A_HUMAN	RPS15A	14.82	100.0	3	3	5	22.30	FLTVMMK	95.0	33.7	25.0	901.45	0	2	0	0	2	37	43
									HGYIGEFEIIDDHR	95.0	46.9	25.0	1700.80	0	0	2	0	2	44	57
									IVVNLTGR	95.0	49.9	25.0	871.54	0	1	0	0	2	61	68
40S ribosomal protein S16	RS16_HUMAN	RPS16	16.43	100.0	7	8	29	37.70	GPLQSVQVFGR	95.0	67.0	25.0	1187.65	0	2	0	0	2	5	15
									LLEPVLLLGK	95.0	41.8	25.0	1094.72	0	9	0	0	2	51	60
									FAGVDIR	95.0	47.1	25.0	777.43	0	9	0	0	2	63	69
									ALVAYYQK	95.0	29.8	25.0	955.52	0	1	0	0	2	91	98
									EIKDILIQYDR	95.0	67.1	25.0	1405.77	0	4	2	0	2	107	117
									DILIQYDR	95.0	36.3	25.0	1035.55	0	1	0	0	2	110	117
									TLLVADPR	95.0	30.2	25.0	884.52	0	1	0	0	2	118	125
40S ribosomal protein S18	RS18_HUMAN	RPS18	17.70	100.0	6	6	37	34.90	VLNTNIDGR	95.0	59.3	25.0	1001.54	0	12	0	0	2	15	23
									IAFAITAIK	95.0	68.7	25.0	947.59	0	6	0	0	2	26	34
									KADIDLTK	95.0	35.4	25.0	903.51	0	3	0	0	2	47	54
									AGELTEDEVER	95.0	40.8	25.0	1247.58	0	4	0	0	2	56	66
									VITIMQNPR	95.0	49.9	25.0	1087.59	0	11	0	0	2	67	75
									LREDLER	95.0	28.2	25.0	930.50	0	1	0	0	2	107	113
40S ribosomal protein S19	RS19_HUMAN	RPS19	16.04	100.0	4	4	10	20.00	DVNQQEFVR	95.0	51.8	25.0	1134.55	0	3	0	0	2	8	16
									RVLQALEGLK	95.0	41.1	25.0	1126.69	0	2	0	0	2	102	111
									VLQALEGLK	95.0	50.5	25.0	970.59	0	4	0	0	2	103	111
									IAGQVAAANK	95.0	35.2	25.0	942.54	0	1	0	0	2	134	143
40S ribosomal protein S2	RS2_HUMAN	RPS2	31.31	100.0	4	5	28	13.00	LSIVPVR	95.0	29.7	25.0	783.51	0	6	0	0	2	160	166
									GTGIVSAPVPK	95.0	42.8	25.0	1025.60	0	8	0	0	2	201	211
									ATFDAISK	95.0	33.0	25.0	852.45	0	1	0	0	2	239	246
									SPYQEFTDHLVK	95.0	56.5	25.0	1463.72	0	7	6	0	2	264	275
40S ribosomal protein S23	RS23_HUMAN	RPS23	15.79	100.0	4	4	17	23.80	ANPFGGASHAK	95.0	31.9	25.0	1056.52	0	3	0	0	2	38	48
									KGHAVGDIPGVR	95.0	21.0	25.0	1205.68	0	0	1	0	2	108	119
									GHAVGDIPGVR	95.0	35.5	25.0	1077.58	0	5	0	0	2	109	119
									VANVSLLALYK	95.0	72.0	25.0	1190.71	0	8	0	0	2	125	135
40S ribosomal protein S25	RS25_HUMAN	RPS25	13.73	100.0	4	4	20	24.00	DKLNNLVLFDK	95.0	60.7	25.0	1318.74	0	4	0	0	2	42	52

									LNNLVLFDK	95.0	43.5	25.0	1075.61	0	3	0	0	2	44	52
									LITPAVVSER	95.0	47.3	25.0	1084.64	0	4	0	0	2	67	76
									AALQELLSK	95.0	69.4	25.0	972.57	0	9	0	0	2	86	94
40S ribosomal protein S3	RS3_HUMAN	RPS3	26.67	100.0	9	10	60	39.50	AELNEFLTR	95.0	68.9	25.0	1092.57	0	15	0	0	2	19	27
									ELAEDGYSGVEVR	95.0	88.6	25.0	1423.67	0	13	0	0	2	28	40
									TEIIILATR	95.0	53.8	25.0	1029.63	0	11	0	0	2	46	54
									ELTAVVQK	95.0	40.2	25.0	887.52	0	1	0	0	2	68	75
									LLGGLAVR	95.0	57.2	25.0	798.52	0	4	0	0	2	109	116
									QGVLGIK	95.0	28.0	25.0	714.45	0	2	0	0	2	179	185
									KPLPDHVSIVEPK	95.0	46.4	25.0	1458.83	0	2	6	0	2	202	214
									DEILPTTPISEQK	95.0	36.2	25.0	1470.77	0	2	0	0	2	215	227
									GGKPEPPAMPQPVPTA	95.0	34.7	25.0	1589.80	0	4	0	0	2	228	243
40S ribosomal protein S3a	RS3A_HUMAN	RPS3A	29.93	100.0	7	7	25	25.40	VVDPFSK	95.0	28.5	25.0	791.43	0	1	0	0	2	21	27
									APAMFNIR	95.0	49.2	25.0	935.48	0	6	0	0	2	35	42
									LITEDVQGK	95.0	28.9	25.0	1002.55	0	1	0	0	2	86	94
									TTDGYLLR	95.0	48.1	25.0	938.49	0	8	0	0	2	129	136
									TSYAQHQQVR	95.0	44.6	25.0	1217.60	0	4	0	0	2	153	162
									LMELHGEGSSSGK	95.0	35.9	25.0	1347.62	0	4	0	0	2	228	240
									ADGYEPPVQESV	95.0	28.6	25.0	1290.58	0	1	0	0	2	253	264
40S ribosomal protein S4, X isoform	RS4X_HUMAN	RPS4X	29.58	100.0	7	7	17	23.60	GIPHLVTHDAR	95.0	27.2	25.0	1215.66	0	1	0	0	2	135	145
									YPDPLIK	95.0	29.7	25.0	845.48	0	1	0	0	2	149	155
									IGVITNR	95.0	27.0	25.0	772.47	0	1	0	0	2	192	198
									HPGSFDVVHVK	95.0	55.0	25.0	1221.64	0	0	2	0	2	201	211
									DANGNSFATR	95.0	46.8	25.0	1052.48	0	4	0	0	2	212	221
									LSNIFVIGK	95.0	71.8	25.0	990.60	0	7	0	0	2	222	230
									LTIAEER	95.0	30.5	25.0	831.46	0	1	0	0	2	246	252
40S ribosomal protein S8	RS8_HUMAN	RPS8	24.19	100.0	4	4	53	23.10	IIDVVYNASNNELVR	95.0	54.9	25.0	1718.91	0	0	2	0	2	78	92
									LTPEEEEILNK	95.0	61.3	25.0	1314.68	0	21	0	0	2	129	139
									ISSLLEEQFQQGK	95.0	79.8	25.0	1506.78	0	23	0	0	2	158	170
									ADGYVLEGK	95.0	47.9	25.0	951.48	0	7	0	0	2	185	193
40S ribosomal protein S9	RS9_HUMAN	RPS9	22.57	100.0	6	6	41	24.20	LIGEYGLR	95.0	55.3	25.0	920.52	0	6	0	0	2	31	38
									LFEGNALLR	95.0	75.4	25.0	1032.58	0	16	0	0	2	71	79
									IGVLDEGK	95.0	56.6	25.0	830.46	0	2	0	0	2	84	91
									LDYILGLK	95.0	42.0	25.0	934.56	0	8	0	0	2	94	101
									IEDFLER	95.0	48.8	25.0	921.47	0	7	0	0	2	102	108
									LQTQVFK	95.0	39.5	25.0	863.50	0	2	0	0	2	110	116
40S ribosomal protein SA	RSSA_HUMAN	RPSA	32.84	100.0	6	7	59	21.70	KSDGIYIINLK	95.0	79.5	25.0	1263.73	0	9	0	0	2	42	52
									SDGIYIINLK	95.0	66.6	25.0	1135.64	0	20	0	0	2	43	52
									AIVAIENPADVSVISSR	95.0	64.4	25.0	1740.95	0	1	0	0	2	64	80
									FAAATGATPIAGR	95.0	94.2	25.0	1203.65	0	12	0	0	2	90	102
									LLVVTDPR	95.0	54.1	25.0	912.55	0	8	0	0	2	121	128
									DPEEIEKEEQAAAEK	95.0	95.0	25.0	1715.80	0	7	2	0	2	206	220
4-aminobutyrate aminotransferase, mitochondrial	GABT_HUMAN	ABAT	56.42	100.0	8	8	11	14.60	VDVEFDYDGPLMK	95.0	62.8	25.0	1543.70	0	1	0	0	2	35	47
									GNYLVDVDGNR	95.0	58.6	25.0	1221.59	0	2	0	0	2	82	92
									QSLLSVAPK	95.0	34.3	25.0	942.56	0	1	0	0	2	145	153
									YPLEEFVK	95.0	36.8	25.0	1024.54	0	1	0	0	2	253	260
									REDLLNNAAHAGK	95.0	46.6	25.0	1408.73	0	0	2	0	2	401	413
									EDLLNNAAHAGK	95.0	28.6	25.0	1252.63	0	1	0	0	2	402	413
									ALLTGLLDLQAR	95.0	72.0	25.0	1283.77	0	2	0	0	2	414	425
									YPQFISR	95.0	30.8	25.0	910.48	0	1	0	0	2	426	432
4F2 cell-surface antigen	4F2_HUMAN	SLC3A2	67.98	100.0	9	9	101	15.40	VAEDEAEAAAAAK	95.0	90.6	25.0	1245.60	0	12	0	0	2	148	160

heavy chain									LDYLSSLK	95.0	43.3	25.0	938.52	0	17	0	0	2	248	255
									GLVLGPIHK	95.0	37.9	25.0	933.59	0	7	0	0	2	258	266
									EDFDSLLQSAK	95.0	65.8	25.0	1252.61	0	18	0	0	2	288	298
									VILDLTPNYR	95.0	56.6	25.0	1203.67	0	25	0	0	2	304	313
									SLVTQYLNATGNR	95.0	41.0	25.0	1436.75	0	2	0	0	2	417	429
									ADLLLSTQPGR	95.0	50.2	25.0	1170.65	0	9	0	0	2	593	603
									EEGSPLELER	95.0	46.5	25.0	1158.56	0	9	0	0	2	604	613
									LKLEPHEGLLLR	95.0	36.6	25.0	1417.85	0	0	2	0	2	614	625
4-trimethylaminobutyraldehyde dehydrogenase	AL9A1_HUMAN	ALDH9A1	53.78	100.0	3	3	6	5.87	ILLEAAR	95.0	32.3	25.0	785.49	0	2	0	0	2	76	82
									GIKPVTLELGGK	95.0	21.4	25.0	1211.74	0	0	2	0	2	247	258
									IGDPLLEDTR	95.0	76.8	25.0	1128.59	0	2	0	0	2	317	326
5'-3' exoribonuclease 2	XRN2_HUMAN	XRN2	108.57	100.0	4	4	6	5.26	LLYMAIDGVAPR	95.0	75.6	25.0	1334.71	0	2	0	0	2	97	108
									NLTVILSDASAPGEGEHK	95.0	31.8	25.0	1837.93	0	0	1	0	2	190	207
									NSLGGDVLFVGK	95.0	55.5	25.0	1205.65	0	2	0	0	2	677	688
									TLGHVMPR	95.0	29.4	25.0	926.49	0	1	0	0	2	817	824
5'-AMP-activated protein kinase subunit gamma-1	AAKG1_HUMAN	PRKAG1	37.56	100.0	3	3	10	9.67	AFFALVTNGVR	95.0	68.2	25.0	1194.66	0	2	0	0	2	60	70
									FDVINLAAEK	95.0	61.0	25.0	1119.60	0	6	0	0	2	244	253
									LVVVDENDVVK	95.0	35.4	25.0	1228.68	0	2	0	0	2	300	310
5'-nucleotidase	5NTD_HUMAN	NT5E	63.35	100.0	4	4	7	8.36	FPILSANIK	95.0	34.0	25.0	1002.60	0	3	0	0	2	137	145
									YPFIVTSDDGR	95.0	55.2	25.0	1269.61	0	2	0	0	2	263	273
									VPVVQAYAFGK	95.0	29.8	25.0	1178.66	0	1	0	0	2	275	285
									HDSGDQDINVVSTYISK	95.0	29.1	25.0	1877.89	0	0	1	0	2	518	534
5-oxoprolinase	OPLA_HUMAN	OPLAH	137.44	100.0	5	5	9	4.11	ILEQEAGMLLPR	95.0	53.6	25.0	1385.75	0	2	0	0	2	54	65
									DQPLDSSHIASIR	95.0	72.9	25.0	1438.73	0	1	0	0	2	66	78
									ITDPEILESR	95.0	57.9	25.0	1172.62	0	2	0	0	2	1145	1154
									EEALLSVLTER	95.0	41.8	25.0	1259.68	0	2	0	0	2	1188	1198
									GLNLLIR	95.0	38.8	25.0	798.52	0	2	0	0	2	1215	1221
60 kDa heat shock protein, mitochondrial	CH60_HUMAN	HSPD1	61.04	100.0	10	10	57	20.10	LVQDVANNTNEEAGDGTTTATVLAR	95.0	52.4	25.0	2560.25	0	0	2	0	2	97	121
									GANPVEIR	95.0	30.1	25.0	855.47	0	2	0	0	2	134	141
									TLNDELEIIEGMK	95.0	74.9	25.0	1520.75	0	6	0	0	2	206	218
									GYISPYFINTSK	95.0	73.3	25.0	1389.70	0	8	0	0	2	222	233
									VGLQVVAVK	95.0	72.7	25.0	912.59	0	10	0	0	2	293	301
									VGEVIVTK	95.0	44.3	25.0	844.51	0	4	0	0	2	345	352
									VGGTSDVEVNEK	95.0	57.4	25.0	1233.60	0	9	0	0	2	406	417
									VTDALNATR	95.0	63.2	25.0	960.51	0	7	0	0	2	421	429
									IGIEIIK	95.0	41.8	25.0	785.51	0	5	0	0	2	463	469
									NAGVEGSLIVEK	95.0	53.8	25.0	1215.66	0	4	0	0	2	482	493
60 kDa SS-A/Ro ribonucleoprotein	RO60_HUMAN	TROVE2	60.65	100.0	4	4	6	8.55	LGLENAEALIR	95.0	82.4	25.0	1198.68	0	2	0	0	2	53	63
									GGMALALAVTK	95.0	53.4	25.0	1047.59	0	2	0	0	2	160	170
									LSHLKPSSEGLAIVTK	95.0	38.4	25.0	1679.97	0	1	0	0	2	185	200
									ALDAAFYK	95.0	27.9	25.0	898.47	0	1	0	0	2	352	359
60S acidic ribosomal protein P0	RLA0_HUMAN	RPLP0	34.26	100.0	5	5	35	17.70	IIQLLDDYPK	95.0	79.7	25.0	1217.68	0	13	0	0	2	17	26
									GHLENNPALEK	95.0	37.2	25.0	1221.62	0	1	0	0	2	67	77
									GNVGFVFTK	95.0	50.3	25.0	968.52	0	11	0	0	2	84	92
									EDLTEIRDMLLANK	95.0	28.5	25.0	1676.85	0	1	0	0	2	93	106
									TSFFQALGITTK	95.0	74.9	25.0	1313.71	0	9	0	0	2	135	146
60S acidic ribosomal protein P2	RLA2_HUMAN	RPLP2	11.65	100.0	3	3	8	24.30	ILDSVGIEADDDR	95.0	83.3	25.0	1417.68	0	2	0	0	2	26	38
									ILDSVGIEADDDRLNK	95.0	76.7	25.0	1772.90	0	2	0	0	2	26	41
									NIEDVIAQGIGK	95.0	92.7	25.0	1256.68	0	4	0	0	2	50	61
60S ribosomal protein L10	RL10_HUMAN	RPL10	24.59	100.0	3	3	6	13.10	IFDLGR	95.0	34.8	25.0	720.40	0	2	0	0	2	33	38
									MLSCAGADR	95.0	27.2	25.0	996.42	0	1	0	0	2	102	110

									FNADEFEDMVAEK	95.0	82.6	25.0	1560.65	0	3	0	0	2	176	188
60S ribosomal protein L10a	RL10A_HUMAN	RPL10A	24.81	100.0	3	4	10	16.10	DTLYEAVR	95.0	44.0	25.0	966.49	0	3	0	0	2	8	15
									KYDAFLASESLIK	95.0	76.7	25.0	1484.80	0	4	0	0	2	106	118
									FPSLLTHNENMVAK	95.0	53.1	25.0	1616.81	0	2	1	0	2	134	147
60S ribosomal protein L11	RL11_HUMAN	RPL11	20.24	100.0	3	3	15	16.90	VLEQLTGQTPVFSK	95.0	92.1	25.0	1546.85	0	6	0	0	2	39	52
									AEEILEK	95.0	39.8	25.0	831.45	0	4	0	0	2	79	85
									YDGIILPGK	95.0	58.6	25.0	975.55	0	5	0	0	2	170	178
60S ribosomal protein L13	RL13_HUMAN	RPL13	24.24	100.0	4	4	32	19.40	GFSLEELR	95.0	45.8	25.0	950.49	0	5	0	0	2	75	82
									TIGISVDPR	95.0	40.8	25.0	957.54	0	20	0	0	2	93	101
									STESLQANVQR	95.0	52.4	25.0	1232.62	0	4	0	0	2	106	116
									LATQLTGPVMPVR	95.0	48.1	25.0	1398.78	0	3	0	0	2	146	158
60S ribosomal protein L17	RL17_HUMAN	RPL17	21.38	100.0	5	6	19	23.90	YSLDPENPTK	95.0	56.7	25.0	1163.56	0	6	0	0	2	4	13
									KSAEFLLHMLK	95.0	19.4	25.0	1332.73	0	0	1	0	2	86	96
									SAEFLLHMLK	95.0	39.2	25.0	1204.64	0	2	1	0	2	87	96
									NAESNAELK	95.0	28.9	25.0	975.47	0	1	0	0	2	97	105
									EQIVPKPEEEVAQK	95.0	54.2	25.0	1623.86	0	8	0	0	2	154	167
60S ribosomal protein L18	RL18_HUMAN	RPL18	21.62	100.0	3	3	9	18.10	TNSTFNQVVLK	95.0	58.9	25.0	1250.67	0	6	0	0	2	39	49
									TNRPPLSLSR	95.0	25.2	25.0	1140.65	0	0	2	0	2	56	65
									TAVVVGTITDDVR	95.0	57.1	25.0	1345.73	0	1	0	0	2	79	91
60S ribosomal protein L26	RL26_HUMAN	RPL26	17.24	100.0	5	5	19	21.40	HFNAPSHIR	95.0	20.5	25.0	1078.55	0	0	1	0	2	18	26
									KDDEVQVVR	95.0	72.7	25.0	1087.57	0	9	0	0	2	51	59
									DDEVQVVR	95.0	47.6	25.0	959.48	0	6	0	0	2	52	59
									VVQVYR	95.0	28.5	25.0	763.45	0	1	0	0	2	70	75
									YVIYIER	95.0	41.1	25.0	955.52	0	2	0	0	2	78	84
60S ribosomal protein L27	RL27_HUMAN	RPL27	15.78	100.0	3	4	14	20.60	VVLVLAGR	95.0	43.4	25.0	826.55	0	4	0	0	2	10	17
									VYNYNHLMPTR	95.0	46.4	25.0	1423.68	0	2	1	0	2	74	84
									YSVDIPLDK	95.0	37.8	25.0	1049.55	0	7	0	0	2	85	93
60S ribosomal protein L30	RL30_HUMAN	RPL30	12.77	100.0	3	3	10	18.30	KSLESINSR	95.0	27.2	25.0	1033.56	0	2	0	0	2	9	17
									KSEIEYYAMLAK	95.0	67.5	25.0	1461.73	0	4	0	0	2	57	68
									SEIEYYAMLAK	95.0	80.5	25.0	1333.63	0	4	0	0	2	58	68
60S ribosomal protein L35a	RL35A_HUMAN	RPL35A	12.52	100.0	3	3	12	25.50	AIFAGYK	95.0	26.8	25.0	769.42	0	2	0	0	2	9	15
									DETEFYLGK	95.0	50.8	25.0	1101.51	0	8	0	0	2	37	45
									NNTVTPGGKPNK	95.0	30.5	25.0	1226.65	0	2	0	0	2	55	66
60S ribosomal protein L5	RL5_HUMAN	RPL5	34.35	100.0	4	4	26	13.10	DIICQIAYAR	95.0	48.1	25.0	1222.63	0	2	0	0	2	59	68
									GAVDGGLSIPHSTK	95.0	89.9	25.0	1338.70	0	11	0	0	2	165	178
									EFNAEVHR	95.0	42.1	25.0	1001.48	0	7	0	0	2	189	196
									QFSQYIK	95.0	34.7	25.0	913.48	0	6	0	0	2	222	228
60S ribosomal protein L6	RL6_HUMAN	RPL6	32.71	100.0	5	5	25	15.60	IDISNVK	95.0	29.7	25.0	788.45	0	2	0	0	2	201	207
									HLTDAYFK	95.0	30.4	25.0	994.50	0	4	0	0	2	211	218
									HQEGEIFDTEK	95.0	58.4	25.0	1332.61	0	10	0	0	2	227	237
									AVDSQILPK	95.0	40.7	25.0	970.56	0	6	0	0	2	252	260
									AIPQLQGYLR	95.0	44.0	25.0	1158.66	0	3	0	0	2	263	272
60S ribosomal protein L7	RL7_HUMAN	RPL7	29.21	100.0	5	5	36	17.30	AGNFYVPAEPK	95.0	60.5	25.0	1192.60	0	12	0	0	2	78	88
									LAFVIR	95.0	34.3	25.0	718.46	0	12	0	0	2	89	94
									ASINMLR	95.0	46.4	25.0	820.43	0	5	0	0	2	128	134
									SVNELIYK	95.0	44.5	25.0	965.53	0	5	0	0	2	149	156
									IALTDNALIAR	95.0	73.6	25.0	1170.68	0	2	0	0	2	167	177
60S ribosomal protein L7a	RL7A_HUMAN	RPL7A	29.98	100.0	4	5	43	14.70	NFGIGQDIQPK	95.0	66.3	25.0	1216.63	0	8	0	0	2	38	48
									VPPAINQFTQALDR	95.0	53.8	25.0	1569.84	0	1	0	0	2	76	89
									AGVNTVTTLVENK	95.0	92.8	25.0	1345.73	0	28	0	0	2	138	150
									AGVNTVTTLVENKK	95.0	74.3	25.0	1473.83	0	4	2	0	2	138	151

60S ribosomal protein L8	RL8_HUMAN	RPL8	28.01	100.0	3	3	11	13.20	AVDFAER	95.0	33.5	25.0	807.40	0	2	0	0	2	31	37
									ASGNYATVISHNPETK	95.0	61.9	25.0	1688.82	0	2	0	0	2	129	144
									AVVGVVAGGGR	95.0	48.4	25.0	941.55	0	7	0	0	2	164	174
6-phosphofructokinase type C	K6PP_HUMAN	PFKP	85.58	100.0	6	6	14	9.95	AIGVLTSGGDAQGMNAAVR	95.0	####	25.0	1803.90	0	4	0	0	2	26	44
									ELVVTQLGYDTR	95.0	89.4	25.0	1393.73	0	4	0	0	2	290	301
									LPDDQIPK	95.0	27.1	25.0	925.50	0	1	0	0	2	401	408
									YLEEIATQMR	95.0	52.3	25.0	1269.61	0	2	0	0	2	487	496
									DLQSNVEHLTEK	95.0	66.0	25.0	1412.70	0	2	0	0	2	614	625
									NVLGHMQQGGAPSPFDR	95.0	19.5	25.0	1826.86	0	0	1	0	2	667	683
6-phosphofructokinase, liver type	K6PL_HUMAN	PFKL	85.00	99.5	2	2	3	6.03	AIGVLTSGGDAQGMNAAVR	95.0	####	25.0	1803.90	0	4	0	0	2	17	35
									IMEVIDAITTTAQSHQR	95.0	58.9	25.0	1929.97	0	0	2	0	2	185	201
									AVAFSPVTELK	95.0	44.0	25.0	1161.65	0	1	0	0	2	716	726
6-phosphogluconate dehydrogenase, decarboxylating	6PGD_HUMAN	PGD	53.12	100.0	9	9	69	18.00	VDDFLANEAK	95.0	76.1	25.0	1121.55	0	9	0	0	2	39	48
									VVGAQSLK	95.0	46.8	25.0	801.48	0	4	0	0	2	52	59
									AGQAVDDFIEK	95.0	64.2	25.0	1192.58	0	11	0	0	2	77	87
									GILFVGSGVSGGEEGAR	95.0	####	25.0	1591.81	0	22	0	0	2	120	136
									YGPSLMPGGNK	95.0	53.7	25.0	1136.54	0	6	0	0	2	137	147
									TIFQGIAAK	95.0	42.0	25.0	948.55	0	4	0	0	2	155	163
									SFLEDIR	95.0	36.6	25.0	879.46	0	4	0	0	2	318	324
									SFLEDIRK	95.0	33.6	25.0	1007.55	0	6	0	0	2	318	325
									HEMLPASLIQAQR	95.0	49.5	25.0	1509.78	0	3	0	0	2	435	447
6-phosphogluconolactonase	6PGL_HUMAN	PGLS	27.53	100.0	5	6	12	24.00	ELPAAVAPAGPASLAR	95.0	41.1	25.0	1490.83	0	2	0	0	2	57	72
									IVAPISDSPKPPPQR	95.0	64.6	25.0	1601.90	0	4	1	0	2	171	185
									VTLTLPVLNAAR	95.0	72.9	25.0	1267.77	0	2	0	0	2	186	197
									TVIFVATGEGK	95.0	57.8	25.0	1121.62	0	2	0	0	2	198	208
									LLTVPFEK	95.0	28.3	25.0	946.56	0	1	0	0	2	247	254
72 kDa type IV collagenase	MMP2_HUMAN	MMP2	73.87	100.0	5	5	11	6.21	FPFLFNGK	95.0	30.3	25.0	969.52	0	2	0	0	2	235	242
									LSQDDIK	95.0	29.3	25.0	818.43	0	1	0	0	2	433	439
									GEIFFFK	95.0	31.7	25.0	887.47	0	3	0	0	2	483	489
									IDAVYEAPQEEK	95.0	66.5	25.0	1391.67	0	4	0	0	2	520	531
									MDPGFPK	95.0	29.7	25.0	807.37	0	1	0	0	2	598	604
78 kDa glucose-regulated protein	GRP78_HUMAN	HSPA5	72.32	100.0	22	25	230	35.50	VEIIANDQGNR	95.0	72.8	25.0	1228.63	0	130	0	0	2	50	60
									ITPSYVAFTPEGER	95.0	70.2	25.0	1566.78	0	2	0	0	2	61	74
									NQLTSNPENTVFDAK	95.0	####	25.0	1677.81	0	47	0	0	2	82	96
									KTKPYIQVDIGGGQTK	95.0	31.8	25.0	1732.96	0	0	2	0	2	123	138
									TKPYIQVDIGGGQTK	95.0	53.0	25.0	1604.86	0	0	2	0	2	124	138
									TFAPEEISAMVLTK	95.0	96.1	25.0	1552.79	0	10	0	0	2	139	152
									MKETAEAYLGK	95.0	69.3	25.0	1256.62	0	6	6	0	2	153	163
									ETAEAYLGK	95.0	37.4	25.0	981.49	0	3	0	0	2	155	163
									DAGTIAGLNVMR	95.0	83.5	25.0	1233.63	0	29	0	0	2	186	197
									IINEPTAAAIAYGLDK	95.0	94.0	25.0	1659.90	0	7	0	0	2	198	213
									VMEHFIK	95.0	39.4	25.0	919.47	0	2	0	0	2	262	268
									FEELNMDLFR	95.0	49.1	25.0	1329.61	0	2	0	0	2	327	336
									VLEDSDLK	95.0	27.1	25.0	918.48	0	2	0	0	2	345	352
									VLEDSDLKK	95.0	40.3	25.0	1046.57	0	3	0	0	2	345	353
									KSDIDEIVLVGGSTR	95.0	####	25.0	1588.85	0	4	4	0	2	353	367
									SDIDEIVLVGGSTR	95.0	89.7	25.0	1460.76	0	11	0	0	2	354	367
									IQQLVK	95.0	40.5	25.0	728.47	1	3	0	0	2	371	376
									EFFNGKEPSR	95.0	38.8	25.0	1210.59	0	2	0	0	2	377	386
									SQIFSTASDNQPTVTIK	95.0	####	25.0	1836.93	0	14	0	0	2	448	464
									VYEGERPLTK	95.0	47.7	25.0	1191.64	0	15	0	0	2	465	474

									ITITNDQNR	95.0	50.9	25.0	1074.55	0	15	0	0	2	524	532
									LTPEEIER	95.0	29.8	25.0	986.52	0	1	0	0	2	533	540
									NELESYAYSLK	95.0	70.9	25.0	1316.64	0	18	0	0	2	563	573
									ELEEIVQPIISK	95.0	76.3	25.0	1397.79	0	26	0	0	2	622	633
Abhydrolase domain-containing protein 11	ABHDB_HUMAN	ABHD11	34.67	100.0	4	5	10	17.80	TAMLLALQRPELVER	95.0	42.9	25.0	1755.98	0	0	2	0	2	146	160
									LADEQLSSVIQDMAVR	95.0	79.8	25.0	1790.90	0	2	0	0	2	201	216
									QHLLTNLVEVDGR	95.0	78.2	25.0	1493.81	0	2	2	0	2	217	229
									VNLDALTQHLDK	95.0	76.0	25.0	1366.73	0	2	0	0	2	234	245
Acetyl-CoA acetyltransferase, cytosolic	THIC_HUMAN	ACAT2	41.33	100.0	3	4	9	6.80	EIVPVLVSTR	95.0	41.0	25.0	1112.67	0	2	0	0	2	201	210
									TDEFPR	95.0	31.7	25.0	764.36	0	2	0	0	2	218	223
									ILVTLLHTLER	95.0	65.8	25.0	1307.80	0	3	2	0	2	362	372
Acidic leucine-rich nuclear phosphoprotein 32 family member A	AN32A_HUMAN	ANP32A	28.57	99.5	2	2	11	13.70	RIHLELR	95.0	33.8	25.0	936.57	0	3	0	0	2	6	12
									IHLELR	95.0	38.9	25.0	780.47	0	4	0	0	2	7	12
									ELVLDNSR	95.0	53.0	25.0	945.50	0	4	0	0	2	21	28
									KLELSDNR	95.0	47.2	25.0	974.53	0	7	0	0	2	68	75
									IKDLSTIEPLK	95.0	46.4	25.0	1256.75	0	4	4	0	2	100	110
									DLSTIEPLK	95.0	38.0	25.0	1015.57	0	4	0	0	2	102	110
Acidic leucine-rich nuclear phosphoprotein 32 family member B	AN32B_HUMAN	ANP32B	28.77	100.0	7	9	47	19.90	RIHLELR	95.0	33.8	25.0	936.57	0	3	0	0	2	6	12
									IHLELR	95.0	38.9	25.0	780.47	0	4	0	0	2	7	12
									KLELSENR	95.0	44.2	25.0	988.54	0	11	0	0	2	68	75
									IFGGLDMLAEK	95.0	64.3	25.0	1209.62	0	10	0	0	2	76	86
									LPNLTHLNLSGNK	95.0	64.9	25.0	1420.79	0	5	2	0	2	87	99
									LKDISTLEPLK	95.0	46.4	25.0	1256.75	0	4	4	0	2	100	110
									DISTLEPLK	95.0	38.0	25.0	1015.57	0	4	0	0	2	102	110
Aconitate hydratase, mitochondrial	ACON_HUMAN	ACO2	85.41	100.0	13	14	37	18.10	NINIVR	95.0	26.8	25.0	728.44	0	1	0	0	2	51	56
									LNRPLTLSEK	95.0	19.9	25.0	1170.68	0	0	1	0	2	59	68
									IVYGHLDDPASQEIER	95.0	33.5	25.0	1841.90	0	0	4	0	2	69	84
									VAGILTVK	95.0	38.9	25.0	800.52	0	3	0	0	2	251	258
									SQFTITPGSEQIR	95.0	52.9	25.0	1463.75	0	2	0	0	2	412	424
									DGYAQILR	95.0	54.8	25.0	935.49	0	4	0	0	2	430	437
									FNPETDYLTGTDGKK	95.0	74.4	25.0	1685.80	0	2	0	0	2	507	521
									FRLEAPDADELPK	95.0	46.8	25.0	1500.77	0	1	0	0	2	522	534
									LEAPDADELPK	95.0	58.6	25.0	1197.60	0	2	0	0	2	524	534
									GEFDPGQDTYQHPPK	95.0	59.5	25.0	1715.77	0	2	0	0	2	535	549
									DSSGQHVDVSPTSQR	95.0	60.4	25.0	1599.74	0	3	2	0	2	550	564
									NAVTQEFGPVPDTAR	95.0	94.8	25.0	1601.79	0	8	0	0	2	634	648
									LTIQGLK	95.0	51.8	25.0	772.49	0	2	0	0	2	724	730
Actin-like protein 6A	ACL6A_HUMAN	ACTL6A	47.44	100.0	5	5	10	13.30	QGGPTYYIDTNALR	95.0	94.2	25.0	1568.77	0	2	0	0	2	63	76
									ENMEAISPLK	95.0	31.2	25.0	1147.57	0	1	0	0	2	80	89
									TAVLTAFANGR	95.0	47.9	25.0	1120.61	0	1	0	0	2	154	164
									IPEGLFDPSNVK	95.0	40.0	25.0	1315.69	0	1	0	0	2	304	315
									LIANNTTVER	95.0	57.3	25.0	1130.62	0	5	0	0	2	380	389
Actin-related protein 2	ARP2_HUMAN	ACTR2	44.74	100.0	7	9	30	19.80	VGNIEIK	95.0	34.4	25.0	772.46	0	5	0	0	2	47	53
									LNIDTR	95.0	31.7	25.3	731.40	0	1	0	0	2	98	103
									ILLTEPPMNPTK	95.0	72.1	25.0	1369.74	0	6	0	0	2	107	118
									RLDIAGR	95.0	48.4	25.0	800.47	0	5	0	0	2	181	187
									GYAFNHSADFETVR	95.0	78.1	25.0	1613.73	0	4	2	0	2	201	214
									HIVLSGGSTMYPGLPSR	95.0	85.4	25.0	1787.91	0	3	0	0	2	300	316
									HMVFLGGAVLADIMK	95.0	59.7	25.0	1633.84	0	2	2	0	2	352	366
Actin-related protein 2/3 complex subunit 1A	ARC1A_HUMAN	ARPC1A	41.55	100.0	3	4	6	9.19	TQIALSPNNHEVHIYK	95.0	62.4	25.0	1863.97	0	1	1	0	2	21	36
									FAVGSGAR	95.0	30.2	25.0	764.40	0	1	0	0	2	111	118

									TLESSIQGLR	95.0	84.9	25.0	1103.61	0	3	0	0	2	359	368
Actin-related protein 2/3 complex subunit 2	ARPC2_HUMAN	ARPC2	34.32	100.0	10	13	51	32.00	MILLEVNNR	95.0	55.4	25.0	1117.60	0	2	0	0	2	1	9
									IIEETLALK	95.0	50.7	25.0	1029.62	0	2	0	0	2	10	18
									ELQAHGADELLK	95.0	73.1	25.0	1323.69	0	5	0	0	2	66	77
									DSIVHQAGMLK	95.0	47.5	25.0	1214.62	0	4	0	0	2	107	117
									YFQFQEEGK	95.0	38.6	25.0	1175.54	0	3	0	0	2	128	136
									YFQFQEEGKEGENR	95.0	79.7	25.0	1760.79	0	2	4	0	2	128	141
									DDETMYVESK	95.0	61.6	25.0	1232.50	0	11	0	0	2	148	157
									VFMQEFK	95.0	45.7	25.0	944.45	0	2	0	0	2	180	186
									ASHTAPQVLFSHR	95.0	43.8	25.0	1450.75	0	4	2	0	2	191	203
									DNTINLIHTFR	95.0	53.2	25.0	1343.71	0	6	4	0	2	238	248
Actin-related protein 2/3 complex subunit 3	ARPC3_HUMAN	ARPC3	20.53	100.0	4	6	32	23.00	PAYHSSLMDPDTK	95.0	40.5	25.0	1477.66	0	2	2	0	1	2	14
									LIGNMALLPIR	95.0	43.0	25.0	1226.73	0	1	0	0	2	15	25
									ANVFFK	95.0	44.8	25.0	725.40	0	10	0	0	2	51	56
									VFDPQNDKPSK	95.0	49.6	25.0	1274.64	0	16	1	0	2	148	158
Actin-related protein 2/3 complex subunit 4	ARPC4_HUMAN	ARPC4	19.65	100.0	5	6	43	28.00	HNKPEVEVR	95.0	48.6	25.0	1107.59	0	15	2	0	2	33	41
									ELLLQPVTISR	95.0	63.4	25.0	1268.76	0	11	0	0	2	45	55
									VLIEGSINSVR	95.0	76.7	25.0	1186.68	0	3	0	0	2	61	71
									AENFFILR	95.0	60.4	25.0	1009.55	0	9	0	0	2	98	105
									IVAEEFLK	95.0	54.0	25.0	948.54	0	3	0	0	2	159	166
Actin-related protein 2/3 complex subunit 5-like protein	ARP5L_HUMAN	ARPC5L	16.92	100.0	3	3	9	20.90	AFHAALR	95.0	31.2	25.0	785.44	0	2	0	0	2	56	62
									SSEIEQAVQSLDR	95.0	97.6	25.0	1461.72	0	4	0	0	2	90	102
									ALAVGGLGSIIR	95.0	67.7	25.0	1126.69	0	3	0	0	2	134	145
Actin-related protein 3	ARP3_HUMAN	ACTR3	47.35	100.0	10	11	40	24.20	LPACVVDCGTGYTK	95.0	70.9	25.0	1540.71	0	2	0	0	2	5	18
									FMEQVIFK	95.0	38.5	25.0	1057.54	0	3	0	0	2	92	99
									DREVGIPPEQSLETAK	95.0	####	25.0	1768.91	0	4	2	0	2	210	225
									EVGIPPEQSLETAK	95.0	41.7	25.0	1497.78	0	1	0	0	2	212	225
									YSYVCPDLVK	95.0	40.9	25.0	1243.60	0	2	0	0	2	231	240
									EFNKYDTDGSK	95.0	42.7	25.0	1303.58	0	3	0	0	2	241	251
									EFSIDVGYER	95.0	48.7	25.0	1214.57	0	4	0	0	2	266	275
									NIVLSGGSTMFR	95.0	75.1	25.0	1297.66	0	8	0	0	2	318	329
									LSEELSGGR	95.0	59.1	25.0	947.48	0	10	0	0	2	349	357
									DYEEIGPSICR	95.0	46.9	25.0	1338.60	0	1	0	0	2	399	409
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1_HUMAN	AHSA1	38.26	100.0	5	5	45	15.70	LDGEASINNR	95.0	73.4	25.0	1088.53	0	24	0	0	2	64	73
									DEPDTNLVALMK	95.0	60.6	25.0	1361.66	0	6	0	0	2	126	137
									EAMGIYISTLK	95.0	46.0	25.0	1241.64	0	9	0	0	2	146	156
									ETFLTSPEELYR	95.0	45.4	25.0	1484.73	0	4	0	0	2	213	224
									QTFGYGAR	94.9	26.6	25.0	899.44	0	2	0	0	2	329	336
Acylamino-acid-releasing enzyme	ACPH_HUMAN	APEH	81.21	100.0	5	5	20	6.97	ALDVSASDDEIAR	95.0	77.7	25.0	1361.65	0	4	0	0	2	181	193
									VTSVVVDVVPR	95.0	55.2	25.0	1169.69	0	2	0	0	2	340	350
									VGFLPSAGK	95.0	30.4	25.0	875.50	0	2	0	0	2	435	443
									TPLLLMLGQEDR	95.0	81.9	25.0	1401.74	0	9	0	0	2	665	676
									LLLYPK	95.0	40.3	25.0	746.48	0	3	0	0	2	699	704
Acyl-protein thioesterase 1	LYPA1_HUMAN	LYPLA1	24.65	100.0	3	3	11	13.90	ALIDQEVK	95.0	53.0	25.0	915.51	0	3	0	0	2	98	105
									ASFPQGPIGGANR	95.0	44.0	25.0	1271.65	0	5	0	0	2	150	162
									TLVNPANVTFK	95.0	47.2	25.0	1203.67	0	3	0	0	2	191	201
Adapter molecule crk	CRK_HUMAN	CRK	33.81	100.0	6	6	16	21.70	QEAVALLQGQR	95.0	59.5	25.0	1212.67	0	2	0	0	2	21	31
									DSSTSPGDYVLSVSENSR	95.0	85.7	25.0	1899.86	0	6	0	0	2	39	56
									QGSGVILR	95.0	35.5	25.0	829.49	0	1	0	0	2	123	130
									QEEAEYVR	95.0	35.4	25.0	1023.47	0	3	0	0	2	131	138
									TALALEVGELVK	95.0	83.0	25.0	1242.73	0	2	0	0	2	254	265

									GHFPFTHVR	95.0	27.1	25.0	1097.56	0	0	2	0	2	284	292
Adenosine kinase	ADK_HUMAN	ADK	40.53	100.0	9	9	19	19.90	YSLKPNDQILAEDKHK	95.0	48.0	25.0	1899.00	0	0	2	0	2	48	63
									HKELFDELVK	95.0	22.4	25.0	1257.68	0	0	2	0	2	62	71
									ELFDELVK	95.0	42.7	25.0	992.53	0	4	0	0	2	64	71
									ELFDELVKK	95.0	28.3	25.0	1120.63	0	1	0	0	2	64	72
									FKVEYHAGGSTQNSIK	95.0	31.1	25.0	1765.89	0	0	1	0	2	73	88
									FGEILK	95.0	29.7	25.0	706.41	0	3	0	0	2	112	117
									HLDLEK	95.0	27.7	25.0	754.41	0	1	0	0	2	166	171
									IVIFTQGR	95.0	40.8	25.0	933.55	0	4	0	0	2	278	285
									AGHYAASIIIR	95.0	53.5	25.0	1171.66	0	1	0	0	2	339	349
Adenosylhomocysteinase	SAHH_HUMAN	AHCY	47.70	100.0	13	17	159	27.80	ALDIAENEMPGLMR	95.0	77.9	25.0	1591.75	0	18	1	0	2	21	34
									YPQLLPGIR	95.0	46.2	25.0	1056.62	0	19	0	0	2	143	151
									GISEETTTGVHNLYK	95.0	81.2	25.0	1648.82	0	7	2	0	2	152	166
									VPAINVNDSVTK	95.0	82.6	25.0	1256.68	0	30	0	0	2	175	186
									ESLIDGIK	95.0	46.2	25.0	874.49	0	6	0	0	2	197	204
									ATDVMIAGK	95.0	75.7	25.0	921.47	0	14	0	0	2	206	214
									VAVVAGYGDVGK	95.0	76.1	25.0	1134.62	0	3	0	0	2	215	226
									VNIKPQVDR	95.0	39.8	25.0	1068.62	0	2	0	0	2	319	327
									RIILLAEGR	95.0	46.0	25.0	1040.66	0	4	0	0	2	335	343
									IILLAEGR	95.0	62.3	25.0	884.56	0	38	0	0	2	336	343
									YPVGVHFLPK	95.0	64.0	25.0	1156.65	0	2	7	0	2	379	388
									KLDEAVAEAHLGK	95.0	97.3	25.0	1380.75	0	3	0	0	2	389	401
									LDEAVAEAHLGK	95.0	61.7	25.0	1252.65	0	2	1	0	2	390	401
Adenylate kinase 2, mitochondrial	KAD2_HUMAN	AK2	26.46	100.0	5	5	12	23.40	AVLLGPPGAGK	95.0	44.0	25.0	979.59	0	2	0	0	2	18	28
									AMVASGSELGK	95.0	33.2	25.0	1065.52	0	2	0	0	2	52	62
									LVSDEMVVELIEK	95.0	77.7	25.0	1519.79	0	4	0	0	2	73	85
									NGFLLDGFPR	95.0	73.2	25.0	1135.59	0	2	0	0	2	94	103
									QAEMLDDLMEK	95.0	64.5	25.0	1354.59	0	2	0	0	2	107	117
Adenylate kinase isoenzyme 1	KAD1_HUMAN	AK1	21.62	100.0	5	5	54	26.80	IIFVVGGPGSGK	95.0	70.2	25.0	1130.66	0	20	0	0	2	10	21
									GFLIDGYPR	95.0	44.9	25.0	1037.54	0	4	0	0	2	89	97
									EVQQGEEFER	95.0	56.7	25.0	1250.56	0	13	0	0	2	98	107
									VDDNEETIKK	95.0	39.3	25.0	1190.59	0	12	0	0	2	139	148
									ATEPVIAFYEK	95.0	66.1	25.0	1267.66	0	5	0	0	2	156	166
Adenylyl cyclase-associated protein 1	CAP1_HUMAN	CAP1	51.84	100.0	6	7	55	11.20	HAEMVHTGLK	95.0	19.9	25.0	1138.57	0	0	1	0	2	72	81
									LSDLLAPISEQIK	95.0	79.7	25.0	1426.82	0	34	1	0	2	101	113
									EMNDAAMFYTNR	95.0	63.0	25.0	1494.60	0	4	0	0	2	156	167
									KEPAVLELEGK	95.0	40.0	25.0	1212.68	0	0	6	0	2	317	327
									EPAVLELEGK	95.0	44.2	25.0	1084.59	0	8	0	0	2	318	327
									QVAYIYK	95.0	27.6	25.0	884.49	0	1	0	0	2	349	355
ADP/ATP translocase 2	ADT2_HUMAN	SLC25A5	32.88	100.0	3	3	5	11.10	DFLAGGVAAAISK	95.0	84.7	25.0	1219.67	0	2	0	0	2	11	23
									QIFLGGVDK	95.0	27.6	25.0	976.55	0	2	0	0	2	97	105
									AAYFGIYDTAK	95.0	34.1	25.0	1219.60	0	1	0	0	2	189	199
ADP-ribosylation factor 1	ARF1_HUMAN	ARF1	20.68	100.0	3	3	20	28.20	ILMVGLDAAGK	95.0	78.2	25.0	1103.61	0	14	0	0	2	20	30
									MLAEDELR	95.0	43.6	25.0	992.47	0	5	0	0	2	110	117
									DAVLLVFANK	95.0	76.9	25.0	1089.63	0	22	0	0	2	118	127
									QDLPNAMNAAEITDK	95.0	81.8	25.0	1646.77	0	7	0	0	2	128	142
									LGLHSLR	95.0	44.3	25.0	795.48	0	8	0	0	2	143	149
ADP-ribosylation factor 4	ARF4_HUMAN	ARF4	20.49	100.0	5	5	26	29.40	ILMVGLDAAGK	95.0	78.2	25.0	1103.61	0	14	0	0	2	20	30
									IQEVADELQK	95.0	55.5	25.0	1172.62	0	3	0	0	2	100	109
									DAVLLLFANK	95.0	48.4	25.0	1103.65	0	2	0	0	2	118	127
									QDLPNAMAISEMTDK	95.0	69.0	25.0	1695.76	0	3	0	0	2	128	142

									LGLQSLR	95.0	34.9	25.0	786.48	0	4	0	0	2	143	149
ADP-ribosylation factor 5	ARF5_HUMAN	ARF5	20.51	100.0	3	3	25	21.10	ILMVGLDAAGK	95.0	78.2	25.0	1103.61	0	14	0	0	2	20	30
									VQESADELQK	95.0	30.5	25.0	1146.56	0	1	0	0	2	100	109
									DAVLLVFANK	95.0	76.9	25.0	1089.63	0	22	0	0	2	118	127
									LGLQHLR	95.0	35.4	25.0	836.51	0	2	0	0	2	143	149
ADP-sugar pyrophosphatase	NUDT5_HUMAN	NUDT5	24.31	100.0	6	7	23	29.70	QYIISEELISEGK	95.0	55.6	25.0	1508.78	0	2	0	0	2	15	27
									TTYMDPTGK	95.0	26.9	25.0	1029.46	0	1	0	0	2	34	42
									EQTADGVAVIPVLQR	95.0	91.4	25.0	1595.88	0	10	2	0	2	56	70
									NDLLQR	95.0	43.0	25.0	758.42	0	2	0	0	2	176	181
									VYSYALALK	95.0	43.7	25.0	1027.58	0	2	0	0	2	197	205
									HANAKPFEVPFLK	95.0	31.0	25.0	1497.82	0	0	4	0	2	206	218
Afadin	AFAD_HUMAN	MLLT4	206.79	100.0	3	3	10	2.08	VSSTATTQDVIETLAEK	95.0	85.5	25.0	1792.92	0	6	0	0	2	62	78
									IVQATTLLTMDK	95.0	73.8	25.0	1349.73	0	2	0	0	2	846	857
									QQQLEEMRK	95.0	32.1	25.0	1205.59	0	0	2	0	2	1613	1621
Agrin	AGRIN_HUMAN	AGRN	214.82	100.0	12	13	66	6.26	VLGAPVPAFEGR	95.0	52.5	25.0	1212.67	0	16	0	0	2	1369	1380
									SFLAFPTLR	95.0	44.9	25.0	1051.59	0	4	0	0	2	1381	1389
									LALEFR	95.0	28.6	25.0	748.44	0	5	0	0	2	1396	1401
									GKDFLALALLDGR	95.0	59.2	25.0	1388.79	0	1	0	0	2	1417	1429
									LLDVNNQR	95.0	31.4	25.0	971.53	0	1	0	0	2	1522	1529
									LELGIGPGAATR	95.0	39.1	25.0	1154.65	0	4	0	0	2	1530	1541
									TDGKGDFVSLALR	95.0	38.4	25.0	1378.73	0	1	1	0	2	1684	1696
									GDFVSLALR	95.0	62.3	25.0	977.54	0	13	0	0	2	1688	1696
									VLGESPVPHTVLNLK	95.0	60.8	25.0	1602.92	0	2	0	0	2	1746	1760
									EPLYVGGAPDFSK	95.0	42.9	25.0	1379.68	0	3	0	0	2	1761	1773
									SAGDVDTLAFDGR	95.0	89.4	25.0	1323.62	0	14	0	0	2	1860	1872
									TFVEYLNAVTESEK	95.0	64.9	25.0	1629.80	0	1	0	0	2	1873	1886
Alanyl-tRNA synthetase, cytoplasmic	SYAC_HUMAN	AARS	106.80	100.0	6	6	18	7.44	VGAEDADGIDMAYR	95.0	77.4	25.0	1498.65	0	6	0	0	2	283	296
									TITVALADGGRPDNTGR	95.0	48.6	25.0	1713.89	0	0	3	0	2	304	320
									DIINEEEVQFLK	95.0	57.7	25.0	1476.76	0	1	0	0	2	373	384
									GLVVDMDGFEEER	95.0	69.4	25.0	1511.67	0	4	0	0	2	433	445
									GLEVTDDSPK	95.0	40.6	25.0	1060.52	0	3	0	0	2	477	486
									FDFTAK	95.0	28.2	25.0	728.36	0	1	0	0	2	636	641
Alcohol dehydrogenase [NADP+]	AK1A1_HUMAN	AKR1A1	36.56	100.0	7	7	25	22.20	YALSVGYR	95.0	42.3	25.0	928.49	0	4	0	0	2	35	42
									EELFVTSK	95.0	34.8	25.0	952.50	0	1	0	0	2	73	80
									ALEALVAK	95.0	58.7	25.0	814.50	0	5	0	0	2	146	153
									GLVQALGLSNFNSR	95.0	24.9	25.0	1475.80	0	0	2	0	2	154	167
									GLEVTAYSPLGSSDR	95.0	56.1	25.0	1551.77	0	8	0	0	2	204	218
									SPAQILLR	95.0	64.3	25.0	897.55	0	4	0	0	2	244	251
									YIVPMLTVDGK	95.0	29.1	25.0	1251.67	0	1	0	0	2	298	308
Aldehyde dehydrogenase family 1 member A3	AL1A3_HUMAN	ALDH1A3	56.09	100.0	10	10	40	18.60	AVEAAQVAFQR	95.0	62.7	25.0	1189.63	0	4	0	0	2	74	84
									RLDALSR	95.0	32.1	25.0	830.48	0	1	0	0	2	90	96
									LLHQLADLVER	95.0	47.3	25.0	1306.75	0	2	0	0	2	99	109
									VTLELGGK	95.0	35.0	25.0	816.48	0	3	0	0	2	277	284
									KRPVGDPFDVK	95.0	28.7	25.0	1257.70	0	0	2	0	2	340	350
									TEQGPQIDQK	95.0	40.6	25.0	1143.56	0	6	0	0	2	351	360
									ILELIESGK	95.0	58.2	25.0	1001.59	0	12	0	0	2	365	373
									ILELIESGKK	95.0	27.4	25.0	1129.68	0	1	0	0	2	365	374
									EEIFGPVQPILK	95.0	37.3	25.0	1369.77	0	2	0	0	2	410	421
									ANSTDYGLTAAVFTK	95.0	####	25.0	1558.77	0	7	0	0	2	432	446
Aldehyde dehydrogenase, mitochondrial	ALDH2_HUMAN	ALDH2	56.36	99.5	2	2	4	7.16	LGPALATGNVVVMK	95.0	67.9	25.0	1385.78	0	2	0	0	2	196	209
									VTLELGGK	95.0	35.0	25.0	816.48	0	3	0	0	2	282	289

									ANNSTYGLAAAVFTK	95.0	59.0	25.0	1527.78	0	2	0	0	2	437	451
Aldo-keto reductase family 1 member B10	AK1BA_HUMAN	AKR1B10	36.00	100.0	9	9	21	25.00	VAIDAGYR	95.0	33.0	25.0	864.46	0	1	0	0	2	34	41
									REDLFIVSK	95.0	55.5	25.0	1106.62	0	4	0	0	2	70	78
									EDLFIVSK	95.0	43.1	25.0	950.52	0	2	0	0	2	71	78
									SGDDLFPK	95.0	54.5	25.0	878.43	0	4	0	0	2	118	125
									ALGVSNFSHFQIEK	95.0	42.2	25.0	1576.81	0	1	0	0	2	156	169
									TAAQVLIR	95.0	53.5	25.0	871.54	0	2	0	0	2	244	251
									NVIVIPK	95.0	27.9	25.0	782.51	0	1	0	0	2	257	263
									IVENIQVFDFK	95.0	77.4	25.0	1351.73	0	2	0	0	2	270	280
									LSDEEMATILSFNR	95.0	96.5	25.0	1641.78	0	4	0	0	2	281	294
Aldo-keto reductase family 1 member C1	AK1C1_HUMAN	AKR1C1	36.77	100.0	9	11	47	19.80	LAIEAGFR	95.0	56.6	25.0	876.49	0	5	0	0	2	40	47
									REDIFYTSK	95.0	31.2	25.0	1158.58	0	2	0	0	2	76	84
									SIGVSNFNR	95.0	35.4	25.0	993.51	0	4	0	0	2	162	170
									RQLEMILNKPGLK	95.0	22.5	25.0	1555.90	0	0	1	0	2	171	183
									QLEMILNKPGLK	95.0	56.6	25.0	1399.80	0	4	0	0	2	172	183
									SKDIVLVAYSALGSHR	95.0	####	25.0	1715.94	0	2	3	0	2	208	223
									DIVLVAYSALGSHR	95.0	####	25.0	1500.82	0	4	2	0	2	210	223
									RTPALIALR	95.0	49.0	25.0	1010.65	0	5	0	0	2	250	258
									TPALIALR	95.0	61.2	25.0	854.55	0	15	0	0	2	251	258
Aldo-keto reductase family 1 member C2	AK1C2_HUMAN	AKR1C2	36.72	99.5	2	2	7	17.30	REDIFYTSK	95.0	31.2	25.0	1158.58	0	2	0	0	2	76	84
									SIGVSNFNHR	95.0	48.1	25.0	1130.57	0	4	0	0	2	162	171
									LLEMILNKPGLK	95.0	46.5	25.0	1384.82	0	3	0	0	2	172	183
									SKDIVLVAYSALGSHR	95.0	####	25.0	1715.94	0	2	3	0	2	208	223
									DIVLVAYSALGSHR	95.0	####	25.0	1500.82	0	4	2	0	2	210	223
									RTPALIALR	95.0	49.0	25.0	1010.65	0	5	0	0	2	250	258
									TPALIALR	95.0	61.2	25.0	854.55	0	15	0	0	2	251	258
Aldo-keto reductase family 1 member C3	AK1C3_HUMAN	AKR1C3	36.83	99.5	2	2	2	22.00	LAIEAGFR	95.0	56.6	25.0	876.49	0	5	0	0	2	40	47
									REDIFYTSK	95.0	31.2	25.0	1158.58	0	2	0	0	2	76	84
									SIGVSNFNR	95.0	35.4	25.0	993.51	0	4	0	0	2	162	170
									RQLEMILNKPGLK	95.0	22.5	25.0	1555.90	0	0	1	0	2	171	183
									QLEMILNKPGLK	95.0	56.6	25.0	1399.80	0	4	0	0	2	172	183
									SKDIVLVAYSALGSQR	95.0	80.9	25.0	1706.94	0	1	0	0	2	208	223
									RTPALIALR	95.0	49.0	25.0	1010.65	0	5	0	0	2	250	258
									TPALIALR	95.0	61.2	25.0	854.55	0	15	0	0	2	251	258
									AIDGLDR	95.0	29.0	25.0	759.40	0	1	0	0	2	295	301
Aldose reductase	ALDR_HUMAN	AKR1B1	35.84	100.0	6	6	58	15.50	SPPGQVTEAVK	95.0	62.7	25.0	1112.59	0	30	0	0	2	23	33
									REELFIVSK	95.0	40.1	25.0	1120.64	0	7	0	0	2	70	78
									TTAQVLIR	95.0	68.5	25.0	901.55	0	12	0	0	2	244	251
									NLVVIPK	95.0	31.4	25.0	782.51	0	5	0	0	2	257	263
									IAENFK	95.0	30.9	25.0	721.39	0	1	0	0	2	270	275
									DYPFHEEF	95.0	35.5	25.0	1083.44	0	3	0	0	2	309	316
Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	MGAT1_HUMAN	MGAT1	50.85	100.0	4	4	8	8.54	LAQDAEVELER	95.0	34.0	25.0	1272.64	0	1	0	0	2	57	67
									WALGQVFR	95.0	29.4	25.0	976.54	0	1	0	0	2	191	198
									VYGAPQLQVEK	95.0	35.3	25.0	1231.67	0	2	0	0	2	362	372
									GIVTFQFR	95.0	39.2	25.0	967.54	0	4	0	0	2	418	425
Alpha-1,6-mannosylglycoprotein 6-beta-N-	MGT5A_HUMAN	MGAT5	84.53	100.0	3	3	6	3.78	TDFNILYSMMK	95.0	27.0	25.0	1394.63	0	1	0	0	2	220	230
									DLQFLLR	95.0	44.5	25.0	904.53	0	1	0	0	2	501	507
									DILVPSFDPK	95.0	31.8	25.0	1130.61	0	4	0	0	2	689	698
Alpha-2-macroglobulin	A2MG_HUMAN	A2M	163.27	100.0	3	3	13	2.24	ATVLNYLPK	95.0	48.3	25.0	1018.59	0	3	0	0	2	812	820
									LPPNVVEESAR	95.0	60.5	25.0	1210.64	0	6	0	0	2	935	945
									MVSGFIPLKPTVK	95.0	66.5	25.0	1432.82	0	4	0	0	2	1385	1397

Alpha-2-macroglobulin-like protein 1	A2ML1_HUMAN	A2ML1	161.09	100.0	5	5	10	3.78	IVTMDSNFVPVNDK	95.0	40.3	25.0	1594.78	0	2	0	0	2	141	154
									ELSTVQESFLVK	95.0	50.7	25.0	1379.74	0	5	0	0	2	228	239
									AGLLTEEIR	95.0	47.7	25.0	1001.56	0	1	0	0	2	991	999
									TFNIQSVNR	95.0	33.1	25.0	1078.56	0	1	0	0	2	1275	1283
									SSSNMAIVEVK	95.0	32.1	25.0	1180.59	0	1	0	0	2	1360	1370
Alpha-actinin-1	ACTN1_HUMAN	ACTN1	103.04	100.0	21	31	363	39.70	DLLLDPAWEK	95.0	37.8	25.0	1199.63	0	1	0	0	2	22	31
									TFTAWCNSHLR	95.0	28.9	25.0	1392.65	0	1	0	0	2	36	46
									KAGTQIENIEEDFR	95.0	95.2	25.0	1649.81	0	2	0	0	2	47	60
									AGTQIENIEEDFR	95.0	77.0	25.0	1521.72	0	2	0	0	2	48	60
									ALDFIASK	95.0	56.1	25.0	864.48	0	53	0	0	2	96	103
									LVSIGAEEIVDGNVK	95.0	60.3	25.0	1542.84	0	1	0	0	2	107	121
									FAIQDISVEETSAK	95.0	97.3	25.0	1537.77	0	95	2	0	2	134	147
									HRPELIDYGK	95.0	48.7	25.0	1227.65	0	2	37	0	2	186	195
									KDDPLTNLNTAFDVAEK	95.0	49.0	25.0	1890.94	0	2	0	0	2	198	214
									YLDIPK	95.0	36.6	25.0	748.42	0	28	0	0	2	215	220
									MLDAEDIVGTARPDEK	95.0	99.9	25.0	1775.85	0	17	32	0	2	221	236
									VLAVNQENEQLMEDYEK	95.0	####	25.0	2067.95	0	6	4	0	2	265	281
									LSNRPAFMPSEGR	95.0	42.0	25.0	1477.72	0	1	23	0	2	347	359
									ASIHEAWTDGK	95.0	43.6	25.0	1214.58	0	2	0	0	2	403	413
									QKDYETATLSEIK	95.0	68.8	25.0	1525.77	0	2	4	0	2	419	431
									KHEAFESDLAAHQDR	95.0	83.7	25.0	1753.83	0	6	9	14	2	436	450
									HEAFESDLAAHQDR	95.0	79.2	25.0	1625.73	0	2	8	0	2	437	450
									ATLPDADKER	95.0	68.8	25.0	1115.57	0	18	11	0	2	556	565
									LAILGIHNEVSK	95.0	65.9	25.0	1293.75	0	14	4	0	2	566	577
									RDQALTEEHAR	95.0	42.2	25.0	1325.66	0	2	8	0	2	614	624
									DQALTEEHAR	95.0	42.0	25.0	1169.55	0	5	0	0	2	615	624
									ISIEMHGTLEDQLSHLR	95.0	69.1	25.0	1995.00	0	0	2	2	2	656	672
									SIVNYKPK	95.0	37.3	25.0	948.55	0	7	0	0	2	677	684
									HTNYTMEHIR	95.0	55.6	25.0	1317.60	0	13	24	0	2	705	714
									TINEVENQILTR	95.0	84.2	25.0	1429.76	0	77	0	0	2	727	738
									GISQEQMNEFR	95.0	56.7	25.0	1354.61	0	66	0	0	2	742	752
									ASFNHFDR	95.0	72.3	25.0	993.45	0	11	0	0	2	753	760
									DHSGTLGPEEFK	95.0	55.4	25.0	1316.61	0	12	0	0	2	761	772
									IMSIVDPNR	95.0	47.4	25.1	1060.55	0	16	0	0	2	795	803
									ETADTDTADQVMASFK	95.0	####	25.0	1745.75	0	47	0	0	2	819	834
									ILAGDKNYITMDELR	95.0	59.2	25.0	1767.89	0	1	2	0	2	835	849
									ELPPDQAEYCIAR	95.0	51.6	25.0	1561.73	0	2	0	0	2	851	863
Alpha-actinin-4	ACTN4_HUMAN	ACTN4	104.84	100.0	42	60	746	45.60	DLLLDPAWEK	95.0	37.8	25.0	1199.63	0	1	0	0	2	41	50
									TFTAWCNSHLR	95.0	28.9	25.0	1392.65	0	1	0	0	2	55	65
									KAGTQIENIDEDFR	95.0	82.8	25.0	1635.80	0	2	2	0	2	66	79
									AGTQIENIDEDFR	95.0	55.3	25.0	1507.70	0	2	0	0	2	67	79
									AGTQIENIDEDFRDGLK	95.0	33.5	25.0	1920.93	0	0	4	0	2	67	83
									ALDFIASK	95.0	56.1	25.0	864.48	0	53	0	0	2	115	122
									LVSIGAEEIVDGNAK	95.0	99.8	25.0	1514.81	0	8	0	0	2	126	140
									FAIQDISVEETSAK	95.0	97.3	25.0	1537.77	0	95	2	0	2	153	166
									DGLAFNALIHR	95.0	50.6	25.0	1226.66	0	18	4	0	2	194	204
									HRPELIEYDK	95.0	51.8	25.0	1299.67	0	2	16	0	2	205	214
									HRPELIEYDKLR	95.0	49.2	25.0	1568.85	0	0	0	4	2	205	216
									KDDPVTNLNNAFEVAEK	95.0	####	25.0	1903.94	0	6	6	0	2	217	233
									DDPVTNLNNAFEVAEK	95.0	70.0	25.0	1775.84	0	1	0	0	2	218	233
									YLDIPK	95.0	36.6	25.0	748.42	0	28	0	0	2	234	239

									MLDAEDIVNTARPDEK	95.0	74.1	25.0	1832.87	0	7	15	0	2	240	255
									VLAVNQENEHLMEDYEK	95.0	69.4	25.0	2076.95	0	6	10	0	2	284	300
									LSNRPAFMPSEGK	95.0	50.0	25.0	1449.72	0	11	13	0	2	366	378
									ASIHEAWTDGK	95.0	43.6	25.0	1214.58	0	2	0	0	2	422	432
									HRDYETATLSDIK	95.0	69.0	25.0	1548.77	0	4	6	0	2	438	450
									DYETATLSDIK	95.0	77.6	25.0	1255.61	0	36	0	0	2	440	450
									KHEAFESDLAAHQDR	95.0	83.7	25.0	1753.83	0	6	9	14	2	455	469
									HEAFESDLAAHQDR	95.0	79.2	25.0	1625.73	0	2	8	0	2	456	469
									QLEAIDQLHLEYAK	95.0	21.5	25.0	1670.88	0	0	1	0	2	522	535
									STLPDADRER	95.0	38.5	25.0	1159.57	0	13	13	0	2	575	584
									EAILAIHK	95.0	50.0	25.0	894.54	0	11	0	0	2	585	592
									LSGSNPYTTVTPQIINSK	95.0	####	25.0	1920.01	0	6	4	0	2	605	622
									VQQLVPK	95.0	45.6	25.0	811.50	0	23	0	0	2	626	632
									RDHALLEEQSK	95.0	53.4	25.0	1325.68	0	8	4	0	2	633	643
									DHALLEEQSK	95.0	64.2	25.0	1169.58	0	4	0	0	2	634	643
									ISIEMNGTLEDQLSHLK	95.0	29.6	25.0	1943.97	0	0	2	0	2	675	691
									HTNYTMEHIR	95.0	55.6	25.0	1317.60	0	13	24	0	2	724	733
									TINEVENQILTR	95.0	84.2	25.0	1429.76	0	77	0	0	2	746	757
									GISQEQMQEFR	95.0	62.5	25.0	1368.62	0	31	0	0	2	761	771
									ASFNHFDK	95.0	47.2	25.0	965.45	0	3	0	0	2	772	779
									DHGGALGPEEFK	95.0	26.5	25.0	1256.59	0	0	1	0	2	780	791
									QGEAEFNR	95.0	54.0	25.0	950.43	0	5	0	0	2	806	813
									ETTDTDTADQVIASFK	95.0	####	25.0	1741.81	0	59	0	0	2	838	853
									VLAGDKNFITAEELR	95.0	####	25.0	1675.90	0	2	2	0	2	854	868
									NFITAEELR	95.0	45.7	25.0	1092.57	0	27	0	0	2	860	868
									NFITAEELRR	95.0	32.8	25.0	1248.67	0	1	2	0	2	860	869
									ELPPDQAEYCIAR	95.0	51.6	25.0	1561.73	0	2	0	0	2	870	882
									MAPYQGPDAVPGALDYK	95.0	74.6	25.0	1808.85	0	4	0	0	2	883	899
Alpha-aminoadipic semialdehyde dehydrogenase	AL7A1_HUMAN	ALDH7A1	58.47	100.0	5	5	10	10.60	IQVLGSLVSLEMGK	95.0	83.6	25.0	1489.83	0	4	0	0	2	125	138
									GAPTTSLISVAVTK	95.0	62.5	25.0	1344.77	0	1	0	0	2	219	232
									VNLLSFTGSTQVGK	95.0	####	25.0	1450.79	0	2	0	0	2	267	280
									QAVSMFLGAVEEAK	95.0	75.9	25.0	1495.75	0	2	0	0	2	376	389
									QAVSMFLGAVEEAKK	95.0	28.7	25.0	1623.84	0	0	1	0	2	376	390
Alpha-centractin	ACTZ_HUMAN	ACTR1A	42.60	100.0	3	3	5	8.51	AGFAGDQIPK	95.0	66.9	25.0	1003.52	0	2	0	0	2	23	32
									VMAGALEGDIFIGPK	95.0	56.8	25.0	1533.80	0	2	0	0	2	47	61
									ISAPQER	95.0	31.8	25.0	800.43	0	1	0	0	2	330	336
Alpha-enolase	ENOA_HUMAN	ENO1	47.15	100.0	22	28	684	42.60	EIFDSR	95.0	34.8	25.0	766.37	0	11	0	0	2	10	15
									GNPTVEVDLFTSK	95.0	####	25.0	1406.72	0	92	0	0	2	16	28
									AAVPSGASTGIYEALELR	95.0	73.5	25.0	1804.94	0	1	0	0	2	33	50
									TIAPALVSK	95.0	52.7	25.0	899.56	0	5	0	0	2	72	80
									KLNVTEQEK	95.0	56.3	25.0	1088.59	0	81	10	0	2	81	89
									LNVTEQEK	95.0	33.6	25.0	960.50	0	16	0	0	2	82	89
									IDKLMIEMDGTENK	95.0	69.8	25.0	1668.78	0	5	2	0	2	90	103
									LMIEMDGTENK	95.0	69.4	25.0	1312.58	0	94	0	0	2	93	103
									GVPLYR	95.0	31.4	25.0	704.41	0	1	0	0	2	127	132
									IGAEVYHNLK	95.0	61.4	25.0	1143.62	0	111	46	0	2	184	193
									DATNVGDEGGFAPNILENK	95.0	####	25.0	1960.92	0	23	2	0	2	203	221
									EGLELLK	95.0	47.4	25.0	801.47	1	17	0	0	2	222	228
									VVIGMDVAASEFFR	95.0	####	25.0	1556.78	0	2	0	0	2	240	253
									SGKYDLDFK	95.0	49.2	25.0	1072.53	0	0	2	0	2	254	262
									YDLDFK	95.0	34.0	25.0	800.38	0	15	0	0	2	257	262

									YDLDFKSPDDPSR	95.0	63.3	25.0	1554.71	0	2	1	0	2	257	269
									SPDDPSR	95.0	35.7	25.0	773.34	0	1	0	0	2	263	269
									YISPDQLADLYK	95.0	77.4	25.0	1425.73	0	36	0	0	2	270	281
									VNQIGSVTESLQACK	95.0	####	25.0	1633.82	0	10	0	0	2	344	358
									LAKYNQLLR	95.0	20.2	25.0	1118.67	0	0	1	0	2	404	412
									YNQLLR	95.0	37.3	25.0	806.45	0	48	0	0	2	407	412
									IEEELGSK	95.0	54.2	25.0	904.46	0	48	0	0	2	413	420
Alpha-parvin	PARVA_HUMAN	PARVA	42.23	100.0	3	3	12	8.60	QIQEEITGNTEALSGR	95.0	####	25.0	1745.87	0	4	0	0	2	229	244
									TLITFVNK	95.0	32.5	25.0	935.56	0	1	0	0	2	267	274
									VLYNLFTK	95.0	47.7	25.0	997.57	0	7	0	0	2	360	367
Alpha-soluble NSF attachment protein	SNAA_HUMAN	NAPA	33.22	100.0	4	5	8	18.60	EAEAMALLAEAER	95.0	80.2	25.0	1419.68	0	1	0	0	2	7	19
									AIAHYEQSADYYKGEESNSSANK	95.0	46.0	25.0	2562.14	0	0	2	0	2	141	163
									KLLEAHEEQNVDSYTESVK	95.0	47.7	25.0	2219.08	0	0	2	0	2	246	264
									LLEAHEEQNVDSYTESVK	95.0	91.2	25.0	2090.99	0	2	1	0	2	247	264
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1_HUMAN	AIMP1	34.34	100.0	3	4	13	11.90	GAEADQIIEYLK	95.0	59.6	25.0	1349.69	0	6	0	0	2	15	26
									AILQATLR	95.0	33.7	25.0	885.55	0	1	0	0	2	36	43
									QQSIAGSADSKPIDVSR	95.0	79.2	25.0	1758.90	0	3	3	0	2	138	154
Aminopeptidase B	AMPB_HUMAN	RNPEP	72.58	100.0	9	10	18	15.80	RPLHSAQAVDVASASNFR	95.0	84.6	25.0	1925.99	0	2	0	2	2	15	32
									AEFGPPGPGAGSR	95.0	35.7	25.0	1199.58	0	2	0	0	2	45	57
									GLSGTAVLDLR	95.0	63.1	25.0	1101.63	0	2	0	0	2	58	68
									KKPFVYTQGQAVLNR	95.0	56.7	25.0	1748.98	0	2	0	0	2	162	176
									KPFVYTQGQAVLNR	95.0	43.5	25.0	1620.89	0	0	2	0	2	163	176
									QHMDITGEENPLNK	95.0	63.7	25.0	1641.75	0	2	0	0	2	381	394
									TYQLVYFLDK	95.0	29.6	25.0	1289.68	0	1	0	0	2	532	541
									SPLPPGNVK	94.8	26.6	25.0	908.52	0	1	0	0	2	546	554
									KLGDTYPSISNAR	95.0	69.7	25.0	1421.74	0	2	0	0	2	555	567
Amyloid beta A4 protein	A4_HUMAN	APP	86.92	100.0	4	4	34	5.84	AVIQHFQEK	95.0	30.6	25.0	1099.59	0	2	0	0	2	430	438
									VESLEQEAANER	95.0	70.9	25.0	1374.65	0	18	0	0	2	439	450
									VEAMLNDR	95.0	50.7	25.0	963.46	0	10	0	0	2	461	468
									ISYGNDALMPSLTETK	95.0	78.9	25.0	1755.85	0	4	0	0	2	586	601
Ankycorbin	RAI14_HUMAN	RAI14	110.03	100.0	4	4	5	4.90	ISSERSGTPK	95.0	27.5	25.0	1061.56	0	1	0	0	2	262	271
									SLEDVTAEYIHK	95.0	60.1	25.0	1404.70	0	1	0	0	2	667	678
									VLNELTQLK	95.0	39.5	25.0	1057.63	0	2	0	0	2	709	717
									EALNSLSQLSYSTSSSK	95.0	95.9	25.0	1801.88	0	1	0	0	2	896	912
Ankyrin repeat and FYVE domain-containing protein 1	ANFY1_HUMAN	ANKFY1	128.38	100.0	5	5	7	4.45	FQLQLLR	95.0	41.2	25.0	917.56	0	2	0	0	2	145	151
									GVMSLVNVR	95.0	42.3	25.0	990.54	0	1	0	0	2	157	165
									RLESIATTLVSHK	95.0	39.9	25.0	1454.83	0	0	2	0	2	267	279
									TQDGETALQLAIR	95.0	66.7	25.0	1415.75	0	1	0	0	2	652	664
									GADMSVPDEK	94.5	26.4	25.0	1064.46	0	1	0	0	2	678	687
Ankyrin-3	ANK3_HUMAN	ANK3	480.39	100.0	3	3	7	0.73	VGLQAQPVPDEIVK	95.0	65.0	25.0	1492.84	0	2	0	0	2	1177	1190
									ATFSPIVTVEPR	95.0	78.1	25.0	1316.72	0	4	0	0	2	1197	1208
									SRIPVK	94.7	26.5	25.0	699.45	0	1	0	0	2	3911	3916
Annexin A1	ANXA1_HUMAN	ANXA1	38.70	100.0	12	13	63	33.20	GVDEATIIDILTK	95.0	68.1	25.0	1387.77	0	2	0	0	2	59	71
									AAYLQETGKPLDETLK	95.0	68.8	25.0	1776.94	0	1	1	0	2	82	97
									AAYLQETGKPLDETLKK	95.0	62.9	25.0	1905.03	0	2	0	0	2	82	98
									TPAQFDADELR	95.0	72.7	25.0	1262.60	0	5	0	0	2	114	124
									DITSDTSGDFR	95.0	82.4	25.0	1213.53	0	8	0	0	2	167	177
									NALLSLAK	95.0	39.5	25.0	829.51	0	3	0	0	2	178	185
									SEDFGVNEDLADSDAR	95.0	####	25.0	1739.74	0	10	0	0	2	189	204
									ALYEAGER	95.0	55.7	25.0	908.45	0	8	0	0	2	205	212
									KGTDVNVFNTILTTR	95.0	####	25.0	1678.91	0	6	0	0	2	214	228

									GTDVNVFNTILTTR	95.0	65.3	25.0	1550.82	0	2	0	0	2	215	228
									VLDLELK	95.0	33.1	25.0	829.50	0	7	0	0	2	251	257
									SEIDMNDIK	95.0	38.7	25.0	1080.49	0	8	0	0	2	304	312
Annexin A11	ANX11_HUMAN	ANXA11	54.37	100.0	7	8	15	15.60	QQILLSFK	95.0	27.1	25.0	976.58	0	1	0	0	2	236	243
									LLISLSQGNR	95.0	69.5	25.0	1100.64	0	2	0	0	2	337	346
									DESTNVDMSLAQR	95.0	64.7	25.0	1481.65	0	2	0	0	2	347	359
									DAQELYAAGENR	95.0	72.8	25.0	1336.61	0	2	0	0	2	360	371
									AHLVAVFNEYQR	95.0	73.4	25.0	1446.75	0	2	2	0	2	389	400
									EMSGDLEEGMLAVVK	95.0	86.7	25.0	1639.76	0	2	0	0	2	413	427
									SETDLLDIR	95.0	53.2	25.0	1061.55	0	2	0	0	2	462	470
Annexin A2	ANXA2_HUMAN	ANXA2	38.59	100.0	17	18	371	45.40	LSLEGDHSTPPSAYGSVK	95.0	85.5	25.0	1844.90	0	6	6	0	2	11	28
									AYTNFDAER	95.0	71.5	25.0	1086.49	0	18	0	0	2	29	37
									DALNIETAIK	95.0	79.6	25.0	1087.60	0	63	0	0	2	38	47
									GVDEVTIVNILTNR	95.0	63.5	25.0	1542.85	0	5	0	0	2	50	63
									QDIAFAYQR	95.0	72.5	25.0	1111.55	0	22	0	0	2	69	77
									ELASALK	95.0	35.8	25.0	731.43	0	9	0	0	2	82	88
									TPAQYDASELK	95.0	75.7	25.0	1222.60	0	64	0	0	2	105	115
									TNQELQEINR	95.0	65.2	25.0	1244.62	0	99	0	0	2	136	145
									DIISDTSGDFR	95.0	62.6	25.0	1225.57	0	7	0	0	2	158	168
									DIISDTSGDFRK	95.0	49.2	25.0	1353.66	0	6	0	0	2	158	169
									LMVALAK	95.0	43.1	25.0	761.46	0	9	0	0	2	170	176
									DLYDAGVKR	95.0	38.0	25.0	1036.54	0	2	0	0	2	197	205
									SVPHLQK	95.0	32.4	25.0	808.47	0	2	0	0	2	221	227
									SYSPYDMLESIR	95.0	55.0	25.0	1476.67	0	4	0	0	2	234	245
									SYSPYDMLESIRK	95.0	53.5	25.0	1604.76	0	2	0	0	2	234	246
									SEVDMLK	95.0	37.5	25.0	837.40	0	4	0	0	2	296	302
									SLYYYIQQDTK	95.0	73.2	25.0	1421.69	0	43	0	0	2	314	324
Annexin A3	ANXA3_HUMAN	ANXA3	36.36	100.0	10	11	30	31.30	MLISILTER	95.0	57.1	25.0	1091.61	0	4	0	0	2	40	48
									DISQAYYTVYK	95.0	46.6	25.0	1350.66	0	2	0	0	2	127	137
									SLGDDISSETSGDFR	95.0	87.7	25.0	1585.70	0	2	0	0	2	139	153
									SLGDDISSETSGDFRK	95.0	87.9	25.0	1713.79	0	2	1	0	2	139	154
									ALLTLADGR	95.0	53.0	25.0	929.54	0	2	0	0	2	155	163
									DESLKVDEHLAK	95.0	54.2	25.0	1383.71	0	2	0	0	2	165	176
									GIGTDEFTLNR	95.0	41.6	25.0	1222.61	0	2	0	0	2	264	274
									SEIDLLDIR	95.0	70.2	25.0	1073.58	0	9	0	0	2	280	288
									HYGYSLYSAIK	95.0	49.6	25.0	1301.65	0	2	0	0	2	294	304
									SDTSGDYEITLLK	95.0	93.8	25.0	1441.71	0	2	0	0	2	305	317
Annexin A4	ANXA4_HUMAN	ANXA4	35.87	100.0	6	6	14	21.60	AASGFNAMEDAQTLR	95.0	91.0	25.0	1597.73	0	2	0	0	2	10	24
									VLVSLSAGGR	95.0	55.8	25.0	958.57	0	3	0	0	2	151	160
									DEGNYLDDALVR	95.0	72.8	25.0	1379.64	0	3	0	0	2	161	172
									QDAQDLYEAGEK	95.0	55.0	25.0	1366.61	0	2	0	0	2	173	184
									NHLLHVFDEYK	95.0	23.2	25.0	1414.71	0	0	2	0	2	203	213
									AEIDMLDIR	95.0	46.1	25.0	1091.54	0	2	0	0	2	276	284
Annexin A5	ANXA5_HUMAN	ANXA5	35.92	100.0	9	9	53	26.90	GTVTDFPGFDER	95.0	70.6	25.0	1340.61	0	6	0	0	2	7	18
									QEISAAFK	95.0	31.6	25.0	893.47	0	2	0	0	2	51	58
									LIVALMKPSR	95.0	38.3	25.0	1143.69	0	2	0	0	2	80	89
									LYDAYELK	95.0	50.4	25.0	1014.51	0	1	0	0	2	90	97
									VLTEIIASR	95.0	79.0	25.0	1001.60	0	11	0	0	2	109	117
									FITIFGTR	95.0	30.3	25.0	954.54	0	3	0	0	2	194	201
									GAGTDDHTLIR	95.0	59.8	25.0	1155.58	0	8	0	0	2	261	271
									SEIDLFNIR	95.0	45.0	25.0	1106.58	0	14	0	0	2	277	285

									NFATSLYSMIK	95.0	59.6	25.0	1290.64	0	6	0	0	2	291	301
Annexin A8	ANXA8_HUMAN	ANXA8	36.86	100.0	10	11	34	36.10	SSSHFNPDPDAETLYK	95.0	68.2	25.0	1807.81	0	5	0	0	2	17	32
									GIGTNEQAIIDVLTK	95.0	74.6	25.0	1571.86	0	2	0	0	2	36	50
									EGVIIEILASR	95.0	60.0	25.0	1199.70	0	4	0	0	2	113	123
									ILVCLLQGSR	95.0	56.0	25.0	1158.67	0	1	0	0	2	158	167
									FITILCTR	95.0	45.7	25.0	1023.57	0	2	0	0	2	201	208
									SATHLLR	95.0	27.1	25.0	797.46	0	1	0	0	2	209	215
									SETHGSLEEAMLTVVK	95.0	68.8	25.0	1746.86	0	2	1	0	2	234	249
									SEIDLNLIK	95.0	53.9	25.0	1044.59	0	6	0	0	2	284	292
									TLSSMIMEDTSGDYK	95.0	99.8	25.0	1709.72	0	6	0	0	2	302	316
									NALLSLVGSDP	95.0	51.0	25.0	1085.58	0	4	0	0	2	317	327
Antithrombin-III	ANT3_HUMAN	SERPINC1	52.59	100.0	3	3	7	5.82	FDTISEK	95.0	29.4	25.0	839.41	0	2	0	0	2	140	146
									TSDQIHFFFAK	95.0	42.8	25.0	1340.66	0	3	0	0	2	147	157
									LPGIVAEGR	95.0	36.5	25.0	911.53	0	2	0	0	2	383	391
AP-1 complex subunit beta-1	AP1B1_HUMAN	AP1B1	104.62	100.0	12	13	67	13.40	KGEIFELK	95.0	50.3	25.0	963.55	0	10	0	0	2	12	19
									LSHANSAVVLSAVK	95.0	77.5	25.0	1395.80	0	6	2	0	2	248	261
									DLDYYGTLLK	95.0	50.4	25.0	1200.61	0	2	0	0	2	273	282
									NINLIVQK	95.0	42.5	25.0	941.58	0	4	0	0	2	305	312
									YNDPIYVK	95.0	45.4	25.0	1011.51	0	8	0	0	2	328	335
									LDIMIR	95.0	36.8	25.0	776.43	0	5	0	0	2	339	344
									LLSTDPVAAK	95.0	34.6	25.0	1014.58	0	3	0	0	2	529	538
									QVGSISMDLQLTNK	95.0	74.9	25.0	1549.79	0	3	0	0	2	741	754
									MEPLNNLQVAVK	95.0	57.2	25.0	1371.73	0	11	0	0	2	806	817
									DIPNENEAQFQIR	95.0	31.3	25.0	1573.76	0	3	0	0	2	852	864
									LQSSNIFTVAK	95.0	28.5	25.0	1207.67	0	1	0	0	2	877	887
									NVEGQDMLYQSLK	95.0	79.3	25.0	1540.73	0	9	0	0	2	889	901
AP-1 complex subunit gamma-1	AP1G1_HUMAN	AP1G1	91.34	100.0	6	6	39	7.06	KVPELMEMFLPATK	95.0	31.7	25.0	1665.86	0	1	0	0	2	167	180
									VLAINILGR	95.0	53.5	25.0	968.63	0	15	0	0	2	307	315
									VLTTAGSYVR	95.0	59.0	25.0	1066.59	0	4	0	0	2	425	434
									GYALTAIMK	95.0	45.0	25.0	983.52	0	4	0	0	2	524	532
									AVEYNALFK	95.0	46.9	25.0	1054.56	0	11	0	0	2	563	571
									IEFTFER	95.0	31.7	25.0	941.47	0	4	0	0	2	717	723
AP-1 complex subunit gamma-like 2	AP1G2_HUMAN	AP1G2	87.10	100.0	5	5	13	7.01	LQDLIEEIR	95.0	48.2	25.0	1128.63	0	6	0	0	2	8	16
									VLAVNILGR	95.0	50.0	25.0	954.61	0	1	0	0	2	308	316
									YVALTSLLR	95.0	38.3	25.0	1035.62	0	1	0	0	2	327	335
									GYALTALMK	95.0	45.0	25.0	983.52	0	4	0	0	2	525	533
									AVEYDTLFR	95.0	39.1	25.0	1113.56	0	4	0	0	2	564	572
									GGLPITQLFR	95.0	38.9	25.0	1101.64	0	1	0	0	2	737	746
AP-1 complex subunit mu-1	AP1M1_HUMAN	AP1M1	48.57	100.0	6	6	15	18.00	HNNLYLVATSK	95.0	49.2	25.0	1259.67	0	2	0	0	2	62	72
									VVQVFSEYFK	95.0	53.2	25.0	1245.65	0	4	0	0	2	87	96
									ILQEYITQEGHK	95.0	19.6	25.0	1458.76	0	0	1	0	2	130	141
									VFLSGMPELR	95.0	53.9	25.0	1164.61	0	4	0	0	2	202	211
									STANNVEIHIPVPNDADSPK	95.0	28.7	25.0	2118.05	0	0	2	0	2	305	324
									AHFGLPSVEAEDK	95.0	59.3	25.0	1399.69	0	2	0	0	2	358	370
AP-1 complex subunit mu-2	AP1M2_HUMAN	AP1M2	48.09	100.0	4	4	6	12.50	HSNLYLVATTSK	95.0	78.0	25.0	1333.71	0	1	0	0	2	62	73
									ILQEYITQQSNK	95.0	63.3	25.0	1464.77	0	2	0	0	2	130	141
									VFLSGMPELR	95.0	53.9	25.0	1164.61	0	4	0	0	2	202	211
									VLFELTGR	95.0	48.9	25.0	934.54	0	2	0	0	2	218	225
									YITQSGDYQLR	95.0	35.5	25.0	1343.66	0	1	0	0	2	411	421
AP-1 complex subunit sigma-1A	AP1S1_HUMAN	AP1S1	18.72	100.0	5	5	13	30.40	FMLLFSR	95.0	28.8	25.0	929.49	0	2	0	0	2	4	10
									ELMQVVLAR	95.0	60.0	25.0	1074.60	0	4	0	0	2	34	42

									YVELLDK	95.0	42.0	25.0	879.48	0	4	0	0	2	87	93
									AIEQADLLQEEDESPR	95.0	74.4	25.0	1842.87	0	1	0	0	2	134	149
									SVLEEMGLA	95.0	47.1	25.0	964.47	0	2	0	0	2	150	158
AP-2 complex subunit alpha-1	AP2A1_HUMAN	AP2A1	107.53	100.0	12	13	45	12.50	GLAVFISDIR	95.0	70.9	25.0	1090.63	0	9	0	0	2	12	21
									ILVAGDSMDSVK	95.0	39.3	25.0	1250.63	0	4	0	0	2	154	165
									THIDTVINALK	95.0	44.5	25.0	1224.69	0	2	0	0	2	368	378
									VLQIVTNR	95.0	44.7	25.0	942.57	0	3	0	0	2	465	472
									DDVQGYAAK	95.0	27.5	25.0	966.45	0	1	0	0	2	473	481
									SSPPVQFSLLHSK	95.0	41.7	25.0	1426.77	0	2	2	0	2	517	529
									ALLLSTYIK	95.0	45.5	25.0	1021.63	0	7	0	0	2	539	547
									FINLFPETK	95.0	41.9	25.0	1108.60	0	5	0	0	2	548	556
									MYLFYGNK	95.0	30.9	25.0	1051.49	0	1	0	0	2	776	783
									YGGAPQALTLK	95.0	64.9	25.0	1118.62	0	6	0	0	2	846	856
									ANHPMDAEVTK	95.0	28.5	25.0	1228.56	0	0	1	0	2	895	905
									LEPNAQAQMYR	95.0	36.1	25.0	1336.63	0	2	0	0	2	945	955
AP-2 complex subunit beta	AP2B1_HUMAN	AP2B1	104.54	100.0	4	4	15	12.00	KGEIFELK	95.0	50.3	25.0	963.55	0	10	0	0	2	12	19
									SQPDMAIMAVNSFVK	95.0	28.1	25.0	1669.79	0	2	0	0	2	79	93
									LSHANSAVVLSAVK	95.0	77.5	25.0	1395.80	0	6	2	0	2	248	261
									FLELLPK	95.0	28.2	25.0	859.53	0	1	0	0	2	266	272
									DSDYYNMLLK	95.0	53.7	25.0	1277.57	0	8	0	0	2	273	282
									NINLIVQK	95.0	42.5	25.0	941.58	0	4	0	0	2	305	312
									YNDPIYVK	95.0	45.4	25.0	1011.51	0	8	0	0	2	328	335
									LDIMIR	95.0	36.8	25.0	776.43	0	5	0	0	2	339	344
									MEPLNNLQVAVK	95.0	57.2	25.0	1371.73	0	11	0	0	2	797	808
									LQNNNVYTIAK	95.0	47.7	25.0	1277.68	0	4	0	0	2	868	878
									NVEGQDMLYQSLK	95.0	79.3	25.0	1540.73	0	9	0	0	2	880	892
AP-2 complex subunit mu	AP2M1_HUMAN	AP2M1	49.64	100.0	4	4	7	8.28	VNVIHAR	95.0	28.6	25.0	808.48	0	1	0	0	2	34	40
									SPVTNIAR	95.0	33.9	25.0	857.48	0	2	0	0	2	45	52
									SNFKPSLLAQK	95.0	41.5	25.0	1232.70	0	2	0	0	2	309	319
									LNYSDHDVIK	95.0	55.4	25.0	1203.60	0	2	0	0	2	411	420
AP-3 complex subunit beta-1	AP3B1_HUMAN	AP3B1	121.31	100.0	3	3	7	3.75	VVNVANVGAVPSGQDNIHR	95.0	40.1	25.0	1946.02	0	0	3	0	2	1026	1044
									EGSTAQLIINTEK	95.0	54.0	25.0	1403.74	0	1	0	0	2	1064	1076
									TVIGSVLLR	95.0	54.4	25.0	957.61	0	3	0	0	2	1077	1085
AP-3 complex subunit delta-1	AP3D1_HUMAN	AP3D1	130.14	100.0	7	7	25	6.68	LFGALTPLEPR	95.0	27.4	25.0	1213.69	0	1	0	0	2	244	254
									ALDLLYGMVSK	95.0	61.6	25.0	1225.65	0	7	0	0	2	360	370
									LYASILQQK	95.0	42.5	25.0	1063.61	0	2	0	0	2	529	537
									GMELSVLDSLNAR	95.0	####	25.0	1420.71	0	6	0	0	2	963	975
									LLESGDLSMSSIK	95.0	85.9	25.0	1395.70	0	4	0	0	2	1061	1073
									MSFQNLLAK	95.0	47.1	25.0	1067.56	0	3	0	0	2	1079	1087
									KGENSVSVDGK	95.0	32.9	25.0	1119.56	0	2	0	0	2	1122	1132
Apoptosis inhibitor 5	API5_HUMAN	API5	57.55	100.0	7	7	25	12.50	NYGILADATEQVGQHK	95.0	####	25.0	1743.87	0	2	0	0	2	10	25
									LAAQFIPK	95.0	52.5	25.0	887.54	0	2	0	0	2	44	51
									ELPQFATGENLPR	95.0	85.4	25.0	1471.75	0	8	0	0	2	85	97
									EVEELILTESK	95.0	58.4	25.0	1289.68	0	6	0	0	2	170	180
									EVEELILTESKK	95.0	53.2	25.0	1417.78	0	2	0	0	2	170	181
									LPDFLTAK	95.0	29.3	25.0	904.51	0	1	0	0	2	357	364
									GLQVYIR	95.0	38.8	25.0	848.50	0	4	0	0	2	383	389
Apoptosis regulator BAX	BAX_HUMAN	BAX	21.17	100.0	3	3	7	18.80	GGGPTSSEQIMK	95.0	36.5	25.0	1207.56	0	2	0	0	2	10	21
									IGDELDSNMELQR	95.0	63.0	25.0	1535.70	0	4	0	0	2	66	78
									MIAAVDTDSPR	95.0	46.6	25.0	1191.57	0	1	0	0	2	79	89
Apoptosis-associated	ASC_HUMAN	PYCARD	21.61	100.0	5	5	21	26.70	LLSVPLR	95.0	44.5	25.0	797.52	0	2	0	0	2	27	33

speck-like protein containing a CARD									GALLSMDALDLTDK	95.0	97.3	25.0	1478.74	0	6	0	0	2	42	55
									VLTDEQYQAVR	95.0	93.3	25.0	1321.67	0	4	0	0	2	140	150
									DLLLQALR	95.0	51.2	25.0	941.58	0	6	0	0	2	175	182
									ESQSYLVEDLER	95.0	80.3	25.0	1467.70	0	3	0	0	2	183	194
Apoptosis-inducing factor 1, mitochondrial	AIFM1_HUMAN	AIFM1	66.88	100.0	10	11	35	15.70	ISGLGLTPEQK	95.0	43.2	25.0	1142.64	0	2	0	0	2	99	109
									AALSASEGEEVPQDK	95.0	61.5	25.0	1530.73	0	6	0	0	2	113	127
									KVVQLDVR	95.0	27.5	25.0	956.59	0	1	0	0	2	232	239
									VVQLDVR	95.0	41.7	25.0	828.49	0	2	0	0	2	233	239
									LNDGSQITYEK	95.0	52.6	25.0	1267.62	0	7	0	0	2	245	255
									VMPNAIVQSVGVSSGK	95.0	88.2	25.0	1588.84	0	4	0	0	2	363	378
									VNAELQAR	95.0	55.7	25.0	900.49	0	3	0	0	2	423	430
									GVIFYLR	95.0	39.2	25.0	867.51	0	6	0	0	2	563	569
									DGEQHEDLNEVAK	95.0	38.0	25.0	1483.67	0	2	1	0	2	594	606
									LFNIHED	95.0	27.3	25.0	887.43	0	1	0	0	2	607	613
Argininosuccinate synthase	ASSY_HUMAN	ASS1	46.51	100.0	4	4	8	7.77	QHGIPIPVTPK	95.0	31.5	25.0	1186.69	0	1	0	0	2	166	176
									APNTPDILEIEFK	95.0	62.2	25.0	1486.78	0	2	0	0	2	216	228
									APNTPDILEIEFKK	95.0	60.7	25.0	1614.87	0	0	3	0	2	216	229
									VQVSVLK	95.0	29.4	25.0	772.49	0	2	0	0	2	349	355
Arginyl-tRNA synthetase, cytoplasmic	SYRC_HUMAN	RARS	75.36	100.0	12	14	43	16.70	NMINIISR	95.0	36.6	25.0	976.52	0	4	0	0	2	72	79
									LQEVFGHAIK	95.0	43.1	25.0	1141.64	0	4	0	0	2	80	89
									STIIGESISR	95.0	62.2	25.0	1062.58	0	2	0	0	2	214	223
									GESFYQDR	95.0	36.5	25.0	1001.43	0	3	0	0	2	334	341
									GFVQVDDGR	95.0	38.5	25.0	992.48	0	1	0	0	2	353	361
									SDGGYTYDTSDLAAIK	95.0	92.3	25.0	1676.77	0	3	0	0	2	378	393
									LMDLLGEGLK	95.0	60.6	25.0	1104.60	0	6	0	0	2	462	471
									LMDLLGEGLKR	95.0	32.5	25.0	1260.70	0	1	1	0	2	462	472
									YADLSHNR	95.0	40.8	25.0	975.46	0	2	0	0	2	505	512
									LANIDEEMLQK	95.0	64.9	25.0	1319.65	0	4	0	0	2	547	557
									FPEILQK	95.0	43.9	25.0	874.50	0	8	0	0	2	581	587
									GFDILGIKPVQR	95.0	49.3	25.0	1342.78	0	3	1	0	2	648	659
Asparagine synthetase [glutamine-hydrolyzing]	ASNS_HUMAN	ASNS	64.35	100.0	9	9	25	16.90	LAVVDPLFGMQPIR	95.0	38.0	25.0	1571.86	0	1	0	0	2	50	63
									MQQHFEFEYQTK	95.0	50.7	25.0	1631.72	0	1	0	0	2	84	95
									VASVEMVK	95.0	30.2	25.0	878.47	0	2	0	0	2	196	203
									DVPLHALYDNVEK	95.0	60.0	25.0	1512.77	0	7	0	0	2	209	221
									APSPEKAEEESER	95.0	54.7	25.0	1458.67	0	2	0	0	2	380	392
									TTAAHGLELR	95.0	31.9	25.0	1068.58	0	0	2	0	2	408	417
									VPFLDHR	95.0	38.1	25.0	883.48	0	3	0	0	2	418	424
									EAFSDGITSVK	95.0	50.1	25.0	1153.57	0	5	0	0	2	468	478
									FPFNTPK	95.0	34.9	25.0	850.45	0	2	0	0	2	505	511
Asparaginyl-tRNA synthetase, cytoplasmic	SYNC_HUMAN	NARS	62.93	100.0	3	3	24	5.11	EPFPTIYVDSQK	95.0	68.6	25.0	1423.71	0	6	0	0	2	39	50
									IGALEGYR	95.0	38.9	25.0	878.47	0	5	0	0	2	117	124
									NLMFLVLR	95.0	42.4	25.0	1021.59	0	13	0	0	2	143	150
Aspartate aminotransferase, cytoplasmic	AATC_HUMAN	GOT1	46.23	100.0	9	11	41	20.60	KVNLGVGAYR	95.0	54.0	25.0	1076.62	0	2	0	0	2	33	42
									VNLGVGAYR	95.0	45.2	25.0	948.53	0	1	0	0	2	34	42
									LALGDDSPALK	95.0	49.4	25.0	1099.60	0	4	0	0	2	87	97
									NFGLYNER	95.0	33.6	25.0	1012.48	0	4	0	0	2	260	267
									VGNLTVVGK	95.0	59.1	25.0	886.54	0	5	0	0	2	268	276
									EPESILQVLSQMEK	95.0	71.7	25.0	1646.83	0	5	2	0	2	277	290
									QVEYLVNEK	95.0	47.6	25.0	1121.58	0	5	0	0	2	370	378
									INVSGLTTK	95.0	45.7	25.0	932.54	0	3	0	0	2	388	396
									NLDYVATSIHEAVTK	95.0	####	25.0	1660.85	0	6	4	0	2	397	411

Aspartate aminotransferase, mitochondrial	AATM_HUMAN	GOT2	47.46	100.0	14	16	64	30.50	KMNLGVGAYR	95.0	36.3	25.0	1124.59	0	2	0	0	2	59	68
									MNLGVGAYR	95.0	52.1	25.0	996.49	0	2	0	0	2	60	68
									DDNGKPYVLPSVR	95.0	23.7	25.0	1459.75	0	0	1	0	2	69	81
									ASAELALGENSEVLK	95.0	99.5	25.0	1530.80	0	4	0	0	2	108	122
									FVTVQTISGTGALR	95.0	####	25.0	1449.81	0	15	1	0	2	126	139
									IGASFLQR	95.0	37.8	25.0	891.50	0	3	0	0	2	140	147
									DAGMQLQGYR	95.0	54.4	25.0	1154.53	0	8	0	0	2	171	180
									EIATVVK	95.0	37.6	25.0	759.46	0	2	0	0	2	228	234
									NMGLYGER	95.0	47.7	25.0	955.43	0	4	0	0	2	280	287
									ILIRPMYSNPPLNGAR	95.0	27.8	25.0	1827.99	0	0	1	0	2	310	325
									IAAAILNTPDLR	95.0	81.9	25.0	1267.74	0	15	0	0	2	326	337
									IAAAILNTPDLRK	95.0	56.7	25.0	1395.83	0	2	2	0	2	326	338
									TQLVSNLKK	95.0	26.8	25.0	1030.63	0	1	0	0	2	356	364
									EFSIYMTK	95.0	40.4	25.0	1034.49	0	1	0	0	2	397	404
Aspartyl aminopeptidase	DNPEP_HUMAN	DNPEP	52.41	100.0	7	9	19	16.40	LLQAGFSELK	95.0	60.2	25.0	1105.63	0	4	0	0	2	42	51
									LLQAGFSELKETEK	95.0	63.5	25.0	1592.85	0	1	1	0	2	42	55
									LEQQLVHVERPILR	95.0	41.1	25.0	1730.01	0	0	1	0	2	150	163
									GTPEPGPLNAVDER	95.0	43.4	25.0	1451.71	0	2	0	0	2	202	215
									YASNAVSEALIR	95.0	74.3	25.0	1293.68	0	4	0	0	2	381	392
									VPLQDLMVR	95.0	56.9	25.0	1086.60	0	4	0	0	2	400	408
									VLDLGSPQLAMHSIR	95.0	68.7	25.0	1652.88	0	1	1	0	2	429	443
Aspartyl-tRNA synthetase, cytoplasmic	SYDC_HUMAN	DARS	57.12	100.0	15	17	59	33.50	EIMDAAEDYAK	95.0	30.2	25.0	1271.55	0	2	0	0	2	16	26
									YGISSMIQSQEKPDR	95.0	50.6	25.0	1754.84	0	2	2	0	2	29	43
									ESIVDVEGVVR	95.0	69.4	25.0	1201.64	0	8	0	0	2	111	121
									IYVISLAEPR	95.0	63.3	25.0	1160.67	0	8	0	0	2	142	151
									TSTSQAVFR	95.0	35.0	25.0	996.51	0	1	0	0	2	189	197
									NNAYLAQSPQLYK	95.0	84.5	25.0	1509.77	0	4	0	0	2	242	254
									VFSIGPVFR	95.0	52.3	25.0	1021.58	0	6	0	0	2	265	273
									FQTEIQTVNK	95.0	51.3	25.0	1207.63	0	8	0	0	2	321	330
									FLEPTLR	95.0	33.6	25.0	875.50	0	2	0	0	2	339	345
									LEYCEALAMLR	95.0	40.3	25.0	1384.66	0	1	0	0	2	346	356
									EAGVEMGDEDDLSTPNEK	95.0	78.7	25.0	1951.81	0	4	0	0	2	357	374
									LLGHLVK	95.0	34.3	25.0	779.51	0	2	0	0	2	375	381
									ALHHGIDLEK	95.0	30.0	25.0	1132.61	0	1	0	0	2	442	451
									FGAPPHAGGGIGLER	95.0	63.2	25.0	1435.74	0	2	4	0	2	461	475
									VTMLFLGLHNVR	95.0	53.8	25.0	1415.78	0	2	0	0	2	476	487
Ataxin-10	ATX10_HUMAN	ATXN10	53.47	100.0	9	9	20	20.80	ALTALFK	95.0	34.3	25.0	763.47	0	3	0	0	2	28	34
									VLDILK	95.0	31.2	25.0	700.46	0	2	0	0	2	50	55
									VEQESLLTAFR	95.0	75.6	25.0	1292.68	0	2	0	0	2	123	133
									SPELVQAMFPK	95.0	62.6	25.0	1262.65	0	2	0	0	2	227	237
									LASEEPPDDEEALATIR	95.0	####	25.0	1855.89	0	2	0	0	2	289	305
									VIDLLR	95.0	31.0	25.0	728.47	0	2	0	0	2	333	338
									AEGDISNVANGFK	95.0	50.5	25.0	1321.64	0	2	0	0	2	359	371
									NLTEDNSQNQDLIAK	95.0	98.5	25.0	1702.82	0	4	0	0	2	424	438
									MEEQGLADASLLK	95.0	67.3	25.0	1420.70	0	1	0	0	2	439	451
ATP synthase subunit beta, mitochondrial	ATPB_HUMAN	ATP5B	56.54	100.0	8	8	25	19.50	TIAMDGTEGLVR	95.0	57.7	25.0	1278.64	0	3	0	0	2	110	121
									IPVGPETLGR	95.0	46.9	25.0	1038.59	0	2	0	0	2	134	143
									IMNVIGEPIDER	95.0	58.2	25.0	1401.70	0	2	0	0	2	144	155
									IGLFGGAGVGK	95.0	55.6	25.0	975.56	0	6	0	0	2	202	212
									TVLIMELINNVAK	95.0	55.4	25.0	1473.83	0	5	0	0	2	213	225
									VALVYGQMNEPPGAR	95.0	84.2	25.0	1617.81	0	2	0	0	2	265	279

									FTQAGSEVSALLGR	95.0	73.2	25.0	1435.75	0	3	0	0	2	311	324
									IMDPNIVGSEHYDVAR	95.0	48.7	25.0	1831.86	0	0	2	0	2	407	422
ATP-citrate synthase	ACLY_HUMAN	ACLY	120.82	100.0	14	15	46	15.10	LGQEATVGK	95.0	43.0	25.0	902.49	0	5	0	0	2	89	97
									LLVGVDEK	95.0	38.8	25.0	872.51	0	2	0	0	2	152	159
									DGVYVLDLAAK	95.0	46.6	25.0	1163.63	0	10	0	0	2	210	220
									LTLLNPK	95.0	28.1	25.0	798.51	0	1	0	0	2	266	272
									TILSLMTR	95.0	49.5	25.0	950.53	0	2	0	0	2	322	329
									DEPSVAAMVYPFTGDHK	95.0	60.8	25.0	1879.85	0	2	0	0	2	522	538
									SAYDSTMETMNYAQIR	95.0	####	25.0	1912.81	0	2	0	0	2	577	592
									IGNTGGMLDNILASK	95.0	72.8	25.0	1519.78	0	5	0	0	2	636	650
									LYRPGSVAYVSR	95.0	44.4	25.0	1367.74	0	2	2	0	2	651	662
									SGGMSNELNNIISR	95.0	63.6	25.0	1507.72	0	5	0	0	2	663	676
									TTDGVYEGVAIGGDR	95.0	####	25.0	1509.72	0	2	0	0	2	677	691
									YPGSTFMDHVLR	95.0	21.4	25.0	1438.68	0	0	2	0	2	692	703
									FGGALDAAAK	95.0	28.2	25.0	920.48	0	2	0	0	2	935	944
									SMGFIGHYLDQK	95.0	23.2	25.0	1411.67	0	0	2	0	2	1066	1077
ATP-dependent DNA helicase Q1	RECQ1_HUMAN	RECQL	73.44	100.0	6	7	14	11.20	VKDILQNVFK	95.0	50.9	25.0	1203.71	0	2	1	0	2	79	88
									EVFLVMPTGGGK	95.0	50.8	25.0	1250.65	0	2	0	0	2	108	119
									QLGISATMLNASSSK	95.0	62.1	25.0	1523.77	0	1	0	0	2	153	167
									SMENYYQESGR	95.0	64.8	25.0	1379.55	0	2	0	0	2	394	404
									ISSMVVMENVGQQK	95.0	33.4	25.0	1581.76	0	2	0	0	2	426	439
									VAGVVAPTLPR	95.0	61.8	25.0	1079.66	0	4	0	0	2	529	539
ATP-dependent RNA helicase A	DHX9_HUMAN	DHX9	140.94	100.0	20	22	86	14.50	LNQYFQK	95.0	37.3	25.0	940.49	0	3	0	0	2	185	191
									YTQVGPDHNR	95.0	42.0	25.0	1186.56	0	1	0	0	2	200	209
									EGETVEPYK	95.0	28.3	25.0	1051.49	0	1	0	0	2	267	275
									LAQFEPSQR	95.0	44.6	25.0	1075.55	0	4	0	0	2	315	323
									RISAVSVAER	95.0	40.2	25.0	1087.62	0	1	0	0	2	447	456
									ISAVSVAER	95.0	63.1	25.0	931.52	0	9	0	0	2	448	456
									GISHVIVDEIHER	95.0	71.2	25.0	1503.79	0	2	1	0	2	504	516
									DVVQAYPEVR	95.0	56.8	25.0	1175.61	0	2	0	0	2	529	538
									LSMSQLNEK	95.0	53.3	25.0	1065.52	0	10	0	0	2	622	630
									YQILPLHSQIPR	95.0	47.0	25.0	1464.83	0	2	0	0	2	681	692
									VFDPVPVGVTK	95.0	51.8	25.0	1157.66	0	9	0	0	2	698	708
									TPLHEIALSIK	95.0	30.4	25.0	1221.72	0	1	1	0	2	796	806
									LGGIGQFLAK	95.0	59.1	25.0	1003.59	0	25	0	0	2	810	819
									LPIEPR	95.0	27.7	25.0	724.44	0	1	0	0	2	858	863
									LGYIHR	95.0	31.2	25.0	758.43	0	1	0	0	2	900	905
									MGGEEAEIR	95.0	35.5	25.0	1007.45	0	2	0	0	2	930	938
									LNMATLR	95.0	33.2	25.0	834.45	0	4	0	0	2	945	951
									AAMEALVVEVTK	95.0	54.2	25.0	1276.68	0	2	0	0	2	1105	1116
									QPAIISQLDPVNER	95.0	55.3	25.0	1579.84	0	2	0	0	2	1117	1130
									YGDGPRPPK	95.0	37.6	25.0	986.51	0	2	0	0	2	1155	1163
ATP-dependent RNA helicase DDX1	DDX1_HUMAN	DDX1	82.42	100.0	6	6	13	7.70	FGFGFGGTGK	95.0	30.8	25.0	974.47	0	4	0	0	2	163	172
									ALIVEPSR	95.0	28.3	25.0	884.52	0	1	0	0	2	289	296
									ELAEQTLNNIK	95.0	37.5	25.0	1272.68	0	1	0	0	2	297	307
									LDDLVSTGK	95.0	42.4	25.0	947.50	0	4	0	0	2	350	358
									LNLSQVR	95.0	27.5	25.0	829.49	0	1	0	0	2	359	365
									MGLAISLVATEK	95.0	73.7	25.0	1248.69	0	2	0	0	2	612	623
ATP-dependent RNA helicase DDX3X	DDX3X_HUMAN	DDX3X	73.23	100.0	5	5	10	9.82	QYPISLVLAPTR	95.0	47.9	25.0	1357.78	0	4	0	0	2	265	276
									YLVLDEADR	95.0	42.8	25.0	1093.55	0	2	0	0	2	343	351
									MLDMGFEPQIR	95.0	55.4	25.0	1368.63	0	18	0	0	2	352	362

									HTMMFSATFPK	95.0	27.4	25.0	1329.60	0	1	0	0	2	377	387
									SPILVATAVAAR	95.0	56.3	25.0	1168.70	0	2	0	0	2	492	503
									DLLDLLVEAK	95.0	28.4	25.0	1128.65	0	1	0	0	2	555	564
ATP-dependent RNA helicase DDX42	DDX42_HUMAN	DDX42	102.96	100.0	4	4	27	4.48	VSYLVFDEADR	95.0	70.3	25.0	1313.64	0	4	0	0	2	401	411
									DILIDPIR	95.0	27.9	25.0	954.56	0	1	0	0	2	451	458
									DIPVLVATDVAAR	95.0	74.0	25.0	1339.76	0	18	0	0	2	548	560
									DSNFAGDLVR	95.0	55.5	25.0	1093.53	0	4	0	0	2	606	615
BAG family molecular chaperone regulator 2	BAG2_HUMAN	BAG2	23.75	100.0	3	3	6	12.30	IIDEVVNK	95.0	31.2	25.0	929.53	0	1	0	0	2	116	123
									FLDDLGNAK	95.0	32.8	25.0	992.50	0	2	0	0	2	124	132
									TLQQNAESR	95.0	32.3	25.0	1046.52	0	3	0	0	2	201	209
Basement membrane-specific heparan sulfate proteoglycan core protein	PGBM_HUMAN	HSPG2	468.76	100.0	27	31	161	6.67	SIEYSPQLEDAGSR	95.0	94.1	25.0	1551.73	0	4	0	0	2	93	106
									LGTVPQFPR	95.0	38.4	25.0	1014.57	0	2	0	0	2	189	197
									VDSYGGSLR	95.0	28.7	25.0	953.47	0	1	0	0	2	607	615
									GHTPTQPGALNQR	95.0	30.2	25.0	1376.70	0	0	1	0	2	648	660
									AGFFGDAMK	95.0	38.4	25.0	959.43	0	4	0	0	2	797	805
									VTSYGGELR	95.0	28.0	25.0	981.50	0	1	0	0	2	1002	1010
									FTVTQR	94.7	26.5	25.0	751.41	0	1	0	0	2	1011	1016
									ASYAQQPAESR	95.0	43.6	25.0	1207.57	0	9	0	0	2	1091	1101
									SYEIMFR	95.0	35.0	25.0	961.44	0	6	0	0	2	1458	1464
									AMDFNGILTIR	95.0	29.3	25.0	1266.65	0	1	0	0	2	1818	1828
									AVLHVHGGGGPR	95.0	38.0	25.0	1156.63	0	0	8	0	2	1946	1957
									IQVVVLSASDASPPPVK	95.0	69.2	25.0	1706.97	0	2	0	0	2	2038	2054
									LSGSHSQGVAYPVR	95.0	72.0	25.0	1457.75	0	2	4	0	2	2524	2537
									VAEGQTLDLK	95.0	42.3	25.0	1073.58	0	2	0	0	2	2838	2847
									HQVHGPLLR	95.0	34.2	25.0	1056.61	0	0	8	0	2	2871	2879
									LEGDTLIIPR	95.0	84.5	25.0	1126.65	0	13	0	0	2	3258	3267
									VGSSLPGR	95.0	38.7	25.0	772.43	0	6	0	0	2	3335	3342
									NELLHFER	95.0	57.7	25.0	1057.54	0	12	6	0	2	3347	3354
									EGGQLPPGHSVQDGVLR	95.0	32.8	25.0	1745.89	0	0	3	0	2	3436	3452
									IAHVELADAGQYR	95.0	83.0	25.0	1442.74	0	7	2	0	2	3542	3554
									LDGSLPPDSR	95.0	34.1	25.0	1056.53	0	4	0	0	2	3611	3620
									AFAHLQVPER	95.0	45.3	25.0	1167.63	0	6	3	0	2	3652	3661
									FDAGSGMATIR	95.0	80.5	25.0	1141.53	0	17	0	0	2	3737	3747
									AGLSSGFIGCVR	95.0	51.2	25.0	1223.62	0	2	0	0	2	3810	3821
									SAEPLALGR	95.0	43.3	25.0	913.51	0	7	0	0	2	4004	4012
									GSIQVDGEELVSGR	95.0	93.0	25.0	1445.72	0	8	0	0	2	4305	4318
									SPGPNVAVNAK	95.0	52.9	25.0	1053.57	0	9	0	0	2	4319	4329
Basic leucine zipper and W2 domain-containing protein 1	BZW1_HUMAN	BZW1	48.03	100.0	3	3	7	12.90	KLLLFLK	95.0	31.3	25.0	874.61	0	2	0	0	2	134	140
									EGVSAAFAVK	95.0	43.1	25.0	978.53	0	1	0	0	2	179	188
									YFTEAGLK	95.0	36.2	25.0	928.48	0	2	0	0	2	232	239
									KEELVAEQAIK	95.0	45.9	25.0	1257.71	0	3	0	0	2	309	319
									IVVLFYK	95.0	42.3	25.0	881.55	0	5	0	0	2	362	368
									AEVLSEEPILK	95.0	66.4	25.0	1227.68	0	4	0	0	2	369	379
Basic leucine zipper and W2 domain-containing protein 2	BZW2_HUMAN	BZW2	48.15	100.0	10	10	28	20.80	FLDSTGSR	95.0	32.4	25.0	882.43	0	4	0	0	2	51	58
									KLLLFLK	95.0	31.3	25.0	874.61	0	2	0	0	2	135	141
									AFSETEQTK	95.0	28.5	25.0	1040.49	0	2	0	0	2	142	150
									EGIAASFAVK	95.0	52.4	25.0	992.54	0	2	0	0	2	180	189
									LLELFPVNR	95.0	53.6	25.0	1100.65	0	5	0	0	2	216	224
									ELSDFLR	95.0	31.2	25.0	879.46	0	2	0	0	2	241	247
									VQQSLGTR	95.0	36.0	25.0	888.49	0	1	0	0	2	248	255
									KEELVAEQALK	95.0	45.9	25.0	1257.71	0	3	0	0	2	310	320

									IVVLFYK	95.0	42.3	25.0	881.55	0	5	0	0	2	363	369
									ADVLSEEAILK	95.0	74.1	25.0	1187.65	0	2	0	0	2	370	380
Basigin	BASI_HUMAN	BSG	42.18	100.0	3	3	3	9.61	FFVSSSQGR	95.0	30.1	25.0	1014.50	0	1	0	0	2	274	282
									GSDQAIITLR	95.0	33.5	25.0	1073.60	0	1	0	0	2	308	317
									RKPEDVLDDDDAGSAPLK	95.0	54.1	25.0	1940.96	0	0	1	0	2	349	366
Beta-2-microglobulin	B2MG_HUMAN	B2M	13.70	100.0	3	5	52	21.80	IQVYSR	95.0	35.7	25.0	765.43	0	5	0	0	2	27	32
									VEHSDLSFSK	95.0	60.0	25.0	1148.56	0	11	7	0	2	69	78
									VNHVTLSQPK	95.0	46.2	25.0	1122.63	0	18	11	0	2	102	111
Beta-lactamase-like protein 2	LACB2_HUMAN	LACTB2	32.79	100.0	3	4	6	12.50	ADIIYPGHGPVIHNAEAK	95.0	52.7	25.0	1901.99	0	1	1	0	2	192	209
									EQQILTLFR	95.0	43.7	25.0	1147.65	0	2	0	0	2	221	229
									SFTVMELVK	95.0	30.6	25.0	1069.56	0	2	0	0	2	235	243
Bifunctional aminoacyl-tRNA synthetase	SYEP_HUMAN	EPRS	170.58	100.0	11	11	46	8.00	FVELPGAEMGK	95.0	34.7	25.0	1193.59	0	4	0	0	2	187	197
									AYVDDTPAEQMK	95.0	29.9	25.0	1383.61	0	1	0	0	2	289	300
									LNLNNTVLSK	95.0	57.3	25.0	1115.64	0	6	0	0	2	426	435
									VAVQGDVVR	95.0	35.3	25.0	942.54	0	2	0	0	2	757	765
									NSEPAGLETPEAK	95.0	34.7	25.0	1342.65	0	2	0	0	2	890	902
									VASQGEVVR	95.0	33.4	25.0	944.52	0	1	0	0	2	908	916
									NQGGGLSSSGAGEGQGPK	95.0	74.0	25.0	1587.74	0	4	0	0	2	992	1009
									LLSVNIR	95.0	31.8	25.0	814.51	0	2	0	0	2	1334	1340
									LTVAENEAETK	95.0	59.4	25.0	1204.61	0	8	0	0	2	1390	1400
									DQDLEPGAPSMGAK	95.0	75.4	25.0	1431.64	0	7	0	0	2	1464	1477
									YYTLFGR	95.0	47.0	25.0	919.47	0	9	0	0	2	1504	1510
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DHAK_HUMAN	DAK	58.96	100.0	8	8	27	17.00	AVAQAGTVGTLLIVK	95.0	94.6	25.0	1440.88	0	4	0	0	2	95	109
									VAGALAEAGVGLEEIAK	95.0	77.5	25.0	1597.88	0	6	0	0	2	163	179
									MATADEIVK	95.0	31.1	25.0	993.49	0	2	0	0	2	231	239
									MALVLER	95.0	26.9	25.0	847.47	0	1	0	0	2	374	380
									EGPPPASPAQLLSK	95.0	47.6	25.0	1391.75	0	2	0	0	2	421	434
									LSVLLLEK	95.0	57.2	25.0	914.59	0	4	0	0	2	435	442
									SPGADLLQVLTK	95.0	81.3	25.0	1241.71	0	6	0	0	2	511	522
									LEQPDPGAVAAAAILR	95.0	97.8	25.0	1591.88	0	2	0	0	2	552	567
Bifunctional purine biosynthesis protein PURH	PUR9_HUMAN	ATIC	64.60	100.0	9	11	27	19.80	APGQLALFSVSDK	95.0	76.8	25.0	1332.72	0	6	0	0	1	2	14
									TLHPAVHAGILAR	95.0	29.2	25.0	1355.79	0	0	2	0	2	67	79
									EALGIPAAASFK	95.0	36.9	25.0	1174.65	0	1	0	0	2	255	266
									HVSPAGAAVGIPLSEDEAK	95.0	97.0	25.0	1847.95	0	3	2	0	2	267	285
									TLTPISAAYAR	95.0	28.8	25.0	1163.64	0	2	0	0	2	295	305
									TLFGLHLSQK	95.0	41.2	25.0	1143.65	0	2	1	0	2	380	389
									SLFSNVVTK	95.0	41.2	25.0	994.56	0	4	0	0	2	398	406
									NGQVIGIGAGQQSR	95.0	65.2	25.0	1384.73	0	2	0	0	2	438	451
									SGVAYIAAPSGSAADK	95.0	57.5	25.0	1464.73	0	2	0	0	2	554	569
Biliverdin reductase A	BIEA_HUMAN	BLVRA	33.41	100.0	7	7	18	20.90	KFGVVVVGVGR	95.0	23.8	25.0	1116.69	0	0	1	0	2	8	18
									FGVVVVGVGR	95.0	77.7	25.0	988.59	0	4	0	0	2	9	18
									GSLLFTAGPLEEER	95.0	56.3	25.0	1518.78	0	2	0	0	2	148	161
									YLSFHFK	95.0	39.8	25.0	941.49	0	2	0	0	2	228	234
									SGSLENVPNVGVNK	95.0	82.8	25.0	1413.73	0	4	0	0	2	235	248
									DQNIFVQK	95.0	46.8	25.0	991.52	0	3	0	0	2	254	261
									LLGQFSEK	95.0	55.8	25.0	921.50	0	2	0	0	2	262	269
Bone morphogenetic protein 1	BMP1_HUMAN	BMP1	111.23	100.0	3	3	20	3.04	GIFLDTIVPK	95.0	40.5	25.0	1102.65	0	11	0	0	2	280	289
									LPEPIVSTDSR	95.0	54.4	25.0	1213.64	0	5	0	0	2	401	411
									AGFAVNFFK	95.0	49.5	25.0	1000.53	0	4	0	0	2	538	546
Brain acid soluble protein 1	BASP1_HUMAN	BASP1	22.68	100.0	9	10	48	62.60	KAEGAATEEEGTPK	95.0	24.9	25.0	1417.68	0	0	1	0	2	25	38
									AEGAATEEEGTPK	95.0	46.1	25.0	1289.59	0	9	0	0	2	26	38

									ESEPQAAAEPAEAK	95.0	48.4	25.0	1427.66	0	10	0	0	2	39	52
									AEPEKTEGAAEAK	95.0	31.2	25.0	1330.65	0	1	0	0	2	85	97
									AEPPKAPEQEQAAPGPAAGGEAPK	95.0	32.0	25.0	2298.14	0	0	1	0	2	98	121
									AAEAAAAPAESAAPAAGEEPSKEEGEPK	95.0	38.3	25.0	2636.23	0	0	12	0	2	122	149
									KTEAPAAPAAQETK	95.0	49.2	25.0	1412.74	0	6	1	0	2	150	163
									SDGAPASDSKPGSSEAAPSSK	95.0	23.8	25.0	1932.88	0	0	2	0	2	164	184
									ETPAATEAPSSTPK	95.0	47.3	25.0	1386.67	0	5	0	0	2	185	198
Branched-chain-amino-acid aminotransferase, cytosolic	BCAT1_HUMAN	BCAT1	42.95	100.0	4	4	8	8.03	AKDLIVTPATILK	95.0	48.6	25.0	1382.86	0	2	0	0	2	27	39
									DLIVTPATILK	95.0	41.7	25.0	1183.73	0	1	0	0	2	29	39
									LFQPNLNMDR	95.0	32.4	25.0	1263.62	0	3	0	0	2	110	119
									LTDIQYGR	95.0	42.7	25.0	965.51	0	2	0	0	2	369	376
BRO1 domain-containing protein BROX	BROX_HUMAN	BROX	46.46	100.0	5	6	11	17.50	IAAGIFK	95.0	33.3	25.0	719.45	0	2	0	0	2	149	155
									ADHTLSSLEPAYSAK	95.0	85.5	25.0	1589.78	0	3	0	0	2	223	237
									GPGPTVKPSGHLFFR	95.0	48.2	25.0	1596.86	0	0	2	0	2	296	310
									IPTEAPQLELK	95.0	48.3	25.0	1238.70	0	2	0	0	2	335	345
									DDSTKPKPEEEVKPVKEPDIKPQK	95.0	29.3	25.0	2761.46	0	0	1	1	2	381	404
BTB/POZ domain-containing protein KCTD12	KCD12_HUMAN	KCTD12	35.68	100.0	6	6	19	20.30	MFTQQQPQELAR	95.0	56.4	25.0	1492.72	0	4	0	0	2	63	74
									DGFLFR	95.0	45.6	25.0	754.39	0	4	0	0	2	85	90
									YILDYLR	94.8	26.5	25.0	955.52	0	1	0	0	2	91	97
									SPSGGAAGPLLTPSQSLDGSR	95.0	####	25.0	1954.98	0	6	0	0	2	185	205
									SGYITIGYR	95.0	36.0	25.0	1029.54	0	3	0	0	2	207	215
									EVFGDTLNESR	95.0	41.5	25.0	1266.60	0	1	0	0	2	247	257
C-1-tetrahydrofolate synthase, cytoplasmic	C1TC_HUMAN	MTHFD1	101.54	100.0	15	15	89	18.30	EQVPGFTPR	95.0	29.4	25.0	1030.53	0	1	0	0	2	29	37
									LAILQVGNR	95.0	75.2	25.0	983.60	0	6	0	0	2	38	46
									DDSNLYINVK	95.0	80.3	25.0	1180.58	0	3	0	0	2	47	56
									GDILVVATGQPEMVK	95.0	39.6	25.0	1572.83	0	2	0	0	2	209	223
									TPVPSDIDISR	95.0	47.3	25.0	1199.63	0	7	0	0	2	314	324
									VLLSALER	95.0	41.3	25.0	900.55	0	22	0	0	2	355	362
									YVVVTGITPTPLGEGK	95.0	70.1	25.0	1630.91	0	1	0	0	2	371	386
									FSDIQIR	95.0	45.2	25.0	878.47	0	4	0	0	2	489	495
									TDPTTLTDEEINR	95.0	81.4	25.0	1504.71	0	15	0	0	2	505	517
									KITIGQAPTEK	95.0	38.6	25.0	1185.68	0	1	0	0	2	543	553
									MHGGGPTVTAGLPLPK	94.7	19.1	25.0	1548.82	0	0	1	0	2	706	721
									TDTESELDLISR	95.0	66.9	25.0	1378.67	0	8	0	0	2	761	772
									GALALAQAVQR	95.0	91.8	25.0	1097.64	0	13	0	0	2	794	804
									THLSLSHNPEQK	95.0	31.6	25.0	1390.71	0	1	0	0	2	867	878
									GVPTGFILPIR	95.0	53.9	25.0	1169.70	0	4	0	0	2	879	889
CAD protein	PYR1_HUMAN	CAD	242.96	100.0	13	13	46	5.93	LGYPVLVR	95.0	41.7	25.0	916.56	0	9	0	0	2	548	555
									ATGYPLAYVAAK	95.0	33.1	25.0	1224.66	0	2	0	0	2	697	708
									SFEEAFQK	95.0	31.2	25.0	985.46	0	1	0	0	2	771	778
									LYELTR	95.0	29.3	25.0	794.44	0	2	0	0	2	826	831
									VLGTSPEAIDSAENR	95.0	####	25.0	1558.77	0	12	0	0	2	1034	1048
									ELSDLESAR	95.0	39.8	25.0	1019.50	0	2	0	0	2	1067	1075
									FLSSAAAVSK	95.0	34.4	25.0	980.54	0	2	0	0	2	1110	1119
									VPQFSFSR	95.0	39.7	25.0	967.50	0	5	0	0	2	1263	1270
									SILEQLAEK	95.0	45.0	25.0	1030.58	0	4	0	0	2	1379	1387
									LSLDDLLQR	95.0	32.7	25.0	1072.60	0	1	0	0	2	1723	1731
									TSSSFAAAMAR	95.0	36.7	25.0	1115.51	0	2	0	0	2	1976	1986
									LGGAVLSFSEATSSVQK	95.0	84.3	25.0	1680.88	0	2	0	0	2	1987	2003
									MALLATVLGR	95.0	38.2	25.0	1060.62	0	2	0	0	2	2215	2224
Cadherin-1	CADH1_HUMAN	CDH1	97.44	100.0	6	7	33	7.37	TAYFSLDTR	95.0	40.6	25.0	1073.53	0	2	0	0	2	66	74

									VGTDGVITVK	95.0	68.6	25.0	988.57	0	2	0	0	2	77	86
									VTEPLDR	95.0	30.1	25.0	829.44	0	2	0	0	2	216	222
									NTGVISVVTTGLDR	95.0	####	25.0	1431.78	0	15	0	0	2	322	335
									GQVPENEANVVITTLK	95.0	95.3	25.0	1711.92	0	9	1	0	2	382	397
									MALEVGDYK	95.0	42.5	25.0	1041.49	0	2	0	0	2	656	664
Calcium-binding protein 39	CAB39_HUMAN	CAB39	39.85	100.0	9	10	25	24.60	KDVAQIFNNILR	95.0	65.3	25.0	1430.81	0	3	0	0	2	96	107
									LLSAEFLEQHYDR	95.0	70.8	25.0	1620.80	0	2	2	0	2	197	209
									LLGELLLDR	95.0	40.3	25.0	1041.63	0	5	0	0	2	232	240
									YISKPENLK	95.0	30.8	25.0	1091.61	0	1	0	0	2	249	257
									NIQFEAFHVFK	95.0	48.5	25.0	1379.71	0	2	0	0	2	269	279
									VFVANPNK	95.0	32.3	25.0	888.49	0	1	0	0	2	280	287
									LIEFLSK	95.0	46.2	25.0	849.51	0	4	0	0	2	302	308
									FQNDRTEDEQFNDEK	95.0	84.5	25.0	1914.81	0	2	0	0	2	309	323
									TEDEQFNDEK	95.0	40.0	25.0	1254.51	0	3	0	0	2	314	323
Calcyclin-binding protein	CYBP_HUMAN	CACYBP	26.19	100.0	3	3	24	7.89	SFDLLVK	95.0	46.1	25.0	821.48	0	21	0	0	2	112	118
									IYEDGDDDMK	95.0	28.4	25.0	1216.47	0	1	0	0	2	198	207
									IYEDGDDDMKR	95.0	32.1	25.0	1372.57	0	0	2	0	2	198	208
Calmodulin	CALM_HUMAN	CALM1	16.82	100.0	4	6	21	15.40	EAFSLFDK	95.0	33.3	25.0	956.47	0	1	0	0	2	15	22
									MKDTDSEEEIR	95.0	47.7	25.0	1368.60	0	4	1	0	2	77	87
									DTDSEEEIR	95.0	44.4	25.0	1093.46	0	11	0	0	2	79	87
									DTDSEEEIREAFR	95.0	47.2	25.0	1596.71	0	3	1	0	2	79	91
Calmodulin-like protein 3	CALL3_HUMAN	CALML3	16.87	99.5	2	2	4	20.80	EAFSLFDK	95.0	33.3	25.0	956.47	0	1	0	0	2	15	22
									SLGQNPTEAELR	95.0	45.8	25.0	1314.66	0	2	0	0	2	39	50
									LSDEEVDEMIR	95.0	60.3	25.0	1351.60	0	2	0	0	2	117	127
Calpain small subunit 1	CPNS1_HUMAN	CAPNS1	28.30	100.0	4	5	41	15.30	THYSNIEANESEEVR	95.0	85.6	25.0	1777.80	0	10	4	0	2	85	99
									SMVAVMDSDTTGK	95.0	70.0	25.0	1373.59	0	18	0	0	2	146	158
									LGFEEFK	95.0	45.5	25.0	869.44	0	3	0	0	2	159	165
									LDAMFR	95.0	37.6	25.0	768.37	0	6	0	0	2	236	241
Calpain-1 catalytic subunit	CAN1_HUMAN	CAPN1	81.87	100.0	16	17	143	16.90	YLGQDYEQLR	95.0	62.0	25.0	1284.62	0	5	0	0	2	37	46
									KAPSDLYQIILK	95.0	71.4	25.0	1388.82	0	13	0	0	2	229	240
									APSDLYQIILK	95.0	61.3	25.0	1260.72	0	26	0	0	2	230	240
									GQVVSLIR	95.0	46.8	25.0	871.54	0	2	0	0	2	286	293
									IRLDETDDPDDYGDR	95.0	59.9	25.0	1794.78	0	2	4	0	2	399	413
									LDETDDPDDYGDR	95.0	60.0	25.0	1525.59	0	5	0	0	2	401	413
									DFFLANASR	95.0	41.5	25.0	1040.52	0	23	0	0	2	463	471
									QLAGEDMEISVK	95.0	73.4	25.0	1335.65	0	8	0	0	2	553	564
									SMVNLMDR	95.0	40.7	25.0	997.44	0	16	0	0	2	592	599
									NYLSIFR	95.0	35.2	25.0	912.49	0	6	0	0	2	619	625
									KFDLDK	95.0	34.0	25.0	765.41	0	5	0	0	2	626	631
									SGSMSAYEMR	95.0	47.2	25.0	1150.45	0	5	0	0	2	632	641
									MAIESAGFK	95.0	31.1	25.0	969.47	0	3	0	0	2	642	650
									KLYELIITR	95.0	40.6	25.0	1148.70	0	4	0	0	2	654	662
									LYELIITR	95.0	65.9	25.0	1020.61	0	14	0	0	2	655	662
									LETMFR	95.0	35.8	25.0	812.40	0	2	0	0	2	682	687
Calpain-2 catalytic subunit	CAN2_HUMAN	CAPN2	80.00	100.0	4	4	16	4.86	DREAAEGLGSHER	95.0	31.0	25.0	1426.67	0	0	2	0	2	11	23
									EAAEGLGSHER	95.0	66.1	25.0	1155.54	0	2	0	0	2	13	23
									SDTFINLR	95.0	62.2	25.0	965.51	0	4	0	0	2	462	469
									IMVDMLDSDGSGK	95.0	66.7	25.0	1399.61	0	8	0	0	2	579	591
Calreticulin	CALR_HUMAN	CALR	48.12	100.0	4	6	28	6.24	FYGDEEKDK	95.0	46.6	25.0	1130.50	0	13	4	0	2	56	64
									KVHVIFNYK	95.0	28.3	25.0	1147.66	0	3	3	0	2	143	151
									VHVIFNYK	95.0	33.3	25.0	1019.57	0	2	0	0	2	144	151

									QIDNPDYK	95.0	32.6	25.0	992.47	0	3	0	0	2	279	286
Calsyntenin-1	CSTN1_HUMAN	CLSTN1	109.77	100.0	10	11	54	9.48	IHGQNVPFDAVVVDK	95.0	81.2	25.0	1637.86	0	3	4	0	2	89	103
									RATEDVLVK	95.0	33.0	25.0	1030.59	0	1	0	0	2	246	254
									ATEDVLVK	95.0	30.5	25.0	874.49	0	3	0	0	2	247	254
									IPDGVVSVSPK	95.0	67.9	25.0	1097.62	0	15	0	0	2	373	383
									LIFLFR	95.0	29.8	25.0	808.51	0	1	0	0	2	427	432
									GNLAGLTLR	95.0	72.0	25.0	914.54	0	13	0	0	2	537	545
									EGLDLQVLEDSGR	95.0	90.4	25.0	1430.71	0	6	0	0	2	563	575
									AMQHISYLNSR	95.0	21.7	25.0	1335.65	0	0	1	0	2	601	611
									QFPTPGIR	95.0	33.0	25.0	915.50	0	3	0	0	2	612	619
									ISLSGVHHFAR	95.0	35.6	25.0	1223.66	0	0	4	0	2	655	665
Calumenin	CALU_HUMAN	CALU	37.09	100.0	3	4	7	11.10	VHHEPQLSDK	95.0	33.1	25.0	1189.60	0	1	2	0	2	28	37
									MADKDGDLIATK	95.0	57.9	25.0	1293.64	0	2	0	0	2	162	173
									DIVVQETMEDIDK	95.0	79.0	25.0	1550.73	0	2	0	0	2	190	202
cAMP-dependent protein kinase catalytic subunit alpha	KAPCA_HUMAN	PRKACA	40.57	100.0	3	3	4	7.12	AKEDFLK	95.0	37.2	25.0	850.47	0	1	0	0	2	23	29
									QIEHTLNEK	95.0	28.5	25.0	1111.57	0	1	0	0	2	85	93
									KVEAPFIPK	95.0	38.3	25.0	1028.61	0	2	0	0	2	310	318
Caprin-1	CAPR1_HUMAN	CAPRIN1	78.35	100.0	4	4	12	6.35	LNQDQLDAVSK	95.0	62.3	25.0	1230.63	0	4	0	0	2	88	98
									YQEVTNNLEFAK	95.0	81.3	25.0	1455.71	0	6	0	0	2	99	110
									SFMALSQDIQK	95.0	28.5	25.0	1283.63	0	1	0	0	2	115	125
									TVLELQYVLDK	95.0	29.7	25.0	1320.74	0	1	0	0	2	148	158
Carbohydrate kinase domain-containing protein	CARKD_HUMAN	CARKD	36.56	100.0	3	3	4	9.80	NVQGILEVSK	95.0	59.1	25.0	1086.62	0	2	0	0	2	163	172
									LYDAVLR	95.0	31.1	25.0	849.48	0	1	0	0	2	213	219
									STTTSDMIAEVGAAFSK	95.0	58.7	25.0	1731.81	0	1	0	0	2	327	343
Carbonic anhydrase 2	CAH2_HUMAN	CA2	29.23	100.0	6	6	20	26.20	ILNNGHAFNVEFDDSQDK	95.0	45.8	25.0	2062.95	0	0	2	0	2	59	76
									GGPLDGTYR	95.0	37.3	25.0	935.46	0	2	0	0	2	81	89
									VGSAKPGLQK	95.0	40.8	25.0	984.58	0	7	0	0	2	149	158
									VVDVLDSIK	95.0	36.9	25.0	987.57	0	4	0	0	2	159	167
									SADFTNFDPR	95.0	50.3	25.0	1169.52	0	4	0	0	2	172	181
									EPISVSSEQVLK	95.0	28.9	25.0	1315.71	0	1	0	0	2	213	224
Carbonyl reductase [NADPH] 1	CBR1_HUMAN	CBR1	30.36	100.0	6	8	29	27.80	GIGLAIVR	95.0	58.9	25.0	798.52	0	4	0	0	2	16	23
									LFSGDVVLTAR	95.0	63.1	25.0	1177.66	0	2	0	0	2	28	38
									GQAAVQQLQAEGLSPR	95.0	####	25.0	1652.87	0	2	2	0	2	43	58
									VADPTPFHIQAEVTMK	95.0	32.4	25.0	1799.90	0	1	2	0	2	97	112
									VVNVSSIMSVR	95.0	63.6	25.0	1206.65	0	8	0	0	2	135	145
									SETITEEELVGLMNK	95.0	95.6	25.0	1708.83	0	8	0	0	2	160	174
Carboxymethylenebutenolidase homolog	CMBL_HUMAN	CMBL	28.03	100.0	5	5	19	18.80	LEYGGLGR	94.6	26.4	25.0	864.46	0	1	0	0	2	16	23
									EISAILK	95.0	37.8	25.0	773.48	0	3	0	0	2	109	115
									AGVSVYGIVK	95.0	70.3	25.0	992.58	0	5	0	0	2	150	159
									DSEDIYNLK	95.0	65.3	25.0	1096.52	0	4	0	0	2	160	168
									TFSGQTHGFVHR	95.0	41.4	25.0	1373.67	0	6	0	0	2	206	217
Carboxypeptidase A4	CBPA4_HUMAN	CPA4	47.33	100.0	3	3	15	6.89	FFGDQVLR	95.0	48.5	25.0	981.52	0	7	0	0	2	21	28
									LSQLVNSNNLK	95.0	37.5	25.0	1229.68	0	2	0	0	2	40	50
									DPAITSILEK	95.0	60.1	25.0	1086.60	0	6	0	0	2	205	214
Casein kinase I isoform alpha	KC1A_HUMAN	CSNK1A1	38.90	100.0	4	4	5	12.50	AEFIVGGK	95.0	31.4	25.0	820.46	0	1	0	0	2	9	16
									HPQLLYESK	95.0	26.9	25.0	1114.59	0	1	0	0	2	54	62
									TVLMLADQMISR	95.0	71.1	25.0	1409.71	0	2	0	0	2	112	123
									DIKPDNFLMGIGR	95.0	26.3	25.0	1491.76	0	0	1	0	2	136	148
Casein kinase II subunit alpha	CSK21_HUMAN	CSNK2A1	45.13	99.5	2	2	2	8.70	ILENLR	95.0	31.3	25.0	757.46	0	1	0	0	2	84	89
									GGPNIITLADIVK	95.0	26.8	25.0	1310.77	0	1	0	0	2	90	102
									TPALVFEHVNNTDFK	95.0	75.0	25.0	1731.87	0	1	0	0	2	108	122

Casein kinase II subunit alpha'	CSK22_HUMAN	CSNK2A2	41.20	100.0	3	3	7	8.86	ILENLR	95.0	31.3	25.0	757.46	0	1	0	0	2	85	90
									VLGTEELYGYLK	95.0	35.4	25.0	1384.74	0	1	0	0	2	249	260
									HLVSPEALDLLDK	95.0	59.4	25.0	1449.80	0	5	0	0	2	292	304
Caspase-6	CASP6_HUMAN	CASP6	33.29	100.0	3	3	7	8.87	GIALIFNHER	95.0	32.1	25.0	1169.64	0	1	0	0	2	45	54
									FSDLGFEVK	95.0	37.5	25.0	1041.53	0	4	0	0	2	78	86
									AEELLLK	95.0	35.7	25.0	815.49	0	2	0	0	2	93	99
Catenin alpha-1	CTNA1_HUMAN	CTNNA1	100.05	100.0	16	17	65	21.00	ALLSAVTR	95.0	53.6	25.0	830.51	0	8	0	0	2	130	137
									LLILADMADVYK	95.0	71.9	25.0	1380.74	0	2	0	0	2	138	149
									NAGNEQDLGIQYK	95.0	61.4	25.0	1449.70	0	2	0	0	2	166	178
									ALKPEVDKLNIMAAK	95.0	35.9	25.0	1656.94	0	0	2	2	2	179	193
									QIIVDPLSFSEER	95.0	57.0	25.0	1532.80	0	2	0	0	2	288	300
									SDALNSAIDK	95.0	30.0	25.0	1033.52	0	2	0	0	2	361	370
									LAQENMDLFK	95.0	52.1	25.0	1224.59	0	4	0	0	2	479	488
									VIHVVTSEMDNYEPGVYTEK	95.0	25.8	25.0	2326.09	0	0	2	0	2	552	571
									AVLMIR	95.0	39.5	25.0	718.43	0	2	0	0	2	628	633
									TSVQTEDDQLIAGQSAR	95.0	99.6	25.0	1818.88	0	11	0	0	2	654	670
									AIMAQLPQEQK	95.0	37.2	25.0	1272.66	0	5	0	0	2	671	681
									IAEQVASFQEEK	95.0	78.6	25.0	1378.68	0	2	0	0	2	684	695
									WDDSGNDIIVLAK	95.0	75.7	25.0	1445.73	0	2	0	0	2	705	717
									NTSDVISAAK	95.0	30.2	25.0	1005.52	0	1	0	0	2	738	747
									QDLLAYLQR	95.0	44.8	25.0	1119.62	0	8	0	0	2	774	782
									NLMNAVVQTVK	95.0	58.1	25.0	1232.67	0	8	0	0	2	824	834
Catenin beta-1	CTNB1_HUMAN	CTNNB1	85.48	100.0	9	11	59	14.10	LLNDEDQVVVNK	95.0	66.4	25.0	1385.73	0	10	0	0	2	159	170
									AAVMVHQLSK	95.0	35.7	25.0	1099.59	0	1	0	0	2	171	180
									SPQMVSAIVR	95.0	34.5	25.0	1103.59	0	1	0	0	2	191	200
									TMQNTNDVETAR	95.0	59.9	25.0	1395.62	0	8	0	0	2	201	212
									EGLLAIFK	95.0	28.4	25.0	890.53	1	0	0	0	2	226	233
									HQEAEMAQNAVR	95.0	44.5	25.0	1399.64	0	4	7	0	2	475	486
									LHYGLPVVVK	95.0	49.0	25.0	1124.68	0	10	8	0	2	487	496
									ATVGLIR	95.0	34.8	25.0	729.46	0	3	0	0	2	509	515
									TSMGGTQQQFVEGVR	95.0	86.4	25.0	1640.77	0	6	0	0	2	551	565
									NEGVATYAAAVLFR	95.0	38.3	25.0	1481.77	0	1	0	0	2	648	661
Cathepsin D	CATD_HUMAN	CTSD	44.54	100.0	7	7	88	18.70	TMSEVGGSVEDLIAK	95.0	93.2	25.0	1551.76	0	17	0	0	2	35	49
									QVFGEATK	95.0	30.7	25.0	879.46	0	1	0	0	2	177	184
									FDGILGMAYPR	95.0	85.0	25.0	1255.61	0	15	0	0	2	195	205
									DPDAQPGGELMLGGTDSK	95.0	####	25.0	1803.81	0	14	0	0	2	236	253
									VSTLPAITLK	95.0	35.8	25.0	1042.65	0	2	0	0	2	332	341
									YYTVFDR	95.0	33.2	25.0	963.46	0	4	0	0	2	393	399
									VGFAEAAR	95.0	50.0	25.0	820.43	0	35	0	0	2	404	411
Cathepsin Z	CATZ_HUMAN	CTSZ	33.85	100.0	3	3	11	10.20	GDGLAPLGR	95.0	34.2	25.0	855.47	0	3	0	0	2	39	47
									NVDGVNYASITR	95.0	82.7	25.0	1308.65	0	6	0	0	2	70	81
									VGDYGSLSGR	95.0	67.5	25.0	1010.49	0	2	0	0	2	190	199
Cation-independent mannose-6-phosphate receptor	MPRI_HUMAN	IGF2R	274.26	100.0	5	5	18	2.01	YDLSALVR	95.0	58.1	25.0	936.51	0	7	0	0	2	484	491
									GTADAFIVR	95.0	37.1	25.0	949.51	0	1	0	0	2	1031	1039
									DGAGNSFDLSSLSR	95.0	42.9	25.0	1425.66	0	2	0	0	2	1373	1386
									DGIIVLK	95.0	52.8	25.0	757.48	0	4	0	0	2	1448	1454
									VPIDGPPIDIGR	95.0	40.0	25.0	1248.70	0	4	0	0	2	1715	1726
Caveolin-1	CAV1_HUMAN	CAV1	20.45	100.0	4	4	13	24.20	YVDSEGHLYTVPIR	95.0	66.4	25.0	1648.83	0	2	0	0	2	6	19
									EQGNIYKPNNK	95.0	28.4	25.0	1304.66	0	1	0	0	2	20	30
									HLNDDVVK	95.0	50.8	25.0	939.49	0	8	0	0	2	58	65
									ASFTTFTVTK	95.0	70.7	25.0	1102.58	0	2	0	0	2	87	96

CCR4-NOT transcription complex subunit 1	CNOT1_HUMAN	CNOT1	266.93	100.0	5	5	6	1.81	DAIAALGLLQK	95.0	30.5	25.0	1112.67	0	1	0	0	2	1654	1664
									NLILSAFPR	95.0	32.0	25.0	1030.60	0	2	0	0	2	2130	2138
									NLILSAFPRNMR	95.0	19.2	25.0	1447.78	0	0	1	0	2	2130	2141
									LPDPFTPNLK	94.7	26.5	25.0	1141.63	0	1	0	0	2	2142	2151
									SPVTFLSDLR	95.0	45.8	25.0	1134.62	0	1	0	0	2	2188	2197
CD109 antigen	CD109_HUMAN	CD109	161.67	100.0	5	5	22	3.81	TSLNILIK	95.0	31.7	25.0	901.57	0	1	0	0	2	162	169
									ADGNQLTLEER	95.0	63.5	25.0	1245.61	0	10	0	0	2	375	385
									SSMAVHSLFK	95.0	37.1	25.0	1122.56	0	1	0	0	2	452	461
									VGSPFELVVSGNK	95.0	48.5	25.0	1332.72	0	4	0	0	2	479	491
									ALSEFAALMNTER	95.0	87.3	25.0	1468.71	0	6	0	0	2	1190	1202
CD166 antigen	CD166_HUMAN	ALCAM	65.09	100.0	9	11	106	13.40	LDVPQNLMFGK	95.0	75.8	25.0	1277.66	0	17	0	0	2	45	55
									KSVQYDDVPEYK	95.0	43.8	25.0	1470.71	0	6	0	0	2	76	87
									SVQYDDVPEYKDR	95.0	63.6	25.0	1613.74	0	15	1	0	2	77	89
									ALFLETEQLK	95.0	62.3	25.0	1191.66	0	14	0	0	2	143	152
									ALFLETEQLKK	95.0	58.8	25.0	1319.76	0	16	4	0	2	143	153
									SSNTYTLTDVR	95.0	67.0	25.0	1256.61	0	28	0	0	2	294	304
									SSNTYTLTDVRR	95.0	36.6	25.0	1412.71	0	1	0	0	2	294	305
									QIGDALPVSCTISASR	95.0	68.3	25.0	1674.85	0	2	0	0	2	345	360
									ESLTLIVEGKPQIK	95.0	76.9	25.0	1554.91	0	2	0	0	2	406	419
CD44 antigen	CD44_HUMAN	CD44	81.54	100.0	5	5	68	8.09	FAGVFHVEK	95.0	45.6	25.0	1033.55	0	32	0	0	2	30	38
									ALSIGFETCR	94.6	26.4	25.0	1153.57	0	1	0	0	2	69	78
									YGFIEGHVVIPR	95.0	48.2	25.0	1386.75	0	0	8	0	2	79	90
									LVINSGNGAVEDR	95.0	60.9	25.0	1343.69	0	12	0	0	2	682	694
									ESSETPDQFMTADETR	95.0	95.4	25.0	1859.76	0	15	0	0	2	716	731
Cell division control protein 2 homolog	CDC2_HUMAN	CDC2	34.07	100.0	4	4	8	18.50	IGEGTYGVVYK	95.0	77.0	25.0	1185.62	0	2	0	0	2	10	20
									LESEEEGVPSTAIR	95.0	39.2	25.0	1516.75	0	2	0	0	2	37	50
									LADFGLAR	95.0	55.9	25.0	862.48	0	9	0	0	2	144	151
									SPEVLLGSAR	95.0	71.8	25.0	1028.57	0	3	0	0	2	171	180
									NLDENGLDLLSK	95.0	42.3	25.0	1330.69	0	1	0	0	2	255	266
Cell division protein kinase 6	CDK6_HUMAN	CDK6	36.92	100.0	6	7	21	20.90	VQTGEEGMPLSTIR	95.0	76.4	25.0	1533.76	0	2	0	0	2	47	60
									HLETFEHPNVVR	95.0	60.0	25.0	1477.75	0	2	2	0	2	67	78
									DMMFQLLR	95.0	40.4	25.0	1085.51	0	2	0	0	2	124	131
									DLKPQNILVTSSGQIK	95.0	67.3	25.0	1740.99	0	2	0	0	2	145	160
									LADFGLAR	95.0	55.9	25.0	862.48	0	9	0	0	2	161	168
									GSSDVDQLGK	95.0	37.4	25.0	1005.48	0	2	0	0	2	221	230
Cellular retinoic acid-binding protein 2	RABP2_HUMAN	CRABP2	15.67	100.0	5	6	27	29.00	SENFEELLK	95.0	57.7	25.0	1108.55	0	15	0	0	2	13	21
									VLGVNVMLR	95.0	68.6	25.0	1016.59	0	5	0	0	2	22	30
									KIAVAAASKPAVEIK	95.0	81.5	25.0	1495.92	0	2	0	0	2	31	45
									IAVAAASKPAVEIK	95.0	60.0	25.0	1367.83	0	2	2	0	2	32	45
									TTEINFK	95.0	30.3	25.0	852.45	0	1	0	0	2	61	67
Charged multivesicular body protein 2a	CHM2A_HUMAN	CHMP2A	25.09	100.0	3	3	7	12.60	ANIQAVSLK	95.0	34.3	25.0	943.56	0	3	0	0	2	81	89
									KAEAAASALADADADLEER	95.0	56.2	25.0	1916.92	0	0	2	0	2	197	215
									AEAAASALADADADLEER	95.0	95.8	25.0	1788.82	0	2	0	0	2	198	215
Chloride intracellular channel protein 1	CLIC1_HUMAN	CLIC1	26.91	100.0	4	4	91	19.50	GVTFNVTTVDTK	95.0	92.6	25.0	1281.67	0	24	0	0	2	38	49
									FSAYIK	95.0	32.3	25.0	728.40	0	7	0	0	2	114	119
									NSNPALNDNLEK	95.0	78.6	25.0	1328.64	0	45	0	0	2	120	131
									GFTIPEAFR	95.0	39.4	25.0	1037.54	0	4	0	0	2	196	204
									YLSNAYAR	95.0	43.9	25.0	957.48	0	18	0	0	2	209	216
Chloride intracellular channel protein 2	CLIC2_HUMAN	CLIC2	28.34	100.0	2	2	8	13.00	AGSDGESIGNCPFCQR	95.0	39.4	25.0	1697.70	0	4	0	0	2	20	35
									FNVTTVDMTR	95.0	62.5	25.0	1199.57	0	4	0	0	2	47	56
									FSAYIK	95.0	32.3	25.0	728.40	0	7	0	0	2	120	125

Chloride intracellular channel protein 4	CLIC4_HUMAN	CLIC4	28.76	100.0	6	6	24	22.10	GVVFSVTTVDLKR	95.0	58.5	25.0	1420.82	0	2	0	0	2	49	61
									FSAYIK	95.0	32.3	25.0	728.40	0	7	0	0	2	125	130
									NSRPEANEALER	95.0	41.4	25.0	1385.68	0	8	0	0	2	131	142
									NFDIPK	95.0	32.4	25.2	733.39	0	2	0	0	2	207	212
									YLTNAYSR	95.0	40.2	25.0	987.49	0	2	0	0	2	220	227
									EVEIAYSDVAK	95.0	38.7	25.0	1223.62	0	3	0	0	2	239	249
Chondroitin sulfate proteoglycan 4	CSPG4_HUMAN	CSPG4	250.52	100.0	16	16	73	7.88	LVLGQEELR	95.0	57.5	25.0	1056.60	0	4	0	0	2	87	95
									LEISVDQYPTHTSNR	94.9	19.2	25.0	1759.86	0	0	1	0	2	296	310
									GVLSYLEPR	95.0	50.9	25.0	1033.57	0	6	0	0	2	311	319
									SQVLFSVTR	95.0	36.4	25.0	1036.58	0	1	0	0	2	466	474
									GGPAQDLTFR	95.0	52.7	25.0	1061.54	0	9	0	0	2	632	641
									VSDGLQASPPATLK	95.0	58.1	25.0	1383.75	0	13	0	0	2	642	655
									VTGALQFGELQK	95.0	66.7	25.0	1290.71	0	2	0	0	2	703	714
									LSDGQGFTQDDIQAGR	95.0	77.9	25.0	1707.79	0	9	0	0	2	841	856
									ASEAVEDTFR	95.0	28.4	25.0	1124.52	0	1	0	0	2	865	874
									TTMVTSFTNEDLLR	95.0	50.7	25.0	1643.79	0	2	0	0	2	954	967
									SPPSAGYLVMVSR	95.0	99.5	25.0	1379.70	0	2	0	0	2	1280	1292
									MVEEQLIR	95.0	40.8	25.0	1033.53	0	4	0	0	2	1424	1431
									GTLDGGFR	95.0	30.7	25.0	822.41	0	1	0	0	2	1550	1557
									ASSSAGTDPQLLLYR	95.0	88.1	25.0	1578.81	0	12	0	0	2	1607	1621
									FTQADVDSGR	95.0	41.7	25.0	1095.51	0	3	0	0	2	1894	1903
									APLEVPQALGR	95.0	54.9	25.0	1150.66	0	3	0	0	2	1948	1958
Chromobox protein homolog 3	CBX3_HUMAN	CBX3	20.79	100.0	3	4	18	13.70	KVEEAEPEEFVVEK	95.0	93.9	25.0	1661.83	0	7	3	0	2	21	34
									VEEAEPEEFVVEK	95.0	75.6	25.0	1533.73	0	4	0	0	2	22	34
									DSDEADLVLAK	95.0	78.0	25.0	1175.58	0	4	0	0	2	144	154
Cingulin	CING_HUMAN	CGN	136.37	99.9	2	2	2	2.01	ATIYGILR	95.0	27.0	25.0	906.54	0	1	0	0	2	310	317
									AVAGQGELTR	95.0	27.4	25.0	1001.54	0	1	0	0	2	351	360
									IEVLQR	95.0	32.5	25.0	757.46	0	3	0	0	2	601	606
Citrate synthase, mitochondrial	CISY_HUMAN	CS	51.70	100.0	6	7	13	13.90	DILADLIPK	95.0	38.9	25.0	997.59	0	3	0	0	2	35	43
									TVVGQITVDMMYGGMR	95.0	79.9	25.0	1805.82	0	2	0	0	2	58	73
									DVSDEKLR	95.0	27.7	25.0	961.50	0	1	0	0	2	322	329
									VVPGYGHAVLR	95.0	36.9	25.0	1167.66	0	2	0	0	2	341	351
									IVPNVLLEQGK	95.0	30.6	25.0	1209.72	0	1	0	0	2	383	393
									ALGFPLERPK	95.0	39.6	25.0	1127.66	0	2	2	0	2	441	450
Clathrin heavy chain 1	CLH1_HUMAN	CLTC	191.60	100.0	24	25	245	13.30	RPISADSAIMNPASK	95.0	54.3	25.0	1573.80	0	4	0	0	2	64	78
									TLQIFNIEMK	95.0	49.5	25.0	1252.66	0	12	0	0	2	87	96
									VVGAMQLYSVDR	95.0	86.5	25.0	1353.68	0	29	0	0	2	177	188
									KVSQPIEGHAASFAQFK	95.0	35.4	25.0	1844.97	0	0	2	0	2	189	205
									VSQPIEGHAASFAQFK	95.0	22.3	25.0	1716.87	0	0	1	0	2	190	205
									HDVVFLITK	95.0	55.6	25.0	1071.62	0	5	0	0	2	270	278
									NNLAGAEELFAR	95.0	####	25.0	1304.66	0	26	0	0	2	355	366
									GQFSTDELVAEVEK	95.0	####	25.0	1551.75	0	6	0	0	2	838	851
									IYIDSNNNPER	95.0	60.1	25.0	1334.63	0	20	0	0	2	882	892
									ENPYYDSR	95.0	39.8	25.0	1043.44	0	3	0	0	2	896	903
									IVLDNSVFSEHR	95.0	91.1	25.0	1415.73	0	18	10	0	2	1011	1022
									NLQNLLILTAIK	95.0	49.9	25.0	1353.85	0	1	0	0	2	1023	1034
									VMEYINR	95.0	40.0	25.0	940.46	0	26	0	0	2	1040	1046
									AYEFAER	95.0	36.3	25.0	885.41	0	3	0	0	2	1095	1101
									EAIDSYIK	95.0	27.3	25.0	938.48	0	2	0	0	2	1123	1130
									LLYNNVSNFGR	95.0	70.5	25.0	1296.67	0	42	0	0	2	1216	1226
									VANVELYYR	95.0	68.7	25.0	1126.59	0	7	0	0	2	1398	1406

									QLPLVKPYLR	95.0	27.3	25.0	1226.76	0	0	1	0	2	1444	1453
									LEKHELIEFR	95.0	30.5	25.0	1313.72	0	0	2	0	2	1499	1508
									HELIEFR	95.0	41.4	25.0	943.50	0	17	0	0	2	1502	1508
									IAAYLFK	95.0	29.0	25.0	825.49	0	1	0	0	2	1510	1516
									DAMQYASESK	95.0	58.3	25.0	1145.48	0	5	0	0	2	1536	1545
									VDKLDASESLR	95.0	31.3	25.0	1232.65	0	1	0	0	2	1610	1620
									LDASESLR	95.0	28.8	25.0	890.46	0	1	0	0	2	1613	1620
Cleavage and polyadenylation specificity factor subunit 5	CPSF5_HUMAN	NUDT21	26.21	100.0	6	7	14	21.10	TVEGVLIVHEHR	95.0	60.5	25.0	1388.76	0	2	1	0	2	79	90
									LPGGELNPGEDEVEGLK	95.0	76.7	25.0	1752.87	0	2	0	0	2	106	122
									LPGGELNPGEDEVEGLKR	95.0	60.1	25.0	1908.97	0	0	2	0	2	106	123
									LMTEILGR	95.0	51.2	25.0	948.52	0	4	0	0	2	124	131
									KLFLVQLQEK	95.0	48.6	25.0	1245.76	0	1	0	0	2	173	182
									LFLVQLQEK	95.0	39.5	25.0	1117.66	0	2	0	0	2	174	182
Cleavage stimulation factor subunit 1	CSTF1_HUMAN	CSTF1	48.34	100.0	4	4	9	14.80	LGMENDDTAVQYAIGR	95.0	97.1	25.0	1768.82	0	4	0	0	2	56	71
									DGQLIATGSADASIK	95.0	77.0	25.0	1446.74	0	2	0	0	2	119	133
									SAMPIEVMMNETAQQNMENHPVIR	95.0	26.5	25.0	2834.26	0	0	1	0	2	144	167
									YIQEAEMLR	95.0	44.5	25.0	1168.57	0	2	0	0	2	213	221
Cleavage stimulation factor subunit 3	CSTF3_HUMAN	CSTF3	82.91	100.0	5	5	13	7.39	LVAQFPSSGR	95.0	27.6	25.0	1061.57	0	1	0	0	2	57	66
									MAQAYDFALDK	95.0	65.3	25.0	1288.59	0	4	0	0	2	122	132
									GVEAVGSYAENQR	95.0	67.8	25.0	1379.65	0	2	0	0	2	152	164
									LFSDEAANIYER	95.0	73.4	25.0	1427.68	0	2	0	0	2	319	330
									IFELGLK	95.0	36.6	25.0	819.50	0	4	0	0	2	432	438
CLIP-associating protein 1	CLAP1_HUMAN	CLASP1	169.44	100.0	4	4	7	2.99	AQIGTVLPSLIDR	95.0	62.2	25.0	1382.80	0	3	0	0	2	87	99
									DAAINSLVEIYR	95.0	47.0	25.0	1363.72	0	1	0	0	2	185	196
									FIVDQTQTPNLK	95.0	57.3	25.0	1403.75	0	1	0	0	2	982	993
									KGALLELLK	95.0	34.7	25.0	984.65	0	2	0	0	2	1322	1330
Clusterin	CLUS_HUMAN	CLU	52.48	100.0	4	4	19	12.20	IDSLLENDR	95.0	42.2	25.0	1074.54	0	2	0	0	2	159	167
									ASSIIDELFQDR	95.0	59.1	25.0	1393.70	0	3	0	0	2	183	194
									ELDESLQVAER	95.0	47.0	25.0	1288.64	0	3	0	0	2	326	336
									VTTVASHTSDSDVPSGVTEVVVK	95.0	46.6	25.0	2314.18	0	0	11	0	2	386	408
Coactosin-like protein	COTL1_HUMAN	COTL1	15.93	100.0	8	9	59	40.10	AAYNLVR	95.0	49.1	25.0	806.45	0	16	0	0	2	12	18
									LFAFVR	95.0	36.3	25.0	752.45	0	12	0	0	2	58	63
									FTTGDAMSK	95.0	38.6	25.0	973.43	0	5	0	0	2	64	72
									EVVQNFAK	95.0	46.1	25.0	934.50	0	10	0	0	2	103	110
									EFVISDRK	95.0	30.4	25.0	993.54	0	3	0	0	2	111	118
									KELEEDFIK	95.0	48.3	25.0	1150.60	0	2	2	0	2	118	126
									ELEEDFIK	95.0	39.4	25.0	1022.50	0	4	0	0	2	119	126
									AGGANYDAQTE	95.0	59.1	25.0	1096.45	0	5	0	0	2	132	142
Coatomer subunit alpha	COPA_HUMAN	COPA	138.33	100.0	14	16	81	12.40	QQPLFVSGGDDYK	95.0	64.9	25.0	1453.70	0	4	0	0	2	62	74
									NLSPGAVESDVR	95.0	47.7	25.0	1243.63	0	4	0	0	2	171	182
									DADSITLFDVQQK	95.0	52.1	25.0	1479.73	0	9	0	0	2	468	480
									YAVTTGDHGIIR	95.0	44.3	25.0	1302.68	0	2	0	0	2	551	562
									TLDLPIYVTR	95.0	40.0	25.0	1190.68	0	7	0	0	2	563	572
									VLTIDPTEFK	95.0	42.8	25.0	1162.64	0	9	0	0	2	589	598
									LALINR	95.0	31.6	25.0	699.45	0	2	0	0	2	601	606
									LVGQSIIAYLQK	95.0	89.0	25.0	1332.79	0	2	0	0	2	620	631
									GFFEGTIASK	95.0	36.7	25.0	1056.54	0	1	0	0	2	816	825
									QLFLQTYAR	95.0	50.8	25.0	1139.62	0	2	0	0	2	957	965
									LNDLIQR	95.0	53.5	25.0	871.50	0	7	0	0	2	1003	1009
									TALNLFFK	95.0	55.0	25.0	953.55	0	17	0	0	2	1107	1114
									LLELGPKPEVAQQTR	95.0	63.8	25.0	1678.95	0	2	9	0	2	1128	1142

									VTTVTEIGKDVIGLR	95.0	67.2	25.0	1600.93	0	2	2	0	2	1203	1217
Coatomer subunit beta	COPB_HUMAN	COPB1	107.13	100.0	19	21	45	24.00	FVLPLQDHTIK	95.0	47.9	25.0	1310.75	0	2	0	0	2	65	75
									DLQHPNEFIR	95.0	31.4	25.0	1268.64	0	2	0	0	2	108	117
									LKEAELLEPLMPAIR	95.0	32.5	25.0	1738.98	0	1	0	0	2	127	141
									EAELLEPLMPAIR	95.0	48.5	25.0	1497.80	0	3	0	0	2	129	141
									NAVLAIYTIYR	95.0	66.8	25.0	1296.73	0	2	0	0	2	154	164
									NAFMMLIHADQDR	94.7	26.5	25.0	1593.72	0	1	0	0	2	192	204
									CIYNLLQSSSPAVK	95.0	74.7	25.0	1579.81	0	2	0	0	2	248	261
									YEAAGTLVTLSSAPTAIK	95.0	####	25.0	1792.97	0	2	0	0	2	262	279
									LIVLDR	95.0	38.4	25.0	728.47	0	4	0	0	2	299	304
									VLQDLVMDILR	95.0	62.5	25.0	1330.74	0	2	0	0	2	317	327
									VLSTPDLEVR	95.0	51.2	25.0	1128.63	0	3	0	0	2	328	337
									TLQLALDLVSSR	95.0	50.5	25.0	1315.76	0	3	0	0	2	340	351
									NVEELVIVLK	95.0	27.2	25.0	1155.70	0	1	0	0	2	352	361
									TNNVSEHEDTDKYR	95.0	67.9	25.0	1707.76	0	2	3	0	2	367	380
									EDIQSVMTEIR	95.0	27.4	25.0	1336.64	0	1	0	0	2	470	480
									SLGEIPIVESEIKK	95.0	58.4	25.0	1541.88	0	4	2	0	2	482	495
									EAGELKPEEEITVGPVQK	95.0	70.5	25.0	1953.02	0	2	0	0	2	496	513
									LVTEMGTYATQSALSSSRPTK	95.0	38.0	25.0	2244.12	0	0	2	0	2	514	534
									KPITDDDVDR	95.0	31.4	25.0	1173.57	0	1	0	0	2	603	612
Coatomer subunit beta'	COPB2_HUMAN	COPB2	102.47	100.0	7	7	71	8.61	TFEVCDLPVR	95.0	39.2	25.0	1235.61	0	2	0	0	2	52	61
									VFNYNTLER	95.0	50.2	25.0	1155.58	0	15	0	0	2	83	91
									DNNQFASASLDR	95.0	67.5	25.0	1337.61	0	14	0	0	2	154	165
									LESTLNYGMER	95.0	37.9	25.0	1328.62	0	2	0	0	2	263	273
									GSNNVALGYDEGSIIVK	95.0	86.8	25.0	1735.89	0	3	0	0	2	282	298
									TMYLLGYIPK	95.0	47.3	25.0	1214.65	0	2	0	0	2	560	569
									LPEAAFLAR	95.0	63.4	25.0	987.56	0	33	0	0	2	751	759
Coatomer subunit delta	COPD_HUMAN	ARCN1	57.19	100.0	9	9	62	20.00	IEGLLAAFPK	95.0	49.0	25.0	1058.62	0	19	0	0	2	29	38
									LYMVLITTK	95.0	59.4	25.0	1097.63	0	7	0	0	2	64	72
									ENVNLAQIR	95.0	52.8	25.0	1056.58	0	7	0	0	2	123	131
									SEGETIMSSSMGK	95.0	37.1	25.0	1375.57	0	3	0	0	2	244	256
									DGGLQNMELHGMIMLR	95.0	39.3	25.0	1862.86	0	0	4	0	2	289	304
									LFTAESLIGLK	95.0	42.1	25.0	1191.70	0	3	0	0	2	337	347
									SFPVNSDVGVLK	95.0	53.4	25.0	1261.68	0	2	0	0	2	352	363
									VTQVDGNSPVR	95.0	64.1	25.0	1171.61	0	16	0	0	2	486	496
									FSTETTFLVDK	95.0	38.5	25.0	1287.65	0	1	0	0	2	497	507
Coatomer subunit epsilon	COPE_HUMAN	COPE	34.46	100.0	3	4	9	8.44	AYLAQR	95.0	30.5	25.0	721.40	0	1	0	0	2	59	64
									MFADYLAHESR	95.0	67.1	25.0	1355.60	0	4	2	0	2	86	96
									LVLQYAPSA	95.0	29.5	25.0	961.54	0	2	0	0	2	300	308
Coatomer subunit gamma	COPG_HUMAN	COPG	97.70	100.0	11	11	37	15.10	KDEESGGGSNPFQHLEK	95.0	39.4	25.0	1858.86	0	0	2	0	2	8	24
									VFNETPINPR	95.0	46.2	25.0	1186.62	0	10	0	0	2	33	42
									LFQSNDPTLR	95.0	57.5	25.0	1190.62	0	2	0	0	2	76	85
									SIATLAITTLLK	95.0	60.2	25.0	1244.78	0	3	0	0	2	339	350
									VVVVQAISALCQK	95.0	53.4	25.0	1414.81	0	2	0	0	2	377	389
									ILHLLGQEGPK	95.0	36.9	25.0	1204.71	0	2	0	0	2	455	465
									AGAVSALAK	95.0	32.5	25.0	787.47	0	1	0	0	2	489	497
									SVPLATAPMAEQR	95.0	35.5	25.0	1386.70	0	3	0	0	2	578	590
									TLEEAVGNIVK	95.0	78.3	25.0	1172.65	0	7	0	0	2	796	806
									NTHTLLLAGVFR	95.0	69.9	25.0	1341.76	0	3	0	0	2	824	835
									LLLLDTVTMQVTAR	95.0	57.2	25.0	1589.89	0	2	0	0	2	846	859
Coatomer subunit gamma-2	COPG2_HUMAN	COPG2	97.61	100.0	2	2	3	5.63	SIATLAITTLLK	95.0	60.2	25.0	1244.78	0	3	0	0	2	339	350

									VVVVQAISALCQK	95.0	53.4	25.0	1414.81	0	2	0	0	2	377	389
									ATFYLNVLQQR	95.0	41.1	25.0	1352.73	0	1	0	0	2	528	538
									SIPLAMAPVFEQK	95.0	53.8	25.0	1446.77	0	2	0	0	2	578	590
Cofilin-1	COF1_HUMAN	CFL1	18.49	100.0	6	6	121	33.70	ASGVAVSDGVIK	95.0	42.4	25.0	1102.61	0	2	0	0	1	2	13
									AVLFCLSEDK	95.0	43.4	25.0	1181.59	0	5	0	0	2	35	44
									AVLFCLSEDKK	95.0	37.3	25.0	1309.68	0	2	0	0	2	35	45
									NIILEEGK	95.0	35.8	25.0	915.51	0	2	0	0	2	46	53
									YALYDATYETK	95.0	72.1	25.0	1337.63	0	98	0	0	2	82	92
									LGGSAVISLEGKPL	95.0	85.5	25.0	1340.78	0	12	0	0	2	153	166
Cohesin subunit SA-2	STAG2_HUMAN	STAG2	141.31	100.0	3	3	4	2.19	GVVTAEMFR	95.0	44.2	25.0	1025.51	0	1	0	0	2	129	137
									SQLIDELADK	95.0	27.4	25.0	1131.59	0	1	0	0	2	655	664
									DGIEFAFK	95.0	32.5	25.0	926.46	0	2	0	0	2	976	983
Collagen alpha-1(V) chain	CO5A1_HUMAN	COL5A1	183.54	100.0	3	4	7	1.58	VLDFHNLPDGITK	95.0	66.4	25.0	1468.78	0	2	1	0	2	45	57
									GPDVAYR	95.0	30.5	25.0	777.39	0	1	0	0	2	70	76
									DAQLSAPTK	95.0	34.3	25.0	930.49	0	3	0	0	2	80	88
Collagen alpha-1(VI) chain	CO6A1_HUMAN	COL6A1	108.51	100.0	10	12	60	9.05	LKPYGALVDK	95.0	50.5	25.0	1103.65	0	0	8	0	2	52	61
									RFIDNLR	95.0	33.2	25.0	933.53	0	1	0	0	2	68	74
									FIDNLR	95.0	35.6	25.0	777.43	0	2	0	0	2	69	74
									GLEQLLVGGSHLK	95.0	68.7	25.0	1350.77	0	14	2	0	2	136	148
									VFSVAITPDHLEPR	95.0	54.8	25.0	1580.84	0	1	3	0	2	186	199
									LSIIATDHTYR	95.0	25.3	25.0	1289.68	0	0	1	0	2	200	210
									DQLLPPSPNNR	95.0	27.4	25.0	1250.65	0	2	0	0	2	712	722
									IALVITDGR	95.0	67.6	25.0	957.57	0	16	0	0	2	723	731
									VPSYQALLR	95.0	44.4	25.0	1046.60	0	2	0	0	2	1006	1014
									GVFHQTVSR	95.0	37.8	25.0	1030.54	0	8	0	0	2	1015	1023
Collagen alpha-1(VII) chain	CO7A1_HUMAN	COL7A1	295.20	100.0	5	5	5	1.56	FATVQYSDDPR	95.0	28.7	25.0	1298.60	0	1	0	0	2	79	89
									LFAVGIK	95.0	28.4	25.0	747.48	0	1	0	0	2	170	176
									QEVNVPAGETSVR	95.0	33.9	25.0	1385.70	0	1	0	0	2	281	293
									VTALVGDR	95.0	27.0	25.0	830.47	0	1	0	0	2	844	851
									VPSIELR	95.0	33.5	25.0	813.48	0	1	0	0	2	957	963
Collagen alpha-1(XII) chain	COCA1_HUMAN	COL12A1	333.13	100.0	5	5	25	2.02	GGNTMTGDAIDYLVK	95.0	54.3	25.0	1570.74	0	5	0	0	2	214	228
									NSDVEIFAVGVK	95.0	80.6	25.0	1277.67	0	13	0	0	2	566	577
									IVEVFDIGPK	95.0	34.9	25.0	1116.63	0	1	0	0	2	1225	1234
									ALALGALQNIR	95.0	62.6	25.0	1139.69	0	5	0	0	2	2385	2395
									GEVQTVTFDTEEVK	95.0	57.2	25.0	1581.76	0	1	0	0	2	2628	2641
Collagen alpha-1(XVII) chain	COHA1_HUMAN	COL17A1	150.40	100.0	5	6	30	4.21	LQGMAPAAGADLDK	95.0	47.0	25.0	1373.67	0	4	0	0	2	524	537
									LMMEQENGNLR	95.0	45.5	25.0	1366.61	0	2	0	0	2	556	566
									GAMGPAGPDGHQGPR	95.0	30.4	25.0	1420.64	0	0	1	0	2	740	754
									SELISYLTSPDVR	95.0	64.9	25.0	1479.77	0	12	0	0	2	1248	1260
									LLSTDASHSR	95.0	51.7	25.0	1086.55	0	5	6	0	2	1281	1290
Collagen alpha-2(IV) chain	CO4A2_HUMAN	COL4A2	167.54	100.0	4	4	45	3.15	GLDGYQGPDGPR	95.0	59.4	25.0	1231.57	0	16	0	0	2	323	334
									GLPGEVLGAQPGPR	95.0	53.7	25.0	1347.74	0	7	0	0	2	771	784
									GEQGFMGNTGPTGAVGDR	95.0	94.7	25.0	1766.78	0	6	0	0	2	1350	1367
									SVSIGYLLVK	95.0	48.8	25.0	1078.65	0	16	0	0	2	1485	1494
Collagenase 3	MMP13_HUMAN	MMP13	53.80	100.0	3	3	13	7.43	EMQSFFGLEVTGK	95.0	56.3	25.0	1488.70	0	1	0	0	2	70	82
									LDDNTLDVMK	95.0	64.2	25.0	1179.56	0	4	0	0	2	83	92
									LIEEDFPGIGDK	95.0	75.3	25.0	1332.67	0	8	0	0	2	419	430
Complement C1r subcomponent	C1R_HUMAN	C1R	80.10	100.0	3	3	6	3.97	YTTTMGVNTYK	95.0	48.2	25.0	1294.60	0	4	0	0	2	389	399
									GGGALLGDR	95.0	27.7	25.0	815.44	0	1	0	0	2	487	495
									VSVHPDYR	95.0	28.5	25.0	972.49	0	1	0	0	2	540	547
Complement C1s	C1S_HUMAN	C1S	76.67	100.0	5	5	20	7.99	LQVIFK	95.0	36.1	25.0	747.48	0	3	0	0	2	106	111

subcomponent									EPTMYVGSTSVQTSR	95.0	37.2	25.0	1658.77	0	1	0	0	2	482	496
									LLEVPEGR	95.0	34.1	25.0	912.52	0	2	0	0	2	516	523
									TNFDNDIALVR	95.0	78.8	25.0	1277.65	0	12	0	0	2	524	534
									GDSGGAFAVQDPNDK	95.0	46.0	25.0	1477.66	0	2	0	0	2	630	644
Complement C3	CO3_HUMAN	C3	187.13	100.0	38	44	407	20.90	TIYTPGSTVLYR	95.0	57.6	25.0	1370.73	0	25	0	0	2	137	148
									TVMVNIENPEGIPVK	95.0	64.7	25.0	1655.87	0	4	0	0	2	162	176
									FYYIYNEK	95.0	40.0	25.0	1139.54	0	4	0	0	2	242	249
									RIPIEDGSGEVVLSR	95.0	37.0	25.0	1626.88	0	2	0	0	2	290	304
									IPIEDGSGEVVLSR	95.0	96.2	25.0	1470.78	0	20	0	0	2	291	304
									KVLLDGVQNPR	95.0	36.0	25.0	1238.72	0	1	2	0	2	305	315
									VLLDGVQNPR	95.0	85.9	25.0	1110.63	0	20	0	0	2	306	315
									LSINTHPSQKPLSITVR	95.0	23.6	25.0	1891.08	0	0	0	1	2	409	425
									KQELSEAEQATR	95.0	63.4	25.0	1389.70	0	8	10	0	2	428	439
									QELSEAEQATR	95.0	54.7	25.0	1261.60	0	9	0	0	2	429	439
									YYTYLIMNK	95.0	57.5	25.0	1224.60	0	25	0	0	2	489	497
									LVAYYTLIGASGQR	95.0	79.1	25.0	1511.82	0	1	0	0	2	531	544
									SGQSEDRQPVPGQQMTLK	95.0	19.7	25.0	2001.97	0	0	1	0	2	567	584
									QPVPGQQMTLK	95.0	42.8	25.0	1242.65	0	3	0	0	2	574	584
									GVFVLNK	95.0	32.9	25.0	776.47	0	5	0	0	2	601	607
									SVQLTEKR	95.0	39.7	25.0	960.55	0	1	0	0	2	672	679
									LMNIFLK	95.0	35.6	25.0	894.51	0	13	0	0	2	790	796
									LPYSVVR	95.0	51.3	25.0	833.49	0	17	0	0	2	835	841
									NEQVEIR	95.0	43.1	25.0	887.46	0	6	0	0	2	842	848
									AVLYNYR	95.0	28.9	25.0	898.48	0	1	0	0	2	849	855
									RHQQTVTIPPK	95.0	37.6	25.0	1304.74	0	0	5	0	2	881	891
									HQQTVTIPPK	95.0	50.2	25.0	1148.64	0	8	0	0	2	882	891
									SSLSVPYVIVPLK	95.0	45.5	25.0	1401.84	0	2	0	0	2	892	904
									TGLQEVEVK	95.0	45.0	25.0	1002.55	0	11	0	0	2	905	913
									AAVYHHFISDGVR	95.0	35.9	25.0	1471.74	0	0	8	1	2	914	926
									QGALELIK	95.0	33.4	25.0	871.52	0	1	0	0	2	1043	1050
									GYTQQLAFR	95.0	61.0	25.0	1083.56	0	36	0	0	2	1052	1060
									QPSSAFAAFVK	95.0	45.2	25.0	1152.60	0	18	0	0	2	1061	1071
									AGDFLEANYMNLQR	95.0	48.3	25.0	1657.76	0	1	0	0	2	1172	1185
									DFDFVPPVVR	95.0	31.4	25.0	1190.62	0	3	0	0	2	1245	1254
									SEETKENEGFTVTAEGK	95.0	96.0	25.0	1855.86	0	4	3	0	2	1321	1337
									ENEGFTVTAEGK	95.0	67.8	25.0	1281.60	0	8	0	0	2	1326	1337
									VTIKPAPETEK	95.0	34.0	25.0	1212.68	0	2	7	0	2	1365	1375
									NTLIIYLDK	95.0	65.1	25.0	1092.63	0	26	0	0	2	1442	1450
									FYHPEKEDGK	95.0	30.2	25.0	1249.58	0	0	9	0	2	1492	1501
									SDDKVTLEER	95.0	50.2	25.0	1191.59	0	11	17	0	2	1523	1532
									SGSDEVQVGQQR	95.0	65.3	25.0	1289.61	0	45	0	0	2	1571	1582
									TFISPIK	95.0	32.8	25.0	805.48	0	2	0	0	2	1583	1589
Complement factor B	CFAB_HUMAN	CFB	85.52	100.0	6	6	17	7.33	VASYGVKPR	95.0	39.7	25.0	976.56	0	3	0	0	2	300	308
									DLLYIGK	95.0	31.1	25.0	821.48	0	2	0	0	2	407	413
									EELLPAQDIK	95.0	33.9	25.0	1155.63	0	1	0	0	2	620	629
									ALFVSEEEKK	95.0	41.5	25.0	1179.63	0	3	0	0	2	630	639
									DISEVVTPR	95.0	44.9	25.0	1015.54	0	6	0	0	2	671	679
									EKLQDEDLGFL	95.0	44.2	25.0	1306.65	0	2	0	0	2	754	764
COP9 signalosome complex subunit 1	CSN1_HUMAN	GPS1	55.52	100.0	5	5	8	9.37	MALSFVQR	95.0	32.4	25.0	967.50	0	2	0	0	2	77	84
									AESTPEIAEQR	95.0	44.8	25.0	1230.60	0	2	0	0	2	225	235
									DSQTQAILTK	95.0	44.3	25.0	1104.59	0	2	0	0	2	239	248

									LFLELEPQVR	95.0	29.0	25.0	1243.70	0	1	0	0	2	318	327
									TLYTQIR	95.0	29.5	25.0	894.50	0	1	0	0	2	364	370
COP9 signalosome complex subunit 2	CSN2_HUMAN	COPS2	51.58	100.0	4	5	10	10.60	AHTDFFEAFK	95.0	38.2	25.0	1212.57	0	2	0	0	2	254	263
									SGINPFDSQEAKPYK	95.0	60.0	25.0	1680.82	0	2	0	0	2	289	303
									IHIPFISK	95.0	38.4	25.0	954.58	0	2	0	0	2	369	376
									IDQVNQLLELDHQK	95.0	78.7	25.0	1692.89	0	2	2	0	2	402	415
COP9 signalosome complex subunit 3	CSN3_HUMAN	COPS3	47.86	100.0	3	3	8	9.46	TFLTLSLQDMASR	95.0	73.9	25.0	1498.76	0	3	0	0	2	313	325
									DGMVSFHDNPEK	95.0	44.5	25.0	1391.59	0	2	0	0	2	355	366
									AMDQEITVNPQFVQK	95.0	85.2	25.0	1763.86	0	3	0	0	2	392	406
COP9 signalosome complex subunit 4	CSN4_HUMAN	COPS4	46.25	100.0	6	6	16	18.70	AIQLSGAEQLEALK	95.0	88.2	25.0	1470.82	0	2	0	0	2	33	46
									VISFEEQVASIR	95.0	59.5	25.0	1377.74	0	2	0	0	2	96	107
									NAAQVLVGIPLETGQK	95.0	####	25.0	1637.92	0	6	0	0	2	122	137
									MLATLFKDER	95.0	49.7	25.0	1239.64	0	2	0	0	2	245	254
									ATTADGSSILDR	95.0	57.2	25.0	1206.60	0	2	0	0	2	291	302
									AVIEHNLLSASK	95.0	66.0	25.0	1281.72	0	2	0	0	2	303	314
COP9 signalosome complex subunit 5	CSN5_HUMAN	COPS5	37.56	100.0	5	5	13	16.20	ISALALLK	95.0	40.5	25.0	828.56	0	4	0	0	2	57	64
									SGGNLEVMGLMLGK	95.0	77.3	25.0	1437.71	0	2	0	0	2	71	84
									VNLGAFR	95.0	28.9	25.0	776.44	0	1	0	0	2	181	187
									LEQSEAQLGR	95.0	48.7	25.0	1130.58	0	4	0	0	2	273	282
									TTIEAIHGLMSQVIK	95.0	67.0	25.0	1656.90	0	2	0	0	2	310	324
COP9 signalosome complex subunit 6	CSN6_HUMAN	COPS6	36.15	100.0	5	5	16	21.10	SQEGRPVQVIGALIGK	95.0	66.4	25.0	1651.95	0	7	0	0	2	60	75
									MTATGSGENSTVAEHLIAQHSAIK	95.0	70.1	25.0	2469.20	0	0	2	0	2	206	229
									LILEYVK	95.0	30.2	25.0	877.54	0	3	0	0	2	237	243
									ASEAGEVPFNHEILR	95.0	43.8	25.0	1668.83	0	1	0	0	2	244	258
									FNVLYDR	95.0	46.7	25.0	926.47	0	3	0	0	2	309	315
COP9 signalosome complex subunit 7a	CSN7A_HUMAN	COPS7A	30.26	100.0	3	3	9	12.40	VTGQNQEQFLLLAK	95.0	57.8	25.0	1588.87	0	4	0	0	2	7	20
									ELAESDFASTFR	95.0	73.4	25.0	1372.64	0	4	0	0	2	54	65
									QDLSAIAR	95.0	30.2	25.0	873.48	0	1	0	0	2	165	172
Copine-1	CPNE1_HUMAN	CPNE1	59.04	100.0	4	4	16	7.08	FGIYDIDNK	95.0	43.8	25.0	1084.53	0	6	0	0	2	76	84
									GTITVSAQELK	95.0	58.5	25.0	1146.64	0	5	0	0	2	125	135
									VVTMEVEAR	95.0	35.7	25.0	1049.53	0	1	0	0	2	139	147
									DIVQFVPYR	95.0	37.9	25.0	1136.61	0	4	0	0	2	479	487
Coproporphyrinogen-III oxidase, mitochondrial	HEM6_HUMAN	CPOX	50.13	100.0	7	8	26	19.40	ATSLGRPEEEEDELAHR	95.0	58.4	25.0	1938.92	0	0	5	0	2	110	126
									AGVSISVVHGNLSEEAAK	95.0	77.6	25.0	1767.92	0	2	2	0	2	203	220
									YFEVEEADGNK	95.0	68.1	25.0	1300.57	0	2	0	0	2	263	273
									AVVPSYIPLVK	95.0	47.6	25.0	1185.72	0	3	0	0	2	360	370
									FGLFTPGSR	95.0	55.4	25.0	981.52	0	5	0	0	2	405	413
									IESILMSLPLTAR	95.0	66.9	25.0	1459.82	0	5	0	0	2	414	426
									EAEILEVLR	95.0	52.9	25.0	1071.60	0	2	0	0	2	439	447
Core histone macro-H2A.1	H2AY_HUMAN	H2AFY	39.60	100.0	5	6	30	20.70	AGVIFPVGR	95.0	48.1	25.0	915.54	0	7	0	0	2	19	27
									AASADSTTEGTPADGFTVLSTK	95.0	####	25.0	2127.01	0	4	0	0	2	168	189
									NGPLEVAGAAVSAGHGLPAK	95.0	88.7	25.0	1815.97	0	3	3	0	2	252	271
									SIAFPSIGSGR	95.0	48.7	25.0	1091.58	0	8	0	0	2	308	318
									AISSYFVSTMSSSIK	95.0	####	25.0	1623.79	0	5	0	0	2	333	347
Coronin-1A	COR1A_HUMAN	CORO1A	51.01	100.0	3	3	20	8.03	EPVVTLEGHTK	95.0	31.5	25.0	1209.65	0	1	0	0	2	122	132
									DAGPLLISLK	95.0	63.9	25.0	1026.62	0	17	0	0	2	384	393
									AAPEASGTPSSDAVSR	95.0	39.5	25.0	1502.71	0	2	0	0	2	417	432
Coronin-1B	COR1B_HUMAN	CORO1B	54.22	100.0	3	3	26	6.95	VFTTGFSR	95.0	34.3	25.0	914.47	0	1	0	0	2	234	241
									DADPILISLR	95.0	50.8	25.0	1112.63	0	21	0	0	2	384	393
									LEEVMQELR	95.0	57.4	25.0	1162.58	0	4	0	0	2	453	461
									LEEQLGR	95.0	31.6	25.0	844.45	0	4	0	0	2	477	483

Coronin-1C	COR1C_HUMAN	CORO1C	53.23	100.0	4	4	24	6.33	NADPILISLK	95.0	60.4	25.0	1083.64	0	13	0	0	2	382	391
									HGYIPGK	95.0	41.5	25.0	771.41	0	8	0	0	2	392	398
									KTTDTASVQNEAK	94.7	19.1	25.0	1392.70	0	0	1	0	2	428	440
									TTDTASVQNEAK	95.0	58.0	25.0	1264.60	0	2	0	0	2	429	440
Creatine kinase B-type	KCRB_HUMAN	CKB	42.63	100.0	5	5	22	16.30	PFSNSHNALK	95.0	59.7	25.0	1114.56	0	2	0	0	1	2	11
									VLTPELYAELR	95.0	29.0	25.0	1303.73	0	1	0	0	2	33	43
									DLFDPIIEDR	95.0	51.7	25.0	1232.62	0	7	0	0	2	87	96
									LAVEALSSLDGDLAGR	95.0	71.3	25.0	1586.84	0	6	0	0	2	157	172
									LEQGQAIDDLMPAQK	95.0	88.1	25.0	1672.82	0	6	0	0	2	367	381
Crk-like protein	CRKL_HUMAN	CRKL	33.76	100.0	4	5	8	16.50	VSHYIINSLPNR	95.0	59.3	25.0	1412.76	0	2	1	0	2	58	69
									IHYLDTTTLIEPAPR	95.0	77.7	25.0	1739.93	0	2	0	0	2	90	104
									VGMIPVPYVEK	95.0	32.1	25.0	1247.67	0	1	0	0	2	170	180
									TALALEVGDIVK	95.0	58.6	25.0	1228.71	0	2	0	0	2	254	265
Cullin-1	CUL1_HUMAN	CUL1	89.66	100.0	3	3	9	3.74	DGEDLMDESVLK	95.0	52.9	25.0	1366.60	0	4	0	0	2	106	117
									SPELLAR	95.0	39.9	25.0	785.45	0	3	0	0	2	418	424
									YIEDKDVFQK	95.0	25.2	25.0	1284.65	0	0	2	0	2	455	464
Cullin-2	CUL2_HUMAN	CUL2	86.97	100.0	6	6	13	10.20	AVVMLEYVER	95.0	32.2	25.0	1224.63	0	3	0	0	2	23	32
									ALTSVVNYR	95.0	46.6	25.0	1022.56	0	2	0	0	2	371	379
									GMTENEVEDR	95.0	37.5	25.0	1195.49	0	3	0	0	2	405	414
									LTSFITVFK	95.0	42.3	25.0	1055.61	0	2	0	0	2	415	423
									LIHGLSMSMDSEEAMINK	95.0	27.8	25.0	2053.92	0	0	2	0	2	443	460
									MYTDMSVSADLNNK	95.0	97.9	25.0	1620.69	0	1	0	0	2	476	489
									FNNFIK	95.0	26.8	25.0	782.42	0	1	0	0	2	490	495
Cullin-3	CUL3_HUMAN	CUL3	88.91	100.0	5	5	9	6.77	NAIQEIQR	95.0	45.6	25.0	971.53	0	1	0	0	2	39	46
									EVVTEHLINK	95.0	39.7	25.0	1181.65	0	4	0	0	2	79	88
									DILMYMDR	94.5	26.4	25.0	1088.48	0	1	0	0	2	121	128
									GLTEQEVETILDK	95.0	92.4	25.0	1474.76	0	1	0	0	2	402	414
									DMSISNTTMDEFR	95.0	79.2	25.0	1578.64	0	2	0	0	2	476	488
Cullin-4A	CUL4A_HUMAN	CUL4A	87.67	99.5	2	2	6	4.87	ESFETFINK	95.0	44.2	25.0	1114.54	0	4	0	0	2	392	400
									DVFEAFYK	95.0	32.7	25.0	1018.49	0	2	0	0	2	447	454
									ETVEEQVSTTER	95.0	82.3	25.0	1407.66	0	2	0	0	2	676	687
									RIESLIDR	95.0	40.7	25.0	1001.57	0	2	0	0	2	735	742
Cullin-4B	CUL4B_HUMAN	CUL4B	103.97	100.0	12	12	28	11.90	FLEETNR	95.0	38.3	25.0	908.45	0	2	0	0	2	389	395
									LITYLDQTTQK	95.0	74.6	25.0	1323.72	0	4	0	0	2	428	438
									GLNNLLDENR	95.0	62.6	25.0	1157.59	0	2	0	0	2	460	469
									AFGSTIVINPEK	95.0	72.9	25.0	1275.69	0	2	0	0	2	500	511
									AFGSTIVINPEKDK	95.0	39.2	25.0	1518.82	0	1	0	0	2	500	513
									EAFETFINK	95.0	55.5	25.0	1098.55	0	4	0	0	2	546	554
									DVFEAFYK	95.0	32.7	25.0	1018.49	0	2	0	0	2	601	608
									DIMIQFK	95.0	27.9	25.0	910.47	0	1	0	0	2	657	663
									QATGIEDGELR	95.0	31.1	25.0	1188.59	0	1	0	0	2	769	779
									ETVEEQASTTER	95.0	75.1	25.0	1379.63	0	6	0	0	2	830	841
									RIESLIDR	95.0	40.7	25.0	1001.57	0	2	0	0	2	889	896
									DKENPNQYNYIA	95.0	39.9	25.0	1468.67	0	1	0	0	2	902	913
Cullin-5	CUL5_HUMAN	CUL5	90.94	100.0	3	3	5	3.97	SNVEDSIVR	95.0	28.5	25.0	1018.52	0	1	0	0	2	128	136
									AVVNDATIFK	95.0	39.8	25.0	1077.59	0	2	0	0	2	375	384
									LATELPDAELRR	95.0	36.5	25.0	1383.76	0	0	2	0	2	621	632
Cullin-associated NEDD8-dissociated protein 1	CAND1_HUMAN	CAND1	136.36	100.0	17	21	123	14.40	NGEVQNLAVK	95.0	27.1	25.0	1071.58	0	1	0	0	2	61	70
									IGEYLEK	95.0	34.2	25.0	851.45	0	2	0	0	2	249	255
									HEMLPEFYK	95.0	48.0	25.0	1209.56	0	5	0	0	2	365	373
									TVSPALISR	95.0	34.9	25.0	943.56	0	8	0	0	2	374	382

									ITSEALLVTQQLVK	95.0	77.8	25.0	1542.91	0	12	2	0	2	535	548
									AADIDQEVK	95.0	41.0	25.0	988.49	0	5	0	0	2	578	586
									AADIDQEVKER	95.0	44.1	25.0	1273.64	0	3	1	0	2	578	588
									ALTLIAGSPLK	95.0	75.6	25.0	1083.68	0	37	0	0	2	631	641
									MLTGPVYSQSTALTHK	95.0	84.4	25.0	1749.88	0	2	5	0	2	778	793
									EGPAVVGQFIQDVK	95.0	41.6	25.0	1486.79	0	3	0	0	2	813	826
									SVILEAFSSPSEEVK	95.0	92.2	25.0	1621.83	0	6	0	0	2	859	873
									TLEDPDLNVR	95.0	31.9	25.0	1171.60	0	1	0	0	2	1014	1023
									VALVTFNSAAHNKPSLIR	95.0	35.0	25.0	1938.09	0	0	2	1	2	1025	1042
									HTVDDGLDIR	95.0	33.7	25.0	1140.56	0	4	0	0	2	1073	1082
									HTVDDGLDIRK	95.0	33.3	25.0	1268.66	0	0	5	0	2	1073	1083
									MLTFLMLVR	95.0	58.8	25.0	1155.63	0	8	0	0	2	1121	1129
									AVAALLTIPEAEK	95.0	44.7	25.0	1325.77	0	10	0	0	2	1179	1191
CWF19-like protein 1	C19L1_HUMAN	CWF19L1	60.60	100.0	3	3	11	6.13	FDILFNR	95.0	37.7	25.0	924.49	0	1	0	0	2	18	24
									FIALANVGNPEK	95.0	74.0	25.0	1272.69	0	6	0	0	2	223	234
									EVLASEAILNVPDK	95.0	91.2	25.0	1497.82	0	4	0	0	2	492	505
Cystathionine gamma-lyase	CGL_HUMAN	CTH	44.49	100.0	3	3	3	6.17	GTLQHAEIFLK	95.0	31.9	25.0	1256.70	0	1	0	0	2	320	330
									NDRDVLGISDTLIR	95.0	59.4	25.0	1586.85	0	1	0	0	2	362	375
									DVLGISDTLIR	95.0	36.2	25.0	1201.68	0	1	0	0	2	365	375
Cystatin-B	CYTB_HUMAN	CSTB	11.12	100.0	4	4	11	39.80	KFPVFK	94.6	26.4	25.0	765.47	0	1	0	0	2	34	39
									SQVVAGTNYFIK	95.0	80.2	25.0	1326.71	0	2	0	0	2	45	56
									VHVGDEDFVHLR	95.0	61.2	25.0	1422.71	0	0	6	0	2	57	68
									AKHDELTYF	95.0	32.2	25.0	1123.54	0	2	0	0	2	90	98
Cystatin-C	CYTC_HUMAN	CST3	15.78	100.0	3	3	28	19.20	LVGGPMDASVEEEGVR	95.0	####	25.0	1660.78	0	6	0	0	2	35	50
									LVGGPMDASVEEEGVRR	95.0	36.5	25.0	1816.89	0	4	0	0	2	35	51
									ALDFAVGEYNK	95.0	65.2	25.0	1226.61	0	18	0	0	2	52	62
Cysteinyl-tRNA synthetase, cytoplasmic	SYCC_HUMAN	CARS	85.46	100.0	7	8	33	11.50	QNHLFEQYR	95.0	24.2	25.0	1234.60	0	0	2	0	2	108	116
									IQHAVQLATEPLEK	95.0	75.9	25.0	1576.87	0	2	4	0	2	155	168
									ALQEGEGDLSISADR	95.0	71.9	25.0	1560.75	0	1	0	0	2	296	310
									APVDITGQFEK	95.0	62.7	25.0	1204.62	0	10	0	0	2	472	482
									VPEILQLSDALR	95.0	70.7	25.0	1353.77	0	7	0	0	2	607	618
									FEDHEGLPTVVK	95.0	50.4	25.0	1370.70	0	3	0	0	2	629	640
									IPPSEMFLSETDK	95.0	71.0	25.0	1509.71	0	4	0	0	2	685	697
Cytochrome c	CYC_HUMAN	CYCS	11.73	100.0	5	7	61	39.00	TGPNLHGLFGR	95.0	31.0	25.0	1168.62	0	2	1	0	2	29	39
									KTGQAPGYSYTAANK	95.0	69.1	25.0	1556.77	0	11	2	0	2	40	54
									TGQAPGYSYTAANK	95.0	78.2	25.0	1428.68	0	16	0	0	2	41	54
									MIFVGIK	94.9	26.6	25.0	823.47	0	1	0	0	2	81	87
									ADLIAYLK	95.0	47.3	25.0	906.53	0	28	0	0	2	93	100
Cytoplasmic aconitate hydratase	ACOC_HUMAN	ACO1	98.38	100.0	5	6	12	6.30	NQDLEFER	95.0	39.9	25.0	1050.49	0	1	0	0	2	142	149
									IDFEKEPLGVNAK	95.0	61.8	25.0	1459.78	0	2	4	0	2	568	580
									LFFWNSK	95.0	32.5	25.0	941.49	0	1	0	0	2	633	639
									YQQAGLPLIVLAGK	95.0	59.7	25.0	1470.87	0	2	0	0	2	759	772
									YTIIIPENLKPQMK	95.0	31.8	25.0	1703.94	0	0	2	0	2	835	848
Cytoplasmic dynein 1 heavy chain 1	DYHC1_HUMAN	DYNC1H1	532.39	100.0	44	44	231	9.19	SNSLAFIK	95.0	40.6	25.0	879.49	0	2	0	0	2	113	120
									DLSSQLLK	95.0	37.0	25.0	903.51	0	3	0	0	2	387	394
									VPLAIVNK	95.0	29.4	25.0	853.55	0	2	0	0	2	760	767
									NTISLLVAGLK	95.0	62.0	25.0	1128.70	0	5	0	0	2	799	809
									LAETVFNFQEK	95.0	38.0	25.0	1325.67	0	3	0	0	2	836	846
									TFSEILNR	95.0	55.1	25.0	979.52	0	6	0	0	2	873	880
									LDMEIER	95.0	45.2	25.0	921.43	0	1	0	0	2	903	909
									NVVHELR	94.6	26.4	25.0	866.48	0	1	0	0	2	957	963

									MVVLSLPR	95.0	39.9	25.0	930.54	0	11	0	0	2	991	998
									EFGPVVIDYGK	95.0	35.2	25.0	1223.63	0	1	0	0	2	1101	1111
									DSAIQQQVANLQMK	95.0	85.3	25.0	1589.80	0	2	0	0	2	1229	1242
									LADLLGK	95.0	35.3	25.0	729.45	0	2	0	0	2	1604	1610
									ALGEYLER	95.0	41.8	25.0	950.49	0	3	0	0	2	1614	1621
									LGGSPFGPAGTGK	95.0	38.5	25.0	1145.60	0	3	0	0	2	1900	1912
									TSAPITCELLNK	95.0	38.2	25.0	1346.70	0	2	0	0	2	1993	2004
									SVLVSAGNVK	95.0	42.3	25.0	973.57	0	5	0	0	2	2095	2104
									DHLYGTLDPNTR	95.0	47.2	25.0	1401.68	0	4	0	0	2	2262	2273
									LLTLPNGER	95.0	33.5	25.0	1012.58	0	1	0	0	2	2324	2332
									IMFEVQDLK	95.0	63.6	25.0	1138.58	0	16	0	0	2	2341	2349
									YATLATVSR	95.0	60.0	25.0	981.54	0	8	0	0	2	2350	2358
									SIPLDEGEDEAQR	95.0	60.8	25.0	1458.67	0	4	0	0	2	2384	2396
									AELGEYIR	95.0	31.7	25.0	950.49	0	3	0	0	2	2512	2519
									VPQIEVETHK	95.0	31.6	25.0	1179.64	0	1	0	0	2	2552	2561
									TMTLFSALR	95.0	53.4	25.0	1055.56	0	19	0	0	2	2602	2610
									TPNGVVLAPVQLGK	95.0	60.4	25.0	1392.82	0	15	0	0	2	2644	2657
									VISFIR	94.9	26.7	25.0	734.46	0	1	0	0	2	2679	2684
									YTGEDFDEDLR	95.0	60.2	25.0	1359.57	0	9	0	0	2	2967	2977
									SMANPPAAVK	95.0	37.7	25.0	1001.51	0	9	0	0	2	3309	3318
									ANEVEQMIR	95.0	37.1	25.0	1105.53	0	1	0	0	2	3430	3438
									DLEASIAR	95.0	36.8	25.0	874.46	0	2	0	0	2	3439	3446
									TEYLSNADER	95.0	38.7	25.0	1197.54	0	4	0	0	2	3550	3559
									TSFLDDAFR	95.0	31.4	25.0	1071.51	0	3	0	0	2	3612	3620
									VTFVNFTVTR	95.0	46.9	25.0	1183.65	0	1	0	0	2	3696	3705
									LQGEFQLR	95.0	49.4	25.0	990.54	0	9	0	0	2	3734	3741
									DLFQVAFNR	95.0	43.5	25.0	1109.57	0	3	0	0	2	3862	3870
									GNEIVLSAGSTPR	95.0	78.7	25.0	1300.69	0	12	0	0	2	3911	3923
									IQGLTVEQAEAVVR	95.0	79.1	25.0	1512.84	0	8	0	0	2	3924	3937
									LFLTMEINPK	95.0	32.4	25.0	1221.66	0	3	0	0	2	4124	4133
									VPVNLLR	95.0	35.4	25.0	810.52	0	16	0	0	2	4134	4140
									TFSSIPVSR	95.0	39.6	25.0	993.54	0	4	0	0	2	4160	4168
									VDNEFDQR	95.0	33.0	25.0	1022.45	0	1	0	0	2	4256	4263
									LLNTFLER	95.0	44.3	25.0	1005.57	0	4	0	0	2	4264	4271
									VLLTTQGVDMISK	95.0	96.5	25.0	1420.77	0	16	0	0	2	4330	4342
									TVENIKDPLFR	95.0	29.7	25.0	1331.73	0	0	2	0	2	4401	4411
Cytoplasmic FMR1-interacting protein 1	CYFP1_HUMAN	CYFIP1	145.17	100.0	12	12	27	10.40	NAFVTGIAR	95.0	51.5	25.0	948.53	0	2	0	0	2	50	58
									TVEVLEPEVTK	95.0	65.9	25.0	1243.68	0	2	0	0	2	111	121
									LMNFMYFQR	95.0	33.0	25.0	1281.58	0	2	0	0	2	122	130
									YSNSEVVTGSGR	95.0	78.1	25.0	1255.59	0	2	0	0	2	366	377
									MESVFNHAIR	95.0	22.6	25.0	1219.59	0	0	2	0	2	468	477
									AVGPSSTQLYMVR	95.0	73.4	25.0	1424.72	0	1	0	0	2	551	563
									TMLESLIADK	95.0	62.8	25.0	1136.59	0	2	0	0	2	564	573
									SSLEGPTILDIEK	95.0	54.4	25.0	1401.75	0	7	0	0	2	582	594
									VMAGSLLLDKR	95.0	30.1	25.0	1218.69	0	0	2	0	2	716	726
									MTHKLLSR	95.0	30.4	25.0	1001.56	0	1	0	0	2	807	814
									LGTPQQIAIAR	95.0	69.2	25.0	1167.68	0	2	0	0	2	1066	1076
									SGDGEGTPVEHVR	95.0	36.4	25.0	1339.62	0	2	0	0	2	1228	1240
Cytoskeleton-associated protein 4	CKAP4_HUMAN	CKAP4	66.00	100.0	6	6	17	12.50	LALQALTEK	95.0	44.0	25.0	986.59	0	5	0	0	2	347	355
									LPEEIR	95.0	27.9	25.0	756.43	0	1	0	0	2	366	371
									LEEELR	95.0	33.5	25.0	788.41	0	2	0	0	2	373	378

									LQHVEDGVLSMQVASAR	95.0	26.9	25.0	1855.93	0	0	1	0	2	413	429
									LAALQGR	95.0	31.5	25.0	728.44	0	2	0	0	2	448	454
									VQEQVHTLLSQDQAQAAR	95.0	44.8	25.0	2022.04	0	0	2	0	2	506	523
									TAVDSLVAYSVK	95.0	69.9	25.0	1252.68	0	6	0	0	2	555	566
Cytoskeleton-associated protein 5	CKAP5_HUMAN	CKAP5	225.48	100.0	17	17	47	9.01	FVTDSNAVVQLK	95.0	56.9	25.0	1320.72	0	1	0	0	2	56	67
									TTGEVVSGVVSK	95.0	43.5	25.0	1162.63	0	3	0	0	2	85	96
									GEAVQEELLK	95.0	38.9	25.0	1115.59	0	3	0	0	2	122	131
									IILLKPIIK	95.0	28.7	25.0	1050.77	0	0	3	0	2	159	167
									LIAVEIYR	95.0	35.3	25.0	976.58	0	4	0	0	2	186	193
									DTNVMLVALAAK	95.0	98.2	25.0	1261.68	0	2	0	0	2	331	342
									HINDSAPEVR	95.0	30.9	25.0	1137.56	0	2	0	0	2	447	456
									DAAFEALGTALK	95.0	90.2	25.0	1206.64	0	5	0	0	2	457	468
									AVNPFLADVDK	95.0	40.7	25.0	1188.63	0	3	0	0	2	474	484
									AVELMDR	94.5	26.3	25.0	849.41	0	1	0	0	2	626	632
									LHIVALIAQK	95.0	56.2	25.0	1105.71	0	1	0	0	2	662	671
									TSAQVVLDGLVDK	95.0	62.6	25.0	1344.74	0	1	0	0	2	677	689
									EFGFSGLNVK	95.0	30.6	25.0	1097.56	0	2	0	0	2	745	754
									TALAATNPAVR	95.0	41.9	25.0	1084.61	0	4	0	0	2	762	772
									MQGQSPPAPTR	95.0	36.7	25.0	1185.57	0	3	0	0	2	812	822
									EGLDEVAGIINDAK	95.0	68.3	25.0	1443.73	0	6	0	0	2	879	892
									FFDTNTSVLMK	95.0	62.0	25.0	1318.63	0	3	0	0	2	1253	1263
Cytosol aminopeptidase	AMPL_HUMAN	LAP3	56.15	100.0	11	11	26	22.20	GLVLGIYSK	95.0	50.5	25.0	949.57	0	2	0	0	2	35	43
									ETLNISGPPLK	95.0	50.5	25.0	1168.66	0	4	0	0	2	69	79
									QLMETPANEMTPTR	95.0	42.8	25.0	1650.75	0	1	0	0	2	201	214
									FAEIIEK	95.0	40.1	25.0	849.47	0	2	0	0	2	215	221
									GSPNANEPPLVFVGK	95.0	62.2	25.0	1525.80	0	4	0	0	2	268	282
									GITFDSGGISIK	95.0	38.5	25.0	1194.64	0	2	0	0	2	283	294
									TIQVDNTDAEGR	95.0	48.1	25.0	1318.62	0	3	0	0	2	357	368
									LFEASIETGDR	95.0	68.0	25.0	1237.61	0	3	0	0	2	418	428
									MPLFEHYTR	95.0	32.0	25.0	1209.57	0	2	0	0	2	432	440
									EFVTHPK	95.0	27.9	25.0	857.45	0	1	0	0	2	470	476
									TLIEFLLR	95.0	36.6	25.0	1004.61	0	2	0	0	2	506	513
Cytosolic acyl coenzyme A thioester hydrolase	BACH_HUMAN	ACOT7	41.78	100.0	6	7	54	22.60	IMRPDDANVAGNVHGGTILK	95.0	46.6	25.0	2094.08	0	0	5	0	2	59	78
									MIEEAGAIISTR	95.0	81.6	25.0	1306.67	0	19	0	0	2	79	90
									VLEVPPVVYSR	95.0	53.1	25.0	1257.72	0	7	0	0	2	173	183
									LMDEVAGIVAAR	95.0	83.8	25.0	1260.66	0	6	0	0	2	253	264
									TNIVTASVDAINFHDK	95.0	91.6	25.0	1744.89	0	7	2	0	2	268	283
									SLPVPQLVPETEDEK	95.0	59.2	25.0	1680.87	0	8	0	0	2	341	355
Cytosolic non-specific dipeptidase	CNDP2_HUMAN	CNDP2	52.86	100.0	8	8	27	20.00	YIDENQDR	95.0	29.6	25.0	1052.46	0	4	0	0	2	10	17
									MMEVAAADVK	95.0	60.4	25.0	1096.50	0	4	0	0	2	44	53
									QLGGSVELVDIGK	95.0	85.6	25.0	1314.73	0	3	0	0	2	54	66
									TGQEIPVNVR	95.0	41.7	25.0	1112.61	0	3	0	0	2	150	159
									KDTFFK	95.0	32.2	25.0	785.42	0	2	0	0	2	181	186
									TVFGVEPDLTR	95.0	47.1	25.0	1233.65	0	5	0	0	2	403	413
									EGGSIPVTLTFQEATGK	95.0	71.8	25.0	1734.89	0	4	0	0	2	414	430
									NVMLLPVGSADDGAHSQNEK	95.0	####	25.0	2097.99	0	2	0	0	2	431	450
Cytosolic purine 5'-nucleotidase	5NTC_HUMAN	NT5C2	64.95	100.0	6	7	34	12.30	LQNAADMPANMDK	95.0	55.4	25.0	1450.63	0	3	0	0	2	9	21
									LPLLLSR	95.0	41.8	25.0	811.54	0	10	0	0	2	232	238
									VFLATNSDYK	95.0	38.0	25.0	1157.58	0	4	0	0	2	245	254
									KPLFFGEGTVLR	95.0	61.6	25.0	1363.77	0	9	3	0	2	292	303
									HLDSSSNERPDISSIQR	95.0	27.2	25.0	1940.94	0	0	3	0	2	405	421

									QTLFASQVMR	95.0	43.3	25.0	1196.61	0	2	0	0	2	447	456
D-3-phosphoglycerate dehydrogenase	SERA_HUMAN	PHGDH	56.63	100.0	6	6	34	12.80	ILQDGGLQVVEK	95.0	73.1	25.0	1298.73	0	5	0	0	2	22	33
									AGTGVDNVDLEAATR	95.0	####	25.0	1488.73	0	7	0	0	2	76	90
									TLGILGLGR	95.0	49.1	25.0	899.57	0	10	0	0	2	147	155
									GGIVDEGALLR	95.0	69.3	25.0	1099.61	0	4	0	0	2	237	247
									GTIQVITQGTSLK	95.0	78.8	25.0	1345.77	0	6	0	0	2	352	364
									DLPLLLFR	95.0	39.8	25.0	986.60	0	2	0	0	2	462	469
dCTP pyrophosphatase 1	DCTP1_HUMAN	DCTPP1	18.66	100.0	3	3	4	14.70	GDTGGEDTAAPGR	95.0	32.7	25.0	1203.52	0	1	0	0	2	10	22
									CRVDLPLAVLSK	95.0	26.9	25.0	1370.78	0	1	0	0	2	110	121
									VDLPLAVLSK	95.0	35.6	25.0	1054.65	0	2	0	0	2	112	121
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1_HUMAN	ECH1	35.80	100.0	3	3	4	10.40	YQETFNVIER	95.0	46.3	25.0	1298.64	0	1	0	0	2	149	158
									EVDVGLAADVGTLQR	95.0	99.7	25.0	1542.81	0	2	0	0	2	197	211
									SPVAVQSTK	95.0	28.0	25.0	916.51	0	1	0	0	2	268	276
Delta-1-pyrroline-5-carboxylate synthase	P5CS_HUMAN	ALDH18A1	87.28	100.0	4	4	7	4.78	LNSLAIGLR	95.0	46.0	25.0	956.59	0	2	0	0	2	433	441
									EAVQLVNTR	95.0	34.0	25.0	1029.57	0	2	0	0	2	531	539
									MIDLIIPR	95.0	40.5	25.0	986.57	0	2	0	0	2	551	558
									GPVGLEGLLTTK	95.0	38.6	25.0	1184.69	0	1	0	0	2	750	761
Desmoglein-2	DSG2_HUMAN	DSG2	122.28	100.0	3	3	26	2.77	ILDVNDNIPVVENK	95.0	74.1	25.0	1581.85	0	20	0	0	2	262	275
									LPDFESR	95.0	37.6	25.0	863.43	0	4	0	0	2	452	458
									IVAISEDYPR	95.0	75.0	25.0	1162.61	0	2	0	0	2	469	478
Desmoplakin	DESP_HUMAN	DSP	331.76	100.0	18	18	33	6.41	YEVTSGGGGTSR	95.0	35.4	25.0	1170.54	0	1	0	0	2	28	39
									AELIVQPELK	95.0	53.3	25.0	1139.67	0	4	0	0	2	85	94
									LLQLQEQMR	95.0	37.4	25.0	1174.63	0	2	0	0	2	142	150
									LASLEELKR	95.0	35.7	25.0	1058.62	0	2	0	0	2	1076	1084
									LTYEIEDEK	95.0	31.2	25.0	1139.55	0	2	0	0	2	1114	1122
									LNDSILQATEQR	95.0	81.5	25.0	1387.72	0	2	0	0	2	1256	1267
									NNYDEEIISLK	95.0	49.2	25.0	1337.66	0	2	0	0	2	1353	1363
									AQIDNLTR	94.6	26.4	25.0	930.50	0	1	0	0	2	1393	1400
									ITNLTQQLEQASIVK	95.0	68.4	25.0	1685.94	0	2	0	0	2	1612	1626
									QLLQEQESVK	95.0	28.0	25.0	1201.64	0	1	0	0	2	1667	1676
									LQSLTENLTK	95.0	44.2	25.0	1146.64	0	2	0	0	2	1706	1715
									LVFDGLR	95.0	33.2	25.0	819.47	0	2	0	0	2	1966	1972
									QQIYAAEK	95.0	29.3	25.0	950.49	0	1	0	0	2	2084	2091
									AITGFDDPFSGK	95.0	35.1	25.0	1254.60	0	2	0	0	2	2092	2103
									IEPHTGLLLLSVQK	95.0	30.5	25.0	1547.92	0	0	2	0	2	2192	2205
									LPVDIAYK	95.0	35.6	25.0	918.53	0	2	0	0	2	2386	2393
									GIVDSITGQR	95.0	40.2	25.0	1045.56	0	2	0	0	2	2640	2649
									SMVEDITGLR	95.0	31.1	25.0	1136.56	0	1	0	0	2	2792	2801
Developmentally-regulated GTP-binding protein 1	DRG1_HUMAN	DRG1	40.53	100.0	4	4	13	15.50	GGGGGGPGEGFDVAK	95.0	44.9	25.0	1261.58	0	3	0	0	2	47	61
									IIENELEGFGIR	95.0	83.3	25.0	1389.74	0	2	0	0	2	160	171
									SDATADDLIDVVEGNR	95.0	97.4	25.0	1689.79	0	6	0	0	2	223	238
									DHTLEDEDVIQIVK	95.0	66.6	25.0	1653.83	0	2	0	0	2	353	366
Dihydrolipoyl dehydrogenase, mitochondrial	DLDH_HUMAN	DLD	54.16	100.0	8	10	24	15.70	AAQLGFK	95.0	30.7	25.0	734.42	0	1	0	0	2	60	66
									GIEMSEVR	95.0	29.4	25.0	936.45	0	3	0	0	2	110	117
									ALTGGIAHLFK	95.0	59.0	25.0	1127.66	0	2	4	0	2	133	143
									ADGGTQVIDTK	95.0	59.3	25.0	1104.55	0	6	0	0	2	167	177
									IDVSIEAASGGK	95.0	66.8	25.0	1146.60	0	1	0	0	2	289	300
									SEEQLKEEGIEYK	95.0	63.7	25.0	1581.76	0	2	2	0	2	405	417
									FPFAANSR	95.0	32.7	25.0	909.46	0	2	0	0	2	421	428
									EANLAASFGK	95.0	47.9	25.0	1007.52	0	1	0	0	2	496	505
Dihydropyrimidinase-	DPYL2_HUMAN	DPYSL2	62.28	100.0	7	8	38	15.60	QIGENLIVPGGVK	95.0	57.5	25.0	1323.76	0	10	0	0	2	44	56

related protein 2									MVIPGGIDVHTR	95.0	60.2	25.0	1310.69	0	2	0	0	2	64	75
									GIQEEMEALVK	95.0	74.8	25.0	1262.63	0	4	0	0	2	147	157
									SSAEVIAQAR	95.0	69.0	25.0	1031.55	0	3	0	0	2	259	268
									MDENQFVAVTSTNAAK	95.0	####	25.0	1741.81	0	8	0	0	2	375	390
									GSPLVVISQGK	95.0	59.6	25.0	1084.64	0	7	0	0	2	441	451
									IVLEDGTLHVTEGSGR	95.0	58.5	25.0	1682.87	0	1	3	0	2	452	467
Dihydropyrimidinase-related protein 3	DPYL3_HUMAN	DPYSL3	61.95	100.0	4	4	20	11.40	QIGDNLIVPGGVK	95.0	43.0	25.0	1309.75	0	1	0	0	2	44	56
									GMTTVDDFFQGTK	95.0	65.4	25.0	1462.65	0	13	0	0	2	82	94
									MDENQFVAVTSTNAAK	95.0	####	25.0	1741.81	0	8	0	0	2	375	390
									IFNLYPR	95.0	33.1	25.0	922.51	0	3	0	0	2	391	397
									IMLEDGNLHVTQGAGR	95.0	33.6	25.0	1726.85	0	0	3	0	2	452	467
Dipeptidyl peptidase 3	DPP3_HUMAN	DPP3	82.57	100.0	12	12	31	16.40	LYAYHLSR	95.0	29.4	25.0	1022.54	0	1	0	0	2	32	39
									AQDPDQLR	95.0	28.7	25.0	942.46	0	3	0	0	2	69	76
									VILGSEAAQQHPEEVR	95.0	98.3	25.0	1762.91	0	4	0	0	2	126	141
									EVDGEGKPYYEVR	95.0	48.7	25.0	1540.73	0	4	0	0	2	203	215
									LASVLGSEPSLDSEVTSK	95.0	54.3	25.0	1818.93	0	4	0	0	2	216	233
									SYEFR	95.0	28.1	25.0	701.33	0	1	0	0	2	236	240
									GEFEGFVAVVNK	95.0	79.3	25.0	1295.66	0	3	0	0	2	326	337
									LVASAEQLLK	95.0	68.2	25.0	1071.64	0	3	0	0	2	346	355
									LFVQDEK	95.0	42.0	25.0	878.46	0	2	0	0	2	460	466
									SVGKPALER	95.0	34.4	25.0	956.55	0	2	0	0	2	612	620
									DTVLLR	95.0	42.7	25.0	716.43	0	3	0	0	2	660	665
									KLIVQPNTR	95.0	28.5	25.0	1068.65	0	1	0	0	2	670	678
Dipeptidyl peptidase 9	DPP9_HUMAN	DPP9	98.25	100.0	8	8	32	9.50	APHDFQFVQK	95.0	30.7	25.0	1216.61	0	0	2	0	2	52	61
									ENSLLYSEIPK	95.0	57.3	25.0	1292.67	0	11	0	0	2	83	93
									NGFMVSPMKPLEIK	95.0	19.3	25.0	1622.83	0	0	1	0	2	168	181
									VEYIAR	95.0	29.9	25.0	750.41	0	1	0	0	2	349	354
									LVYFQGTK	94.9	26.6	25.0	955.52	0	1	0	0	2	512	519
									LSGPDDDPLHK	95.0	45.3	25.0	1193.58	0	0	2	0	2	577	587
									YGFIDLSR	95.0	38.7	25.0	970.50	0	13	0	0	2	716	723
									AGKPYQLQIYPNER	95.0	49.0	25.0	1676.88	0	1	0	0	2	826	839
DNA damage-binding protein 1	DDB1_HUMAN	DDB1	126.95	100.0	15	16	78	13.10	IAVMELFRPK	95.0	33.3	25.0	1219.69	0	0	3	0	2	61	70
									QSGESIDIITR	95.0	44.0	25.0	1218.63	0	1	0	0	2	93	103
									DNKELK	95.0	28.6	25.0	746.40	0	1	0	0	2	148	153
									LEELHVIDVK	95.0	26.8	25.0	1194.67	0	1	0	0	2	159	168
									TYEVSLR	95.0	43.8	25.0	867.46	0	7	0	0	2	192	198
									YLLGDMEGR	95.0	49.3	25.0	1069.50	0	2	0	0	2	271	279
									LGDSQLVK	95.0	44.4	25.0	859.49	0	2	0	0	2	328	335
									LPSFELLHK	95.0	50.5	25.0	1083.62	0	3	2	0	2	571	579
									EMLGGEIIPR	95.0	68.3	25.0	1130.59	0	11	0	0	2	580	589
									VTLGTQPTVLR	95.0	77.1	25.0	1184.70	0	7	0	0	2	629	639
									LVFSNVNLK	95.0	54.3	25.0	1033.60	0	12	0	0	2	666	674
									IVVFQYSDGK	95.0	64.1	25.0	1155.60	0	14	0	0	2	848	857
									TKGDFILVGDLMR	95.0	52.8	25.0	1480.78	0	1	0	0	2	916	928
									MQEVVANLQYDDGSGMK	95.0	####	25.0	1916.84	0	4	0	0	2	1105	1121
									EATADDLIK	95.0	52.0	25.0	975.50	0	7	0	0	2	1123	1131
DNA repair protein RAD50	RAD50_HUMAN	RAD50	153.88	100.0	3	3	4	2.44	SYENELDPLK	95.0	42.4	25.0	1207.58	0	2	0	0	2	243	252
									YELQQLEGSSDR	95.0	56.3	25.0	1424.67	0	1	0	0	2	462	473
									GQDIEYIEIR	95.0	47.5	25.0	1235.63	0	1	0	0	2	1157	1166
DNA replication complex GINS protein PSF3	PSF3_HUMAN	GINS3	24.52	100.0	3	3	3	17.60	LGAFFLER	95.0	28.9	25.0	952.53	0	1	0	0	2	43	50
									TVFSADPNVVDLHK	95.0	40.2	25.0	1541.80	0	1	0	0	2	98	111

								GQASQITASNLVQNYK	95.0	86.6	25.0	1721.88	0	1	0	0	2	192	207
DNA replication licensing factor MCM2	MCM2_HUMAN	MCM2	101.88	100.0	9	9	52	12.30	ESLVVNYEDLAAR	95.0	59.1	25.0	1478.75	0	1	0	0	2	228	240
									ISHLPLVEELR	95.0	33.4	25.0	1305.75	0	0	2	0	2	285	295
									VAVGELTDEDVK	95.0	75.5	25.0	1274.65	0	9	0	0	2	451	462
									GLALALFGGEPK	95.0	75.2	25.0	1172.67	0	21	0	0	2	494	505
									DTVDPVQDEMLAR	95.0	48.7	25.0	1504.70	0	1	0	0	2	665	677
									FVVGSHVR	95.0	33.2	25.0	900.50	0	2	0	0	2	678	685
									ESMATGSIPITVR	95.0	57.8	25.0	1377.70	0	6	0	0	2	753	765
									VMLESFIDTQK	95.0	68.6	25.0	1326.66	0	8	0	0	2	797	807
									FGAQQDTIEVPEKDLVDK	95.0	58.0	25.0	2032.02	0	0	2	0	2	851	868
DNA replication licensing factor MCM3	MCM3_HUMAN	MCM3	90.96	100.0	5	5	15	6.93	ELISDNQYR	95.0	51.1	25.0	1137.55	0	6	0	0	2	38	46
									LIVNVNDLR	95.0	47.9	25.0	1055.62	0	4	0	0	2	47	55
									GDINILLIGDPSVAK	95.0	51.5	25.0	1524.86	0	2	0	0	2	337	351
									TPMENIGLQDSLLSR	95.0	99.1	25.0	1689.85	0	2	0	0	2	464	478
									VALLDVFR	95.0	40.8	25.0	932.56	0	1	0	0	2	749	756
DNA replication licensing factor MCM6	MCM6_HUMAN	MCM6	92.87	100.0	3	4	5	4.38	ESEDFIVEQYK	95.0	49.4	25.0	1386.64	0	2	0	0	2	589	599
									ISNLIVLHLR	95.0	35.0	25.0	1177.74	0	1	1	0	2	723	732
									EIESEIDSEEELINK	95.0	82.8	25.0	1776.84	0	1	0	0	2	755	769
DNA topoisomerase 2-alpha	TOP2A_HUMAN	TOP2A	174.37	100.0	5	5	13	3.85	IFDEILVNAADNK	95.0	71.5	25.0	1461.76	0	1	0	0	2	84	96
									HVDYVADQIVTK	95.0	60.9	25.0	1387.72	0	2	0	0	2	325	336
									TLAVSGLGVVGR	95.0	61.3	25.0	1128.67	0	3	0	0	2	467	478
									ELILFSNSDNER	95.0	56.4	25.0	1436.70	0	6	0	0	2	702	713
									KYDTVLDILR	95.0	29.6	25.0	1235.70	0	1	0	0	2	1011	1020
DNA-(apurinic or apyrimidinic site) lyase	APEX1_HUMAN	APEX1	35.54	100.0	4	4	18	15.70	EAAGEGPALYEDPPDQK	95.0	80.2	25.0	1786.81	0	5	0	0	2	36	52
									EEAPDILCLQETK	95.0	63.0	25.0	1545.75	0	2	0	0	2	86	98
									EGYSGVGLLSR	95.0	70.6	25.0	1137.59	0	6	0	0	2	126	136
									NAGFTPQER	95.0	34.5	25.0	1019.49	0	5	0	0	2	229	237
DNA-dependent protein kinase catalytic subunit	PRKDC_HUMAN	PRKDC	469.08	100.0	15	15	53	3.83	SLNSIEFR	95.0	41.0	25.0	965.51	0	2	0	0	2	72	79
									AFLGELK	95.0	37.8	25.0	777.45	0	5	0	0	2	199	205
									DYVDLFR	95.0	32.4	25.0	927.46	0	1	0	0	2	526	532
									AYVPALQMAFK	95.0	35.0	25.0	1254.66	0	2	0	0	2	747	757
									VVQMLGSLGGQINK	95.0	45.3	25.0	1459.79	0	3	0	0	2	855	868
									NLLTVTSSDEMMK	95.0	49.2	25.0	1500.69	0	2	0	0	2	869	881
									LSFAVPFR	95.0	40.0	25.0	936.53	0	1	0	0	2	892	899
									VTELALTASDR	95.0	93.1	25.0	1175.63	0	5	0	0	2	914	924
									FVPLLPGNR	95.0	30.4	25.0	1012.59	0	2	0	0	2	1194	1202
									MAVLALLAK	95.0	47.0	25.0	945.58	0	10	0	0	2	1643	1651
									LNESTFDTQITK	95.0	69.2	25.0	1396.70	0	12	0	0	2	1858	1869
									SLGPPQGEEDSVPR	95.0	54.2	25.0	1467.71	0	3	0	0	2	2107	2120
									QITQSALLAEAR	95.0	40.7	25.0	1300.72	0	1	0	0	2	2951	2962
									YPEETLSLMTK	95.0	53.2	25.0	1327.65	0	2	0	0	2	3475	3485
									MSTSPEAFLALR	95.0	46.3	25.0	1338.67	0	2	0	0	2	3890	3901
DNA-directed RNA polymerase II subunit RPB7	RPB7_HUMAN	POLR2G	19.28	100.0	3	3	6	20.90	GFVLYPVK	95.0	39.7	25.0	922.54	0	1	0	0	2	64	71
									GEVVDAVVTQVNK	95.0	####	25.0	1357.73	0	4	0	0	2	82	94
									TMDEDIVIQQDDEIR	95.0	####	25.0	1835.83	0	1	0	0	2	130	144
DNA-directed RNA polymerases I, II, and III subunit RPABC3	RPAB3_HUMAN	POLR2H	17.13	100.0	3	3	21	26.70	ADQFEYVMYGK	95.0	69.5	25.0	1366.60	0	2	0	0	2	85	95
									IEGDETSTEAATR	95.0	74.9	25.0	1379.63	0	15	0	0	2	99	111
									LQGDANNLHGFEVDSR	95.0	81.1	25.0	1771.84	0	4	0	0	2	125	140
DnaJ homolog subfamily B member 11	DJB11_HUMAN	DNAJB11	40.50	100.0	6	7	18	17.60	LALQLHPDRNPDDPQAQEK	95.0	38.2	25.0	2185.10	0	0	2	0	2	48	66
									QYDTYGEEGLK	95.0	40.3	25.0	1302.59	0	2	0	0	2	85	95
									TLEVEIEPGVR	95.0	51.8	25.0	1241.67	0	2	0	0	2	207	217

									KGEGLPNFDNNNIK	95.0	56.4	25.0	1559.78	0	2	1	0	2	302	315
									GEGLPNFDNNNIK	95.0	36.0	25.0	1431.69	0	2	0	0	2	303	315
									EQLTEEAR	95.0	44.5	25.0	975.47	0	7	0	0	2	329	336
DnaJ homolog subfamily C member 13	DJC13_HUMAN	DNAJC13	254.42	100.0	3	3	4	1.43	MQELALSEGALPR	95.0	####	25.0	1430.73	0	2	0	0	2	600	612
									TQSILFNR	95.0	28.6	25.0	978.54	0	1	0	0	2	1375	1382
									LAVASVTEILK	95.0	21.5	25.0	1143.70	0	0	1	0	2	1621	1631
DnaJ homolog subfamily C member 7	DNJC7_HUMAN	DNAJC7	56.42	100.0	3	3	10	7.29	YPEAQSVASDILR	95.0	72.0	25.0	1448.74	0	4	0	0	2	192	204
									AVQFFVQALR	95.0	49.4	25.0	1178.67	0	3	0	0	2	229	238
									EVGEAFTILSDPK	95.0	76.3	25.0	1405.72	0	3	0	0	2	430	442
DnaJ homolog subfamily C member 9	DNJC9_HUMAN	DNAJC9	29.89	100.0	4	4	7	11.90	FQILGK	95.0	26.9	25.0	705.43	0	1	0	0	2	59	64
									VYSVLSDR	95.0	43.9	25.0	938.49	0	2	0	0	2	65	72
									GSEEELADIK	95.0	44.7	25.0	1090.53	0	2	0	0	2	122	131
									QAYLDFK	95.0	32.9	25.0	884.45	0	2	0	0	2	132	138
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1_HUMAN	RPN1	68.55	100.0	6	6	15	11.50	VTAEVVLAHLGGGSTSR	95.0	68.5	25.0	1653.89	0	2	0	0	2	49	65
									LAHLGVQVK	95.0	42.3	25.0	964.59	0	2	0	0	2	81	89
									GEDEEENNLEVR	95.0	52.6	25.0	1432.62	0	2	0	0	2	90	101
									NIEIDSPYEISR	95.0	75.3	25.0	1435.71	0	2	0	0	2	380	391
									ALTSEIALLQSR	95.0	69.5	25.0	1301.74	0	5	0	0	2	525	536
									IDHILDAL	95.0	34.8	25.0	909.50	0	2	0	0	2	600	607
Double-stranded RNA-specific adenosine deaminase	DSRAD_HUMAN	ADAR	135.95	100.0	3	3	4	1.96	QIEFLK	95.0	27.8	25.0	777.45	0	1	0	0	2	43	48
									DGSAFEDGLR	95.0	47.2	25.0	1066.48	0	2	0	0	2	1087	1096
									KNIFLLFK	95.0	27.0	25.0	1022.64	0	1	0	0	2	1159	1166
Dual specificity mitogen-activated protein kinase kinase 1	MP2K1_HUMAN	MAP2K1	43.42	100.0	7	8	13	19.80	KLEELELDEQQR	95.0	93.5	25.0	1529.78	0	2	1	0	2	36	47
									VGELKDDDFEK	94.8	19.1	25.0	1294.62	0	0	1	0	2	60	70
									ISELGAGNGGVVFK	95.0	79.6	25.0	1347.73	0	5	0	0	2	71	84
									KLIHLEIKPAIR	95.0	23.5	25.0	1430.92	0	0	0	1	2	97	108
									IPEQILGK	95.0	29.4	25.0	897.54	0	1	0	0	2	161	168
									DVKPSNILVNSR	95.0	46.1	25.0	1341.75	0	1	0	0	2	190	201
									YPIPPPDAK	95.0	33.6	25.0	997.54	0	1	0	0	2	261	269
Dual specificity protein phosphatase 3	DUS3_HUMAN	DUSP3	20.46	100.0	5	6	22	30.30	IYVGNASVAQDIPK	95.0	82.4	25.0	1474.79	0	2	0	0	2	37	50
									LGITHVLNAAEGR	95.0	73.3	25.0	1350.75	0	4	4	0	2	54	66
									DSGITYLGIK	95.0	59.6	25.0	1066.58	0	4	0	0	2	80	89
									AADFIDQALAQK	95.0	70.6	25.0	1290.67	0	6	0	0	2	105	116
									SALSIVR	95.0	41.7	25.0	745.46	0	2	0	0	2	149	155
Dynactin subunit 1	DCTN1_HUMAN	DCTN1	141.68	100.0	9	9	17	9.00	MQEQQADLQR	95.0	31.5	25.0	1262.58	0	1	0	0	2	265	274
									AESLQQEVEALK	95.0	44.8	25.0	1344.70	0	1	0	0	2	318	329
									GSDGAASSYQLK	95.0	46.4	25.0	1183.56	0	4	0	0	2	350	361
									VEAAQETVADYQQTIK	95.0	75.2	25.0	1793.89	0	1	0	0	2	503	518
									ELTNQQEASVER	95.0	46.8	25.0	1403.68	0	2	0	0	2	533	544
									DQLDETVNVEPLTK	95.0	38.8	25.0	1600.81	0	2	0	0	2	709	722
									IKGEELSEANVR	95.0	21.2	25.0	1344.71	0	0	1	0	2	961	972
									DSPLLLQQISAMR	95.0	60.7	25.0	1487.79	0	4	0	0	2	1089	1101
									SPSAQLMEQVAQLK	95.0	46.5	25.0	1545.79	0	1	0	0	2	1180	1193
Dynactin subunit 2	DCTN2_HUMAN	DCTN2	44.21	100.0	3	4	10	9.23	LLHEVQELTTEVEK	95.0	73.7	25.0	1667.89	0	4	1	0	2	106	119
									LLLQLEATK	95.0	51.0	25.0	1028.64	0	3	0	0	2	177	185
									DNTTLLTQVQTTMR	95.0	97.9	25.0	1637.82	0	2	0	0	2	366	379
Dynamin-1-like protein	DNM1L_HUMAN	DNM1L	81.86	100.0	4	4	14	4.89	SSVLESLVGR	95.0	53.9	25.0	1046.58	0	2	0	0	2	39	48
									LGIIGVVNR	95.0	78.5	25.0	940.59	0	5	0	0	2	239	247
									SATLLQLITK	95.0	51.2	25.0	1087.67	0	5	0	0	2	330	339
									SYFLIVR	95.0	29.5	25.0	897.52	0	2	0	0	2	653	659
Dynamin-2	DYN2_HUMAN	DNM2	98.05	100.0	8	8	18	9.43	GMEELIPLVNK	95.0	79.6	25.0	1258.67	0	2	0	0	2	5	15

									SSVLENFVGR	95.0	49.8	25.0	1107.58	0	4	0	0	2	45	54
									GISPVPINLR	95.0	42.7	25.0	1065.64	0	4	0	0	2	114	123
									DMILQFISR	95.0	46.7	25.0	1138.59	0	1	0	0	2	158	166
									LDLMDEGTDAR	95.0	53.1	25.0	1251.55	0	2	0	0	2	207	217
									LQSQLLSLEK	95.0	46.3	25.0	1158.67	0	2	0	0	2	300	309
									YMLPLDNLK	95.0	29.9	25.0	1122.59	0	2	0	0	2	563	571
									NLVDSYVAIINK	95.0	53.8	25.0	1348.75	0	1	0	0	2	658	669
Dynamin-like 120 kDa protein, mitochondrial	OPA1_HUMAN	OPA1	111.62	100.0	10	10	21	11.10	VVVVGDQSAGK	95.0	36.2	25.0	1058.58	0	2	0	0	2	291	301
									IQQIIEGK	95.0	36.6	25.0	928.55	0	1	0	0	2	482	489
									ALGYFAVVTGK	95.0	60.4	25.0	1125.63	0	2	0	0	2	495	505
									GNSSESIEAIR	95.0	50.9	25.0	1162.57	0	1	0	0	2	506	516
									EYEEEFFQNSK	95.0	68.2	25.0	1449.62	0	4	0	0	2	517	527
									ESVEQQADSFK	95.0	54.3	25.0	1267.58	0	2	0	0	2	558	568
									ELDRNELFEK	95.0	32.1	25.0	1292.65	0	1	0	0	2	587	596
									MLAITANTLR	95.0	44.7	25.0	1119.62	0	2	0	0	2	886	895
									EVLEDFAEDGEK	95.0	88.0	25.0	1380.62	0	4	0	0	2	912	923
									LDAFIEALHQEK	95.0	69.6	25.0	1413.74	0	2	0	0	2	949	960
E3 SUMO-protein ligase RanBP2	RBP2_HUMAN	RANBP2	358.18	100.0	4	4	5	1.52	FKTPEEAALFK	95.0	19.4	25.0	1280.69	0	0	1	0	2	1285	1295
									TPELAEEFK	95.0	31.9	25.0	1063.53	0	1	0	0	2	2128	2136
									SGEEDEEILFK	95.0	31.3	25.0	1295.60	0	1	0	0	2	2925	2935
									ITMELFSNIVPR	95.0	39.3	25.0	1435.76	0	2	0	0	2	3080	3091
									TAENFR	95.0	27.5	25.0	737.36	0	1	0	0	2	3092	3097
E3 ubiquitin/ISG15 ligase TRIM25	TRI25_HUMAN	TRIM25	70.97	100.0	3	3	15	4.44	RDEFEFLEK	95.0	43.7	25.0	1212.59	0	8	0	0	2	302	310
									VLETFLAK	95.0	49.0	25.0	920.55	0	4	0	0	2	440	447
									VILDYNTAHNK	95.0	34.7	25.0	1287.67	0	3	0	0	2	459	469
E3 ubiquitin-protein ligase UBR4	UBR4_HUMAN	UBR4	573.82	100.0	9	9	18	1.74	HLILLIK	95.0	28.5	25.0	849.59	0	1	0	0	2	128	134
									LLQTLPQLR	94.8	26.6	25.0	1081.67	0	1	0	0	2	2981	2989
									AVEILR	95.0	42.2	25.0	700.44	0	6	0	0	2	3493	3498
									ELFDYNLR	95.0	51.7	25.0	1069.53	0	2	0	0	2	3908	3915
									SNPSVLQGLLR	95.0	45.7	25.0	1183.68	0	1	0	0	2	4608	4618
									VLGIYTFTK	95.0	29.9	25.0	1041.60	0	1	0	0	2	4852	4860
									EPTYQLNIHDIK	95.0	34.0	25.0	1470.76	0	2	0	0	2	4951	4962
									FAMEQSFSADTGGGGR	95.0	95.9	25.0	1633.69	0	2	0	0	2	4968	4983
									HNDMPIYEAADK	95.0	40.4	25.0	1419.62	0	2	0	0	2	5129	5140
Early endosome antigen 1	EEA1_HUMAN	EEA1	162.45	100.0	19	19	44	15.10	LSASETSLHR	95.0	22.0	25.0	1100.57	0	0	1	0	2	353	362
									LKEELSEVETK	95.0	53.5	25.0	1304.69	0	4	0	0	2	377	387
									LMDKEQQVADLQLK	95.0	25.1	25.0	1674.87	0	0	1	0	2	448	461
									EAQNDLEQVLR	95.0	43.8	25.0	1314.66	0	2	0	0	2	506	516
									IQNLEALLQK	95.0	44.8	25.0	1169.69	0	1	0	0	2	525	534
									NHTLQEQVTQLTEK	95.0	42.4	25.0	1668.86	0	0	2	0	2	570	583
									TELLLSAEAAK	95.0	33.3	25.0	1145.64	0	1	0	0	2	648	658
									ADLQNHLDTAQNALQDK	95.0	45.7	25.0	1894.93	0	0	2	0	2	663	679
									ITTQLDQVTAK	95.0	66.7	25.0	1217.67	0	4	0	0	2	686	696
									KLEADSLEVK	95.0	28.4	25.0	1131.63	0	1	0	0	2	734	743
									EQALQDLQQQR	95.0	50.7	25.0	1356.69	0	5	0	0	2	747	757
									QLNTDLELR	95.0	34.9	25.0	1101.59	0	2	0	0	2	758	766
									IQHEELNNR	95.0	28.3	25.0	1152.58	0	0	2	0	2	825	833
									IQTTVTELQK	95.0	37.9	25.0	1160.65	0	2	0	0	2	834	843
									EALMTELSTVK	95.0	65.3	25.0	1237.63	0	4	0	0	2	849	859
									QIEALQGELK	95.0	38.7	25.0	1128.63	0	1	0	0	2	974	983
									LSLAQEDLISNR	95.0	69.3	25.0	1358.73	0	6	0	0	2	1056	1067

									LTMQITALNENLGTVK	95.0	79.0	25.0	1761.94	0	2	0	0	2	1239	1254
									VLELQR	95.0	48.2	25.0	757.46	0	1	0	0	2	1313	1318
Echinoderm microtubule-associated protein-like 2	EMAL2_HUMAN	EML2	70.66	100.0	3	3	11	6.32	EVIFSVEDGSVK	95.0	69.4	25.0	1308.67	0	6	0	0	2	11	22
									SAGFHPSGSVLAVGTVTGR	95.0	73.7	25.0	1799.94	0	2	0	0	2	423	441
									LLASADDFGK	95.0	48.3	25.0	1036.53	0	3	0	0	2	587	596
EF-hand domain-containing protein D2	EFHD2_HUMAN	EFHD2	26.68	100.0	9	10	52	35.80	RADLNQGIGEPQSPSR	95.0	45.6	25.0	1724.87	0	1	0	0	2	62	77
									ADLNQGIGEPQSPSR	95.0	58.6	25.0	1568.77	0	6	0	0	2	63	77
									DGFIDLMELK	95.0	45.8	25.0	1196.59	0	2	0	0	2	109	118
									LGAPQTHLGLK	95.0	55.7	25.0	1134.66	0	10	6	0	2	124	134
									EVDEDFDSK	95.0	35.9	25.0	1083.45	0	1	0	0	2	139	147
									EFLLIFR	95.0	28.7	25.0	937.55	0	1	0	0	2	152	158
									LSEIDVSSEGVK	95.0	97.9	25.0	1262.65	0	20	0	0	2	177	188
									VQAINVSSR	95.0	40.6	25.0	973.54	0	3	0	0	2	198	206
									FEEEIKAEQEER	95.0	45.4	25.0	1536.72	0	2	0	0	2	207	218
EGF-containing fibulin-like extracellular matrix protein 1	FBLN3_HUMAN	EFEMP1	54.62	100.0	4	4	47	8.32	IPSNPSHR	95.0	27.9	25.0	907.47	0	1	0	0	2	149	156
									ELPQSIVYK	95.0	31.2	25.0	1076.60	0	2	0	0	2	388	396
									SGNENGEFYLR	95.0	73.7	25.0	1285.58	0	13	0	0	2	430	440
									QTSPVSAMLVLVK	95.0	93.3	25.0	1388.78	0	31	0	0	2	441	453
EH domain-containing protein 1	EHD1_HUMAN	EHD1	60.61	100.0	14	16	78	25.30	LLPLEEHYR	94.9	26.6	25.0	1169.63	0	1	0	0	2	33	41
									HLIEQDFPGMR	95.0	38.7	25.0	1358.65	0	4	0	0	2	77	87
									KLNAFGNAFLNR	95.0	28.4	25.0	1364.74	0	0	2	0	2	124	135
									LNAFGNAFLNR	95.0	61.4	25.0	1236.65	0	7	0	0	2	125	135
									IILLFDAHK	95.0	50.6	25.0	1069.64	0	2	6	0	2	185	193
									ADQIETQQLMR	95.0	58.2	25.0	1348.65	0	11	0	0	2	221	231
									LFEAEEQDLFK	95.0	57.5	25.0	1368.67	0	3	0	0	2	270	280
									KLNDLIK	95.0	36.8	25.0	843.53	0	2	0	0	2	293	299
									ELVNNLGEIYQK	95.0	84.9	25.0	1419.75	0	10	0	0	2	330	341
									EHQISPGDFPSLR	95.0	57.7	25.0	1482.73	0	6	9	0	2	345	357
									KMQELLQTQDFSK	95.0	84.6	25.0	1611.81	0	2	0	0	2	358	370
									MQELLQTQDFSK	95.0	58.2	25.0	1483.71	0	2	0	0	2	359	370
									LLDTVDDMLANDIAR	95.0	####	25.0	1690.83	0	9	0	0	2	378	392
									QEESLMPSQVVK	95.0	43.8	25.0	1390.69	0	2	0	0	2	399	410
EH domain-containing protein 2	EHD2_HUMAN	EHD2	61.15	100.0	4	4	6	8.66	LLPLEEHYR	94.9	26.6	25.0	1169.63	0	1	0	0	2	33	41
									GYDFPAVLR	94.7	26.5	25.0	1037.54	0	1	0	0	2	168	176
									VVGTPEVLR	95.0	35.7	25.0	969.57	0	1	0	0	2	243	251
									LPNSVLGR	95.0	48.4	25.0	855.50	0	2	0	0	2	481	488
									LEGHGLPANLPR	95.0	45.4	25.0	1273.70	0	0	2	0	2	517	528
ELAV-like protein 1	ELAV1_HUMAN	ELAVL1	36.07	100.0	3	3	20	10.10	SLFSSIGEVESAK	95.0	81.3	25.0	1353.69	0	8	0	0	2	38	50
									AINTLNGLR	95.0	43.9	25.0	971.56	0	4	0	0	2	77	85
									VLVDQTTGLSR	95.0	76.8	25.0	1188.66	0	8	0	0	2	137	147
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA_HUMAN	ETFA	35.06	100.0	5	5	8	21.00	VLVAQHDVYK	95.0	33.5	25.0	1171.65	0	2	0	0	2	76	85
									LEVAPISDIIAIK	95.0	27.7	25.0	1381.83	0	1	0	0	2	127	139
									GTSFDAAATSGGSASSEK	95.0	75.9	25.0	1630.72	0	2	0	0	2	170	187
									SDRPELTGAK	95.0	27.4	25.0	1073.56	0	0	1	0	2	207	216
									AAVDAGFVPNDMQVGQTGK	95.0	66.7	25.0	1920.91	0	2	0	0	2	250	268
Electron transfer flavoprotein subunit beta	ETFB_HUMAN	ETFB	27.83	100.0	5	5	9	18.40	LGPLQVAR	95.0	29.1	25.0	853.53	0	2	0	0	2	99	106
									EIDGGLETLR	95.0	38.7	25.0	1102.57	0	2	0	0	2	165	174
									LKLPAVVTADLR	95.0	22.7	25.0	1295.80	0	0	1	0	2	175	186
									LPAVVTADLR	95.0	38.7	25.0	1054.63	0	2	0	0	2	177	186
									KIEVIKPGDLGVDLTSK	95.0	24.7	25.0	1812.05	0	0	2	0	2	205	221
ELKS/Rab6-	RB6I2_HUMAN	ERC1	128.07	100.0	3	3	5	2.42	DLKDLK	95.0	34.5	25.0	731.43	0	3	0	0	2	653	658

interacting/CAST family member 1									LLEILKEVENEK	95.0	32.6	25.0	1456.83	0	1	0	0	2	761	772
									IEELEEALR	95.0	34.0	25.0	1101.58	0	1	0	0	2	839	847
Elongation factor 1-delta	EF1D_HUMAN	EEF1D	31.10	100.0	3	3	12	11.70	IASLEVENQSLR	95.0	69.7	25.0	1358.73	0	2	0	0	2	84	95
									GVVQELQQAISK	95.0	59.5	25.0	1299.73	0	6	0	0	2	96	107
									LVPVGYGIR	95.0	42.0	25.0	973.58	0	4	0	0	2	233	241
Elongation factor 1-gamma	EF1G_HUMAN	EEF1G	50.10	100.0	16	20	231	27.90	ALIAAQYSGAQVR	95.0	90.3	25.0	1347.74	0	28	0	0	2	18	30
									VLSAPPHFHFGQTNR	95.0	78.3	25.0	1707.87	0	2	4	0	2	31	45
									TPEFLR	95.0	39.4	25.0	762.41	0	11	0	0	2	46	51
									ILGLLDAYLK	95.0	69.5	25.0	1118.68	0	11	0	0	2	138	147
									TFLVGER	95.0	43.0	25.0	821.45	0	18	0	0	2	150	156
									QVLEPSFR	95.0	29.8	25.0	975.53	0	1	0	0	2	174	181
									QAFPNTNR	95.0	27.4	25.0	947.47	0	1	0	0	2	182	189
									AVLGEVK	95.0	37.5	25.0	715.43	0	2	0	0	2	202	208
									MAQFDAK	95.0	28.6	25.0	826.38	0	1	0	0	2	213	219
									FAETQPK	95.0	35.3	25.0	820.42	0	7	0	0	2	221	227
									AKDPFAHLPK	95.0	52.0	25.0	1123.63	0	8	22	0	2	276	285
									DPFAHLPK	95.0	32.4	25.0	924.49	0	3	0	0	2	278	285
									STFVLDEFK	95.0	44.5	25.0	1085.55	0	22	0	0	2	286	294
									STFVLDEFKR	95.0	50.5	25.0	1241.65	0	9	10	0	2	286	295
									KLDPGSEETQTLVR	95.0	89.7	25.0	1572.82	0	26	17	0	2	401	414
									LDPGSEETQTLVR	95.0	87.4	25.0	1444.73	0	28	0	0	2	402	414
Elongation factor 2	EF2_HUMAN	EEF2	95.32	100.0	30	37	493	29.50	MVNFTVDQIR	95.0	30.3	25.0	1238.62	0	1	0	0	2	1	10
									VNFTVDQIR	95.0	83.9	25.0	1091.58	0	60	0	0	1	2	10
									NMSVIAHVDHGK	95.0	73.5	25.0	1323.65	0	13	2	0	2	21	32
									AGIIASAR	95.0	62.2	25.0	758.45	0	25	0	0	2	43	50
									IKPVLMMNK	95.0	25.5	25.0	1105.61	0	0	7	0	2	151	159
									QFAEMYVAK	95.0	31.2	25.0	1102.52	0	1	0	0	2	227	235
									GEGQLGPAER	95.0	52.1	25.0	1013.50	0	36	0	0	2	240	249
									VFDAIMNFK	95.0	52.0	25.0	1100.54	0	65	0	0	2	300	308
									VFDAIMNFKK	95.0	39.0	25.0	1228.64	0	2	3	0	2	300	309
									GPLMMYISK	95.0	39.6	25.0	1071.52	0	9	0	0	2	392	400
									FYAFGR	95.0	27.5	25.0	760.38	0	1	0	0	2	410	415
									VFSGLVSTGLK	95.0	84.6	25.0	1107.64	0	87	0	0	2	416	426
									IMGPNYTPGK	95.0	47.8	25.0	1093.53	0	22	0	0	2	429	438
									IMGPNYTPGKK	95.0	29.8	25.0	1221.63	0	0	7	0	2	429	439
									KEDLYLKPIQR	95.0	63.8	25.0	1402.81	0	6	22	0	2	439	449
									EDLYLKPIQR	95.0	26.8	25.0	1274.71	0	0	8	0	2	440	449
									TILMMGR	95.0	40.4	25.0	853.43	0	7	0	0	2	450	456
									TGTITTFEHAHNMR	95.0	61.9	25.0	1631.76	0	10	12	0	2	482	495
									FSVSPVVR	95.0	43.3	25.0	890.51	0	4	0	0	2	499	506
									NPADLPK	95.0	40.7	25.0	754.41	0	13	0	0	2	513	519
									KSDPVVSYR	95.0	36.8	25.0	1050.56	0	3	0	0	2	572	580
									SDPVVSYR	95.0	41.2	25.0	922.46	0	4	0	0	2	573	580
									ETVSEESNVLCLSK	95.0	88.8	25.0	1594.76	0	2	0	0	2	581	594
									ARPFPDGLAEDIDK	95.0	78.7	25.0	1543.78	0	2	1	0	2	606	619
									ARPFPDGLAEDIDKGEVSAR	95.0	72.1	25.0	2143.08	0	0	2	0	2	606	625
									GVQYLNEIK	95.0	63.0	25.0	1063.58	0	25	0	0	2	668	676
									EGALCEENMR	95.0	34.7	25.0	1224.50	0	2	0	0	2	689	698
									GGGQIIPTAR	95.0	44.4	25.0	969.55	0	22	0	0	2	717	726
									CLYASVLTAQPR	95.0	64.0	25.0	1378.71	0	2	2	0	2	728	739
									GHVFEESQVAGTPMFVVK	95.0	####	25.0	1977.97	0	2	1	0	2	768	785

Elongation factor Tu, mitochondrial	EFTU_HUMAN	TUFM	49.52	100.0	3	3	17	5.31	TTLTAAITK	95.0	33.0	25.0	919.55	0	2	0	0	2	71	79
									ELLTEFGYK	95.0	40.0	25.0	1099.57	0	2	0	0	2	201	209
									FNLILR	95.0	47.4	25.0	775.48	0	13	0	0	2	406	411
Endoplasmic reticulum aminopeptidase 2	ERAP2_HUMAN	ERAP2	110.45	100.0	5	5	8	5.62	LGDGFEGFYK	95.0	31.2	25.0	1132.53	0	1	0	0	2	172	181
									ILAVTDFEPTQAR	95.0	56.5	25.0	1460.77	0	2	0	0	2	193	205
									ETSLLFDPK	95.0	36.4	25.0	1049.55	0	2	0	0	2	346	354
									ILYALSTSK	95.0	37.0	25.0	995.58	0	2	0	0	2	824	832
									MIISGTTAHFSSK	95.0	62.5	25.0	1395.69	0	1	0	0	2	896	908
Endoplasmic reticulum resident protein 29	ERP29_HUMAN	ERP29	28.98	100.0	5	5	10	23.80	GALPLDTVTFYK	95.0	60.0	25.0	1324.71	0	2	0	0	2	37	48
									FDTQYPYGEK	95.0	33.2	25.0	1247.56	0	2	0	0	2	60	69
									DGDFENPVPYTGAVK	95.0	76.0	25.0	1608.75	0	2	0	0	2	123	137
									ILDQGEDFPASEMTR	95.0	####	25.0	1724.78	0	2	0	0	2	209	223
									SLNILTAFQK	95.0	42.7	25.0	1134.65	0	2	0	0	2	244	253
Endoplasmic reticulum resident protein 44	ERP44_HUMAN	ERP44	46.95	100.0	3	3	4	8.87	ALADYIR	95.0	47.3	25.0	821.45	0	4	0	0	2	131	137
									DLAEITTLDR	95.0	56.3	25.0	1146.60	0	1	0	0	2	149	158
									NIIGYFEQK	95.0	42.7	25.0	1111.58	0	1	0	0	2	162	170
									QFVFDLHSGK	95.0	41.7	25.0	1177.60	0	0	2	0	2	346	355
Endoplasmin	ENPL_HUMAN	HSP90B1	92.45	100.0	16	17	110	20.40	LIINSLYK	95.0	48.4	25.0	963.59	0	6	0	0	2	88	95
									ELISNASDALDK	95.0	82.0	25.0	1275.64	0	85	0	0	2	103	114
									ELISNASDALDKIR	95.0	####	25.0	1544.83	0	4	2	0	2	103	116
									NLLHVTDTGVGMTR	95.0	77.4	25.0	1529.77	0	2	0	0	2	143	156
									SGTSEFLNK	95.0	58.1	25.0	982.48	0	4	0	0	2	169	177
									EEASDYLELDTIK	95.0	####	25.0	1525.73	0	11	0	0	2	253	265
									SILFVPTSAPR	95.0	55.9	25.0	1187.68	0	25	0	0	2	385	395
									GLFDEYGSK	95.0	37.1	25.0	1015.47	0	5	0	0	2	396	404
									VFITDDFHDMMPK	95.0	54.4	25.0	1627.71	0	1	0	0	2	416	428
									GVVDSDDLPLNVSR	95.0	97.9	25.0	1485.75	0	26	0	0	2	435	448
									LGVIEDHSNR	95.0	65.5	25.0	1139.58	0	4	2	0	2	494	503
									KEAESSPFVER	95.0	43.7	25.0	1278.63	0	3	0	0	2	547	557
									EAESSPFVER	95.0	41.7	25.0	1150.54	0	4	0	0	2	548	557
									DISTNYYASQK	95.0	57.5	25.0	1289.60	0	6	0	0	2	672	682
									KTFEINPR	95.0	27.6	25.0	1004.55	0	1	0	0	2	683	690
									TFEINPR	95.0	39.0	25.0	876.46	0	2	0	0	2	684	690
									SGYLLPDTK	95.0	42.8	25.0	993.53	0	4	0	0	2	725	733
									LSLNIDPDAK	95.0	51.5	25.0	1085.58	0	4	0	0	2	745	754
Enoyl-CoA hydratase domain-containing protein 1	ECHD1_HUMAN	ECHDC1	33.68	100.0	4	4	9	16.90	TLQQFPGGSIDLQK	95.0	40.0	25.0	1531.81	0	1	0	0	2	46	59
									EDNGIGILTLNNPSR	95.0	57.2	25.0	1612.83	0	4	0	0	2	60	74
									QFIQGPPEVIR	95.0	37.9	25.0	1283.71	0	2	0	0	2	251	261
									ELYLEEALQNER	95.0	66.9	25.0	1506.74	0	2	0	0	2	272	283
Enoyl-CoA hydratase, mitochondrial	ECHM_HUMAN	ECHS1	31.37	100.0	4	4	8	12.80	NNTVGLIQLNRPK	95.0	80.5	25.0	1466.84	0	3	0	0	2	44	56
									SLAMEMVLTGDR	95.0	63.7	25.0	1354.63	0	2	0	0	2	186	197
									LFYSTFATDDR	95.0	78.7	25.0	1335.62	0	2	0	0	2	262	272
									LFYSTFATDDRK	95.0	20.5	25.0	1463.72	0	0	1	0	2	262	273
Ephrin type-B receptor 2	EPHB2_HUMAN	EPHB2	117.48	99.5	2	2	8	2.84	SPTNTVTVQGLK	95.0	48.7	25.0	1244.68	0	3	0	0	2	488	499
									AGAIYVFQVR	95.0	50.4	25.0	1123.63	0	5	0	0	2	500	509
									VSDFGLSR	95.0	45.1	25.0	880.45	0	2	0	0	2	762	769
Epidermal growth factor receptor	EGFR_HUMAN	EGFR	134.26	100.0	6	6	80	5.12	NYDLSFLK	95.0	45.3	25.0	999.51	0	13	0	0	2	73	80
									IPLENLQIIR	95.0	81.3	25.0	1208.74	0	47	0	0	2	99	108
									NLQEILHGAVR	95.0	55.7	25.0	1249.70	0	2	0	0	2	139	149
									EISDGDVIISGNK	95.0	53.8	25.0	1346.68	0	6	0	0	2	455	467
									VLGSGAFGTVYK	95.0	64.7	25.0	1198.65	0	10	0	0	2	717	728

									GMNYLEDR	95.0	34.7	25.0	1013.44	0	2	0	0	2	824	831
Epidermal growth factor receptor substrate 15	EPS15_HUMAN	EPS15	98.64	100.0	4	4	8	5.13	SGLPDLILGK	95.0	28.6	25.0	1012.60	0	1	0	0	2	46	55
									LPVDILGR	95.0	44.8	25.0	882.54	0	4	0	0	2	160	167
									NIIGSSPVADFSAIK	95.0	30.0	25.0	1518.82	0	1	0	0	2	319	333
									TSEVQDLQDEVQR	95.0	72.0	25.0	1546.73	0	2	0	0	2	367	379
Epidermal growth factor receptor substrate 15-like 1	EP15R_HUMAN	EPS15L1	94.24	100.0	3	3	13	3.36	VGASEAALFLK	95.0	71.0	25.0	1105.63	0	3	0	0	2	34	44
									SGLSDIILGK	95.0	53.6	25.0	1002.58	0	4	0	0	2	46	55
									LPLDVLGR	95.0	37.8	25.0	882.54	0	6	0	0	2	159	166
Epiplakin	EPIPL_HUMAN	EPPK1	553.07	100.0	5	5	6	2.11	APGSGLALLPLK	94.8	26.5	25.0	1136.70	0	1	0	0	2	196	207
									LAAVDVSAR	95.0	28.1	25.0	901.51	0	1	0	0	2	241	249
									LLEAQIATGGVIDPVHSHR	95.0	43.9	25.0	2013.09	0	0	1	0	2	694	712
									VPVDVAYR	95.0	47.6	25.0	918.50	0	6	0	0	2	713	720
									QVSARDLFR	95.0	27.3	25.0	1091.60	0	1	0	0	2	1502	1510
									GYFDEEMNR	95.0	32.4	25.0	1176.46	0	2	0	0	2	2341	2349
									VLADPSDDTK	95.0	47.3	25.0	1060.52	0	14	0	0	2	2350	2359
									GSAVHQLSEELR	95.0	45.6	25.0	1325.68	0	2	0	0	2	2396	2407
									EGQGEGETQEAAAAAAAAR	95.0	86.3	25.0	1787.82	0	1	0	0	2	2589	2607
ERO1-like protein alpha	ERO1A_HUMAN	ERO1L	54.38	100.0	3	3	15	7.26	LLESDYFR	95.0	54.3	25.0	1042.52	0	6	0	0	2	68	75
									LGAVDESLSEETQK	95.0	97.2	25.0	1505.73	0	6	0	0	2	137	150
									FDGILTEGEGPR	95.0	53.2	25.0	1290.63	0	3	0	0	2	288	299
ES1 protein homolog, mitochondrial	ES1_HUMAN	C21orf33	28.15	100.0	3	3	5	13.10	NLSTFAVDGK	95.0	38.2	25.0	1051.54	0	1	0	0	2	142	151
									GVEVTVGHEQEEGGK	95.0	47.2	25.0	1554.74	0	1	0	0	2	189	203
									EVVEAHVDQK	95.0	48.9	25.0	1153.58	0	3	0	0	2	224	233
Eukaryotic initiation factor 4A-I	IF4A1_HUMAN	EIF4A1	46.14	100.0	14	16	215	34.00	GYDVIAQAQSGTGK	95.0	####	25.0	1394.69	0	32	0	0	2	69	82
									ATQALVLAPTR	95.0	66.8	25.0	1140.67	0	5	0	0	2	100	110
									ELAQQIQK	95.0	32.3	25.0	957.54	0	12	0	0	2	111	118
									LQMEAPHIIVGTPGR	95.0	54.4	25.0	1634.87	0	6	23	0	2	147	161
									VFDMLNR	95.0	39.4	25.0	910.45	0	12	0	0	2	162	168
									MFVLDEADEMLSR	95.0	95.8	25.0	1587.70	0	36	0	0	2	178	190
									DQIYDIFQK	95.0	56.9	25.0	1169.58	0	20	0	0	2	194	202
									KEELTLEGIR	95.0	51.5	25.0	1187.66	0	6	1	0	2	238	247
									EELTLEGIR	95.0	43.2	25.0	1059.57	0	4	0	0	2	239	247
									QFYINVER	95.0	37.2	25.0	1068.55	0	4	0	0	2	248	255
									DFTVSAMHGDMDQK	95.0	54.0	25.0	1613.66	0	11	0	0	2	296	309
									VLITTDLLAR	95.0	60.4	25.0	1114.68	0	34	0	0	2	325	334
									ENYIHR	95.0	37.6	25.0	831.41	0	6	0	0	2	354	359
									GVAINMVTEEDKR	95.0	51.2	25.0	1477.73	0	3	0	0	2	370	382
Eukaryotic initiation factor 4A-II	IF4A2_HUMAN	EIF4A2	46.39	100.0	6	7	20	33.90	GYDVIAQAQSGTGK	95.0	####	25.0	1394.69	0	32	0	0	2	70	83
									ETQALVLAPTR	95.0	52.1	25.0	1198.68	0	3	0	0	2	101	111
									ELAQQIQK	95.0	32.3	25.0	957.54	0	12	0	0	2	112	119
									LQAEAPHIVVGTPGR	95.0	80.0	25.0	1544.85	0	4	0	0	2	148	162
									VFDMLNR	95.0	39.4	25.0	910.45	0	12	0	0	2	163	169
									MFVLDEADEMLSR	95.0	95.8	25.0	1587.70	0	36	0	0	2	179	191
									DQIYEIFQK	95.0	44.7	25.0	1183.60	0	3	0	0	2	195	203
									KEELTLEGIK	95.0	49.1	25.0	1159.66	0	3	2	0	2	239	248
									QFYINVER	95.0	37.2	25.0	1068.55	0	4	0	0	2	249	256
									DFTVSALHGDMDQK	95.0	58.4	25.0	1579.71	0	3	0	0	2	297	310
									VLITTDLLAR	95.0	60.4	25.0	1114.68	0	34	0	0	2	326	335
									ENYIHR	95.0	37.6	25.0	831.41	0	6	0	0	2	355	360
									GVAINFVTEEDKR	95.0	80.8	25.0	1477.76	0	2	0	0	2	371	383
Eukaryotic initiation factor	IF4A3_HUMAN	EIF4A3	46.85	100.0	7	7	24	16.80	DVIAQSQSGTGK	95.0	59.0	25.0	1190.60	0	4	0	0	2	77	88

4A-III									ETQALILAPTR	95.0	53.6	25.0	1212.69	0	7	0	0	2	106	116
									KLDYGQHVVAGTPGR	95.0	29.5	25.0	1597.84	0	0	4	0	2	152	166
									MLVLDEADEMLNK	95.0	65.5	25.0	1552.72	0	4	0	0	2	183	195
									RDELTLEGIK	95.0	36.1	25.0	1173.65	0	2	0	0	2	243	252
									DELTLEGIK	95.0	27.0	25.0	1017.55	0	1	0	0	2	244	252
									QFFVAVER	95.0	33.7	25.0	995.53	0	2	0	0	2	253	260
Eukaryotic peptide chain release factor subunit 1	ERF1_HUMAN	ETF1	49.01	100.0	5	5	36	11.70	LSVLGAITSVQQR	95.0	72.4	25.0	1371.80	0	14	0	0	2	69	81
									FTVDLPK	95.0	41.7	25.0	819.46	0	3	0	0	2	172	178
									YFDEISQDTGK	95.0	70.6	25.0	1302.59	0	6	0	0	2	290	300
									ILYLTPEQEK	95.0	44.8	25.0	1233.67	0	3	0	0	2	343	352
									GFGGIGGILR	95.0	46.0	25.0	946.55	0	10	0	0	2	405	414
Eukaryotic translation elongation factor 1 epsilon-1	MCA3_HUMAN	EEF1E1	19.79	100.0	3	3	9	17.20	EYLLGSTAEEK	95.0	45.5	25.0	1239.61	0	3	0	0	2	58	68
									DLNSYLEDK	95.0	38.0	25.0	1096.52	0	2	0	0	2	97	105
									QHLSSVVFIK	95.0	28.9	25.0	1157.67	0	0	4	0	2	157	166
Eukaryotic translation initiation factor 2 subunit 1	IF2A_HUMAN	EIF2S1	36.09	100.0	9	9	35	28.90	TVYSILR	95.0	33.8	25.0	851.50	0	3	0	0	2	107	113
									HVAEVLEYTK	95.0	27.7	25.0	1188.63	0	1	0	0	2	114	123
									DEQLESLFQR	95.0	57.3	25.0	1264.62	0	2	0	0	2	124	133
									RPGYGAYDAFK	95.0	32.0	25.0	1244.61	0	2	0	0	2	144	154
									RLTPQAVK	95.0	32.7	25.0	912.56	0	1	0	0	2	183	190
									INLIAPPR	95.0	37.8	25.0	893.56	0	5	0	0	2	227	234
									TEGLSVLSQAMAVIK	95.0	62.8	25.0	1562.85	0	5	0	0	2	245	259
									GVFNVQMEPK	95.0	50.7	25.0	1164.57	0	5	0	0	2	267	276
									VVTDTDETELAR	95.0	96.3	25.0	1348.66	0	11	0	0	2	277	288
Eukaryotic translation initiation factor 2 subunit 2	IF2B_HUMAN	EIF2S2	37.77	100.0	3	3	10	12.80	EVEPEPTEDKDLEADEEDTR	95.0	50.8	25.0	2346.01	0	0	2	0	2	43	62
									IFDIDEAEEGVK	95.0	78.3	25.0	1364.66	0	3	0	0	2	88	99
									DYTYEELLNR	95.0	48.0	25.0	1315.62	0	5	0	0	2	167	176
Eukaryotic translation initiation factor 2 subunit 3	IF2G_HUMAN	EIF2S3	51.09	100.0	7	8	27	16.30	LTPLSHEVISR	95.0	48.4	25.0	1251.71	0	3	0	0	2	28	38
									AISGVHTVR	95.0	55.0	25.0	939.54	0	5	0	0	2	60	68
									HILILQNK	95.0	37.2	25.0	978.61	0	2	0	0	2	184	191
									GGVAGGSILK	95.0	44.9	25.0	858.50	0	3	0	0	2	276	285
									VGQEIEVRPGIVSK	95.0	51.2	25.0	1510.86	0	6	2	0	2	290	303
									IVLTNPVCTEVGEK	95.0	57.7	25.0	1558.81	0	2	0	0	2	427	440
									GVTIKPTVDDD	95.0	53.5	25.0	1159.58	0	4	0	0	2	462	472
Eukaryotic translation initiation factor 2A	EIF2A_HUMAN	EIF2A	64.97	100.0	4	4	7	8.03	VNIISVTNK	95.0	43.7	25.0	987.58	0	2	0	0	2	59	67
									GLLHSFDLLK	95.0	20.9	25.0	1142.66	0	0	1	0	2	68	77
									INDFVLSPGPQPYK	95.0	35.8	25.0	1574.82	0	1	0	0	2	170	183
									ATAVLVIASTDVDK	95.0	65.2	25.0	1402.78	0	3	0	0	2	232	245
Eukaryotic translation initiation factor 3 subunit A	EIF3A_HUMAN	EIF3A	166.56	100.0	10	10	25	8.10	PAYFQRPENALK	95.0	25.1	25.0	1433.75	0	0	2	0	1	2	13
									ANEFLEVGK	95.0	33.9	25.0	1006.52	0	2	0	0	2	15	23
									QPALDVLYDVMK	95.0	40.5	25.0	1407.72	0	3	0	0	2	25	36
									LLLTPWVK	95.0	26.9	25.0	969.61	0	1	0	0	2	144	151
									SGNALFHASTLHR	95.0	56.3	25.0	1410.72	0	0	2	0	2	286	298
									NLTQDEMQR	95.0	36.5	25.0	1150.52	0	1	0	0	2	309	317
									LLDMDGIIVEK	95.0	54.2	25.0	1261.67	0	2	0	0	2	341	351
									EDAPIGPHLQSMPSEQIR	95.0	39.9	25.0	2020.98	0	0	4	0	2	503	520
									NQLTAMSSVLAK	95.0	72.9	25.0	1278.67	0	4	0	0	2	521	532
									LESLNIQR	95.0	56.1	25.0	972.55	0	4	0	0	2	582	589
Eukaryotic translation initiation factor 3 subunit B	EIF3B_HUMAN	EIF3B	92.46	100.0	12	14	84	14.10	AQAVSEDAGGNEGR	95.0	####	25.0	1360.61	0	20	0	0	2	121	134
									ITNDFYPEEDGK	95.0	72.5	25.0	1427.63	0	8	0	0	2	217	228
									ITNDFYPEEDGKTK	95.0	36.4	25.0	1656.78	0	1	0	0	2	217	230
									VNLFTDFDK	95.0	44.1	25.0	1098.55	0	14	0	0	2	263	271

									DQYSVIFESGDR	95.0	51.1	25.0	1415.64	0	2	0	0	2	304	315
									DPVSIEER	95.0	30.8	25.0	944.47	0	1	0	0	2	325	332
									GTYLATFHQR	95.0	51.1	25.0	1193.61	0	4	1	0	2	346	355
									VTLMQLPTR	95.0	50.6	25.0	1074.60	0	8	0	0	2	493	501
									QVPVDVVEMK	95.0	40.6	25.0	1159.60	0	4	0	0	2	553	562
									FAVLHGEAPR	95.0	32.5	25.0	1096.59	0	0	6	0	2	577	586
									ISVSFYHVK	95.0	35.9	25.0	1079.59	0	5	3	0	2	587	595
									MAQELYMEQK	95.0	51.5	25.0	1302.57	0	7	0	0	2	763	772
Eukaryotic translation initiation factor 3 subunit C	EIF3C_HUMAN	EIF3C	105.33	100.0	10	11	46	11.80	FEELTNLIR	95.0	63.0	25.0	1134.62	0	13	0	0	2	57	65
									DFESHITSYK	95.0	28.7	25.0	1226.57	0	1	0	0	2	151	160
									GTEITHAVVIK	95.0	45.7	25.0	1167.67	0	2	0	0	2	321	331
									ILHTYYK	95.0	32.3	25.0	937.51	0	1	0	0	2	507	513
									SEQDQAENEGEDSAVLMER	95.0	####	25.0	2152.89	0	2	2	0	2	532	550
									DAHNALLDIQSSGR	95.0	93.7	25.0	1496.75	0	4	0	0	2	628	641
									AKELLGQGLLLR	95.0	42.4	25.0	1310.82	0	0	2	0	2	642	653
									ELLGQGLLLR	95.0	61.6	25.0	1111.68	0	9	0	0	2	644	653
									TEPTAQQNLALQLAEK	95.0	####	25.0	1754.93	0	6	0	0	2	847	862
									LGSLVENNER	95.0	58.8	25.0	1130.58	0	4	0	0	2	863	872
Eukaryotic translation initiation factor 3 subunit E	EIF3E_HUMAN	EIF3E	52.20	100.0	7	8	18	17.80	NLYSDDIPHALR	95.0	62.0	25.0	1413.71	0	2	3	0	2	60	71
									QLQAETEPIVK	95.0	43.3	25.0	1255.69	0	4	0	0	2	83	93
									MFEDPETTR	95.0	38.4	25.0	1141.48	0	1	0	0	2	94	102
									MLFDYLADK	95.0	43.6	25.0	1131.54	0	2	0	0	2	112	120
									ETIDNNSVSSPLQSLQQR	95.0	96.1	25.0	2016.00	0	3	0	0	2	194	211
									YLTTAVITNK	95.0	39.2	25.0	1123.64	0	2	0	0	2	256	265
									LNMTPEEAER	95.0	30.9	25.0	1205.55	0	1	0	0	2	360	369
Eukaryotic translation initiation factor 3 subunit F	EIF3F_HUMAN	EIF3F	37.55	100.0	6	6	13	21.80	VIGTLLGTVDK	95.0	70.8	25.0	1115.67	0	6	0	0	2	116	126
									EAPNPIHLTVDTSLQNGR	95.0	40.3	25.0	1962.00	0	0	1	0	2	193	210
									AYVSTLMGVPGR	95.0	49.5	25.0	1266.65	0	2	0	0	2	215	226
									VIGLSSDLQQVGGASAR	95.0	23.3	25.0	1657.89	0	0	1	0	2	262	278
									VSADNTVGR	95.0	57.1	25.0	918.46	0	1	0	0	2	298	306
									FLMSLVNQVPK	95.0	82.0	25.0	1291.71	0	2	0	0	2	307	317
Eukaryotic translation initiation factor 3 subunit G	EIF3G_HUMAN	EIF3G	35.59	100.0	3	3	17	11.20	ELAEQLGLSTGEK	95.0	72.3	25.0	1374.71	0	13	0	0	2	181	193
									LPGELEPVQATQNK	95.0	55.8	25.0	1523.81	0	2	0	0	2	196	209
									VTNLSEDTR	95.0	30.3	25.0	1034.51	0	2	0	0	2	243	251
Eukaryotic translation initiation factor 3 subunit H	EIF3H_HUMAN	EIF3H	39.91	100.0	7	8	15	22.70	EGTGSTATSSSSTAGAAGK	95.0	63.9	25.0	1627.74	0	3	0	0	2	6	24
									SAVADKHELLSLASSNHLGK	95.0	75.7	25.0	2077.10	0	0	2	2	2	222	241
									HELLSLASSNHLGK	95.0	53.6	25.0	1505.81	0	0	2	0	2	228	241
									VDEMSQDIVK	95.0	56.8	25.0	1179.56	0	2	0	0	2	250	259
									LFKPPQPPAR	95.0	20.1	25.0	1150.67	0	0	1	0	2	304	313
									EFTAQNLGK	95.0	38.0	25.0	1007.52	0	1	0	0	2	332	340
									LFMAQALQEYNN	95.0	35.4	25.0	1457.67	0	2	0	0	2	341	352
Eukaryotic translation initiation factor 3 subunit I	EIF3I_HUMAN	EIF3I	36.48	100.0	6	6	20	21.20	EGDLLFTVAK	95.0	50.8	25.0	1092.59	0	11	0	0	2	21	30
									DPSQIDNNEPYMK	95.0	29.4	25.0	1566.67	0	2	0	0	2	129	141
									SGEVLVNVK	95.0	37.8	25.0	944.54	0	1	0	0	2	177	185
									QINDIQLSR	95.0	69.7	25.0	1086.59	0	2	0	0	2	190	198
									GHFGPINSVAFHPDGK	95.0	41.0	25.0	1679.83	0	0	2	0	2	283	298
									SYSSGGEDGYVR	95.0	49.1	25.0	1276.54	0	2	0	0	2	299	310
Eukaryotic translation initiation factor 3 subunit J	EIF3J_HUMAN	EIF3J	29.05	100.0	3	4	7	12.40	VLTPEEQLADKLR	95.0	58.8	25.0	1511.84	0	2	2	0	2	107	119
									LQEESDLELAK	95.0	50.3	25.0	1274.65	0	2	0	0	2	123	133
									DDFTEFGK	95.0	30.1	25.0	958.42	0	1	0	0	2	154	161
Eukaryotic translation	EIF3L_HUMAN	EIF3L	66.71	100.0	8	8	29	10.80	TVSDLIDQK	95.0	29.2	25.0	1018.54	0	1	0	0	2	62	70

initiation factor 3 subunit L									VYELQASR	95.0	35.5	25.0	965.51	0	3	0	0	2	71	78
									VSGGPSLEQR	95.0	65.2	25.0	1029.53	0	6	0	0	2	144	153
									KSEEEIDFLR	95.0	53.0	25.0	1265.64	0	4	0	0	2	207	216
									SEEEIDFLR	95.0	55.7	25.0	1137.54	0	5	0	0	2	208	216
									VLENIELNK	95.0	35.9	25.0	1071.60	0	1	0	0	2	293	301
									EPFLQQLK	95.0	35.7	25.0	1002.56	0	4	0	0	2	438	445
									YGDFFIR	95.0	46.6	25.0	917.45	0	5	0	0	2	539	545
Eukaryotic translation initiation factor 3 subunit M	EIF3M_HUMAN	EIF3M	42.49	100.0	3	4	11	11.00	LQLLSNLFHGMDK	95.0	77.2	25.0	1531.79	0	6	2	0	2	103	115
									DFIDSLGLLHEQNMAK	95.0	39.9	25.0	1846.90	0	1	0	0	2	261	276
									LLTFMGMAVENK	95.0	53.9	25.0	1385.68	0	2	0	0	2	279	290
Eukaryotic translation initiation factor 4 gamma 1	IF4G1_HUMAN	EIF4G1	175.48	100.0	15	17	51	9.38	DITEEIMSGAR	95.0	39.2	25.0	1237.57	0	2	0	0	2	191	201
									EAVGDLLDAFK	95.0	53.2	25.0	1177.61	0	1	0	0	2	525	535
									QVTQLAIDTEER	95.0	79.7	25.0	1402.72	0	2	0	0	2	782	793
									GVIDLIFEK	95.0	52.3	25.0	1033.59	0	11	0	0	2	796	804
									VPTTEKPTVTVNFR	95.0	47.1	25.0	1588.87	0	2	2	0	2	827	840
									EMDEAATAEER	95.0	30.3	25.0	1267.51	0	2	0	0	2	867	877
									LKEELEEAR	95.0	31.6	25.0	1116.59	0	2	0	0	2	880	888
									EAALPPVSPLK	95.0	46.9	25.0	1121.66	0	4	0	0	2	1224	1234
									AALSEEELEK	95.0	44.6	25.0	1118.56	0	1	0	0	2	1235	1244
									AALSEEELEKK	95.0	31.7	25.0	1246.65	0	0	2	0	2	1235	1245
									AIIEEYLHLNDMK	95.0	62.5	25.0	1604.80	0	4	0	0	2	1248	1260
									HGVESTLER	95.0	33.3	25.0	1027.52	0	4	0	0	2	1281	1289
									VEYTLGEESEAPGQR	95.0	90.9	25.0	1664.78	0	8	2	0	2	1422	1436
									VDVAVLK	95.0	33.0	25.0	743.47	0	1	0	0	2	1499	1505
									SVTAFFK	95.0	27.2	25.0	799.43	0	1	0	0	2	1581	1587
Eukaryotic translation initiation factor 4 gamma 2	IF4G2_HUMAN	EIF4G2	102.35	100.0	5	5	18	4.74	GVILLIVDK	95.0	38.3	25.0	969.63	0	4	0	0	2	113	121
									LQDEFENR	95.0	28.9	25.0	1050.49	0	1	0	0	2	171	178
									VIILSLDR	95.0	35.7	25.0	928.58	0	1	0	0	2	585	592
									ASSLISLLK	95.0	43.2	25.0	931.58	0	6	0	0	2	600	608
									LEVDIPLVK	95.0	42.0	25.0	1025.62	0	6	0	0	2	632	640
Eukaryotic translation initiation factor 5	IF5_HUMAN	EIF5	49.21	100.0	5	5	20	12.30	TVIVNMVDVAK	95.0	48.7	25.0	1204.66	0	3	0	0	2	34	44
									LQDMLDGFIK	95.0	53.0	25.0	1195.60	0	5	0	0	2	85	94
									VLTLSDDLER	95.0	45.9	25.0	1160.62	0	7	0	0	2	225	234
									VNILFDFVK	95.0	36.1	25.0	1094.62	0	3	0	0	2	240	248
									SDNKDDDIDIDAI	95.0	29.0	25.0	1448.64	0	2	0	0	2	419	431
Eukaryotic translation initiation factor 5A-1	IF5A1_HUMAN	EIF5A	16.81	100.0	6	8	57	24.00	NGFVVLK	95.0	56.0	25.0	776.47	0	18	0	0	2	28	34
									VHLVGIDIFTGK	95.0	45.1	25.0	1298.75	0	3	0	0	2	56	67
									VHLVGIDIFTGKK	95.0	48.2	25.0	1426.84	0	2	2	0	2	56	68
									EDLRLPEGDLGK	95.0	41.9	25.0	1341.70	0	10	2	0	2	110	121
									LPEGDLGK	95.0	47.8	25.0	828.45	0	19	0	0	2	114	121
									LPEGDLGKEIEQK	95.0	60.6	25.0	1455.77	0	1	0	0	2	114	126
Eukaryotic translation initiation factor 5B	IF2P_HUMAN	EIF5B	138.81	100.0	6	7	17	6.07	SPDSDVAATLKK	95.0	35.8	25.0	1231.65	0	0	2	0	2	767	778
									DELIHELK	95.0	29.5	25.0	996.54	0	1	0	0	2	961	968
									TSEVPYAGINIGPVHK	95.0	77.7	25.0	1681.89	0	4	2	0	2	1000	1015
									DAQEMADSLGVR	95.0	46.7	25.0	1307.59	0	2	0	0	2	1044	1055
									DPIVMGVTVEAGQVK	95.0	97.6	25.0	1558.81	0	4	0	0	2	1106	1120
									HFEATDILVSK	95.0	50.2	25.0	1259.66	0	2	0	0	2	1175	1185
Eukaryotic translation initiation factor 6	IF6_HUMAN	EIF6	26.58	100.0	3	5	16	15.90	HGLLVPNNTTDQELQHIR	95.0	77.7	25.0	2085.08	0	2	5	2	2	68	85
									NSLPDTVQIR	95.0	28.6	25.0	1142.62	0	1	0	0	2	86	95
									ETEEILADVLK	95.0	74.5	25.0	1259.67	0	6	0	0	2	124	134
Exosome complex	EXOS7_HUMAN	EXOSC7	31.82	100.0	4	4	7	15.50	VYIVHGVQEDLR	95.0	68.9	25.0	1427.76	0	2	0	0	2	12	23

exonuclease RRP42									LGHTDILVGVK	95.0	34.0	25.0	1151.68	0	2	0	0	2	53	63
									GGDDLGTEIANTLYR	95.0	56.4	25.0	1594.77	0	2	0	0	2	97	111
									AALFNTR	95.0	33.8	25.0	792.44	0	1	0	0	2	158	164
Exosome complex exonuclease RRP44	RRP44_HUMAN	DIS3	108.99	100.0	7	8	23	8.46	SLTANPELIDR	95.0	40.3	25.0	1228.65	0	5	0	0	2	200	210
									SGTYLQGTFR	95.0	33.3	25.0	1129.56	0	1	0	0	2	243	252
									AVHEDIVAVELLPK	95.0	34.5	25.0	1532.87	0	1	0	0	2	286	299
									ASLTYAEAQLR	95.0	34.3	25.0	1222.64	0	1	0	0	2	586	596
									IDSANMNDDITTSLR	95.0	78.0	25.0	1681.77	0	2	0	0	2	597	611
									NAIVVLIPK	95.0	51.5	25.0	966.63	0	4	0	0	2	858	866
									IEDTVFHVFDK	95.0	60.6	25.0	1349.67	0	5	4	0	2	896	906
Exportin-1	XPO1_HUMAN	XPO1	123.37	100.0	12	15	59	12.50	PAIMTMLADHAAR	95.0	22.0	25.0	1429.69	0	0	1	0	1	2	14
									QLLDFSQK	95.0	29.7	25.0	978.53	0	1	0	0	2	15	22
									MAQEVLTHLK	95.0	54.2	25.0	1185.63	0	5	4	0	2	45	54
									VDTILEFSQNMNTK	95.0	88.7	25.0	1655.79	0	14	1	0	2	63	76
									KYVVGLIIK	95.0	41.7	25.0	1032.68	0	2	0	0	2	104	112
									MAKPEEVLVVENDQGEVVR	95.0	26.6	25.0	2157.09	0	0	1	0	2	424	442
									FLVTVIK	95.0	39.5	25.0	819.53	0	6	0	0	2	516	522
									NVDILKDPETVK	95.0	49.8	25.0	1370.75	0	6	0	0	2	675	686
									QLGSILK	95.0	43.7	25.0	758.48	0	2	0	0	2	687	693
									EPEVLSTMAIIVNK	95.0	78.0	25.0	1559.84	0	8	0	0	2	797	810
									DFEEYPEHR	95.0	28.8	25.0	1221.52	0	2	0	0	2	837	845
									SAFPHLQDAQVK	95.0	59.3	25.0	1340.70	0	5	1	0	2	984	995
Exportin-2	XPO2_HUMAN	CSE1L	110.40	100.0	19	20	147	18.30	TLDPDPAIR	95.0	26.9	25.0	997.53	0	1	0	0	2	18	26
									QLSDAISIIGR	95.0	77.3	25.0	1172.66	0	7	0	0	2	110	120
									SQICDNAALYAQK	95.0	72.1	25.0	1481.71	0	1	0	0	2	269	281
									YDEEFQR	95.0	44.8	25.0	986.42	0	4	0	0	2	282	288
									VIVPNMEFR	95.0	41.7	25.0	1120.58	0	6	0	0	2	347	355
									DLEGSDIDTR	95.0	47.4	25.0	1120.51	0	9	0	0	2	373	382
									HKDAAIYLVTSLASK	95.0	43.6	25.0	1616.90	0	0	1	0	2	426	440
									DAAIYLVTSLASK	95.0	52.9	25.0	1351.75	0	2	0	0	2	428	440
									SANVNEFPVLK	95.0	53.1	25.0	1217.65	0	13	0	0	2	471	481
									ALTLPGSSENEYIMK	95.0	84.3	25.0	1668.82	0	8	0	0	2	560	574
									TGNIPALVR	95.0	56.3	25.0	940.56	0	15	0	0	2	698	706
									LLQAFLER	95.0	56.8	25.0	989.58	0	54	0	0	2	707	714
									GSNTIASAAADK	95.0	67.2	25.0	1105.55	0	4	0	0	2	715	726
									IPGLLGVFQK	95.0	27.9	25.0	1071.66	0	2	0	0	2	727	736
									MFGMVLEK	95.0	29.7	25.0	986.47	0	1	0	0	2	817	824
									IIIPEIQK	95.0	30.7	25.0	953.60	0	9	0	0	2	825	832
									KEHDPVGQMVNNPK	95.0	20.6	25.0	1608.78	0	0	1	0	2	912	925
									EHDPVGQMVNNPK	95.0	60.0	25.0	1480.69	0	7	1	0	2	913	925
									IHLAQSLHK	95.0	27.6	25.0	1046.61	0	1	0	0	2	926	934
Exportin-4	XPO4_HUMAN	XPO4	130.13	100.0	9	9	15	10.30	VLMAPPSMVNNEQR	95.0	38.5	25.0	1617.77	0	1	0	0	2	21	34
									ENLNAQMSSVFQR	95.0	74.0	25.0	1539.72	0	2	0	0	2	213	225
									VMELFFTVHR	95.0	46.6	25.0	1294.66	0	2	0	0	2	274	283
									HQQQLLASPGSSTVDNK	95.0	32.6	25.0	1809.91	0	0	2	0	2	514	530
									ADLTHLLSPQMGK	95.0	45.5	25.0	1426.74	0	2	0	0	2	624	636
									SPPLNFLSSPVQR	95.0	74.3	25.0	1441.78	0	2	0	0	2	737	749
									ALVLGGFAHMDTETK	95.0	60.4	25.0	1605.79	0	2	0	0	2	754	768
									AQETDSPLFLATR	95.0	71.2	25.0	1448.74	0	1	0	0	2	1039	1051
									LVFDMLVLQK	95.0	27.1	25.0	1221.69	0	1	0	0	2	1056	1065
Exportin-5	XPO5_HUMAN	XPO5	136.30	100.0	6	6	15	6.06	AVTVMMDPNSTQR	95.0	37.4	25.0	1481.67	0	1	0	0	2	16	28

									DIQQTLTQNMER	95.0	51.9	25.0	1492.71	0	2	0	0	2	177	188
									DPLLLAIIPK	95.0	41.4	25.0	1092.70	0	6	0	0	2	387	396
									QLLSNELLLTQMEK	95.0	93.3	25.0	1675.89	0	1	0	0	2	632	645
									THNTLYAPEMLAK	95.0	20.0	25.0	1504.75	0	0	2	0	2	782	794
									AVMEQIPEIQK	95.0	46.4	25.0	1301.68	0	3	0	0	2	1113	1123
Exportin-7	XPO7_HUMAN	XPO7	123.89	100.0	4	4	6	3.50	TNNPLPLEQR	95.0	41.5	25.0	1181.63	0	2	0	0	2	74	83
									SNYQLGELVK	95.0	28.0	25.0	1150.61	0	1	0	0	2	339	348
									TTFYTALGR	95.0	32.0	25.0	1029.54	0	1	0	0	2	666	674
									ILTLGEVPK	95.0	32.8	25.0	969.60	0	2	0	0	2	813	821
Exportin-T	XPOT_HUMAN	XPOT	109.95	100.0	10	10	22	11.00	YSELTTVQQQLIR	95.0	62.8	25.0	1578.85	0	4	0	0	2	68	80
									GVDLYLR	95.0	33.9	25.0	835.47	0	2	0	0	2	138	144
									ILMAIDSELVDR	95.0	71.3	25.0	1390.72	0	2	0	0	2	145	156
									DVVHTSEEAR	95.0	30.9	25.0	1142.54	0	1	0	0	2	157	166
									NAQEALQAIETK	95.0	71.1	25.0	1315.69	0	4	0	0	2	317	328
									ANVEAIMLAVMK	95.0	85.4	25.0	1321.69	0	2	0	0	2	370	381
									LAQVSPELLLASVR	95.0	41.0	25.0	1495.88	0	2	0	0	2	415	428
									FMEVEVAIR	95.0	57.4	25.0	1109.57	0	2	0	0	2	443	451
									ASALQDMMR	95.0	37.4	25.0	1054.47	0	2	0	0	2	475	483
									TCFIILSK	95.0	41.2	25.0	981.54	0	1	0	0	2	844	851
Extracellular matrix protein 1	ECM1_HUMAN	ECM1	60.66	100.0	4	4	17	8.70	LLPAQLPAEK	95.0	30.0	25.0	1079.65	0	2	0	0	2	91	100
									EVGPPLPQEAVPLQK	95.0	58.5	25.0	1601.89	0	6	0	0	2	101	115
									FCEAEFSVK	95.0	30.7	25.0	1116.50	0	1	0	0	2	244	252
									NVALVSGDTENAK	95.0	95.1	25.0	1317.66	0	8	0	0	2	506	518
Ezrin	EZRI_HUMAN	EZR	69.40	100.0	18	23	308	33.60	PKPINVR	95.0	37.8	25.0	823.51	0	1	0	0	1	2	8
									QLFDQVVK	95.0	47.4	25.0	976.55	0	10	0	0	2	28	35
									VSAQEVR	95.0	44.9	25.0	788.43	0	1	0	0	2	65	71
									KENPLQFK	94.6	26.4	25.0	1003.56	0	1	0	0	2	72	79
									ENPLQFK	95.0	46.2	25.0	875.46	0	2	0	0	2	73	79
									LFFLQVK	95.0	46.6	25.0	894.54	0	7	0	0	2	101	107
									SGYLSSER	95.0	58.0	25.0	898.43	0	27	0	0	2	144	151
									DNAMLEYLK	95.0	45.5	25.0	1112.53	0	18	0	0	2	185	193
									NISFNDKK	95.0	31.6	25.0	965.51	0	3	0	0	2	247	254
									FVIKPIDK	95.0	40.5	25.0	959.59	0	18	0	0	2	255	262
									FVIKPIDKK	95.0	29.4	25.0	1087.69	0	2	3	0	2	255	263
									KAPDFVFYAPR	95.0	55.3	25.0	1310.69	0	14	7	0	2	263	273
									APDFVFYAPR	95.0	75.6	25.0	1182.59	0	41	0	0	2	264	273
									RKPDTIEVQQMK	95.0	55.2	25.0	1488.78	0	21	54	0	2	295	306
									KPDTIEVQQMK	95.0	56.1	25.0	1332.68	0	17	2	0	2	296	306
									EKEELMLR	95.0	31.3	25.0	1063.55	0	4	0	0	2	343	350
									ELSEQIQR	95.0	55.7	25.0	1002.52	0	29	0	0	2	364	371
									ALQLEEER	95.0	48.0	25.0	987.51	0	40	0	0	2	372	379
									AQEEAERLEADR	95.0	39.2	25.0	1416.67	0	5	3	0	2	382	393
									SQEQLAAELAEYTAK	95.0	####	25.0	1651.82	0	27	8	0	2	413	427
									IALLEEAR	95.0	64.5	25.0	914.53	0	73	0	0	2	428	435
									AKEAQDDLVK	95.0	40.8	25.0	1116.59	0	5	2	0	2	449	458
									EAQDDLVK	95.0	39.7	25.0	917.46	0	4	0	0	2	451	458
									QLLTLSSELSQAR	95.0	94.3	25.0	1445.80	0	29	0	0	2	530	542
									RTHNDIIHNENMR	95.0	26.7	25.0	1665.79	0	0	0	2	2	547	559
									THNDIIHNENMR	95.0	68.3	25.0	1509.69	0	12	10	2	2	548	559
									QRIDEFEAL	95.0	31.1	25.0	1120.56	0	3	0	0	2	578	586
FACT complex subunit	SP16H_HUMAN	SUPT16H	119.90	100.0	8	8	37	8.12	GNENANGAPAITLLIR	95.0	56.9	25.0	1623.88	0	10	0	0	2	93	108

SPT16									AASITSEVFNK	95.0	71.1	25.0	1166.61	0	10	0	0	2	186	196
									VMEIVDADEK	95.0	43.0	25.0	1164.55	0	8	0	0	2	202	211
									NLGFGMGIEFR	95.0	37.2	25.0	1256.61	0	2	0	0	2	347	357
									ELAAQLNEEAK	95.0	63.8	25.0	1215.62	0	3	0	0	2	480	490
									IYIDK	95.0	28.8	25.0	651.37	1	0	0	0	2	529	533
									GDKVDILYNNIK	95.0	56.5	25.0	1391.75	0	1	0	0	2	694	705
									NFDMVIVYK	95.0	29.1	25.0	1144.57	0	2	0	0	2	854	862
FACT complex subunit SSRP1	SSRP1_HUMAN	SSRP1	81.06	100.0	6	6	18	8.32	LFLLPHK	95.0	36.2	25.0	867.55	0	1	0	0	2	242	248
									NMSGSLYEMVSR	95.0	72.5	25.0	1405.61	0	5	0	0	2	305	316
									ASSGLLYPLER	95.0	49.5	25.0	1205.65	0	3	0	0	2	347	357
									SFDFEIETK	95.0	39.9	25.0	1115.53	0	4	0	0	2	388	396
									QGTQYTFSSIER	95.0	57.5	25.0	1416.68	0	2	0	0	2	397	408
									LFDFVNAK	95.0	32.5	25.0	953.51	0	3	0	0	2	414	421
F-actin-capping protein subunit alpha-1	CAZA1_HUMAN	CAPZA1	32.91	100.0	4	5	37	14.70	LLLNNDNLLR	95.0	71.9	25.0	1197.70	0	4	0	0	2	38	47
									KEASDPQPEEADGGLK	95.0	39.3	25.0	1670.79	0	1	0	0	2	103	118
									EASDPQPEEADGGLK	95.0	70.7	25.0	1542.69	0	14	0	0	2	104	118
									DVQDSLTVSNEAQTAK	95.0	96.6	25.0	1705.82	0	16	2	0	2	211	226
F-actin-capping protein subunit beta	CAPZB_HUMAN	CAPZB	31.33	100.0	7	8	51	25.30	RLPPQQIEK	95.0	40.6	25.0	1108.65	0	13	0	0	2	15	23
									DYLLCDYNR	95.0	43.9	25.0	1231.54	0	2	0	0	2	58	66
									YDPPLEDGAMPSAR	95.0	70.6	25.0	1534.68	0	4	0	0	2	79	92
									KLEVEANNAFDQYR	95.0	####	25.0	1696.83	0	4	2	0	2	95	108
									LEVEANNAFDQYR	95.0	79.0	25.0	1568.73	0	2	0	0	2	96	108
									SGSGTMNLGGSLTR	95.0	87.5	25.0	1353.64	0	6	0	0	2	182	195
									STLNEIYFGK	95.0	62.4	25.0	1171.60	0	18	0	0	2	226	235
Far upstream element-binding protein 1	FUBP1_HUMAN	FUBP1	67.54	100.0	9	9	44	15.70	VPDGMVGFIIGR	95.0	60.9	25.0	1276.67	0	3	0	0	2	107	118
									IQIAPDSGGLPER	95.0	61.0	25.0	1352.72	0	13	0	0	2	134	146
									LLDQIVEK	95.0	27.0	25.0	957.56	0	1	0	0	2	163	170
									MVMIQDGPQNTGADKPLR	95.0	50.6	25.0	2002.97	0	0	2	0	2	219	236
									EMVLELIR	95.0	48.4	25.0	1018.56	0	7	0	0	2	249	256
									IGGNEGIDVPIPR	95.0	88.5	25.0	1336.72	0	7	0	0	2	272	284
									FAVGIVIGR	95.0	52.8	25.0	931.57	0	4	0	0	2	285	293
									IQFKPDDGTTPER	95.0	69.3	25.0	1503.74	0	2	0	0	2	309	321
									TGLIIGK	95.0	50.1	25.0	701.46	0	5	0	0	2	388	394
Far upstream element-binding protein 2	FUBP2_HUMAN	KHSRP	73.13	100.0	4	4	15	6.48	VPDGMVGLIIGR	95.0	34.7	25.0	1242.69	0	2	0	0	2	151	162
									VQISPDSGGLPER	95.0	53.0	25.0	1354.70	0	4	0	0	2	178	190
									IGGGIDVPVPR	95.0	61.3	25.0	1079.62	0	2	0	0	2	321	331
									IINDLLQSLR	95.0	70.1	25.0	1184.70	0	7	0	0	2	385	394
Farnesyl pyrophosphate synthase	FPPS_HUMAN	FDPS	48.26	100.0	5	7	21	12.40	QDFVQHFSQIVR	95.0	54.7	25.0	1503.77	0	2	5	0	2	81	92
									VLTEDEMGHPEIGDAIAR	95.0	66.2	25.0	1968.93	0	3	2	0	2	93	110
									LKEVLEYNAIGGK	95.0	51.2	25.0	1433.80	0	0	4	0	2	111	123
									EVLEYNAIGGK	95.0	57.2	25.0	1192.62	0	3	0	0	2	113	123
									IGTDIQDNK	95.0	32.3	25.0	1003.51	0	2	0	0	2	324	332
FAS-associated factor 1	FAF1_HUMAN	FAF1	73.94	100.0	4	4	4	5.69	TGDVEDSTVLK	95.0	38.7	25.0	1163.58	0	1	0	0	2	147	157
									LSLEADR	95.0	28.8	25.0	803.43	0	1	0	0	2	517	523
									LSLEQALPPEPK	94.6	26.4	25.0	1321.74	0	1	0	0	2	555	566
									LLSTFPR	95.0	32.2	25.0	833.49	0	1	0	0	2	615	621
Fascin	FSCN1_HUMAN	FSCN1	54.51	100.0	13	18	332	24.50	YLTAEAFGFK	95.0	56.7	25.0	1146.58	0	32	0	0	2	23	32
									VNASASSLK	95.0	47.6	25.0	876.48	0	21	0	0	2	33	41
									VNASASSLKK	95.0	29.8	25.0	1004.57	0	4	0	0	2	33	42
									FLIVAHDDGR	95.0	59.9	25.0	1142.60	0	54	33	0	2	91	100
									WSLQSEAHR	95.0	50.3	25.0	1113.54	0	2	2	0	2	101	109

									YFGGTEDR	95.0	55.3	25.0	944.41	0	19	0	0	2	111	118
									YSVQTADHR	95.0	52.0	25.0	1076.51	0	64	10	0	2	186	194
									LVARPEPATGYTLEFR	95.0	47.6	25.0	1819.97	0	0	2	0	2	202	217
									YLAPSGPSGTLK	95.0	55.3	25.0	1190.64	0	3	0	0	2	230	241
									YWTLTATGGVQSTASSK	95.0	88.5	25.0	1757.87	0	2	0	0	2	314	330
									LINRPIIVFR	95.0	44.0	25.0	1240.79	0	20	45	0	2	380	389
									KVTGTLDANR	95.0	56.8	25.0	1074.59	0	8	1	0	2	399	408
									VTGTLDANR	95.0	50.9	25.0	946.50	0	10	0	0	2	400	408
Fatty acid synthase	FAS_HUMAN	FASN	273.41	100.0	18	18	102	8.04	AGLYGLPR	95.0	39.8	25.0	846.48	0	2	0	0	2	42	49
									FDASFFGVHPK	95.0	23.9	25.0	1251.62	0	0	1	0	2	60	70
									SEGVVAVLLTK	95.0	43.3	25.0	1115.67	0	3	0	0	2	225	235
									VGDPQELNGITR	95.0	63.6	25.0	1298.67	0	3	0	0	2	299	310
									LQVVDQPLPVR	95.0	60.9	25.0	1263.74	0	15	0	0	2	374	384
									SDEAVKPFGLK	95.0	31.7	25.0	1190.64	0	0	6	0	2	523	533
									GTPLISPLIK	95.0	27.8	25.0	1038.66	0	1	0	0	2	826	835
									TGTVSLEVR	95.0	68.6	25.0	961.53	0	7	0	0	2	928	936
									AQVADVVVSR	95.0	46.2	25.0	1043.58	0	1	0	0	2	1073	1082
									GLVQALQTK	95.0	54.2	25.0	957.57	0	6	0	0	2	1143	1151
									MVVPGLDGAQIPR	95.0	27.9	25.0	1368.73	0	1	0	0	2	1159	1171
									VVEVLAGHGHLYSR	95.0	18.9	25.0	1536.83	0	0	0	1	2	1242	1255
									GDLSSIR	95.0	31.0	25.0	747.40	0	2	0	0	2	1539	1545
									FPQLDSTSFANSR	95.0	68.1	25.0	1469.70	0	4	0	0	2	1712	1724
									GNAGQSNYGFANSAMER	95.0	70.5	25.0	1789.76	0	1	0	0	2	2027	2043
									EDGLAQQQTQLNLR	95.0	82.5	25.0	1613.82	0	6	0	0	2	2207	2220
									SLLVNPEGPTLMR	95.0	57.8	25.0	1442.77	0	22	0	0	2	2221	2233
									VLEALLPLK	95.0	57.1	25.0	995.65	0	20	0	0	2	2383	2391
Fatty acid-binding protein, epidermal	FABP5_HUMAN	FABP5	15.15	100.0	3	4	19	14.10	ELGVGIALR	95.0	58.2	25.0	927.56	0	7	0	0	2	25	33
									FEETTADGR	95.0	51.8	25.0	1025.45	0	7	0	0	2	73	81
									FEETTADGRK	95.0	41.4	25.0	1153.55	0	3	2	0	2	73	82
F-box/LRR-repeat protein 18	FXL18_HUMAN	FBXL18	88.32	100.0	6	6	15	8.57	SLIHTVLLQK	95.0	20.8	25.0	1151.71	0	0	1	0	2	67	76
									LAPGYINQEVVR	95.0	38.9	25.0	1358.74	0	2	0	0	2	237	248
									LYLAVLSDR	95.0	75.7	25.0	1049.60	0	4	0	0	2	249	257
									NVVLDALQLPK	95.0	52.2	25.0	1209.72	0	5	0	0	2	289	299
									VVYMPALSDMLK	95.0	41.6	25.0	1398.70	0	2	0	0	2	574	585
									SGTLQPDAVLAFMAR	95.0	40.4	25.0	1592.81	0	1	0	0	2	625	639
Fermitin family homolog 1	FERM1_HUMAN	FERMT1	77.42	100.0	3	3	11	5.02	YGVQADAK	95.0	32.4	25.0	851.43	0	2	0	0	2	80	87
									VSFSAVVFK	95.0	50.7	25.0	983.56	0	6	0	0	2	111	119
									ILEAHQNVAQMPLVEAK	95.0	45.0	25.0	1907.01	0	0	3	0	2	536	552
Ferritin heavy chain	FRIH_HUMAN	FTH1	21.21	100.0	5	5	19	27.90	QNYHQDSEAAINR	95.0	33.4	25.0	1545.70	0	0	1	0	2	11	23
									YFLHQSHEER	95.0	33.9	25.0	1345.63	0	1	0	0	2	55	64
									IFLQDIK	95.0	39.6	25.0	876.52	0	12	0	0	2	81	87
									NVNQSLLELHK	95.0	40.0	25.0	1294.71	0	2	0	0	2	110	120
									ELGDHVTNLR	95.0	43.4	25.0	1153.60	0	3	0	0	2	148	157
Fibronectin	FINC_HUMAN	FN1	262.58	100.0	21	24	209	9.89	VGDTYERPK	95.0	49.8	25.0	1064.54	0	8	0	0	2	108	116
									ISCTIANR	95.0	40.0	25.0	934.48	0	1	0	0	2	133	140
									HTSVQTTSSGSGPFTDVR	95.0	34.3	25.0	1863.88	0	0	5	0	2	273	290
									EATIPGHLNSYTIK	95.0	43.6	25.0	1543.81	0	5	0	0	2	656	669
									SDTVPSPR	94.5	26.4	25.0	858.43	0	1	0	0	2	904	911
									DLQFVEVTDVK	95.0	84.9	25.0	1292.67	0	14	0	0	2	912	922
									VDVIPVNLPGEHGQR	95.0	66.1	25.0	1629.87	0	11	21	0	2	939	953
									VFAVSHGR	95.0	34.8	25.0	872.47	0	7	0	0	2	977	984

									AQITGYR	95.0	29.2	25.0	808.43	0	1	0	0	2	1022	1028
									LTVGLTR	95.0	42.2	25.0	759.47	0	7	0	0	2	1029	1035
									LGVRPSQGGEAPR	95.0	58.7	25.0	1323.71	0	1	36	0	2	1117	1129
									STTPDITGYR	95.0	53.2	25.0	1110.54	0	4	0	0	2	1198	1207
									FTNIGPDTMR	95.0	45.8	25.0	1167.55	0	19	0	0	2	1275	1284
									GDSPASSKPISINYR	95.0	73.1	25.0	1591.81	0	8	8	0	2	1525	1539
									GLAFTDVDVDSIK	95.0	85.5	25.0	1379.71	0	17	0	0	2	1637	1649
									YEVSVYALK	95.0	30.2	25.0	1071.57	0	1	0	0	2	1788	1796
									SYTITGLQPGTDYK	95.0	71.8	25.0	1543.76	0	4	0	0	2	1867	1880
									IYLYTLNDNAR	95.0	72.0	25.0	1355.70	0	18	0	0	2	1881	1891
									YEKPGSPPR	95.0	32.4	25.0	1030.53	0	2	0	0	2	1937	1945
									VPGTSTSATLTGLTR	95.0	82.6	25.0	1461.79	0	5	0	0	2	2150	2164
									GATYNIIVEALK	95.0	58.3	25.0	1291.73	0	5	0	0	2	2165	2176
Fibulin-1	FBLN1_HUMAN	FBLN1	77.19	100.0	6	6	61	9.82	SQETGDLDVGGLQETDK	95.0	####	25.0	1791.82	0	13	0	0	2	147	163
									GYHLNEEGTR	95.0	35.4	25.0	1175.54	0	7	0	0	2	344	353
									TGYYFDGISR	95.0	75.8	25.0	1178.55	0	21	0	0	2	386	395
									DSFDIIK	95.0	30.3	25.0	837.44	0	2	0	0	2	643	649
									YMDGMTVGVVR	95.0	38.7	25.0	1259.58	0	8	0	0	2	651	661
									LEMNYVVGGVVSHR	95.0	81.2	25.0	1575.79	0	0	10	0	2	676	689
Filamin-A	FLNA_HUMAN	FLNA	280.71	100.0	71	90	1432	29.90	AGQSAAGAAPGGGVDTR	95.0	53.2	25.0	1442.70	0	2	0	0	2	8	24
									KIQQNTFTR	95.0	37.9	25.0	1135.62	0	6	0	0	2	43	51
									IQQNTFTR	95.0	53.7	25.0	1007.53	0	25	0	0	2	44	51
									IANLQTDLSDGLR	95.0	99.6	25.0	1415.75	0	85	0	0	2	64	76
									LIALLEVLSQK	95.0	66.1	25.0	1226.77	0	2	0	0	2	77	87
									LVSIDSK	95.0	40.5	25.0	761.44	0	7	0	0	2	121	127
									AIVDGNLK	95.0	37.3	25.0	829.48	0	6	0	0	2	128	135
									LKPGAPLRPK	95.0	23.7	25.0	1076.69	0	0	4	0	2	269	278
									AYGPGIEPTGNMVK	95.0	61.6	25.0	1449.70	0	55	0	0	2	286	299
									RAEFTVETR	95.0	44.1	25.0	1108.57	0	7	0	0	2	301	309
									AEFTVETR	95.0	52.4	25.0	952.47	0	29	0	0	2	302	309
									SAGQGEVLVYVEDPAGHQEEAK	95.0	42.2	25.0	2313.10	0	0	1	0	2	310	331
									VTVLFAGQHIAK	95.0	72.3	25.0	1283.75	0	15	6	0	2	356	367
									SPFEVYVDK	95.0	59.1	25.0	1083.54	0	53	0	0	2	368	376
									SPFEVYVDKSQGDASK	95.0	29.4	25.0	1756.84	0	0	2	0	2	368	383
									VTAQGPGLEPSGNIANK	95.0	99.9	25.0	1652.86	0	63	0	0	2	384	400
									GTVEPQLEAR	95.0	50.1	25.0	1099.57	0	14	0	0	2	428	437
									VKETADFK	95.0	34.0	25.0	937.50	0	4	0	0	2	497	504
									SPFEVK	95.0	33.0	25.0	706.38	0	1	0	0	2	564	569
									LSPFMADIR	95.0	48.3	25.0	1065.54	0	19	0	0	2	656	664
									DAPQDFHPDR	95.0	51.9	25.0	1197.53	0	25	3	0	2	665	674
									TGVAVNKPAEFTVDAK	95.0	86.3	25.0	1646.87	0	21	31	0	2	685	700
									VQVQDNEGCPVEALVK	95.0	77.3	25.0	1784.88	0	2	0	0	2	709	724
									VNVGAGSHPNK	95.0	47.0	25.0	1079.56	0	36	0	0	2	761	771
									NDNDTFTVK	95.0	43.7	25.0	1053.48	0	19	0	0	2	829	837
									AEGPGLSR	95.0	33.1	25.0	786.41	0	5	0	0	2	877	884
									TGVELGKPTHFTVNAK	95.0	71.1	25.0	1698.92	0	8	11	4	2	885	900
									GKLDVQFSGLTK	95.0	64.6	25.0	1292.72	0	27	2	0	2	905	916
									LDVQFSGLTK	95.0	75.3	25.0	1107.60	0	19	0	0	2	907	916
									DVDIIDHHDNTYTVK	95.0	79.7	25.0	1784.85	0	19	11	0	2	922	936
									SPFSVAVSPSLDLSK	95.0	66.4	25.0	1533.82	0	3	0	0	2	959	973
									VDVGKDQEFTVK	95.0	71.7	25.0	1364.71	0	22	12	0	2	983	994

									DQEFTVK	95.0	32.1	25.0	866.43	0	2	0	0	2	988	994
									VEPGLGADNSVVR	95.0	80.3	25.0	1312.69	0	26	0	0	2	1020	1032
									AFGPGLQGGSAGSPAR	95.0	####	25.0	1429.72	0	64	0	0	2	1072	1087
									YGGQPVPNFPSK	95.0	66.4	25.0	1290.65	0	44	0	0	2	1235	1246
									EATTEFSVDAR	95.0	70.3	25.0	1225.57	0	12	0	0	2	1273	1283
									ALTQTGGPHVK	95.0	36.5	25.0	1108.61	0	6	0	0	2	1284	1294
									VANPSGNLTETYVQDR	95.0	####	25.0	1763.86	0	51	2	0	2	1297	1312
									VHGPGIQSGTTNKPNK	95.0	36.9	25.0	1634.86	0	2	10	0	2	1360	1375
									FTVETR	95.0	34.7	25.0	752.39	0	19	0	0	2	1376	1381
									GAGTGGLGLAVEGPSEAK	95.0	####	25.0	1570.81	0	47	0	0	2	1382	1399
									VPVHDVTDASK	95.0	58.0	25.0	1167.60	0	29	22	0	2	1440	1450
									ANLPQSFQVDTSK	95.0	93.9	25.0	1434.72	0	18	0	0	2	1465	1477
									AGVAPLQVK	95.0	56.5	25.0	882.54	0	8	0	0	2	1478	1486
									DAGEGLLAVQITDPEGKPK	95.0	68.4	25.0	1938.02	0	4	5	0	2	1574	1592
									YGGDEIPFSPYR	95.0	32.9	25.0	1400.65	0	1	0	0	2	1622	1633
									KGEITGEVR	95.0	37.0	25.0	988.54	0	2	0	0	2	1801	1809
									VAQPTITDNK	95.0	57.5	25.0	1086.58	0	9	0	0	2	1815	1824
									VAQPTITDNKDGTVTVR	95.0	81.3	25.0	1814.96	0	9	14	0	2	1815	1831
									DAGEGGLSLAIEGPSK	95.0	####	25.0	1500.75	0	35	0	0	2	1892	1907
									YNEQHVPGSPFTAR	95.0	65.4	25.0	1602.77	0	7	4	0	2	1938	1951
									NGHVGISFVPK	95.0	54.3	25.0	1154.63	0	6	13	0	2	2004	2014
									ETGEHLVHVK	95.0	35.1	25.0	1148.61	0	2	0	0	2	2015	2024
									FADQHVPGSPFSVK	95.0	40.1	25.0	1515.76	0	3	4	0	2	2120	2133
									IPEISIQDMTAQVTSPSGK	95.0	####	25.0	2018.01	0	4	0	0	2	2166	2184
									FVPAEMGTHTVSVK	95.0	63.4	25.0	1518.76	0	29	0	0	2	2202	2215
									AGGPGLER	95.0	38.8	25.0	756.40	0	2	0	0	2	2243	2250
									EAGAGGLAIAVEGPSK	95.0	####	25.0	1426.75	0	25	0	0	2	2265	2280
									AEISFEDR	95.0	36.2	25.0	966.45	0	7	0	0	2	2281	2288
									AEISFEDRK	95.0	36.2	25.0	1094.55	0	1	13	0	2	2281	2289
									RLTVSSLQESGLK	95.0	77.4	25.0	1417.80	0	3	0	0	2	2334	2346
									LTVSSLQESGLK	95.0	79.1	25.0	1261.70	0	35	0	0	2	2335	2346
									VNQPASFAVSLNGAK	95.0	61.0	25.0	1502.80	0	1	0	0	2	2347	2361
									ENGVYLIDVK	95.0	71.4	25.0	1149.62	0	32	0	0	2	2396	2405
									YGGPYHIGGSPFK	95.0	73.5	25.0	1379.67	0	5	15	0	2	2501	2513
									LVSNHSLHETSSVFVDSLTK	95.0	47.9	25.0	2200.12	0	0	1	0	2	2521	2540
									AGNNMLLVGVHGPR	95.0	65.6	25.0	1450.76	0	10	43	0	2	2585	2598
									TPCEEILVK	95.0	51.6	25.0	1088.57	0	2	0	0	2	2599	2607
									LYSVSYLLK	95.0	35.8	25.0	1085.62	0	9	0	0	2	2613	2621
									DKGEYTLVVK	95.0	49.7	25.0	1151.63	0	29	0	0	2	2622	2631
Filamin-B	FLNB_HUMAN	FLNB	278.14	100.0	62	76	795	28.70	KIQQNTFTR	95.0	37.9	25.0	1135.62	0	6	0	0	2	16	24
									IQQNTFTR	95.0	53.7	25.0	1007.53	0	25	0	0	2	17	24
									IGNLQTDLSDGLR	95.0	76.5	25.0	1401.73	0	33	0	0	2	37	49
									LIALLEVLSQK	95.0	66.1	25.0	1226.77	0	2	0	0	2	50	60
									LVSIDSK	95.0	40.5	25.0	761.44	0	7	0	0	2	94	100
									AIVDGNLK	95.0	37.3	25.0	829.48	0	6	0	0	2	101	108
									LKPGAPLKPK	95.0	28.7	25.0	1048.69	0	0	12	0	2	242	251
									GIEPTGNMVK	95.0	29.7	25.0	1061.53	0	1	0	0	2	263	272
									TYSVEYLPK	95.0	68.9	25.0	1099.57	0	6	0	0	2	314	322
									VTVLFAGQHISK	95.0	88.5	25.0	1299.74	0	12	4	0	2	329	340
									SPFEVSVDK	95.0	40.2	25.0	1007.50	0	7	0	0	2	341	349
									NTVELLVEDK	95.0	86.1	25.0	1159.62	0	23	0	0	2	400	409

IFFAGDTIPK	95.0	64.3	25.0	1108.60	0	42	0	0	2	430	439
AAGSGELGVTMK	95.0	84.6	25.0	1136.56	0	55	0	0	2	481	492
GLEELVK	95.0	53.5	25.0	787.46	0	17	0	0	2	496	502
SPFEVQVGPEAGMQK	95.0	84.4	25.0	1619.77	0	37	4	0	2	537	551
AYGPGLEK	95.0	29.2	25.0	834.44	0	1	0	0	2	650	657
IFAQDGEGQR	95.0	46.6	25.0	1120.54	0	24	0	0	2	682	691
MDGTYACSYTPVK	95.0	62.4	25.0	1508.64	0	2	0	0	2	700	712
VNIGQGSHPQK	95.0	28.2	25.0	1164.61	0	5	2	0	2	734	744
VFGPGVER	95.0	48.2	25.0	860.46	0	9	0	0	2	747	754
VKAEGPGLSK	95.0	35.0	25.0	985.57	0	5	0	0	2	848	857
SPFTVGVAAPLDLSK	95.0	50.4	25.0	1501.83	0	1	0	0	2	932	946
VEVGKDQEFTVDTR	95.0	81.8	25.0	1622.80	0	13	16	0	2	956	969
DQEFTVDTR	95.0	40.4	25.0	1110.51	0	3	0	0	2	961	969
GAGTGGLGLTVEGPCEAK	95.0	86.8	25.0	1673.82	0	2	0	0	2	1067	1084
ADIEMPFDPSK	95.0	73.5	25.0	1265.57	0	22	0	0	2	1125	1135
VVASGPGLEHGK	95.0	69.0	25.0	1150.62	0	18	22	0	2	1136	1147
YGGELVPHFPAR	95.0	34.7	25.0	1342.69	0	0	4	0	2	1208	1219
VKVEPAVDTSR	95.0	30.3	25.0	1200.66	0	6	0	0	2	1220	1230
VEPAVDTSR	95.0	28.4	25.0	973.49	0	1	0	0	2	1222	1230
VFGPGIEGK	95.0	31.3	25.0	903.49	0	2	0	0	2	1233	1241
VAVTEGCQPSR	95.0	39.1	25.0	1203.58	0	1	0	0	2	1320	1330
VQAQGPGLK	95.0	32.3	25.0	897.52	0	5	0	0	2	1331	1339
GAGIGGLGITVEGPSESK	95.0	82.7	25.0	1628.85	0	14	0	0	2	1355	1372
VPVKDVVDPSK	95.0	39.4	25.0	1182.67	0	0	3	0	2	1413	1423
IAGPGLGSGVR	95.0	77.0	25.0	983.56	0	25	0	0	2	1426	1436
VLQSFTVDSSK	95.0	79.8	25.0	1210.63	0	12	0	0	2	1439	1449
AGLAPLEVR	95.0	62.2	25.0	925.55	0	5	0	0	2	1450	1458
YADEEIPR	95.0	47.0	25.0	992.47	0	9	0	0	2	1497	1504
DAGEGLLAVQITDQEGKPK	95.0	43.8	25.0	1969.02	0	1	3	0	2	1546	1564
DGTYAVTYIPDK	95.0	43.7	25.0	1342.65	0	1	0	0	2	1573	1584
CLATGPGIASTVK	95.0	58.2	25.0	1274.68	0	4	0	0	2	1617	1629
TGEEVGFVVDAK	95.0	88.7	25.0	1250.63	0	21	0	0	2	1630	1641
KGEITGEVHMPSGK	95.0	44.1	25.0	1485.74	0	1	2	0	2	1757	1770
TATPEIVDNK	95.0	43.5	25.0	1087.56	0	2	0	0	2	1771	1780
TATPEIVDNKDGTVTVR	95.0	86.2	25.0	1815.94	0	4	4	0	2	1771	1787
YAPTEVGLHEMHIK	95.0	59.6	25.0	1640.81	0	6	0	3	2	1788	1801
EVGEHLVSIK	95.0	38.7	25.0	1110.62	0	3	0	0	2	1970	1979
TFEMSDFIVDTR	95.0	67.7	25.0	1476.67	0	9	0	0	2	2017	2028
DAGYGGISLAVEGPSK	95.0	####	25.0	1520.76	0	20	0	0	2	2029	2044
FADEHVPGSPFTVK	95.0	42.5	25.0	1530.76	0	2	2	0	2	2075	2088
IPEINSSDMSAHVTSPSGR	95.0	72.2	25.0	2000.93	0	4	37	0	2	2121	2139
VTEAEIVPMGK	95.0	63.3	25.0	1189.61	0	21	0	0	2	2140	2150
FVPQEMGVHTVSVK	95.0	79.9	25.0	1573.80	0	16	0	0	2	2157	2170
AGGPGLER	95.0	38.8	25.0	756.40	0	2	0	0	2	2198	2205
EAGAGGLSIAVEGPSK	95.0	####	25.0	1442.75	0	39	0	0	2	2220	2235
AEITFDDHK	95.0	30.4	25.0	1075.51	0	1	0	0	2	2236	2244
RLTVMSLQESGLK	95.0	28.7	25.0	1477.80	0	0	1	0	2	2289	2301
LTVMSLQESGLK	95.0	64.4	25.0	1321.70	0	6	0	0	2	2290	2301
VNQPASFAIR	95.0	66.2	25.0	1102.60	0	19	0	0	2	2302	2311
FNGSHVVGSPFK	95.0	49.5	25.0	1275.65	0	1	6	0	2	2361	2372
AGPGTLSVTIEGPSK	95.0	91.3	25.0	1413.76	0	33	0	0	2	2412	2426

									YGGPNHIVGSPFK	95.0	81.2	25.0	1372.70	0	14	2	0	2	2456	2468
									LVSPGSANETSSILVESVTR	95.0	88.2	25.0	2046.07	0	2	0	0	2	2476	2495
									SSFLVDCSK	95.0	41.0	25.0	1042.49	0	2	0	0	2	2531	2539
									HVGNQQYNVTYVVK	95.0	71.4	25.0	1648.84	0	12	1	0	2	2563	2576
									ERGDYVLAVK	95.0	33.9	25.0	1149.63	0	0	5	0	2	2577	2586
Filamin-C	FLNC_HUMAN	FLNC	291.00	100.0	16	17	71	10.60	KIQQNTFTR	95.0	37.9	25.0	1135.62	0	6	0	0	2	36	44
									IQQNTFTR	95.0	53.7	25.0	1007.53	0	25	0	0	2	37	44
									LIALLEVLSQK	95.0	66.1	25.0	1226.77	0	2	0	0	2	70	80
									LVSIDSK	95.0	40.5	25.0	761.44	0	7	0	0	2	114	120
									AIVDGNLK	95.0	37.3	25.0	829.48	0	6	0	0	2	121	128
									VTVLFAGQNIER	95.0	59.8	25.0	1346.74	0	5	0	0	2	350	361
									SPFEVNVGMALGDANK	95.0	58.0	25.0	1664.80	0	1	0	0	2	362	377
									SPFEVQVSPEAGVQK	95.0	####	25.0	1601.82	0	13	0	0	2	559	573
									VNVGEGSHPER	95.0	33.0	25.0	1180.57	0	2	2	0	2	756	766
									NDNDTFTVK	95.0	43.7	25.0	1053.48	0	19	0	0	2	824	832
									VAVGQEQAFSVNTR	95.0	####	25.0	1505.77	0	5	0	0	2	978	991
									GAGGQGQLDVR	95.0	57.4	25.0	1057.54	0	6	0	0	2	992	1002
									GGLVGTPAPFSIDTK	95.0	59.7	25.0	1459.78	0	2	0	0	2	1074	1088
									GAGTGGLGLTVEGPCEAK	95.0	86.8	25.0	1673.82	0	2	0	0	2	1089	1106
									VSGPGVEPHGVLR	95.0	40.4	25.0	1303.71	0	0	2	0	2	1255	1267
									AFGPGLEGGLVNK	95.0	59.9	25.0	1258.68	0	4	0	0	2	1355	1367
									FTVETR	95.0	34.7	25.0	752.39	0	19	0	0	2	1371	1376
									GAGTGGLGLAIEGPSEAK	95.0	96.7	25.0	1584.82	0	12	0	0	2	1377	1394
									DAGEGGLSLAVEGPSK	95.0	97.8	25.0	1486.74	0	2	0	0	2	1886	1901
									HIGISFTPK	95.0	31.3	25.0	999.56	0	2	0	0	2	2000	2008
									ILVGPSEIGDASK	95.0	60.2	25.0	1285.70	0	2	0	0	2	2031	2043
									LGSFGSITR	95.0	43.6	25.0	937.51	0	4	0	0	2	2231	2239
									EAGAGGLSIAVEGPSK	95.0	####	25.0	1442.75	0	39	0	0	2	2341	2356
									GPGLSQAFVGQK	95.0	51.4	25.0	1188.64	0	6	0	0	2	2642	2653
									VYNVTYTVK	95.0	29.3	25.0	1086.58	0	1	0	0	2	2691	2699
Flap endonuclease 1	FEN1_HUMAN	FEN1	42.58	100.0	5	6	26	11.60	LIADVAPSAIR	95.0	57.2	25.0	1125.66	0	11	0	0	2	9	19
									QLQQAQAAGAEQEVEK	95.0	####	25.0	1727.86	0	5	0	0	2	110	125
									KLPIQEFHLSR	95.0	70.4	25.0	1367.78	0	2	4	0	2	201	211
									LPIQEFHLSR	95.0	35.6	25.0	1239.68	0	0	2	0	2	202	211
									LDDFFK	95.0	29.7	25.0	784.39	0	2	0	0	2	340	345
Flavin reductase	BLVRB_HUMAN	BLVRB	22.10	100.0	3	5	24	16.00	NDLSPTTVMSEGAR	95.0	79.6	25.0	1493.69	0	7	0	0	2	79	92
									LQAVTDDHIR	95.0	58.7	25.0	1167.61	0	8	4	0	2	125	134
									HDLGHFMLR	95.0	28.8	25.0	1141.56	0	1	4	0	2	179	187
Focal adhesion kinase 1	FAK1_HUMAN	PTK2	119.22	100.0	6	6	11	5.42	LIQQTFR	95.0	28.3	25.0	905.52	0	1	0	0	2	223	229
									FLQEALTMR	95.0	52.2	25.0	1124.58	0	4	0	0	2	468	476
									LGDFGLSR	95.0	39.8	25.0	864.46	0	2	0	0	2	562	569
									AQLSTILEEEK	95.0	57.9	25.0	1260.67	0	2	0	0	2	674	684
									LLNSDLGELINK	95.0	37.8	25.0	1328.74	0	1	0	0	2	989	1000
									NLLDVIDQAR	95.0	36.0	25.0	1156.63	0	1	0	0	2	1033	1042
Fructose-bisphosphate aldolase A	ALDOA_HUMAN	ALDOA	39.40	100.0	17	25	517	46.70	PYQYPALTPEQK	95.0	64.2	25.0	1434.73	0	85	0	0	1	2	13
									KELSDIAHR	95.0	75.7	25.0	1068.58	0	4	6	0	2	14	22
									ELSDIAHR	95.0	48.0	25.0	940.48	0	39	0	0	2	15	22
									GILAADESTGSIAK	95.0	92.8	25.0	1332.70	0	119	0	0	2	29	42
									LQSIGTENTEENR	95.0	78.1	25.0	1490.71	0	44	0	0	2	44	56
									LQSIGTENTEENRR	95.0	39.5	25.0	1646.81	0	7	19	0	2	44	57
									QLLLTADDR	95.0	80.4	25.0	1044.57	0	19	0	0	2	61	69

								ADDGRPFPQVIK	95.0	40.4	25.0	1342.71	0	20	37	0	2	88	99
								GVVPLAGTNGETTTQGLDGLSER	95.0	####	25.0	2272.14	0	1	1	0	2	112	134
								DGADFAK	95.0	34.0	25.0	723.33	0	1	0	0	2	141	147
								IGEHTPSALAIMENANVLAR	95.0	70.5	25.0	2123.09	0	1	1	0	2	154	173
								VLAAVYK	95.0	45.6	25.0	763.47	0	7	0	0	2	209	215
								FSHEEIAMATVTALR	95.0	####	25.0	1691.84	0	10	6	0	2	244	258
								ALQASALK	95.0	44.0	25.0	801.48	1	19	0	0	2	305	312
								AAQEEYVK	95.0	59.9	25.0	937.46	0	28	0	0	2	323	330
								AAQEEYVKR	95.0	91.8	25.0	1093.56	0	34	2	0	2	323	331
								ALANSLACQGK	95.0	59.0	25.0	1132.58	0	6	0	0	2	332	342
Fumarate hydratase, mitochondrial	FUMH_HUMAN	FH	54.62	100.0	8	9	23	16.10	IEYDTFGELK	95.0	61.3	25.0	1214.59	0	2	0	0	2	52	61
								IGGVTER	95.0	40.2	25.5	731.40	0	2	0	0	2	81	87
								AFGILK	95.0	28.8	25.0	648.41	1	0	0	0	2	95	100
								AAAEVNQDYGLDPK	95.0	88.9	25.0	1490.71	0	5	0	0	2	102	115
								IANAIMK	95.0	32.8	25.0	776.43	0	2	0	0	2	116	122
								IPVHPNDHVNK	95.0	41.0	25.0	1269.67	0	4	1	0	2	173	183
								SKEFAQIIK	95.0	33.9	25.0	1063.61	0	2	0	0	2	222	230
								IYELAAGGTAVGTGLNTR	95.0	####	25.0	1763.93	0	4	0	0	2	269	286
Fumarylacetoacetase	FAAA_HUMAN	FAH	46.36	100.0	4	4	11	10.30	VFLQNLLSVSQAR	95.0	63.6	25.0	1474.84	0	4	0	0	2	83	95
								ASSVVVSGTPIR	95.0	30.1	25.0	1172.66	0	1	0	0	2	163	174
								LGEPIPISK	95.0	43.9	25.0	953.57	0	4	0	0	2	212	220
								IGFGQCAGK	95.0	27.4	25.0	937.46	0	2	0	0	2	403	411
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAH2A_HUMAN	FAHD2A	34.58	100.0	4	4	6	17.50	ALAAQLPVLPR	95.0	42.1	25.0	1148.72	0	2	0	0	2	83	93
								SEVTFLAPVTRPDK	95.0	35.6	25.0	1559.84	0	1	0	0	2	94	107
								ATDAMAHVAGFTVAHDVSAR	95.0	42.5	25.0	2042.97	0	0	2	0	2	175	194
								DSVADPHNLK	95.0	27.2	25.0	1095.54	0	1	0	0	2	225	234
Galactocerebrosidase	GALC_HUMAN	GALC	77.02	100.0	3	3	11	5.11	EFDGIGAVSGGGATSR	95.0	####	25.0	1480.70	0	6	0	0	2	54	69
								LLVNYPEPYR	95.0	50.3	25.0	1263.67	0	4	0	0	2	70	79
								MLNYQGLQR	95.0	30.9	25.0	1138.57	0	1	0	0	2	212	220
Galectin-1	LEG1_HUMAN	LGALS1	14.70	100.0	4	4	54	28.10	VRGEVAPDAK	95.0	32.0	25.0	1041.57	0	8	0	0	2	20	29
								SFVLNLGK	95.0	50.7	25.0	877.51	0	33	0	0	2	30	37
								DSNNLCLHFNPR	95.0	32.3	25.0	1486.69	0	0	3	0	2	38	49
								LPDGYEFK	95.0	54.6	25.0	968.47	0	10	0	0	2	101	108
Galectin-3	LEG3_HUMAN	LGALS3	26.13	100.0	5	11	53	25.60	MLITILGTVKPNANR	95.0	64.1	25.0	1656.95	0	9	10	0	2	130	144
								GNDVAFHFNPR	95.0	57.8	25.0	1273.61	0	5	6	0	2	152	162
								QSVFPFESGKPFK	95.0	52.6	25.0	1497.77	0	2	2	0	2	187	199
								IQVLVEPDHFK	95.0	41.8	25.0	1324.73	0	2	2	0	2	200	210
								VAVNDAHLLQYNHR	95.0	74.6	25.0	1649.85	0	3	11	1	2	211	224
Galectin-3-binding protein	LG3BP_HUMAN	LGALS3BP	65.31	100.0	10	12	125	13.80	VEIFYR	94.9	26.7	25.0	826.45	0	1	0	0	2	37	42
								STHTLDLSR	95.0	31.8	25.0	1029.53	0	3	0	0	2	129	137
								ELSEALGQIFDSQR	95.0	92.6	25.0	1592.79	0	3	1	0	2	138	151
								RIDITLSSVK	95.0	49.1	25.0	1131.67	0	13	0	0	2	216	225
								IDITLSSVK	95.0	57.7	25.0	975.57	0	19	0	0	2	217	225
								LASAYGAR	95.0	44.9	25.0	808.43	0	12	0	0	2	230	237
								SDLAVPSELALLK	95.0	49.0	25.0	1355.78	0	10	0	0	2	311	323
								ASHEEVEGLVEK	95.0	69.8	25.0	1326.65	0	28	25	0	2	334	345
								KSQLVYQSR	95.0	47.4	25.0	1108.61	0	5	0	0	2	427	435
								SQLVYQSR	95.0	32.2	25.0	980.52	0	5	0	0	2	428	435
Gamma-adducin	ADDG_HUMAN	ADD3	79.14	100.0	3	4	24	5.81	GLSFSEATASNLVK	95.0	89.6	25.0	1423.74	0	5	0	0	2	178	191
								VNIIGEVVDQGSTNLK	95.0	99.2	25.0	1685.91	0	12	3	0	2	192	207
								VGEIEFEGLMR	95.0	59.5	25.0	1295.63	0	4	0	0	2	366	376

Gamma-enolase	ENOG_HUMAN	ENO2	47.25	100.0	4	4	6	15.00	GNPTVEVDLYTAK	95.0	42.4	25.0	1406.72	0	1	0	0	2	16	28
									AAVPSGASTGIYEALELR	95.0	73.5	25.0	1804.94	0	1	0	0	2	33	50
									LGAEVYHTLK	95.0	28.7	25.0	1130.62	0	0	2	0	2	184	193
									DGKYDLDFK	95.0	27.5	25.0	1100.53	0	1	0	0	2	254	262
									YDLDFK	95.0	34.0	25.0	800.38	0	15	0	0	2	257	262
									VNQIGSVTEAIQACK	95.0	####	25.0	1617.83	0	2	0	0	2	344	358
Gamma-glutamyl hydrolase	GGH_HUMAN	GGH	35.95	100.0	6	7	50	19.50	KPIIGILMQK	95.0	43.1	25.0	1156.71	0	10	1	0	2	33	42
									YYIAASYVK	95.0	41.0	25.0	1077.56	0	8	0	0	2	54	62
									DYEILFK	95.0	28.0	25.0	927.48	0	3	0	0	2	82	88
									FFNVLTTNTDGK	95.0	82.5	25.0	1356.68	0	16	0	0	2	213	224
									IEFISTMEGYK	95.0	50.8	25.0	1333.63	0	2	0	0	2	225	235
									NLDGISHAPNAVK	95.0	61.0	25.0	1335.70	0	10	0	0	2	254	266
Gamma-glutamylcyclotransferase	GGCT_HUMAN	GGCT	20.99	100.0	7	7	34	39.40	NPSAAFFCVAR	95.0	73.4	25.0	1239.59	0	2	0	0	2	35	45
									LDFGNSQGK	95.0	48.3	25.0	965.47	0	11	0	0	2	51	59
									SNLNSLDEQEGVK	95.0	77.5	25.0	1432.69	0	7	0	0	2	89	101
									SGMYVVIEVK	95.0	60.4	25.0	1140.60	0	2	0	0	2	102	111
									ENGLPLEYQEK	95.0	44.7	25.0	1319.65	0	2	0	0	2	149	159
									AIEPNDYTGK	95.0	41.1	25.0	1107.53	0	8	0	0	2	162	171
									VSEEIEDIIK	95.0	29.1	25.0	1174.62	0	2	0	0	2	172	181
Gamma-synuclein	SYUG_HUMAN	SNCG	13.31	100.0	4	4	8	35.40	TKENVVQSVTSVAEK	95.0	80.1	25.0	1618.86	0	2	0	0	2	44	58
									ENVVQSVTSVAEK	95.0	70.9	25.0	1389.72	0	2	0	0	2	46	58
									TVEEAENIAVTSGVVR	95.0	98.0	25.0	1673.87	0	3	0	0	2	81	96
									EKEEVAEEAQSGGD	95.0	33.1	25.0	1477.63	0	1	0	0	2	114	127
GDH/6PGL endoplasmic bifunctional protein	G6PE_HUMAN	H6PD	88.88	100.0	3	3	4	3.92	QAVAQILPFR	95.0	71.9	25.0	1142.67	0	2	0	0	2	209	218
									LANDIEATAVR	95.0	60.5	25.0	1172.63	0	1	0	0	2	567	577
									MSLSLPLINR	95.0	49.2	25.0	1159.65	0	1	0	0	2	729	738
GDP-L-fucose synthase	FCL_HUMAN	TSTA3	35.87	100.0	4	4	16	15.00	ILVTGGSGLVGK	95.0	67.5	25.0	1100.67	0	6	0	0	2	10	21
									DADLTDTAQTR	95.0	58.2	25.0	1206.56	0	6	0	0	2	45	55
									NVHMNDNVLHSAFEVGAR	95.0	34.2	25.0	2025.96	0	0	2	0	2	90	107
									TYLPDFR	95.0	34.4	25.0	911.46	0	2	0	0	2	291	297
Gelsolin	GELS_HUMAN	GSN	85.68	100.0	9	11	46	14.60	GGVASGFK	95.0	31.0	25.0	722.38	0	1	0	0	2	170	177
									HVVPNEVVVQR	95.0	45.6	25.0	1275.72	0	3	2	0	2	178	188
									QTQVSVLPEGGETPLFK	95.0	73.8	25.0	1829.96	0	6	0	0	2	374	390
									VPFDAATLHTSTAMAAQHGMDDDGTGQK	95.0	43.8	25.0	2905.27	0	0	1	0	2	420	447
									AVEVLPK	95.0	49.7	25.0	755.47	0	4	0	0	2	578	584
									AGALNSNDAFVLK	95.0	51.8	25.0	1319.70	0	4	0	0	2	585	597
									TGAQELLR	95.0	71.3	25.0	887.49	0	7	0	0	2	616	623
									DSQEEEKTEALTSAK	95.0	83.8	25.0	1665.78	0	8	4	0	2	714	728
									TPITVVK	95.0	40.8	25.0	757.48	0	6	0	0	2	742	748
General vesicular transport factor p115	USO1_HUMAN	USO1	107.88	100.0	12	12	52	14.30	LLTSLLK	95.0	28.1	25.0	787.53	0	1	0	0	2	145	151
									LMDLLADSR	95.0	65.2	25.0	1049.53	0	2	0	0	2	171	179
									NDGVLLLQALTR	95.0	76.3	25.0	1312.76	0	11	0	0	2	184	195
									IVAFENAFER	95.0	56.5	25.0	1195.61	0	10	0	0	2	203	212
									NNNSNQNFFK	95.0	58.4	25.0	1226.55	0	2	0	0	2	242	251
									TLEQHDNIVTHYK	95.0	40.2	25.0	1597.80	0	0	3	0	2	644	656
									NQELLQSQLTEK	95.0	90.1	25.0	1430.75	0	2	0	0	2	745	756
									SSQTSGTNEQSSAIVSAR	95.0	95.0	25.0	1809.86	0	8	0	0	2	765	782
									DSEQVAELK	95.0	58.8	25.0	1018.51	0	4	0	0	2	783	791
									SQLNSQSVEITK	95.0	77.0	25.0	1333.70	0	5	0	0	2	799	810
									LSALLQETK	95.0	60.1	25.0	1002.58	0	2	0	0	2	850	858
									EQLDSSNSTIAILQTEK	95.0	84.6	25.0	1876.95	0	2	0	0	2	876	892

Gephyrin	GEPH_HUMAN	GPHN	79.73	100.0	3	3	5	4.35	TLIINLPGSK	95.0	29.2	25.0	1055.65	0	2	0	0	2	139	148
									MSPFPLTSMDK	95.0	33.7	25.0	1285.58	0	2	0	0	2	318	328
									DNLPPFPASVK	95.0	27.1	25.0	1184.63	0	1	0	0	2	363	373
Geranylgeranyl transferase type-2 subunit alpha	PGTA_HUMAN	RABGGTA	65.05	100.0	9	9	27	14.80	LYQSATQAVFQK	95.0	75.0	25.0	1383.73	0	3	0	0	2	27	38
									EVLQQLETQK	95.0	34.4	25.0	1215.66	0	1	0	0	2	71	80
									SPEELAALVK	95.0	74.6	25.0	1056.59	0	6	0	0	2	81	90
									FLEVDER	95.0	35.7	25.0	907.45	0	2	0	0	2	135	141
									DSTTDEQLFR	95.0	55.1	25.0	1211.55	0	2	0	0	2	344	353
									ALDPLLYEK	95.0	39.0	25.0	1061.59	0	5	0	0	2	394	402
									ETLQYFQTLK	95.0	30.7	25.0	1270.67	0	1	0	0	2	403	412
									FLLENSVLK	95.0	41.2	25.0	1062.62	0	5	0	0	2	429	437
									MEYAEVR	95.0	28.4	25.0	913.41	0	2	0	0	2	438	444
Glia-derived nexin	GDN_HUMAN	SERPINE2	43.99	100.0	11	12	55	27.10	NKDIVTVANAVFVK	95.0	30.5	25.0	1517.87	0	0	3	0	2	104	117
									DIVTVANAVFVK	95.0	86.1	25.0	1275.73	0	11	0	0	2	106	117
									NASEIEVPFVTR	95.0	53.2	25.0	1361.71	0	6	0	0	2	118	129
									LVLVNAVYFK	95.0	62.5	25.0	1165.70	0	6	0	0	2	181	190
									VQVILPK	95.0	41.2	25.0	796.53	0	6	0	0	2	289	295
									FTAVAQTDLK	95.0	33.6	25.0	1093.59	0	2	0	0	2	296	305
									FTAVAQTDLKEPLK	95.0	72.6	25.0	1560.86	0	2	2	0	2	296	309
									VLGITDMFDSSK	95.0	64.0	25.0	1328.64	0	3	0	0	2	310	321
									AKIEVSEDGTK	95.0	37.0	25.0	1176.61	0	1	0	0	2	343	353
									ASAATTAILIAR	95.0	95.2	25.0	1158.68	0	11	0	0	2	354	365
									HNPTGAVLFMGQINKP	95.0	56.6	25.0	1739.89	0	2	0	0	2	383	398
Glucosamine-6-phosphate isomerase 1	GNPI1_HUMAN	GNPDA1	32.65	100.0	3	4	17	12.80	TFNMDEYVGLPR	95.0	69.5	25.0	1457.67	0	6	0	0	2	68	79
									VPTMALTVGVGTVMDAR	95.0	87.5	25.0	1749.89	0	4	4	0	2	181	197
									GLMLVHNK	95.0	38.4	25.0	927.51	0	3	0	0	2	257	264
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1_HUMAN	GFPT1	78.79	100.0	10	10	25	15.60	GYDFESETDTETIAK	95.0	####	25.0	1705.74	0	2	0	0	2	140	154
									ESQDTSFTTLVER	95.0	74.6	25.0	1512.72	0	6	0	0	2	164	176
									GSPLLIGVR	95.0	34.8	25.0	911.57	0	2	0	0	2	204	212
									LSTDHIPILYR	95.0	33.1	25.0	1327.74	0	0	2	0	2	217	227
									AVQTLQMELQQIMK	95.0	75.9	25.0	1692.87	0	2	0	0	2	323	336
									EIFEQPESVVNTMR	95.0	78.2	25.0	1694.81	0	2	0	0	2	346	359
									EIMLGLK	95.0	39.2	25.0	819.46	0	2	0	0	2	523	529
									RLPDLIK	95.0	27.0	25.0	854.55	0	1	0	0	2	530	536
									EVLSMDDEIQK	95.0	40.7	25.0	1322.61	0	2	0	0	2	537	547
									GYDVDFPR	95.0	41.1	25.0	968.45	0	4	0	0	2	683	690
Glucose 1,6-bisphosphate synthase	PGM2L_HUMAN	PGM2L1	70.44	100.0	3	3	4	4.82	GFVVGYDTR	95.0	36.1	25.0	1013.51	0	1	0	0	2	110	118
									DVPVYLFSR	95.0	36.0	25.0	1095.58	0	2	0	0	2	142	150
									NVYMLATTVSSK	95.0	43.7	25.0	1329.67	0	1	0	0	2	381	392
Glucose-6-phosphate 1-dehydrogenase	G6PD_HUMAN	G6PD	59.24	100.0	23	27	261	33.80	LTVADIR	95.0	48.0	25.0	787.47	0	43	0	0	2	75	81
									LTVADIRK	95.0	45.3	25.0	915.56	0	3	0	0	2	75	82
									KQSEPFFK	95.0	41.1	25.0	1010.53	0	3	0	0	2	82	89
									QSEPFFK	95.0	36.5	25.0	882.44	0	1	0	0	2	83	89
									LKLEDFFAR	95.0	51.0	25.0	1138.63	0	15	13	0	2	96	104
									LEDFFAR	95.0	39.1	25.0	897.45	0	19	0	0	2	98	104
									NSYVAGQYDDAASYQR	95.0	####	25.0	1807.79	0	12	0	0	2	105	120
									LNSHMNALHLGSQANR	95.0	64.6	25.0	1778.87	0	4	6	0	2	121	136
									IIVEKPFGR	95.0	42.6	25.0	1058.64	0	12	3	0	2	167	175
									LSNHISSLFR	95.0	48.8	25.0	1173.64	0	17	1	0	2	183	192
									IDHYLGK	95.0	41.8	25.0	845.45	0	5	0	0	2	199	205
									EMVQNLMVLR	95.0	62.9	25.0	1264.64	0	14	0	0	2	206	215

									IFGPIWNR	95.0	45.8	25.0	1002.55	0	4	0	0	2	220	227
									DNIACVILTFK	95.0	28.6	25.0	1293.69	0	1	0	0	2	228	238
									EPFGTEGR	95.0	29.7	25.0	892.42	0	3	0	0	2	239	246
									GYLDDPTVPR	95.0	42.3	25.0	1132.56	0	17	0	0	2	321	330
									RNELVIR	95.0	34.2	25.0	899.54	0	5	0	0	2	387	393
									VQPNEAVYTK	95.0	28.4	25.0	1148.59	0	1	0	0	2	394	403
									LPDAYER	95.0	47.0	25.0	863.43	0	17	0	0	2	433	439
									GPTEADELMK	95.0	47.2	25.0	1106.50	0	27	0	0	2	488	497
									GPTEADELMKR	95.0	41.9	25.0	1262.60	0	3	0	0	2	488	498
									RVGFQYEGTYK	95.0	49.8	25.0	1347.67	0	4	0	0	2	498	508
									VGFQYEGTYK	95.0	47.5	25.0	1191.57	0	8	0	0	2	499	508
Glucose-6-phosphate isomerase	G6PI_HUMAN	GPI	63.13	100.0	11	13	77	21.10	SELNLR	95.0	28.5	25.5	731.40	0	1	0	0	2	22	27
									LFDANKDR	95.0	43.6	25.0	978.50	0	4	0	0	2	29	36
									NLVTEDVMR	95.0	62.8	25.0	1092.54	0	5	0	0	2	58	66
									MLVDLAK	95.0	39.2	25.0	805.45	0	4	0	0	2	67	73
									INYTEGR	95.0	36.0	25.0	852.42	0	11	0	0	2	90	96
									AVLHVALR	95.0	56.5	25.0	878.56	0	3	0	0	2	97	104
									SNTPILVDGKDVMPEVNK	95.0	61.5	25.0	1972.01	0	2	3	0	2	107	124
									VWYVSNIDGTHIAK	95.0	23.6	25.0	1602.83	0	0	1	0	2	181	194
									TFTTQETITNAETAK	95.0	####	25.0	1655.81	0	33	1	0	2	212	226
									HFVALSTNTTK	95.0	63.9	25.0	1218.65	0	7	0	0	2	242	252
									FAAYFQQGDMESNGK	95.0	88.9	25.0	1708.73	0	2	0	0	2	348	362
Glucosidase 2 subunit beta	GLU2B_HUMAN	PRKCSH	59.41	100.0	8	8	36	14.60	ESLQQMAEVTR	95.0	57.0	25.0	1307.63	0	6	0	0	2	125	135
									KLIELQAGK	95.0	52.8	25.0	999.62	0	1	0	0	2	158	166
									LIELQAGKK	95.0	30.5	25.0	999.62	0	2	0	0	2	159	167
									SLEDQVEMLR	95.0	54.8	25.0	1235.59	0	3	0	0	2	168	177
									TVKEEAEKPER	95.0	37.3	25.0	1315.69	0	0	3	0	2	178	188
									LWEEQLAAAK	95.0	35.7	25.0	1158.62	0	1	0	0	2	197	206
									AQQEQELAADAFK	95.0	97.2	25.0	1448.70	0	5	0	0	2	207	219
									ETMVTSTTEPSR	95.0	63.7	25.0	1354.62	0	15	0	0	2	488	499
Glutamate dehydrogenase 1, mitochondrial	DHE3_HUMAN	GLUD1	61.38	100.0	9	9	19	17.20	MVEGFFDR	95.0	34.5	25.0	1016.45	0	2	0	0	2	69	76
									GASIVEDKLVEDLR	95.0	60.4	25.0	1543.83	0	2	0	0	2	77	90
									YSTDVSVDEVK	95.0	54.1	25.0	1241.59	0	1	0	0	2	152	162
									ALASLMTYK	95.0	35.7	25.0	1013.53	0	1	0	0	2	163	171
									NYTDNELEK	95.0	27.0	25.0	1125.51	0	1	0	0	2	192	200
									LQHGSILGFPK	95.0	39.0	25.0	1196.68	0	0	2	0	2	353	363
									IIAEGANGPTTPEADK	95.0	43.8	25.0	1583.79	0	3	0	0	2	400	415
									YNLGLDLR	95.0	68.4	25.0	963.53	0	5	0	0	2	528	535
									VYNEAGVTFT	95.0	35.9	25.0	1100.53	0	2	0	0	2	549	558
Glutamate--cysteine ligase catalytic subunit	GSH1_HUMAN	GCLC	72.75	100.0	6	6	22	9.42	SLFFPDEAINK	95.0	37.0	25.0	1280.65	0	1	0	0	2	172	182
									VVINVPIFK	95.0	58.9	25.0	1028.65	0	2	0	0	2	201	209
									SRYDSIDSYLSK	95.0	61.4	25.0	1433.69	0	2	0	0	2	327	338
									DPLTLFEEK	95.0	53.0	25.0	1091.56	0	12	0	0	2	378	386
									LDFLIPLSK	95.0	49.4	25.0	1045.63	0	2	0	0	2	457	465
									ASGELMTVAR	95.0	74.6	25.0	1050.52	0	3	0	0	2	566	575
Glutamine-dependent NAD(+) synthetase	NADE1_HUMAN	NADSYN1	79.27	100.0	7	7	20	11.50	VDLVTMVTSK	95.0	61.5	25.0	1108.59	0	2	0	0	2	213	222
									NGGIYLLANQK	95.0	75.9	25.0	1190.65	0	2	0	0	2	223	233
									SGNEEVLADVR	95.0	52.2	25.0	1188.59	0	2	0	0	2	382	392
									TIVNQISYTPQDPR	95.0	72.8	25.0	1631.84	0	4	0	0	2	393	406
									AVMGIFSLVTGK	95.0	64.6	25.0	1238.68	0	7	0	0	2	453	464
									SPLFAAHGGSSR	95.0	38.5	25.0	1186.60	0	1	0	0	2	465	476

									ENLALQNVQAR	95.0	71.4	25.0	1255.68	0	2	0	0	2	477	487
Glutaminyl-tRNA synthetase	SYQ_HUMAN	QARS	87.78	100.0	13	14	47	19.40	EAATQAQQTLGSTIDK	95.0	####	25.0	1661.83	0	4	0	0	2	35	50
									ATGILLYGLASR	95.0	89.6	25.0	1234.72	0	4	0	0	2	51	62
									NEVDMQVLHLLGPK	95.0	61.4	25.0	1608.84	0	2	0	0	2	167	180
									TPGYVVTPHTMNLLK	95.0	30.9	25.0	1686.89	0	0	2	0	2	240	254
									AINFNFGYAK	95.0	47.4	25.0	1144.58	0	1	0	0	2	283	292
									FDDTNPEKEEAK	95.0	28.2	25.0	1422.64	0	1	0	0	2	302	313
									FSEGEATLR	95.0	40.3	25.0	1009.49	0	1	0	0	2	395	403
									LFTLTALR	95.0	60.2	25.0	934.57	0	15	0	0	2	516	523
									DVLNDTAPR	95.0	48.2	25.0	1000.51	0	5	0	0	2	559	567
									AMAVLESLR	95.0	35.8	25.0	1005.54	0	2	0	0	2	568	576
									VIITNFPAAK	95.0	44.7	25.0	1073.64	0	2	0	0	2	577	586
									TDFKEEPEPGFK	95.0	52.4	25.0	1423.67	0	3	0	0	2	617	628
									LGYFSVDPDSHQGK	95.0	57.6	25.0	1549.73	0	3	2	0	2	746	759
Glutaredoxin-3	GLRX3_HUMAN	GLRX3	37.41	100.0	5	5	18	19.70	LEAEGVPEVSEK	95.0	42.0	25.0	1286.65	0	3	0	0	2	68	79
									IDRLDGAHAPELTK	95.0	47.5	25.0	1535.82	0	1	0	0	2	97	110
									HASSGSFLPSANEHLK	95.0	32.0	25.0	1681.83	0	0	4	0	2	115	130
									GELVGGLDIVK	95.0	45.7	25.0	1099.64	0	7	0	0	2	309	319
									ELKENGELLPILR	95.0	59.8	25.0	1523.88	0	3	0	0	2	320	332
Glutathione reductase, mitochondrial	GSHR_HUMAN	GSR	56.24	100.0	8	9	40	16.50	LNAIYQNNLTK	95.0	58.7	25.0	1291.70	0	4	0	0	2	154	164
									SHIEIIR	95.0	28.4	25.0	867.50	0	2	0	0	2	165	171
									GHAAFTSDPKPTIEVSGK	95.0	68.2	25.0	1841.94	0	2	2	0	2	172	189
									TSLMIR	95.0	35.0	25.0	736.40	0	2	0	0	2	257	262
									KTLSGLEVSMVTAVPGR	95.0	29.1	25.0	1760.96	0	0	2	0	2	300	316
									TLSGLEVSMVTAVPGR	95.0	45.3	25.0	1632.86	0	2	0	0	2	301	316
									ALLTPVAIAAGR	95.0	76.7	25.0	1152.71	0	21	0	0	2	380	391
									TYSTSFTPMYHAVTK	95.0	62.1	25.0	1749.82	0	3	0	0	2	442	456
Glutathione S-transferase omega-1	GSTO1_HUMAN	GSTO1	27.55	100.0	11	12	50	37.80	GSAPPGPVPEGSIR	95.0	40.1	25.0	1320.69	0	2	0	0	2	12	25
									HEVININLK	95.0	52.2	25.0	1079.62	0	5	0	0	2	49	57
									KLLPDDPYEK	95.0	44.8	25.0	1217.64	0	3	0	0	2	101	110
									LLPDDPYEK	95.0	28.3	25.0	1089.55	0	2	0	0	2	102	110
									MILELFSK	95.0	38.5	25.0	996.54	0	8	0	0	2	115	122
									VPSLVGSFIR	95.0	50.3	25.0	1074.63	0	11	0	0	2	123	132
									SQNKEDYAGLK	95.0	53.6	25.0	1252.62	0	2	1	0	2	133	143
									EDYAGLKEEFR	95.0	51.1	25.0	1356.64	0	2	0	0	2	137	147
									EFTKLEEVLTNK	95.0	66.3	25.0	1450.78	0	2	0	0	2	149	160
									LEEVLTNK	95.0	28.4	25.0	945.53	0	1	0	0	2	153	160
									EDPTVSALLTSEK	95.0	78.3	25.0	1389.71	0	11	0	0	2	208	220
Glutathione synthetase	GSHB_HUMAN	GSS	52.37	100.0	7	7	15	13.90	ALAEGVLLR	95.0	69.1	25.0	941.58	0	4	0	0	2	26	34
									SDYMFQR	95.0	44.2	25.0	962.40	0	3	0	0	2	126	132
									HVLSVLSK	95.0	32.9	25.0	882.54	0	1	0	0	2	165	172
									AIENELLAR	95.0	71.2	25.0	1028.57	0	2	0	0	2	222	230
									RTFEDISEK	95.0	28.5	25.0	1124.56	0	1	0	0	2	237	245
									FVLKPQR	95.0	28.0	25.0	887.55	0	2	0	0	2	361	367
									EGGGNNLYGEEMVQALK	95.0	70.8	25.0	1824.84	0	2	0	0	2	368	384
Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	GAPDH	36.04	100.0	7	8	85	21.80	VGVNGFGR	95.0	50.9	25.0	805.43	0	1	0	0	2	6	13
									IISNASCTTNCLAPLAK	95.0	78.0	25.0	1833.92	0	2	0	0	2	146	162
									GALQNIIPASTGAAK	95.0	84.4	25.0	1411.79	0	56	0	0	2	201	215
									LTGMAFR	95.0	31.6	25.0	811.41	0	7	0	0	2	228	234
									VPTANVSVVDLTCR	95.0	76.8	25.0	1530.79	0	2	0	0	2	235	248
									VVDLMAHMASK	95.0	34.2	25.0	1233.60	0	3	0	0	2	324	334

									VVDLMAHMASKE	95.0	60.0	25.0	1362.64	0	10	4	0	2	324	335
Glycogen debranching enzyme	GDE_HUMAN	AGL	174.75	100.0	5	6	18	3.85	SGGGYIVVDPILR	95.0	39.3	25.0	1345.75	0	1	0	0	2	102	114
									IEEVVLEAR	95.0	62.9	25.0	1057.59	0	2	0	0	2	772	780
									SGSLAVDNADPILK	95.0	73.6	25.0	1399.74	0	4	0	0	2	876	889
									IPFASLASR	95.0	54.0	25.0	961.55	0	8	0	0	2	890	898
									LFHVSEDPSDLNEK	95.0	61.9	25.0	1629.78	0	1	2	0	2	1338	1351
Glycogen phosphorylase, brain form	PYGB_HUMAN	PYGB	96.68	100.0	16	21	57	25.00	GLAGLGDVAEVR	95.0	79.7	25.0	1156.63	0	4	0	0	2	18	29
									YEFGIFNQK	95.0	43.3	25.0	1145.56	0	8	0	0	2	162	170
									ARPEYMLPVHFYGR	95.0	61.3	25.0	1751.87	0	0	2	2	2	193	206
									NLAENISR	95.0	40.9	25.0	916.48	0	4	0	0	2	271	278
									VLYPNDNFFEGK	95.0	64.3	25.0	1442.70	0	4	0	0	2	279	290
									ILVDVEK	94.6	26.4	25.0	815.49	0	1	0	0	2	353	359
									HLEIIYAINQR	95.0	33.2	25.0	1369.76	0	1	0	0	2	400	410
									HLDHVAALFPGDVDR	95.0	39.0	25.0	1661.84	0	0	2	2	2	411	425
									DFYELEPEK	95.0	31.4	25.0	1169.54	0	5	0	0	2	471	479
									DFYELEPEKFQNK	95.0	49.2	25.0	1686.80	0	2	0	0	2	471	483
									IGEEFLTDLSQLKK	95.0	70.9	25.0	1620.88	0	2	2	0	2	508	521
									KLLPLVSDEVFIR	95.0	26.9	25.0	1528.91	0	0	2	0	2	521	533
									LLPLVSDEVFIR	95.0	65.3	25.0	1400.81	0	2	0	0	2	522	533
									INPSSMFDVHVK	95.0	57.1	25.0	1389.68	0	4	0	0	2	558	569
									LVTSIGDVVNHDPVVGDR	95.0	79.6	25.0	1891.99	0	3	3	0	2	623	640
									VIFLENYR	95.0	54.5	25.0	1053.57	0	47	0	0	2	643	650
									VIPAADLSQQISTAGTEASGTGNMK	95.0	73.8	25.0	2463.20	0	1	1	0	2	657	681
									QAVDQISSGFFSPK	95.0	98.2	25.0	1510.75	0	6	0	0	2	741	754
									TITEYAR	95.0	38.2	25.0	853.44	0	2	0	0	2	817	823
Glycogen phosphorylase, liver form	PYGL_HUMAN	PYGL	97.13	100.0	22	25	142	24.80	GIVGVENVAELK	95.0	65.7	25.0	1227.69	0	3	0	0	2	18	29
									GIVGVENVAELKK	95.0	28.3	25.0	1355.79	0	0	2	0	2	18	30
									DYYFALAHTVR	95.0	68.4	25.0	1355.67	0	4	4	0	2	51	61
									YEYGIFNQK	95.0	41.8	25.0	1161.56	0	4	0	0	2	162	170
									NLAENISR	95.0	40.9	25.0	916.48	0	4	0	0	2	271	278
									VLYPNDNFFEGK	95.0	64.3	25.0	1442.70	0	4	0	0	2	279	290
									WPVDLVEK	95.0	37.2	25.0	985.54	0	3	0	0	2	388	395
									HLEIIYEINQK	95.0	46.0	25.0	1399.76	0	2	0	0	2	400	410
									IVALFPK	95.0	31.0	25.0	787.51	0	5	0	0	2	415	421
									MSLIEEEGSK	95.0	47.6	25.0	1138.53	0	4	0	0	2	429	438
									MSLIEEEGSKR	95.0	58.7	25.0	1294.63	0	7	2	0	2	429	439
									DFSELEPDKFQNK	95.0	39.6	25.0	1596.75	0	2	0	0	2	471	483
									FSQFLETEYK	95.0	68.1	25.0	1291.62	0	13	0	0	2	546	555
									INPSSMFDVQVK	95.0	38.4	25.0	1380.68	0	1	0	0	2	558	569
									LITSVADVVNNDPMVGSK	95.0	####	25.0	1874.95	0	8	2	0	2	623	640
									VIFLENYR	95.0	54.5	25.0	1053.57	0	47	0	0	2	643	650
									IDDVAALDKK	95.0	29.2	25.0	1087.60	0	0	1	0	2	716	725
									EYYEALPELK	95.0	38.8	25.0	1254.63	0	9	0	0	2	731	740
									DIINMLFYHDR	95.0	52.9	25.0	1452.69	0	2	0	0	2	761	771
									VFADYEAYVK	95.0	43.6	25.0	1204.59	0	3	0	0	2	774	783
									VSQLYMNPK	95.0	59.5	25.0	1095.55	0	4	0	0	2	788	796
									ISLSNESNK	95.0	39.7	25.0	991.51	0	2	0	0	2	835	843
Glycyl-tRNA synthetase	SYG_HUMAN	GARS	83.12	100.0	12	12	54	14.30	APQVDVDK	95.0	53.1	25.0	871.45	0	8	0	0	2	86	93
									LLEFNQGK	95.0	43.8	25.0	948.52	0	5	0	0	2	311	318
									LPFAAAQIGNSFR	95.0	48.5	25.0	1391.74	0	1	0	0	2	319	331
									IYLYLTK	95.0	41.5	25.0	913.54	0	2	0	0	2	413	419

									VPLVAEKPLKEPK	95.0	28.9	25.0	1447.89	0	0	3	0	2	478	490
									TVNVVQFEPSK	95.0	65.6	25.0	1247.66	0	12	0	0	2	491	501
									GEFTIETEGK	95.0	50.2	25.0	1110.53	0	3	0	0	2	538	547
									TFQLTK	95.0	40.0	25.0	737.42	0	2	0	0	2	548	553
									ELSEALTR	95.0	41.3	25.0	918.49	0	2	0	0	2	633	640
									VDDSSGSIGR	95.0	67.4	25.0	992.46	0	10	0	0	2	647	656
									YPLFEGQETGK	95.0	68.2	25.0	1268.62	0	2	0	0	2	723	733
									YPLFEGQETGKK	95.0	36.8	25.0	1396.71	0	0	4	0	2	723	734
Glyoxalase domain-containing protein 4	GLOD4_HUMAN	GLOD4	34.78	100.0	6	7	19	18.50	ALHFVFK	95.0	30.8	25.0	861.50	0	2	0	0	2	6	12
									SLPQSDPVLK	95.0	31.4	25.0	1083.60	0	2	0	0	2	146	155
									LELQGVK	95.0	29.1	25.0	786.47	0	2	0	0	2	199	205
									GGVDHAAAFGR	95.0	56.3	25.0	1057.52	0	4	1	0	2	206	216
									ELPDLEDLMK	95.0	55.5	25.0	1218.59	0	2	0	0	2	225	234
									ILTPLVSLDTPGK	95.0	61.4	25.0	1353.80	0	6	0	0	2	240	252
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_HUMAN	GRHPR	35.65	100.0	3	3	5	11.30	ILDAAGANLK	94.6	26.4	25.0	985.57	0	1	0	0	2	67	76
									GDVVNQDDLYQALASGK	95.0	81.0	25.0	1792.87	0	2	0	0	2	246	262
									GEPMPSELKL	95.0	30.8	25.0	1116.56	0	2	0	0	2	319	328
Glypican-1	GPC1_HUMAN	GPC1	61.66	100.0	7	8	33	13.10	SHAELETALR	95.0	38.1	25.0	1126.59	0	5	1	0	2	81	90
									VLQAMLATQLR	95.0	69.3	25.0	1259.71	0	2	0	0	2	95	105
									DLYSELR	95.0	29.5	25.0	895.45	0	1	0	0	2	143	149
									SFVQGLGVASDVVR	95.0	97.1	25.0	1433.77	0	13	0	0	2	222	235
									VNPQGPGPEEK	95.0	33.8	25.0	1151.57	0	5	0	0	2	348	358
									ERPPSGTLEK	95.0	36.2	25.0	1113.59	0	3	0	0	2	368	377
									MALSTASDDR	95.0	50.6	25.0	1082.48	0	3	0	0	2	405	414
GMP synthase [glutamine-hydrolyzing]	GUAA_HUMAN	GMPS	76.70	100.0	8	8	33	12.10	GLQKEEVVLLTHGDSVDK	95.0	53.3	25.0	1967.04	0	0	2	0	2	142	159
									EEVVLLTHGDSVDK	95.0	85.1	25.0	1540.79	0	2	0	0	2	146	159
									SGNIVAGIANESK	95.0	86.4	25.0	1259.66	0	4	0	0	2	170	182
									ESQSVEEALKK	95.0	29.6	25.0	1247.65	0	1	0	0	2	279	289
									TLNMTTSPEEK	95.0	43.2	25.0	1266.59	0	3	0	0	2	326	336
									THHNDTELIR	95.0	45.6	25.0	1235.61	0	0	1	0	2	390	399
									ELGLPEELVSR	95.0	50.0	25.0	1241.67	0	11	0	0	2	425	435
									VVYIFGPPVK	95.0	39.9	25.0	1118.66	0	9	0	0	2	560	569
Golgi reassembly-stacking protein 2	GORS2_HUMAN	GORASP2	47.13	100.0	3	3	9	9.51	DNDTLKDLLK	95.0	38.7	25.0	1174.63	0	2	0	0	2	51	60
									ISLPGQMAGTPITPLK	95.0	41.8	25.0	1639.91	0	6	0	0	2	213	228
									ADAASSLTVDVTPPTAK	95.0	53.2	25.0	1643.85	0	1	0	0	2	404	420
Golgi resident protein GCP60	GCP60_HUMAN	ACBD3	60.57	100.0	3	3	7	10.00	GPGASGEQPEPGEAAAGGAAEEAR	95.0	26.8	25.0	2165.97	0	0	1	0	2	50	73
									QQEVVVAGSSLPTSSK	95.0	79.7	25.0	1616.85	0	2	0	0	2	307	322
									IQQDADSVITVGR	95.0	81.3	25.0	1401.73	0	4	0	0	2	387	399
Growth arrest-specific protein 6	GAS6_HUMAN	GAS6	79.66	100.0	5	5	8	8.46	MFSGTPVIR	95.0	35.7	25.0	1023.53	0	2	0	0	2	343	351
									IAVAGDLFQPER	95.0	43.1	25.0	1315.70	0	1	0	0	2	446	457
									AVPLSVALVDYHSTK	95.0	34.5	25.0	1599.87	0	1	0	0	2	575	589
									DGEATLEVDGTR	95.0	41.8	25.0	1262.59	0	2	0	0	2	626	637
									GQSEVSAAQLQER	95.0	78.8	25.0	1402.69	0	2	0	0	2	638	650
GTP-binding nuclear protein Ran	RAN_HUMAN	RAN	24.41	100.0	5	5	13	14.40	LVLVGDGGTGK	95.0	37.5	25.0	1015.58	0	3	0	0	2	13	23
									HLTGEFEK	95.0	31.8	25.0	960.48	0	4	0	0	2	30	37
									HLTGEFEKK	95.0	41.8	25.0	1088.57	0	0	4	0	2	30	38
									KNLQYYDISAK	95.0	26.8	25.0	1342.70	0	1	0	0	2	142	152
									NLQYYDISAK	95.0	32.7	25.0	1214.61	0	1	0	0	2	143	152
GTP-binding protein SAR1a	SAR1A_HUMAN	SAR1A	22.35	100.0	3	3	9	15.70	LVFLGLDNAGK	95.0	36.7	25.0	1146.65	0	4	0	0	2	28	38
									EIFGLYGQTTGK	95.0	72.3	25.0	1313.67	0	4	0	0	2	149	160
									QGYGEGFR	95.0	30.6	25.0	913.42	0	1	0	0	2	184	191

Guanine nucleotide exchange factor VAV2	VAV2_HUMAN	VAV2	101.27	100.0	4	4	8	5.13	VFLDFKER	95.0	27.8	25.0	1053.57	0	2	0	0	2	272	279
									LQDLLVVPMQR	95.0	50.9	25.0	1327.74	0	4	0	0	2	325	335
									EIIELLFHK	95.0	35.0	25.0	1141.66	0	1	0	0	2	448	456
									FTSPADLDASGAGPGPK	95.0	97.6	25.0	1587.77	0	1	0	0	2	574	590
Guanine nucleotide-binding protein subunit beta-2-like 1	GBLP_HUMAN	GNB2L1	35.06	100.0	5	5	53	12.00	DETNYGIPQR	95.0	57.2	25.0	1192.56	0	9	0	0	2	48	57
									DVLSVAFSSDNR	95.0	90.8	25.0	1309.64	0	24	0	0	2	107	118
									IIVDELK	95.0	43.7	25.0	829.50	0	2	0	0	2	265	271
									IIVDELKQEVISTSSK	95.0	####	25.0	1789.00	0	17	0	0	2	265	280
									QEVISTSSK	95.0	28.5	25.0	978.51	0	1	0	0	2	272	280
HEAT repeat-containing protein 2	HEAT2_HUMAN	HEATR2	93.48	100.0	3	3	5	4.09	LFDDVPQVR	95.0	38.6	25.0	1088.57	0	2	0	0	2	254	262
									TPSASGLLVLASAMR	95.0	38.4	25.0	1489.80	0	2	0	0	2	447	461
									AIQDAILEVLK	95.0	36.4	25.0	1212.72	0	1	0	0	2	804	814
Heat shock 70 kDa protein 1A/1B	HSP71_HUMAN	HSPA1A	70.04	100.0	20	26	494	35.60	VEIIANDQGNR	95.0	72.8	25.0	1228.63	0	130	0	0	2	26	36
									TTPSYVAFTDTER	95.0	81.7	25.0	1487.70	0	122	0	0	2	37	49
									NQVALNPQNTVFDAK	95.0	####	25.0	1658.85	0	107	0	0	2	57	71
									KFGDPVVQSDMK	95.0	41.5	25.0	1366.67	0	4	4	0	2	77	88
									FGDPVVQSDMK	95.0	67.6	25.0	1238.57	0	16	0	0	2	78	88
									VQVSYK	95.0	25.4	25.0	723.40	1	0	0	0	2	103	108
									AFYPEEISSMVLTK	95.0	81.4	25.0	1630.80	0	4	0	0	2	113	126
									DAGVIAGLNVLR	95.0	96.3	25.0	1197.70	0	73	0	0	2	160	171
									ATAGDTHLGGEDFDNR	95.0	87.7	25.0	1675.73	0	25	9	0	2	221	236
									LVNHFVEEFK	95.0	48.3	25.0	1261.66	0	11	2	0	2	237	246
									LVNHFVEEFKR	95.0	60.2	25.0	1417.76	0	0	15	1	2	237	247
									FEELCSDLFR	95.0	56.6	25.0	1315.60	0	4	0	0	2	302	311
									STLEPVEK	95.0	31.0	25.0	902.48	0	3	0	0	2	312	319
									AQIHDLVLVGGSTR	95.0	87.4	25.0	1465.81	0	22	4	0	2	329	342
									LLQDFFNGR	95.0	63.4	25.0	1109.57	0	38	0	0	2	349	357
									DNNLLGR	95.0	46.5	25.0	801.42	0	23	0	0	2	452	458
									FELSGIPPAPR	95.0	38.4	25.0	1183.65	0	1	0	0	2	459	469
									ITITNDK	95.0	34.5	25.0	804.45	1	1	0	0	2	501	507
									ITITNDKGR	95.0	38.4	25.0	1017.57	0	3	0	0	2	501	509
									LSKEEIER	95.0	57.1	25.0	1003.54	0	16	0	0	2	510	517
									YKAEDEVQR	95.0	51.0	25.0	1137.55	0	26	20	0	2	525	533
									NALESYAFNMK	95.0	82.4	25.0	1303.60	0	43	0	0	2	540	550
									SAVEDEGLK	95.0	73.8	25.0	947.47	0	19	0	0	2	551	559
									GGSGSGPTIEEVD	95.0	45.1	25.0	1204.53	0	3	0	0	2	629	641
Heat shock 70 kDa protein 4	HSP74_HUMAN	HSPA4	94.31	100.0	22	25	145	28.20	AGGIETIANEYSDR	95.0	83.8	25.0	1495.70	0	15	0	0	2	20	33
									AFSDPFVEAEK	95.0	53.6	25.0	1239.59	0	25	0	0	2	74	84
									VTYMEEER	95.0	31.1	25.0	1072.46	0	2	0	0	2	103	110
									NFTTEQVTAMLLSK	95.0	####	25.0	1598.81	0	16	0	0	2	111	124
									LKETAESVLK	95.0	31.7	25.0	1117.65	0	1	2	0	2	125	134
									ETAESVLK	95.0	33.5	25.0	876.47	0	1	0	0	2	127	134
									QDLPALEEKPR	95.0	60.9	25.0	1295.70	0	4	0	0	2	186	196
									VLATAFDTTLGGR	95.0	####	25.0	1321.71	0	30	0	0	2	222	234
									EDIYAVEIVGGATR	95.0	76.9	25.0	1492.76	0	6	0	0	2	333	346
									VLTFYR	95.0	33.6	25.0	798.45	0	2	0	0	2	431	436
									SEENEEPMETDQNAK	95.0	41.5	25.0	1766.70	0	1	0	0	2	503	517
									SEENEEPMETDQNAKEEEK	95.0	20.0	25.0	2281.93	0	0	1	0	2	503	521
									MQVDQEEPHVEEQQQQTPAENK	95.0	40.8	25.0	2638.17	0	0	4	0	2	522	543
									EMLNLYIENEGK	95.0	62.7	25.0	1468.70	0	2	0	0	2	592	603
									NAVEEYVYEMR	95.0	65.0	25.0	1418.63	0	6	0	0	2	619	629

									FVSEDDRNSFTLK	95.0	62.4	25.0	1557.75	0	4	0	0	2	639	651
									FQESEERPK	95.0	39.5	25.0	1149.55	0	3	8	0	2	689	697
									LFEELGK	95.0	48.8	25.0	835.46	0	3	0	0	2	698	704
									NKEDQYDHLDAADMTK	95.0	42.9	25.0	1909.82	0	1	3	0	2	718	733
									QSLTMDPVVK	95.0	38.5	25.0	1133.59	0	3	0	0	2	755	764
									VEPPKEEQK	95.0	34.6	25.0	1083.57	0	1	0	0	2	790	798
									KLPEMDID	95.0	26.7	25.0	976.47	0	1	0	0	2	833	840
Heat shock cognate 71 kDa protein	HSP7C_HUMAN	HSPA8	70.88	100.0	26	38	770	35.10	VEIIANDQGNR	95.0	72.8	25.0	1228.63	0	130	0	0	2	26	36
									TTPSYVAFTDTER	95.0	81.7	25.0	1487.70	0	122	0	0	2	37	49
									NQVAMNPTNTVFDAK	95.0	####	25.0	1665.79	0	83	0	0	2	57	71
									RFDDAVVQSDMK	95.0	64.2	25.0	1426.66	0	17	5	0	2	77	88
									FDDAVVQSDMK	95.0	74.1	25.0	1270.56	0	11	0	0	2	78	88
									VQVEYK	95.0	42.8	25.0	765.41	0	13	0	0	2	103	108
									VQVEYKGETK	95.0	48.7	25.0	1180.62	0	5	4	0	2	103	112
									SFYPEEVSSMVLTK	95.0	73.8	25.0	1632.78	0	6	2	0	2	113	126
									MKEIAEAYLGK	95.0	63.6	25.0	1268.66	0	5	1	0	2	127	137
									EIAEAYLGK	95.0	45.1	25.0	993.53	0	9	0	0	2	129	137
									DAGTIAGLNVLR	95.0	####	25.0	1199.67	0	74	0	0	2	160	171
									IINEPTAAAIAYGLDK	95.0	94.0	25.0	1659.90	0	7	0	0	2	172	187
									IINEPTAAAIAYGLDKK	95.0	99.2	25.0	1787.99	0	5	0	0	2	172	188
									STAGDTHLGGEDFDNR	95.0	76.5	25.0	1691.73	0	30	4	0	2	221	236
									MVNHFIAEFK	95.0	46.5	25.0	1251.62	0	10	13	0	2	237	246
									MVNHFIAEFKR	95.0	41.2	25.0	1407.72	0	2	2	2	2	237	247
									ARFEELNADLFR	95.0	48.2	25.0	1480.75	0	2	2	0	2	300	311
									FEELNADLFR	95.0	56.5	25.0	1253.62	0	9	0	0	2	302	311
									GTLDPVEK	95.0	29.7	25.0	858.46	0	5	0	0	2	312	319
									SQIHDIVLVGGSTR	95.0	91.7	25.0	1481.81	0	35	23	0	2	329	342
									LLQDFFNGK	95.0	57.9	25.0	1081.57	0	24	0	0	2	349	357
									ITITNDK	95.0	34.5	25.0	804.45	1	1	0	0	2	501	507
									ITITNDKGR	95.0	38.4	25.0	1017.57	0	3	0	0	2	501	509
									LSKEDIER	95.0	56.1	25.0	989.53	0	7	0	0	2	510	517
									NSLESYAFNMK	95.0	89.0	25.0	1319.59	0	54	0	0	2	540	550
									NQTAEKEEFEHQQK	95.0	58.5	25.0	1745.81	0	16	26	0	2	584	597
Heat shock protein 105 kDa	HS105_HUMAN	HSPH1	96.85	100.0	17	20	132	20.50	AGGIETIANEFSDR	95.0	70.1	25.0	1479.71	0	10	0	0	2	20	33
									NQQITHANNTVSNFK	95.0	63.9	25.0	1715.85	0	2	2	0	2	54	68
									AFNDPFIQK	95.0	43.8	25.0	1079.55	0	30	0	0	2	74	82
									EKENLSYDLVPLK	95.0	34.0	25.0	1547.83	0	0	7	0	2	83	95
									ENLSYDLVPLK	95.0	72.1	25.0	1290.69	0	8	0	0	2	85	95
									LKETAENSLK	95.0	30.7	25.0	1132.62	0	2	2	0	2	125	134
									VLGTAFDPFLGGK	95.0	55.0	25.0	1321.72	0	4	0	0	2	222	234
									VEDVSAVEIVGGATR	95.0	####	25.0	1501.79	0	6	2	0	2	332	346
									DISTTLNADEAVAR	95.0	94.1	25.0	1475.73	0	5	0	0	2	361	374
									VLTFLR	95.0	43.3	25.0	748.47	0	6	0	0	2	431	436
									FVVQNVSAQK	95.0	37.8	25.0	1119.62	0	6	0	0	2	462	471
									DLLNMYIETEGK	95.0	66.2	25.0	1441.69	0	12	0	0	2	609	620
									FQEAEERPK	95.0	51.1	25.0	1133.56	0	13	0	0	2	706	714
									MFEELGQR	95.0	50.1	25.0	1025.47	0	9	0	0	2	715	722
									YNHIDESEMK	95.0	29.6	25.0	1281.54	0	4	0	0	2	740	749
									SLDQDPVVR	95.0	37.0	25.0	1028.54	0	1	0	0	2	773	781
									TPNGPNIDK	95.0	28.7	25.0	955.48	0	1	0	0	2	815	823
Heat shock protein 75 kDa,	TRAP1_HUMAN	TRAP1	80.09	100.0	12	12	50	19.00	KLLDIVAR	95.0	47.4	25.0	927.60	0	3	0	0	2	96	103

mitochondrial									LLDIVAR	95.0	53.4	25.0	799.50	0	4	0	0	2	97	103
									ELISNASDALEK	95.0	88.7	25.0	1289.66	0	4	0	0	2	115	126
									AFLDALQNQAEASSK	95.0	####	25.0	1592.79	0	14	0	0	2	182	196
									TDAPLNIR	95.0	45.0	25.0	899.49	0	2	0	0	2	333	340
									ELGSSVALYSR	95.0	48.1	25.0	1181.62	0	2	0	0	2	358	368
									ATDILPK	95.0	35.5	25.0	757.45	0	2	0	0	2	376	382
									GVVDSEDIPLNLSR	95.0	####	25.0	1513.79	0	149	1	0	2	389	402
									ELLQESALIR	95.0	30.2	25.0	1171.67	0	1	0	0	2	403	412
									EGIVTATEQEVK	95.0	57.4	25.0	1303.67	0	5	0	0	2	450	461
									LDTHPAMVTVLEMGAAR	95.0	33.8	25.0	1843.90	0	0	3	0	2	603	619
									AQLLQPTLEINPR	95.0	69.3	25.0	1492.85	0	8	0	0	2	635	647
									LNELLVK	95.0	33.5	25.0	828.52	0	2	0	0	2	693	699
Heat shock protein beta-1	HSPB1_HUMAN	HSPB1	22.76	100.0	5	5	10	23.40	VPFSLLR	95.0	37.9	25.0	831.51	0	4	0	0	2	6	12
									LFDQAFGLPR	95.0	51.9	25.0	1163.62	0	1	0	0	2	28	37
									QLSSGVSEIR	95.0	48.4	25.0	1075.57	0	2	0	0	2	80	89
									TKDGVVEITGK	95.0	45.8	25.0	1146.64	0	1	0	0	2	113	123
									AQLGGPEAAK	95.0	30.4	25.0	941.51	0	2	0	0	2	189	198
Heat shock protein HSP 90-alpha	HS90A_HUMAN	HSP90AA1	84.65	100.0	36	53	1579	36.70	ELISNSSDALDK	95.0	78.8	25.0	1291.64	0	107	0	0	2	47	58
									ELISNSSDALDKIR	95.0	99.0	25.0	1560.82	0	11	0	0	2	47	60
									IRYESLTDPSK	95.0	38.1	25.0	1308.68	0	1	6	0	2	59	69
									YESLTDPSK	95.0	58.4	25.0	1039.49	0	31	0	0	2	61	69
									YESLTDPSKLDSGK	95.0	73.2	25.0	1539.75	0	6	1	0	2	61	74
									ELHINLIPNK	95.0	45.1	25.0	1190.69	0	8	6	0	2	75	84
									ELHINLIPNKQDR	95.0	51.3	25.0	1589.88	0	13	8	5	2	75	87
									TLTIVDTGIGMTK	95.0	####	25.0	1365.73	0	189	0	0	2	88	100
									ADLINNLGTIAK	95.0	71.5	25.0	1242.71	0	137	1	0	2	101	112
									VILHLK	95.0	42.5	25.0	722.49	0	19	0	0	2	186	191
									VILHLKEDQTEYLEER	95.0	74.5	25.0	2015.04	0	2	2	1	2	186	201
									EDQTEYLEER	95.0	69.7	25.0	1311.57	0	83	0	0	2	192	201
									EDQTEYLEERR	95.0	26.3	25.0	1467.67	0	0	1	0	2	192	202
									ESEDKPEIEDVGSDEEEEK	95.0	23.3	25.0	2192.92	0	0	1	0	2	251	269
									EKYIDQEELNK	95.0	54.2	25.0	1408.70	0	3	0	0	2	282	292
									YIDQEELNK	95.0	60.6	25.0	1151.56	0	100	0	0	2	284	292
									SLTNDWEDHLAVK	95.0	99.1	25.0	1527.74	0	4	0	0	2	315	327
									HFSVEGQLEFR	95.0	73.2	25.0	1348.66	0	7	0	0	2	328	338
									ALLFVPR	95.0	47.2	25.0	815.51	0	100	0	0	2	339	345
									RAPFDLFENR	95.0	49.2	25.0	1264.64	0	43	1	0	2	346	355
									APFDLFENR	95.0	80.3	25.0	1108.54	0	27	0	0	2	347	355
									APFDLFENRK	95.0	33.2	25.0	1236.64	0	2	4	0	2	347	356
									GVVDSEDLPLNISR	95.0	####	25.0	1513.79	0	149	1	0	2	387	400
									KFYEQFSK	95.0	40.6	25.0	1076.54	0	2	0	0	2	436	443
									FYEQFSK	95.0	49.1	25.0	948.45	0	54	0	0	2	437	443
									LGIHEDSQNR	95.0	59.1	25.0	1168.57	0	26	48	0	2	447	456
									LGIHEDSQNRK	95.0	25.9	25.0	1296.67	0	0	4	0	2	447	457
									LSELLR	95.0	45.0	25.0	730.45	0	49	0	0	2	459	464
									YYTSASGDEMVSLK	95.0	93.9	25.0	1566.70	0	42	0	0	2	465	478
									HIYYITGETK	95.0	54.5	25.0	1224.63	0	50	1	0	2	490	499
									DQVANSAFVER	95.0	82.6	25.0	1235.60	0	113	0	0	2	500	510
									EGLELPEDEEEK	95.0	60.0	25.0	1416.64	0	60	0	0	2	547	558
									EGLELPEDEEEKK	95.0	48.9	25.0	1544.73	0	10	0	0	2	547	559
									DNSTMGYMAAK	95.0	31.7	25.0	1220.49	0	1	0	0	2	621	631

									KHLEINPDHSIIETLR	95.0	90.0	25.0	1915.04	0	2	1	1	2	632	647
									HLEINPDHSIIETLR	95.0	93.4	25.0	1786.94	0	7	26	2	2	633	647
Heat shock protein HSP 90-beta	HS90B_HUMAN	HSP90AB1	83.25	100.0	22	31	488	40.90	ELISNASDALDK	95.0	82.0	25.0	1275.64	0	85	0	0	2	42	53
									ELISNASDALDKIR	95.0	####	25.0	1544.83	0	4	2	0	2	42	55
									IRYESLTDPSK	95.0	38.1	25.0	1308.68	0	1	6	0	2	54	64
									YESLTDPSK	95.0	58.4	25.0	1039.49	0	31	0	0	2	56	64
									YESLTDPSKLDSGK	95.0	73.2	25.0	1539.75	0	6	1	0	2	56	69
									IDIIPNPQER	95.0	58.2	25.0	1194.65	0	20	0	0	2	73	82
									TLTLVDTGIGMTK	95.0	####	25.0	1365.73	0	189	0	0	2	83	95
									ADLINNLGTIAK	95.0	71.5	25.0	1242.71	0	137	1	0	2	96	107
									VVVITK	95.0	38.1	25.0	658.45	1	0	0	0	2	143	148
									VILHLK	95.0	42.5	25.0	722.49	0	19	0	0	2	181	186
									VILHLKEDQTEYLEER	95.0	74.5	25.0	2015.04	0	2	2	1	2	181	196
									EDQTEYLEER	95.0	69.7	25.0	1311.57	0	83	0	0	2	187	196
									EDQTEYLEERR	95.0	26.3	25.0	1467.67	0	0	1	0	2	187	197
									IEDVGSDEEDDSGK	95.0	65.5	25.0	1494.61	0	7	0	0	2	250	263
									IEDVGSDEEDDSGKDK	95.0	90.0	25.0	1737.73	0	8	9	0	2	250	265
									EKYIDQEELNK	95.0	54.2	25.0	1408.70	0	3	0	0	2	274	284
									YIDQEELNK	95.0	60.6	25.0	1151.56	0	100	0	0	2	276	284
									NPDDITQEEYGEFYK	95.0	82.1	25.0	1847.80	0	2	0	0	2	292	306
									SLTNDWEDHLAVK	95.0	99.1	25.0	1527.74	0	4	0	0	2	307	319
									HFSVEGQLEFR	95.0	73.2	25.0	1348.66	0	7	0	0	2	320	330
									ALLFIPR	95.0	47.1	25.0	829.53	0	35	0	0	2	331	337
									RAPFDLFENK	95.0	49.5	25.0	1236.64	0	38	0	0	2	338	347
									APFDLFENK	95.0	46.3	25.0	1080.54	0	39	0	0	2	339	347
									APFDLFENKK	95.0	50.6	25.0	1208.63	0	8	6	0	2	339	348
									GVVDSEDLPLNISR	95.0	####	25.0	1513.79	0	149	1	0	2	379	392
									FYEAFSK	95.0	29.5	25.0	891.42	0	1	0	0	2	429	435
									LGIHEDSTNR	95.0	51.0	25.0	1141.56	0	17	29	0	2	439	448
									LGIHEDSTNRR	95.0	32.5	25.0	1297.66	0	0	10	0	2	439	449
									RLSELLR	95.0	33.9	25.0	886.55	0	6	0	0	2	450	456
									LSELLR	95.0	45.0	25.0	730.45	0	49	0	0	2	451	456
									YHTSQSGDEMTSLSEYVSR	95.0	####	25.0	2192.94	0	6	38	0	2	457	475
									SIYYITGESK	95.0	65.8	25.0	1160.58	0	29	0	0	2	482	491
									EQVANSAFVER	95.0	66.2	25.0	1249.62	0	48	0	0	2	492	502
									SLVSVTK	95.0	39.4	25.0	733.45	0	6	0	0	2	532	538
									EGLELPEDEEEK	95.0	60.0	25.0	1416.64	0	60	0	0	2	539	550
									EGLELPEDEEEKK	95.0	48.9	25.0	1544.73	0	10	0	0	2	539	551
									DNSTMGYMMAK	95.0	53.3	25.0	1296.49	0	7	0	0	2	613	623
									KHLEINPDHPIVETLR	95.0	75.2	25.0	1911.04	0	2	2	4	2	624	639
									HLEINPDHPIVETLR	95.0	92.1	25.0	1782.95	0	4	14	1	2	625	639
Heat shock-related 70 kDa protein 2	HSP72_HUMAN	HSPA2	70.01	100.0	3	3	15	21.00	VEIIANDQGNR	95.0	72.8	25.0	1228.63	0	130	0	0	2	27	37
									TTPSYVAFTDTER	95.0	81.7	25.0	1487.70	0	122	0	0	2	38	50
									VQVEYK	95.0	42.8	25.0	765.41	0	13	0	0	2	104	109
									VQVEYKGETK	95.0	48.7	25.0	1180.62	0	5	4	0	2	104	113
									DAGTITGLNVLR	95.0	47.0	25.0	1229.69	0	6	0	0	2	161	172
									IINEPTAAAIAYGLDK	95.0	94.0	25.0	1659.90	0	7	0	0	2	173	188
									IINEPTAAAIAYGLDKK	95.0	99.2	25.0	1787.99	0	5	0	0	2	173	189
									STAGDTHLGGEDFDNR	95.0	76.5	25.0	1691.73	0	30	4	0	2	224	239
									ARFEELNADLFR	95.0	48.2	25.0	1480.75	0	2	2	0	2	303	314
									FEELNADLFR	95.0	56.5	25.0	1253.62	0	9	0	0	2	305	314

									GQIQEIVLVGGSTR	95.0	91.9	25.0	1456.81	0	3	0	0	2	332	345
									LLQDFFNGK	95.0	57.9	25.0	1081.57	0	24	0	0	2	352	360
									ITITNDK	95.0	34.5	25.0	804.45	1	1	0	0	2	504	510
									ITITNDKGR	95.0	38.4	25.0	1017.57	0	3	0	0	2	504	512
									NALESYTYNIK	95.0	75.2	25.0	1315.65	0	6	0	0	2	543	553
Heme oxygenase 2	HMOX2_HUMAN	HMOX2	36.02	100.0	3	3	5	9.18	MADLSELLK	95.0	40.6	25.0	1035.54	0	2	0	0	2	30	38
									AENTQFVK	95.0	33.7	25.0	936.48	0	1	0	0	2	48	55
									YMGDLSGGQVLK	95.0	46.3	25.0	1283.63	0	2	0	0	2	157	168
Heme-binding protein 1	HEBP1_HUMAN	HEBP1	21.08	100.0	4	4	18	24.30	GDKEEVAYEER	95.0	41.5	25.0	1324.60	0	3	0	0	2	24	34
									IPNQFQSDPPAPSDK	95.0	68.8	25.0	1640.79	0	4	0	0	2	104	118
									EADYVAQATR	95.0	52.4	25.0	1123.54	0	3	0	0	2	141	150
									AALEGTATYR	95.0	59.5	25.0	1052.54	0	8	0	0	2	153	162
Hepatocyte growth factor receptor	MET_HUMAN	MET	155.53	100.0	7	8	27	5.68	TEFTTALQR	95.0	40.9	25.0	1066.55	0	5	0	0	2	418	426
									GDLTIANLGTSEGR	95.0	83.3	25.0	1403.71	0	5	0	0	2	448	461
									VFPNSAPLEGGTR	95.0	32.5	25.0	1344.69	0	1	0	0	2	568	580
									EDPIVYEIHPTK	95.0	32.0	25.0	1440.74	0	1	1	0	2	740	751
									SFISGGSTITGVGK	95.0	87.6	25.0	1310.70	0	5	0	0	2	752	765
									NLNSVSVPR	95.0	54.4	25.0	985.54	0	5	0	0	2	766	774
									VADFGLAR	95.0	41.8	25.0	848.46	0	4	0	0	2	1220	1227
Hepatoma-derived growth factor	HDGF_HUMAN	HDGF	26.77	100.0	5	5	18	27.50	CGDLVFAK	95.0	36.3	25.0	909.45	0	1	0	0	2	12	19
									IDEMPEAAVK	95.0	53.6	25.0	1118.54	0	7	0	0	2	30	39
									DLFPYEESKEK	95.0	53.1	25.0	1384.66	0	4	0	0	2	62	72
									GNAEGSSDEEGKLVIDEPAK	95.0	41.6	25.0	2044.97	0	0	4	0	2	127	146
									EAATLEVERPLPMEVEK	95.0	49.1	25.0	1956.99	0	2	0	0	2	181	197
Heterogeneous nuclear ribonucleoprotein A/B	ROAA_HUMAN	HNRNPAB	36.21	100.0	4	4	12	11.10	DLKDYFTK	95.0	29.5	25.0	1029.53	0	2	0	0	2	84	91
									GFGFILFK	95.0	30.2	25.0	928.53	0	1	0	0	2	111	118
									GFVFITFK	95.0	29.4	25.0	958.54	0	1	0	0	2	196	203
									EVYQQQQYGSGGR	95.0	78.3	25.0	1499.69	0	8	0	0	2	233	245
Heterogeneous nuclear ribonucleoprotein A3	ROA3_HUMAN	HNRNPA3	39.58	99.5	2	2	19	7.14	KIFVGGIK	95.0	28.2	25.0	861.56	0	2	0	0	2	127	134
									IFVGGIK	95.0	30.1	25.0	733.46	0	1	0	0	2	128	134
									EDTEEYNLR	95.0	46.9	25.0	1168.51	0	9	0	0	2	135	143
									IETIEVMEDR	95.0	62.1	25.0	1250.59	0	10	0	0	2	152	161
Heterogeneous nuclear ribonucleoprotein D0	HNRPD_HUMAN	HNRNPD	38.42	100.0	6	6	67	18.00	IDASKNEEDEGHSNSSPR	95.0	20.5	25.0	1971.86	0	0	1	0	2	68	85
									DLKDYFSK	95.0	29.6	25.0	1015.51	0	2	0	0	2	112	119
									LDPITGR	95.0	42.7	25.0	771.44	0	2	0	0	2	130	136
									GFGFVLFK	95.0	38.5	25.0	914.51	0	8	0	0	2	139	146
									IFVGGLSPDTPEEK	95.0	88.6	25.0	1488.76	0	52	0	0	2	184	197
									KYHNVGLSK	95.0	27.8	25.0	1045.58	0	2	0	0	2	243	251
Heterogeneous nuclear ribonucleoprotein D-like	HNRDL_HUMAN	HNRPDL	46.42	99.5	2	2	17	7.62	DLTEYLSR	95.0	44.8	25.0	996.50	0	10	0	0	2	163	170
									GFGFVLFK	95.0	38.5	25.0	914.51	0	8	0	0	2	190	197
									VFVGGLSPDTSEEQIK	95.0	72.6	25.0	1705.86	0	7	0	0	2	235	250
Heterogeneous nuclear ribonucleoprotein F	HNRPF_HUMAN	HNRNPF	45.65	99.5	2	3	18	10.10	QSGEAFVELGSEDDVK	95.0	76.0	25.0	1709.79	0	4	0	0	2	53	68
									HSGPNSADSANDGFVR	95.0	76.3	25.0	1630.72	0	11	3	0	2	99	114
									VHIEIGPDGR	95.0	46.9	25.0	1092.58	0	10	0	0	2	317	326
Heterogeneous nuclear ribonucleoprotein G	HNRPG_HUMAN	RBMX	42.32	100.0	3	3	12	7.42	LFIGGLNTETNEK	95.0	70.4	25.0	1435.74	0	6	0	0	2	10	22
									ALEAVFGK	95.0	38.5	25.0	834.47	0	1	0	0	2	23	30
									IVEVLLMK	95.0	51.2	25.0	960.58	0	5	0	0	2	34	41
Heterogeneous nuclear ribonucleoprotein K	HNRPK_HUMAN	HNRNPK	50.96	100.0	7	7	77	17.10	RPAEDMEEEQAFKR	95.0	45.4	25.0	1751.80	0	0	4	0	2	22	35
									NTDEMVELR	95.0	44.0	25.0	1122.51	0	5	0	0	2	38	46
									ILLQSK	95.0	27.8	25.0	701.46	0	1	0	0	2	47	52
									TDYNASVSVPDSSGPER	95.0	91.7	25.0	1780.80	0	20	0	0	2	70	86

									VVLIGGKPDR	95.0	61.5	25.0	1053.64	0	21	0	0	2	192	201
									IILDLISESPIK	95.0	90.4	25.0	1340.80	0	17	0	0	2	208	219
									IDEPLEGSEDR	95.0	65.3	25.0	1259.58	0	9	0	0	2	423	433
Heterogeneous nuclear ribonucleoprotein L	HNRPL_HUMAN	HNRNPL	64.11	100.0	4	6	20	7.98	TPASPVVHIR	95.0	58.2	25.0	1076.62	0	6	5	0	2	98	107
									ISRPGDSDDSR	95.0	32.6	25.0	1204.56	0	4	0	0	2	179	189
									IEYAKPTR	95.0	34.8	25.0	977.54	0	1	0	0	2	265	272
									SKPGAAMVEMADGYAVDR	95.0	61.8	25.0	1899.86	0	2	2	0	2	417	434
Heterogeneous nuclear ribonucleoprotein Q	HNRPQ_HUMAN	SYNCRIP	69.59	100.0	9	10	93	14.40	DSDLSHVQNK	95.0	45.8	25.0	1142.54	0	8	0	0	2	82	91
									TGYTLDVTTGQR	95.0	74.1	25.0	1311.65	0	25	0	0	2	131	142
									LMMDPLTGLNR	95.0	51.4	25.0	1292.63	0	11	0	0	2	193	203
									LYNNHEIR	95.0	42.1	25.0	1058.54	0	6	0	0	2	222	229
									LFVGSIPK	95.0	34.9	25.0	860.52	0	3	0	0	2	245	252
									TKEQILEEFSK	95.0	72.5	25.0	1351.71	0	5	3	0	2	255	265
									EQILEEFSK	95.0	39.1	25.0	1122.57	0	4	0	0	2	257	265
									VTEGLTDVILYHQPDDK	95.0	24.4	25.0	1942.98	0	0	1	0	2	266	282
									NLANTVTEEILEK	95.0	83.2	25.0	1473.78	0	27	0	0	2	344	356
Heterogeneous nuclear ribonucleoprotein R	HNRPR_HUMAN	HNRNPR	70.93	100.0	5	5	36	10.30	ESDLSHVQNK	95.0	27.8	25.0	1156.56	0	1	0	0	2	85	94
									TGYTLDVTTGQR	95.0	74.1	25.0	1311.65	0	25	0	0	2	134	145
									LMMDPLSGQNR	95.0	48.8	25.0	1293.59	0	12	0	0	2	196	206
									LFVGSIPK	95.0	34.9	25.0	860.52	0	3	0	0	2	248	255
									TKENILEEFSK	95.0	39.5	25.0	1337.69	0	2	0	0	2	258	268
									ENILEEFSK	95.0	47.9	25.0	1108.55	0	6	0	0	2	260	268
									NLATTVTEEILEK	95.0	90.3	25.0	1460.78	0	15	0	0	2	347	359
Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	HNRNPU	90.57	100.0	3	3	29	4.24	DIDIHEVR	95.0	27.3	25.0	996.51	0	1	0	0	2	353	360
									YNILGTNTIMDK	95.0	67.6	25.0	1398.69	0	20	0	0	2	525	536
									NFILDQTNVSAAAQR	95.0	####	25.0	1647.84	0	8	0	0	2	576	590
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRL2_HUMAN	HNRNPUL2	85.09	100.0	4	4	8	6.29	YGGQPLFSEK	95.0	33.5	25.0	1125.56	0	1	0	0	2	264	273
									YNVLGAETVLNQMR	95.0	75.8	25.0	1623.82	0	3	0	0	2	481	494
									LVQIASR	95.0	30.4	25.0	786.48	0	2	0	0	2	522	528
									EVEGDDVPESIMLEMK	95.0	73.2	25.0	1852.82	0	2	0	0	2	578	593
Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	HNRNPA2B1	37.41	100.0	10	12	126	24.10	EESGKPGAHVTVK	95.0	57.7	25.0	1338.70	0	12	0	0	2	100	112
									KLFVGGIK	95.0	28.2	25.0	861.56	0	2	0	0	2	113	120
									LFVGGIK	95.0	30.1	25.0	733.46	0	1	0	0	2	114	120
									LFVGGIKEDTEEHHLR	95.0	66.9	25.0	1879.97	0	2	9	3	2	114	129
									EDTEEHHLR	95.0	33.4	25.0	1165.52	0	1	0	0	2	121	129
									DYFEEYGK	95.0	44.8	25.0	1050.44	0	5	0	0	2	130	137
									IDTIEIITDR	95.0	####	25.0	1188.65	0	67	0	0	2	138	147
									YHTINGHNAEVR	95.0	63.6	25.0	1410.69	0	6	0	0	2	174	185
									GGNFGFGDSR	95.0	37.2	25.0	1013.44	0	8	0	0	2	204	213
									GGGGNFGPGPGSNFR	95.0	60.9	25.0	1377.63	0	10	0	0	2	214	228
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_HUMAN	HNRNPC	33.65	100.0	7	8	31	23.20	VFIGNLNTLVVK	95.0	49.8	25.0	1316.79	0	4	0	0	2	18	29
									KSDVEAIFSK	95.0	51.9	25.0	1123.60	0	7	0	0	2	30	39
									SDVEAIFSK	95.0	61.0	25.0	995.50	0	10	0	0	2	31	39
									GFAFVQYVNER	95.0	54.0	25.0	1329.66	0	2	0	0	2	51	61
									MIAGQVLDINLAAEPK	95.0	82.0	25.0	1698.91	0	2	0	0	2	74	89
									LKGDDLQAIK	95.0	36.9	25.0	1100.63	0	2	1	0	2	188	197
									QKVDSLLENLEK	95.0	39.0	25.0	1415.77	0	3	0	0	2	205	216
Hexokinase-1	HXK1_HUMAN	HK1	102.47	100.0	17	17	44	17.90	DFNPTATVK	95.0	40.1	25.0	992.50	0	2	0	0	2	54	62
									ASGVEGADVVK	95.0	28.4	25.0	1031.54	0	1	0	0	2	177	187
									HIDLVEGDEGR	95.0	52.0	25.0	1239.60	0	4	0	0	2	244	254
									MVSGMYLGELVR	95.0	54.5	25.0	1386.68	0	2	0	0	2	296	307

									EGLLFEGR	95.0	58.8	25.0	920.48	0	2	0	0	2	316	323
									ITPELLTR	95.0	47.0	25.0	942.56	0	2	0	0	2	324	331
									FNTSDVSAIEK	95.0	57.8	25.0	1210.60	0	2	0	0	2	334	344
									TTVGVDGSLYK	95.0	36.5	25.0	1139.59	0	4	0	0	2	408	418
									FLLSESGSGK	95.0	38.6	25.0	1024.53	0	2	0	0	2	442	451
									DMLLEVK	95.0	48.5	25.0	863.45	0	4	0	0	2	482	488
									AEMELGLR	95.0	42.0	25.0	934.47	0	1	0	0	2	493	500
									LVDEYSLNAGK	95.0	73.9	25.0	1208.62	0	2	0	0	2	728	738
									MISGMYLGEIVR	95.0	55.7	25.0	1400.69	0	3	0	0	2	744	755
									GQISETLK	95.0	29.0	25.0	875.48	0	1	0	0	2	770	777
									FLSQIESDR	95.0	60.4	25.0	1094.55	0	4	0	0	2	786	794
									LALLQVR	95.0	34.7	25.0	812.54	0	2	0	0	2	795	801
									GAALITAVGVR	95.0	91.5	25.0	1027.63	0	6	0	0	2	900	910
Hexokinase-2	HXK2_HUMAN	HK2	102.36	100.0	4	4	7	6.00	DVVALIR	95.0	34.5	25.0	785.49	0	1	0	0	2	184	190
									MISGMYMGELVR	95.0	42.7	25.0	1434.64	0	2	0	0	2	296	307
									DISDIEGEKDGIR	95.0	39.4	25.0	1446.71	0	1	0	0	2	338	350
									NVELVEGEEGR	95.0	54.1	25.0	1230.60	0	3	0	0	2	692	702
									MISGMYLGEIVR	95.0	55.7	25.0	1400.69	0	3	0	0	2	744	755
Histidyl-tRNA synthetase, cytoplasmic	SYHC_HUMAN	HARS	57.39	100.0	8	9	30	17.50	ASAELIEEEVAK	95.0	81.8	25.0	1288.66	0	2	0	0	2	26	37
									VFDVIIR	95.0	40.1	25.0	861.52	0	4	0	0	2	76	82
									HGAEVIDTPVFELK	95.0	84.6	25.0	1554.82	0	6	1	0	2	87	100
									DQGGELLSLR	95.0	70.5	25.0	1087.57	0	6	0	0	2	119	128
									QALEGLGDLK	95.0	42.7	25.0	1043.57	0	1	0	0	2	294	303
									IFSIVEQR	95.0	59.8	25.0	991.56	0	6	0	0	2	389	396
									TTETQVLVASAQK	95.0	79.3	25.0	1375.74	0	3	0	0	2	406	418
									KLLEER	95.0	32.1	25.0	787.47	0	1	0	0	2	419	424
									REDLVEEIK	95.0	33.2	25.0	1130.61	0	1	0	0	2	491	499
Histone acetyltransferase type B catalytic subunit	HAT1_HUMAN	HAT1	49.50	100.0	4	4	13	10.70	FPEDLENDIR	95.0	41.1	25.0	1247.59	0	2	0	0	2	40	49
									DFVLVK	95.0	28.6	25.0	720.43	0	1	0	0	2	287	292
									LMQGFNEDMAIEAQQK	95.0	79.6	25.0	1884.85	0	2	0	0	2	305	320
									LLVTDMSDAEQYR	95.0	92.7	25.0	1556.73	0	8	0	0	2	337	349
Histone H1.1	H11_HUMAN	HIST1H1A	21.83	99.5	2	2	4	18.60	KKPAGPSVSELIVQAASSSK	95.0	47.1	25.0	1984.11	0	0	2	0	2	36	55
									GGVSLAALK	95.0	35.3	25.0	815.50	0	2	0	0	2	58	66
									ALAAAGYDVEK	95.0	57.6	25.0	1107.57	0	8	0	0	2	68	78
Histone H1.3	H13_HUMAN	HIST1H1D	22.33	100.0	3	3	23	14.90	KASGPPVSELITK	95.0	67.4	25.0	1326.76	0	2	0	0	2	35	47
									SGVSLAALK	95.0	51.7	25.0	845.51	0	13	0	0	2	56	64
									ALAAAGYDVEK	95.0	57.6	25.0	1107.57	0	8	0	0	2	66	76
Histone H1.5	H15_HUMAN	HIST1H1B	22.56	100.0	3	3	16	14.20	ATGPPVSELITK	95.0	59.8	25.0	1212.68	0	3	0	0	2	38	49
									NGLSLAALK	95.0	67.0	25.0	886.54	0	2	0	0	2	58	66
									ALAAGGYDVEK	95.0	45.0	25.0	1093.55	0	11	0	0	2	68	78
Histone H2A.V	H2AV_HUMAN	H2AFV	13.49	100.0	4	4	133	31.20	AGLQFPVGR	95.0	76.1	25.0	944.53	0	80	0	0	2	24	32
									HLQLAIR	95.0	40.7	25.0	850.53	0	42	0	0	2	86	92
									GDEELDSLIK	95.0	68.4	25.0	1118.56	0	9	0	0	2	93	102
									ATIAGGGVIPHIHK	95.0	57.3	25.0	1370.79	0	0	2	0	2	103	116
Histone H2B type 1-C/E/F/G/I	H2B1C_HUMAN	HIST1H2BC	13.89	100.0	5	6	127	29.40	KESYSVYVYK	95.0	54.9	25.0	1265.64	0	2	0	0	2	35	44
									ESYSVYVYK	95.0	39.1	25.0	1137.55	0	2	0	0	2	36	44
									QVHPDTGISSK	95.0	48.3	25.0	1168.60	0	11	32	0	2	48	58
									EIQTAVR	95.0	50.9	25.0	816.46	0	17	0	0	2	94	100
									LLLPGELAK	95.0	59.1	25.0	953.60	0	63	0	0	2	101	109
Histone H3.1t	H31T_HUMAN	HIST3H3	15.49	100.0	6	6	105	30.10	YRPGTVALR	95.0	29.4	25.0	1032.59	0	3	0	0	2	42	50
									STELLIR	95.0	65.0	25.0	831.49	0	80	0	0	2	58	64

									KLPFQR	95.0	34.3	25.0	788.48	0	7	0	0	2	65	70
									EIAQDFK	95.0	48.4	25.0	850.43	0	11	0	0	2	74	80
									VTIMPK	95.0	33.7	25.0	704.40	0	2	0	0	2	118	123
									VTIMPKDIQLAR	95.0	21.4	25.0	1400.79	0	0	2	0	2	118	129
Histone H4	H4_HUMAN	HIST1H4A	11.35	100.0	6	9	252	51.50	DNIQGITKPAIR	95.0	69.6	25.0	1325.75	0	23	16	0	2	25	36
									ISGLIYEETR	95.0	78.7	25.0	1180.62	0	44	0	0	2	47	56
									VFLENVIR	95.0	56.2	25.0	989.58	0	78	0	0	2	61	68
									DAVTYTEHAK	95.0	52.9	25.0	1134.54	0	59	5	0	2	69	78
									KTVTAMDVVYALK	95.0	74.3	25.0	1454.79	0	5	2	0	2	80	92
									TVTAMDVVYALK	95.0	77.8	25.0	1326.70	0	20	0	0	2	81	92
Histone-arginine methyltransferase CARM1	CARM1_HUMAN	CARM1	63.44	100.0	3	3	7	5.30	LLTIGDANGEIQR	95.0	75.4	25.0	1399.75	0	2	0	0	2	37	49
									MLESYLHAK	95.0	31.6	25.0	1107.55	0	1	0	0	2	268	276
									YTVNFLEAK	95.0	45.2	25.0	1084.57	0	4	0	0	2	355	363
Histone-binding protein RBBP4	RBBP4_HUMAN	RBBP4	47.64	100.0	5	5	23	11.80	EAAFDDAVEER	95.0	46.0	25.0	1251.55	0	2	0	0	2	5	15
									GEFGGFGSVSGK	95.0	82.3	25.0	1128.53	0	4	0	0	2	103	114
									IEIEIK	95.0	30.8	25.0	744.45	0	4	0	0	2	115	120
									TPSSDVLVFDYTK	95.0	####	25.0	1471.73	0	11	0	0	2	144	156
									TVALWDLR	95.0	57.4	25.0	973.55	0	2	0	0	2	297	304
Histone-binding protein RBBP7	RBBP7_HUMAN	RBBP7	47.80	100.0	3	3	5	12.90	EMFEDTVEER	95.0	49.3	25.0	1300.54	0	3	0	0	2	5	14
									GEFGGFGSVTGK	95.0	50.1	25.0	1142.55	0	1	0	0	2	102	113
									YMPQNPHIIATK	95.0	33.3	25.0	1428.73	0	1	0	0	2	131	142
									TPSSDVLVFDYTK	95.0	####	25.0	1471.73	0	11	0	0	2	143	155
									TVALWDLR	95.0	57.4	25.0	973.55	0	2	0	0	2	296	303
HLA class I histocompatibility antigen, A-31 alpha chain	1A31_HUMAN	HLA-A	40.99	100.0	3	3	5	6.03	FDSDAASQR	95.0	32.8	25.0	996.44	0	1	0	0	2	60	68
									VDLGTLR	95.0	36.2	25.0	773.45	0	2	0	0	2	100	106
									VAEQLR	95.0	33.8	25.0	715.41	0	2	0	0	2	176	181
Hsc70-interacting protein	F10A1_HUMAN	ST13	41.31	100.0	6	6	72	17.10	VAAIEALNDGELQK	95.0	####	25.0	1470.78	0	20	0	0	2	119	132
									AIDLFTDAIK	95.0	49.9	25.0	1106.61	0	13	0	0	2	133	142
									LAILYAK	95.0	38.0	25.0	791.50	0	8	0	0	2	147	153
									AIEINPDSAQPYK	95.0	57.7	25.0	1445.73	0	19	0	0	2	174	186
									LDYDEDASAMLK	95.0	92.3	25.0	1386.61	0	7	0	0	2	211	222
									VMNLISK	95.0	38.7	25.0	820.46	0	5	0	0	2	354	360
Hsp70-binding protein 1	HPBP1_HUMAN	HSPBP1	39.46	100.0	6	7	30	18.50	YLEAGAAGLR	95.0	63.4	25.0	1020.55	0	3	0	0	2	156	165
									ALFAISCLVR	95.0	33.8	25.0	1149.64	0	2	0	0	2	211	220
									EQEAGLLQFLR	95.0	72.8	25.0	1303.70	0	6	0	0	2	221	231
									LDGFSVLMR	95.0	47.8	25.0	1053.54	0	10	0	0	2	232	240
									SAFLLQNLLVGHPEHK	95.0	42.9	25.0	1802.99	0	2	1	0	2	253	268
									EPELGLEELLR	95.0	44.0	25.0	1297.70	0	6	0	0	2	315	325
Hsp90 co-chaperone Cdc37	CDC37_HUMAN	CDC37	44.45	100.0	5	5	32	14.60	ELEVAEGGK	95.0	37.5	25.0	931.47	0	2	0	0	2	70	78
									LQAEAQQLR	95.0	36.0	25.0	1056.58	0	8	0	0	2	84	92
									DVQMLQDAISK	95.0	60.7	25.0	1263.63	0	5	0	0	2	313	323
									EGEEAGPGDPLLEAVPK	95.0	96.9	25.0	1707.84	0	15	0	0	2	353	369
									TGDEKDVSV	95.0	33.5	25.0	949.45	0	2	0	0	2	370	378
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_HUMAN	HADH	34.26	100.0	3	3	5	8.28	VKNELFK	95.0	43.3	25.0	877.51	0	2	0	0	2	126	132
									TFESLVDFSK	95.0	52.6	25.0	1172.58	0	2	0	0	2	193	202
									DTPGFIVNR	95.0	26.8	25.0	1018.53	0	1	0	0	2	213	221
Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMCS1_HUMAN	HMGCS1	57.28	100.0	6	6	28	13.80	LEVGTETIIDK	95.0	68.9	25.0	1217.66	0	2	0	0	2	90	100
									MLLNDFLNDQNR	95.0	76.3	25.0	1508.72	0	6	0	0	2	278	289
									NSIYSGLEAFGDVK	95.0	93.3	25.0	1499.74	0	2	0	0	2	292	305
									ASSELFSQK	95.0	40.9	25.0	996.50	0	2	0	0	2	322	330
									VTQDATPGSALDK	95.0	58.3	25.0	1302.65	0	12	0	0	2	388	400

									TGVAPDVFAENMK	95.0	67.7	25.0	1394.66	0	4	0	0	2	416	428
Hypoxanthine-guanine phosphoribosyltransferase	HPRT_HUMAN	HPRT1	24.56	100.0	4	5	16	21.60	VFIPHGLIMDR	95.0	47.0	25.0	1313.70	0	2	3	0	2	35	45
									VIGGDDLSTLTGK	95.0	96.5	25.0	1275.68	0	3	0	0	2	116	128
									NVLIVEDIIDTGK	95.0	79.7	25.0	1428.79	0	3	0	0	2	129	141
									TMQTLLSLVR	95.0	48.9	25.0	1177.66	0	5	0	0	2	142	151
Immunoglobulin-binding protein 1	IGBP1_HUMAN	IGBP1	39.20	100.0	4	4	6	13.90	LPELFETGR	95.0	33.5	25.0	1061.56	0	2	0	0	2	12	20
									QLLDEVEVATEPAGSR	95.0	93.2	25.0	1713.87	0	2	0	0	2	21	36
									NEDLEEIASTDLK	95.0	96.2	25.0	1476.71	0	1	0	0	2	65	77
									EYYLLHLQR	95.0	29.2	25.0	1234.66	0	1	0	0	2	191	199
Importin subunit alpha-2	IMA2_HUMAN	KPNA2	57.84	100.0	5	5	23	11.20	NVSSFPDDATSPLQENR	95.0	87.8	25.0	1876.87	0	2	0	0	2	52	68
									GINSSNVENQLQATQAAR	95.0	####	25.0	1900.95	0	6	0	0	2	84	101
									FVSFLGR	95.0	33.8	25.0	825.46	0	4	0	0	2	124	130
									TGVVPQLVK	95.0	42.8	25.0	940.58	0	5	0	0	2	292	300
									ASLSLIEK	95.0	56.2	25.0	860.51	0	6	0	0	2	487	494
Importin subunit alpha-3	IMA3_HUMAN	KPNA3	57.79	100.0	6	7	31	11.70	HRNEVTVELR	95.0	41.7	25.0	1252.68	0	0	2	0	2	28	37
									LLSSDRNPPIDDLIK	95.0	38.2	25.0	1695.93	0	2	1	0	2	98	112
									NPPIDDLIK	95.0	43.0	25.0	1024.57	0	11	0	0	2	104	112
									SGILPILVK	95.0	34.9	25.0	939.62	0	5	0	0	2	113	121
									DSQVVQVVLDGLK	95.0	89.8	25.0	1399.78	0	8	0	0	2	424	436
									IEVLQQHENEDIYK	95.0	22.2	25.0	1757.87	0	0	2	0	2	462	475
Importin subunit beta-1	IMB1_HUMAN	KPNB1	97.15	100.0	15	17	103	19.10	TVSPDRLELEAAQK	95.0	53.0	25.0	1556.83	0	2	0	0	2	10	23
									LELEAAQK	95.0	35.0	25.0	901.50	0	2	0	0	2	16	23
									VLANPGNSQVAR	95.0	65.6	25.0	1225.66	0	8	0	0	2	43	54
									VAAGLQIK	95.0	55.1	25.0	799.50	0	3	0	0	2	55	62
									NSLTSKDPDIK	95.0	33.7	25.0	1217.64	0	2	0	0	2	63	73
									WLAIDANAR	95.0	47.8	25.0	1029.55	0	2	0	0	2	80	88
									SNEILTAIIQGMR	95.0	65.9	25.0	1461.77	0	13	0	0	2	170	182
									LAATNALLNSLEFTK	95.0	####	25.0	1605.88	0	3	0	0	2	192	206
									VAALQNLVK	95.0	54.9	25.0	955.59	0	21	0	0	2	235	243
									DPSVVVR	95.0	28.6	25.0	771.44	0	2	0	0	2	419	425
									SSAYESLMEIVK	95.0	80.8	25.0	1372.67	0	29	0	0	2	526	537
									TTLVIMER	95.0	48.9	25.0	978.53	0	6	0	0	2	550	557
									LQQVLQMESHIQSTSDR	95.0	80.8	25.0	2015.98	0	1	2	0	2	558	574
									GDQENVHPDVMLVQPR	95.0	64.1	25.0	1849.89	0	4	1	0	2	778	793
									LVEARPMIHELLTEGR	95.0	36.1	25.0	1880.01	0	0	2	0	2	836	851
Importin-4	IPO4_HUMAN	IPO4	118.70	100.0	4	4	10	3.89	QFAAVLTR	95.0	38.6	25.0	905.52	0	1	0	0	2	55	62
									SLILTALQR	95.0	50.5	25.0	1014.63	0	6	0	0	2	82	90
									LIMAMQTLIPIDEAK	95.0	60.2	25.0	1718.91	0	2	0	0	2	206	220
									GLEDPSQVVR	95.0	34.9	25.0	1099.57	0	1	0	0	2	402	411
Importin-5	IPO5_HUMAN	IPO5	123.61	100.0	13	14	65	10.70	KQAEETYENIPGQSK	95.0	57.1	25.0	1721.83	0	2	0	0	2	27	41
									QAEETYENIPGQSK	95.0	87.1	25.0	1593.74	0	4	0	0	2	28	41
									ITFLLQAIR	95.0	55.4	25.0	1074.67	0	9	0	0	2	42	50
									QMAAVLLR	95.0	31.5	25.0	917.52	0	4	0	0	2	60	67
									SLVEIADTVPK	95.0	76.5	25.0	1171.66	0	18	0	0	2	239	249
									VIAALLQTMEDQGNQR	95.0	96.6	25.0	1802.91	0	1	3	0	2	442	457
									HLHSIMVLK	95.0	21.8	25.0	1093.62	0	0	2	0	2	488	496
									FMQDASDVMQLLLK	95.0	####	25.0	1670.81	0	5	0	0	2	573	586
									EGFVEYTEQVVK	95.0	65.5	25.0	1427.71	0	9	0	0	2	694	705
									LMVPLLK	95.0	34.3	25.0	829.52	0	4	0	0	2	706	712
									FYFHDGVR	95.0	38.1	25.0	1040.49	0	1	0	0	2	713	720
									AKLEEHFK	95.0	36.5	25.0	1001.54	0	2	0	0	2	799	806

									LEEHFK	95.0	27.9	25.0	802.41	0	1	0	0	2	801	806
Importin-7	IPO7_HUMAN	IPO7	119.50	100.0	9	9	53	8.86	QAGVIYLK	95.0	34.4	25.0	891.53	0	2	0	0	2	54	61
									SPLVAAMQHFLPVLK	95.0	62.0	25.0	1666.94	0	4	0	0	2	168	182
									YGSPGNVSK	95.0	33.8	25.0	908.45	0	5	0	0	2	275	283
									AFAVGVQQVLLK	95.0	87.7	25.0	1272.77	0	18	0	0	2	295	306
									SDQNLQTALELTR	95.0	61.9	25.0	1488.77	0	5	0	0	2	490	502
									ETENDDLTNVIQK	95.0	75.3	25.0	1518.73	0	12	0	0	2	552	564
									AIFQTIQNR	95.0	47.8	25.0	1090.60	0	3	0	0	2	964	972
									QLQDIATLADQR	95.0	85.9	25.0	1371.72	0	2	0	0	2	991	1002
									QLQDIATLADQRR	95.0	29.4	25.0	1527.82	0	0	2	0	2	991	1003
Importin-9	IPO9_HUMAN	IPO9	115.95	100.0	7	8	30	8.45	LIPTLVSIMQAPADK	95.0	77.6	25.0	1612.90	0	7	0	0	2	647	661
									TSEFTAAFVGR	95.0	####	25.0	1185.59	0	5	0	0	2	755	765
									ELGENLDQILR	95.0	35.7	25.0	1299.69	0	7	0	0	2	777	787
									LLQHGINADDKR	95.0	37.0	25.0	1379.74	0	1	5	0	2	866	877
									VKGEEIYSMDEGIR	95.0	49.4	25.0	1641.78	0	2	0	0	2	883	896
									WTNIPLLVK	95.0	27.0	25.0	1083.66	0	1	0	0	2	908	916
									LIINELSNVMEANAAR	95.0	81.5	25.0	1773.92	0	2	0	0	2	920	935
Inhibin beta A chain	INHBA_HUMAN	INHBA	47.42	100.0	6	6	21	12.90	KTLHFEISK	95.0	46.7	25.0	1102.63	0	2	0	0	2	134	142
									EGSDLSVVER	95.0	52.8	25.0	1090.54	0	5	0	0	2	143	152
									HPQGSLDTGEEAEEVGLK	95.0	70.0	25.0	1895.90	0	4	0	0	2	181	198
									HPQGSLDTGEEAEEVGLKGER	95.0	93.7	25.0	2238.06	0	0	3	0	2	181	201
									SELLLSEK	95.0	36.5	25.0	918.51	0	6	0	0	2	202	209
									QFFVSFK	95.0	34.7	25.0	902.48	0	1	0	0	2	325	331
Inorganic pyrophosphatase	IPYR_HUMAN	PPA1	32.64	100.0	4	5	23	12.10	AAPFSLEYR	95.0	30.5	25.0	1053.54	0	2	0	0	2	10	18
									YVANLFPYK	95.0	33.9	25.0	1114.59	0	7	0	0	2	80	88
									GEIIGVK	95.0	33.1	25.0	715.44	0	2	0	0	2	133	139
									DKDFAIDIIK	95.0	53.8	25.0	1177.65	0	10	2	0	2	212	221
Inorganic pyrophosphatase 2, mitochondrial	IPYR2_HUMAN	PPA2	37.90	100.0	2	2	4	10.20	YVANIFPYK	95.0	33.9	25.0	1114.59	0	7	0	0	2	128	136
									LIAINANDPEASK	95.0	61.4	25.0	1355.72	0	3	0	0	2	204	216
									SLVESVSSSPNK	95.0	34.7	25.0	1233.63	0	1	0	0	2	309	320
Inosine-5'-monophosphate dehydrogenase 2	IMDH2_HUMAN	IMPDH2	55.79	100.0	4	4	15	10.50	EDLVVAPAGITLK	95.0	56.6	25.0	1325.77	0	2	0	0	2	183	195
									NLIDAGVDALR	95.0	45.7	25.0	1156.63	0	9	0	0	2	312	322
									VAQGVSGAVQDK	95.0	47.8	25.0	1158.61	0	2	0	0	2	439	450
									TSSAQVEGGVHSLHSYEK	95.0	37.2	25.0	1915.91	0	0	2	0	2	494	511
Inositol monophosphatase 1	IMPA1_HUMAN	IMPA1	30.17	100.0	3	3	11	13.40	SSPVDLVTATDQK	95.0	93.7	25.0	1360.70	0	5	0	0	2	37	49
									SLLVTELGSSR	95.0	89.5	25.0	1161.65	0	4	0	0	2	157	167
									EIQVIPLQRDDED	95.0	38.3	25.0	1569.78	0	2	0	0	2	265	277
Inositol-3-phosphate synthase 1	INO1_HUMAN	ISYNA1	61.05	100.0	3	3	6	4.66	ADNLIPGSR	95.0	37.8	25.0	942.50	0	1	0	0	2	192	200
									AQQLEQIR	95.0	38.8	25.0	985.54	0	2	0	0	2	201	208
									VFVGGDDFK	95.0	35.2	25.0	983.48	0	3	0	0	2	297	305
Insulin-degrading enzyme	IDE_HUMAN	IDE	117.96	100.0	13	13	44	11.90	VLLISDPTTDK	95.0	43.6	25.0	1201.67	0	3	0	0	2	75	85
									ESLDDLTNLVVK	95.0	56.4	25.0	1345.72	0	3	0	0	2	262	273
									LFSEVENK	95.0	43.2	25.0	965.49	0	1	0	0	2	274	281
									DLNAVAFR	95.0	49.1	25.0	905.48	0	6	0	0	2	416	423
									QDDKFFLPK	95.0	20.1	25.0	1137.59	0	0	1	0	2	563	571
									MATFEIDEK	95.0	38.0	25.0	1099.50	0	3	0	0	2	649	657
									RFEIIK	95.0	27.1	25.0	805.49	0	1	0	0	2	658	663
									EALDDVTLPR	95.0	47.8	25.0	1128.59	0	3	0	0	2	702	711
									AFIPQLLSR	95.0	34.7	25.0	1044.62	0	2	0	0	2	714	722
									VEAFLITMEK	95.0	72.4	25.0	1196.62	0	6	0	0	2	863	872
									SIEDMTEEAFQK	95.0	86.4	25.0	1443.63	0	4	0	0	2	873	884

									EMLAVDAPR	95.0	55.8	25.0	1017.50	0	9	0	0	2	942	950
									VSVHVLAR	95.0	36.1	25.0	880.54	0	2	0	0	2	954	961
Insulin-like growth factor-binding protein 7	IBP7_HUMAN	IGFBP7	29.11	100.0	4	6	43	10.60	TELLPGDRDNLAIQTR	95.0	61.1	25.0	1811.96	0	5	15	0	2	206	221
									DNLAIQTR	95.0	28.5	25.0	930.50	0	1	0	0	2	214	221
									ITVVDALHEIPVK	95.0	62.8	25.0	1433.84	0	12	0	0	2	263	275
									ITVVDALHEIPVKK	95.0	62.3	25.0	1561.93	0	6	4	0	2	263	276
Integrin alpha-2	ITA2_HUMAN	ITGA2	129.28	100.0	7	7	16	6.60	FVQGLDIGPTK	95.0	31.3	25.0	1174.65	0	1	0	0	2	198	208
									VVFNLNTYK	95.0	57.5	25.0	1097.60	0	4	0	0	2	222	230
									TSHGHLIFPK	95.0	41.1	25.0	1136.62	0	0	3	0	2	412	421
									VYLFTIK	95.0	34.6	25.0	883.53	0	2	0	0	2	527	533
									QIPAAQEQPFIVSNQNK	95.0	77.6	25.0	1911.99	0	2	0	0	2	805	821
									NPLMYLTGVQTDK	95.0	53.2	25.0	1495.75	0	2	0	0	2	1001	1013
									IGQTSSSVSFK	95.0	38.1	25.0	1140.59	0	2	0	0	2	1028	1038
Integrin alpha-6	ITA6_HUMAN	ITGA6	126.62	100.0	11	11	26	11.10	LLLVGAPR	95.0	36.5	25.0	838.55	0	2	0	0	2	61	68
									IEFDNDADPTSESK	95.0	58.4	25.0	1567.68	0	1	0	0	2	97	110
									GIVSKDEITFVSGAPR	95.0	27.4	25.0	1675.90	0	0	1	0	2	306	321
									DSMFGIAVK	95.0	29.7	25.0	983.49	0	1	0	0	2	413	421
									TAHIDVHFLK	95.0	37.2	25.0	1180.65	0	0	3	0	2	653	662
									EGNQDKFSYLPIQK	95.0	19.6	25.0	1666.84	0	0	1	0	2	685	698
									LETTSNQDNLAPITAK	95.0	70.1	25.0	1715.88	0	3	0	0	2	812	827
									FSLFAER	95.0	34.6	25.0	869.45	0	2	0	0	2	954	960
									LNYLDILMR	95.0	50.2	25.0	1166.62	0	5	0	0	2	1007	1015
									AFIDVTAAAENIR	95.0	75.7	25.0	1390.73	0	5	0	0	2	1016	1028
									LPNAGTQVR	95.0	29.9	25.0	955.53	0	2	0	0	2	1029	1037
Integrin alpha-V	ITAV_HUMAN	ITGAV	116.02	100.0	3	3	9	2.67	MFLLVGAPK	95.0	39.4	25.0	991.56	0	5	0	0	2	64	72
									LNGFEVFAR	95.0	34.7	25.0	1052.55	0	2	0	0	2	361	369
									AGTQLLAGLR	95.0	43.1	25.0	999.59	0	2	0	0	2	719	728
Integrin beta-1	ITB1_HUMAN	ITGB1	88.40	100.0	7	7	45	9.02	SGEPQTFTLK	95.0	39.7	25.0	1107.57	0	6	0	0	2	125	134
									SLGTDLMNEMR	95.0	54.2	25.0	1298.57	0	7	0	0	2	164	174
									IGFGSFVEK	95.0	69.1	25.0	983.52	0	12	0	0	2	182	190
									TVMPYISTTPAK	95.0	34.7	25.0	1324.68	0	2	0	0	2	191	202
									GEVFNELVGK	95.0	42.0	25.0	1091.57	0	7	0	0	2	229	238
									DNTNEIYSGK	95.0	44.2	25.0	1140.52	0	9	0	0	2	542	551
									SAVTTVVNPK	95.0	40.5	25.0	1015.58	0	2	0	0	2	785	794
Integrin beta-4	ITB4_HUMAN	ITGB4	202.13	100.0	9	9	42	5.71	TQDYPSVPTLVR	95.0	36.2	25.0	1375.72	0	6	0	0	2	301	312
									GNIHLKPSFSDGLK	95.0	27.3	25.0	1512.82	0	0	1	0	2	432	445
									QEVEENLNEVYR	95.0	75.8	25.0	1521.72	0	5	0	0	2	845	856
									VAPGYYTLTADQDAR	95.0	####	25.0	1640.79	0	6	0	0	2	916	930
									LVNITIIK	95.0	32.8	25.0	913.61	0	2	0	0	2	978	985
									FHVQLSNPK	95.0	21.0	25.0	1069.58	0	0	1	0	2	1079	1087
									MLLIENLR	95.0	42.4	25.0	1017.58	0	11	0	0	2	1282	1289
									MDFAFPGSTNSLHR	95.0	34.2	25.0	1595.73	0	0	4	0	2	1447	1460
									LVFSALGPTSLR	95.0	62.7	25.0	1260.73	0	6	0	0	2	1534	1545
Interferon-induced 17 kDa protein	UCRP_HUMAN	ISG15	17.87	100.0	4	5	11	23.00	IGVHAFQQR	95.0	27.5	25.0	1055.57	0	1	2	0	2	36	44
									LAVHPSGVALQDR	95.0	42.0	25.0	1362.75	0	2	0	0	2	45	57
									SSTYEVR	95.0	30.0	25.0	841.40	0	1	0	0	2	93	99
									LTQTVAHLK	95.0	45.2	25.0	1010.60	0	5	0	0	2	100	108
Interferon-induced guanylate-binding protein 1	GBP1_HUMAN	GBP1	67.89	100.0	9	9	15	13.70	LMANPEALK	95.0	30.4	25.0	1002.53	0	3	0	0	2	21	29
									GFSLGSTVQSHTK	95.0	72.4	25.0	1348.69	0	2	0	0	2	64	76
									AIAHYEQQMGQK	94.8	26.6	25.0	1419.67	0	1	0	0	2	331	342
									EAIEVFIR	95.0	31.8	25.0	976.55	0	1	0	0	2	363	370

									ELAAQLEK	95.0	31.7	25.0	901.50	0	1	0	0	2	383	390
									SKESMTDAILQTDQTLTEK	95.0	38.6	25.0	2155.04	0	0	1	0	2	467	485
									ESMTDAILQTDQTLTEK	95.0	97.9	25.0	1939.92	0	2	0	0	2	469	485
									IMKNEIQDLQTK	95.0	28.4	25.0	1476.77	0	2	0	0	2	571	582
									NEIQDLQTK	95.0	29.7	25.0	1088.56	0	2	0	0	2	574	582
Interferon-induced guanylate-binding protein 2	GBP2_HUMAN	GBP2	67.19	99.4	2	2	4	5.41	GQLVVNPEALK	95.0	62.6	25.0	1167.67	0	2	0	0	2	19	29
									AIAHYEQQMGQK	94.8	26.6	25.0	1419.67	0	1	0	0	2	329	340
									KLGAQLEAR	94.9	26.6	25.0	985.58	0	2	0	0	2	381	389
Interleukin enhancer-binding factor 2	ILF2_HUMAN	ILF2	43.04	100.0	9	13	62	24.90	VKPAPDETSFSEALLK	95.0	77.3	25.0	1731.92	0	4	2	0	2	44	59
									GTMTTGHNVADLVVILK	95.0	69.8	25.0	1784.96	0	3	2	0	2	111	127
									ILPTLEAVAALGNK	95.0	73.4	25.0	1409.84	0	19	3	0	2	128	141
									ILITTVPPNLR	95.0	52.1	25.0	1236.77	0	12	0	0	2	175	185
									KLDPELHLDIK	95.0	53.1	25.0	1320.75	0	0	4	0	2	186	196
									LDPELHLDIK	95.0	27.1	25.0	1192.66	0	1	1	0	2	187	196
									VLQSALAAIR	95.0	85.1	25.0	1041.64	0	7	0	0	2	197	206
									QPLALNVAYR	95.0	56.1	25.0	1144.65	0	2	0	0	2	260	269
									ILSHGGFR	95.0	45.8	25.0	886.49	0	2	0	0	2	320	327
Interleukin enhancer-binding factor 3	ILF3_HUMAN	ILF3	95.32	100.0	8	9	26	9.84	CLAALASLR	95.0	39.6	25.0	974.55	0	1	0	0	2	203	211
									EATDAIGHLDR	95.0	34.5	25.0	1197.59	0	2	0	0	2	298	308
									EDITQSAQHALR	95.0	63.8	25.0	1368.69	0	3	2	0	2	312	323
									LAAFGQLHK	95.0	39.5	25.0	984.56	0	4	0	0	2	324	332
									VLQDMGLPTGAEGR	95.0	63.8	25.0	1459.72	0	2	0	0	2	461	474
									NPVMELNEK	95.0	31.1	25.0	1089.52	0	1	0	0	2	527	535
									FVMEVEVDGQK	95.0	45.5	25.0	1296.61	0	3	0	0	2	555	565
									LFPDTPLALDANK	95.0	44.4	25.0	1414.76	0	8	0	0	2	588	600
Interstitial collagenase	MMP1_HUMAN	MMP1	53.99	100.0	8	8	27	17.90	IENYTPDLPR	95.0	53.0	25.0	1217.62	0	2	0	0	2	118	127
									ADVDHAIEK	95.0	47.2	25.0	997.50	0	6	0	0	2	128	136
									SQNPVQPIGPQTPK	95.0	63.1	25.0	1490.80	0	6	0	0	2	263	276
									LTFDAITTIR	95.0	53.4	25.0	1150.65	0	2	0	0	2	282	291
									HIDAALSEENTGK	95.0	70.3	25.0	1384.67	0	5	0	0	2	376	388
									TYFFVANK	95.0	39.8	25.0	989.51	0	2	0	0	2	389	396
									SMDPGYPK	95.0	31.9	25.0	910.40	0	2	0	0	2	406	413
									MIAHDFPGIGHK	95.0	44.8	25.0	1338.66	0	2	0	0	2	414	425
Inverted formin-2	INF2_HUMAN	INF2	135.61	100.0	4	4	5	3.20	FDVEVLK	95.0	29.2	25.0	849.47	0	1	0	0	2	667	673
									VSASVAEVQEQYTER	95.0	70.4	25.0	1695.82	0	1	0	0	2	854	868
									ALDELFEAIEQK	95.0	33.3	25.0	1405.72	0	2	0	0	2	878	889
									KLCVIQ	95.0	31.1	25.1	703.42	0	1	0	0	2	1244	1249
Iron-responsive element-binding protein 2	IREB2_HUMAN	IREB2	105.03	100.0	3	3	3	2.80	AVEAGLR	95.0	29.6	25.0	715.41	0	1	0	0	2	531	537
									EFNSYGARR	95.0	20.0	25.0	1099.53	0	0	1	0	2	780	788
									EGIPLIILAGK	95.0	31.3	25.0	1123.71	0	1	0	0	2	837	847
Isocitrate dehydrogenase [NADP] cytoplasmic	IDHC_HUMAN	IDH1	46.64	100.0	9	9	39	24.40	ISGGSVVEMQGDEMTR	95.0	92.0	25.0	1727.76	0	4	0	0	2	5	20
									NILGGTVFR	95.0	45.5	25.0	976.56	0	4	0	0	2	101	109
									ATDFVVPGPGK	95.0	50.5	25.0	1087.58	0	2	0	0	2	141	151
									VEITYTPSDGTQK	95.0	67.1	25.0	1438.71	0	4	0	0	2	152	164
									DIFQEIYDK	95.0	49.5	25.0	1170.57	0	4	0	0	2	225	233
									LIDDMVAQAMK	95.0	46.4	25.0	1266.61	0	6	0	0	2	250	260
									TVEAEAAHGTVTR	95.0	85.2	25.0	1341.68	0	12	0	0	2	302	314
									GLPNVQR	95.0	26.8	25.0	783.45	0	1	0	0	2	382	388
									SDYLNTFEFMDK	95.0	81.1	25.0	1525.65	0	2	0	0	2	389	400
Isocitrate dehydrogenase [NADP], mitochondrial	IDHP_HUMAN	IDH2	50.89	100.0	4	4	7	13.10	YFDLGLPNR	95.0	49.3	25.0	1094.56	0	2	0	0	2	81	89
									DQTDDQVTIDSALATQK	95.0	####	25.0	1848.88	0	1	0	0	2	90	106

									NILGGTVFR	95.0	45.5	25.0	976.56	0	4	0	0	2	141	149
									LIDDMVAQVLK	95.0	58.0	25.0	1260.69	0	2	0	0	2	289	299
									TIEAEAAHGTVTR	95.0	46.5	25.0	1355.69	0	2	0	0	2	341	353
Isoleucyl-tRNA synthetase, cytoplasmic	SYIC_HUMAN	IARS	144.48	100.0	13	13	34	10.50	LLILMEAR	95.0	39.2	25.0	974.57	0	4	0	0	2	255	262
									LESDYEILER	95.0	54.6	25.0	1266.62	0	3	0	0	2	269	278
									SDTPLIYK	95.0	27.6	25.0	936.50	0	1	0	0	2	403	410
									VENMVDQLLR	95.0	62.4	25.0	1232.63	0	4	0	0	2	419	428
									YGADALR	95.0	47.7	25.0	765.39	0	5	0	0	2	618	624
									LYLINSPVVR	95.0	30.8	25.0	1173.70	0	2	0	0	2	625	634
									FLIQNVLR	95.0	35.2	25.0	1002.61	0	2	0	0	2	662	669
									VLIDPVSVQDK	95.0	48.7	25.0	1212.68	0	2	0	0	2	786	796
									TESAVSQMQSVIELGR	95.0	####	25.0	1750.86	0	2	0	0	2	818	833
									EIVVIHQDPEALK	95.0	55.6	25.0	1490.82	0	2	0	0	2	849	861
									YIIEELNVR	95.0	35.2	25.0	1148.63	0	2	0	0	2	869	877
									APLKPYPVSPSDK	95.0	27.8	25.0	1398.76	0	2	0	0	2	1039	1051
									SVVTSIFGVK	95.0	31.9	25.0	1036.60	0	3	0	0	2	1116	1125
Isoleucyl-tRNA synthetase, mitochondrial	SYIM_HUMAN	IARS2	113.78	100.0	10	10	26	11.00	QQPDTELEIQQK	95.0	42.6	25.0	1456.73	0	2	0	0	2	79	90
									VLSELGR	95.0	39.0	25.0	773.45	0	2	0	0	2	164	170
									SGDLYVLAADK	95.0	75.4	25.0	1151.59	0	2	0	0	2	326	336
									ASPLLPANHVTMAK	95.0	39.9	25.0	1465.78	0	2	0	0	2	373	386
									TKDEYLINSQTTEHIVK	95.0	42.0	25.0	2019.04	0	0	3	0	2	539	555
									ADLYLEGK	95.0	48.1	25.0	908.47	0	2	0	0	2	618	625
									TVIVHGFTLGEK	95.0	58.6	25.0	1300.73	0	3	0	0	2	650	661
									EPPYGADVLR	95.0	33.7	25.0	1116.57	0	1	0	0	2	688	697
									DSFLGSIPGK	95.0	66.0	25.0	1020.54	0	7	0	0	2	887	896
									EMTADVIELK	95.0	49.2	25.0	1164.58	0	2	0	0	2	948	957
Junction plakoglobin	PLAK_HUMAN	JUP	81.73	100.0	12	12	83	16.80	LAEPSQLLK	95.0	55.8	25.0	998.59	0	12	0	0	2	116	124
									LLNDEDPVVVTK	95.0	72.9	25.0	1341.73	0	9	0	0	2	150	161
									ALMGSPQLVAAVVR	95.0	72.9	25.0	1427.80	0	11	0	0	2	178	191
									TMQNTSDLDTAR	95.0	29.4	25.0	1368.61	0	1	0	0	2	192	203
									EGLLAIFK	95.0	28.4	25.0	890.53	1	0	0	0	2	217	224
									QEGLESVLK	95.0	43.7	25.0	1002.55	0	1	0	0	2	386	394
									HPEAEMAQNSVR	95.0	33.8	25.0	1384.63	0	1	0	0	2	466	477
									LNYGIPAIVK	95.0	44.7	25.0	1087.65	0	8	0	0	2	478	487
									ATIGLIR	95.0	43.1	25.0	743.48	0	6	0	0	2	500	506
									LVQLLVK	95.0	37.4	25.0	812.56	0	14	0	0	2	527	533
									NEGTATYAAAVLFR	95.0	76.8	25.0	1483.75	0	10	0	0	2	638	651
									VSVELTNSLFK	95.0	62.3	25.0	1236.68	0	9	0	0	2	664	674
Kinectin	KTN1_HUMAN	KTN1	156.26	100.0	18	18	49	14.40	SGVIQDALKK	95.0	30.3	25.0	1058.62	0	2	0	0	2	312	321
									DAVSNTTNQLESK	95.0	98.6	25.0	1406.68	0	10	0	0	2	431	443
									TAEHEAAQQDLQSK	95.0	53.0	25.0	1555.73	0	2	0	0	2	508	521
									ENEVQSLHSK	95.0	30.1	25.0	1170.57	0	1	0	0	2	526	535
									LMQLMESEQK	95.0	30.9	25.0	1268.59	0	3	0	0	2	550	559
									QTEDSLASER	95.0	37.5	25.0	1135.52	0	2	0	0	2	618	627
									MQQSVYVK	95.0	28.8	25.0	998.50	0	1	0	0	2	671	678
									LLEEQLQHEISNK	95.0	76.7	25.0	1580.83	0	2	0	0	2	684	696
									LQTLVSEQPNKDVVEQMEK	95.0	42.1	25.0	2231.12	0	0	3	0	2	717	735
									EEELNAIR	95.0	27.3	25.0	973.49	0	1	0	0	2	762	769
									EVQDLK	95.0	28.4	25.0	731.39	0	1	0	0	2	778	783
									VQELQNLLK	95.0	33.4	25.0	1084.64	0	6	0	0	2	862	870
									TQLLQDVQDENK	95.0	80.4	25.0	1430.71	0	4	0	0	2	960	971

									SVLAETEGILQK	95.0	69.7	25.0	1287.72	0	2	0	0	2	1141	1152
									QMQSSFTSSEQELER	95.0	82.8	25.0	1802.79	0	2	0	0	2	1177	1191
									STYVTEVR	94.8	26.5	25.0	954.49	0	1	0	0	2	1221	1228
									DLLTELQK	95.0	37.1	25.0	959.54	0	2	0	0	2	1232	1239
									AQQSLELIQSK	95.0	71.6	25.0	1244.68	0	4	0	0	2	1286	1296
Kinesin-1 heavy chain	KINH_HUMAN	KIF5B	109.67	100.0	4	4	9	4.15	TGAEGAVLDEAK	95.0	57.6	25.0	1160.58	0	2	0	0	2	241	252
									STLLFGQR	95.0	52.5	25.0	921.52	0	2	0	0	2	314	321
									LITDLQDQNQK	95.0	32.7	25.0	1315.69	0	1	0	0	2	729	739
									LFVQDLATR	95.0	46.5	25.0	1062.59	0	4	0	0	2	802	810
Kinetochore-associated protein 1	KNTC1_HUMAN	KNTC1	250.74	100.0	4	4	5	1.77	TALIYSDGLK	95.0	32.5	25.0	1080.59	0	1	0	0	2	504	513
									ALEMVPLLTSTK	95.0	30.8	25.0	1318.73	0	2	0	0	2	1498	1509
									SLILNNIINK	95.0	33.0	25.0	1141.69	0	1	0	0	2	2126	2135
									EFGILAK	95.0	27.5	25.0	777.45	0	1	0	0	2	2137	2143
Kunitz-type protease inhibitor 1	SPIT1_HUMAN	SPINT1	58.38	100.0	3	3	5	6.81	EGFINYLTR	95.0	31.4	25.0	1112.57	0	1	0	0	2	135	143
									GSSGAQATFPQGPSMER	95.0	38.9	25.0	1723.77	0	1	0	0	2	310	326
									YTSGFDELQR	95.0	39.0	25.0	1215.56	0	3	0	0	2	372	381
Kynurenine--oxoglutarate transaminase 3	KAT3_HUMAN	CCBL2	51.38	100.0	3	3	6	8.15	IAAIDSLNQYTR	95.0	82.9	25.0	1364.72	0	2	0	0	2	88	99
									AIILNTPHNPLGK	95.0	61.7	25.0	1387.81	0	2	0	0	2	210	222
									DSTLDAAEEIIK	95.0	41.3	25.0	1304.66	0	2	0	0	2	436	447
Lactoylglutathione lyase	LGUL_HUMAN	GLO1	20.76	100.0	5	5	30	19.00	DFLLQQTMLR	95.0	67.6	25.0	1280.67	0	14	0	0	2	29	38
									KSLDFYTR	95.0	38.8	25.0	1029.54	0	1	0	0	2	44	51
									SLDFYTR	95.0	36.5	25.0	901.44	0	1	0	0	2	45	51
									VLGMTLIQK	95.0	62.7	25.0	1018.60	0	9	0	0	2	52	60
									RFEELGVK	95.0	36.0	25.0	977.54	0	5	0	0	2	141	148
Lamin-A/C	LMNA_HUMAN	LMNA	74.12	100.0	34	41	321	43.10	LQEKEDLQELNDR	95.0	81.1	25.0	1629.81	0	4	2	0	2	29	41
									EDLQELNDR	95.0	57.8	25.0	1131.53	0	4	0	0	2	33	41
									LAVYIDR	95.0	47.1	25.0	849.48	0	4	0	0	2	42	48
									SLETENAGLR	95.0	59.3	25.0	1089.55	0	7	0	0	2	51	60
									ITESEEVVSR	95.0	89.9	25.0	1148.58	0	35	0	0	2	63	72
									AAYEAELGDAR	95.0	72.6	25.0	1165.55	0	11	0	0	2	79	89
									AAYEAELGDARK	95.0	33.9	25.0	1293.64	0	1	0	0	2	79	90
									LQLELSK	95.0	34.6	25.0	830.50	0	3	0	0	2	102	108
									KEGDLIAAQAR	95.0	45.3	25.0	1171.64	0	4	0	0	2	123	133
									EGDLIAAQAR	95.0	82.6	25.0	1043.55	0	8	0	0	2	124	133
									LKDLEALLNSK	95.0	30.1	25.0	1243.73	0	0	1	0	2	134	144
									DLEALLNSK	95.0	65.0	25.0	1002.55	0	10	0	0	2	136	144
									EAALSTALSEK	95.0	64.2	25.0	1119.59	0	16	0	0	2	145	155
									EAALSTALSEKR	95.0	55.7	25.0	1275.69	0	4	0	0	2	145	156
									RTLEGELHDLR	95.0	40.5	25.0	1338.71	0	0	3	0	2	156	166
									TLEGELHDLR	95.0	67.3	25.0	1182.61	0	8	10	0	2	157	166
									LEAALGEAK	95.0	46.3	25.0	901.50	0	6	0	0	2	172	180
									KQLQDEMLR	95.0	36.9	25.0	1176.60	0	6	2	0	2	181	189
									QLQDEMLR	95.0	54.1	25.0	1048.51	0	2	0	0	2	182	189
									LQTMKEELDFQK	95.0	50.4	25.0	1525.76	0	2	3	0	2	197	208
									EELDFQK	95.0	40.8	25.0	908.44	0	2	0	0	2	202	208
									NIYSEELR	95.0	39.5	25.0	1023.51	0	2	0	0	2	209	216
									LADALQELR	95.0	83.3	25.0	1028.57	0	5	0	0	2	241	249
									AQHEDQVEQYKK	95.0	20.0	25.0	1502.72	0	0	1	0	2	250	261
									NSNLVGAAHEELQQSR	95.0	87.5	25.0	1752.86	0	6	5	0	2	281	296
									IDSLSAQLSQLQK	95.0	84.7	25.0	1430.79	0	48	0	0	2	299	311
									LRDLEDSLAR	95.0	48.2	25.0	1187.64	0	4	3	0	2	320	329

									LALDMEIHAYR	95.0	24.3	25.0	1347.67	0	0	2	0	2	367	377
									LLEGEEER	95.0	28.3	25.0	974.48	0	1	0	0	2	379	386
									VAVEEVDEEGK	95.0	77.1	25.0	1203.57	0	35	0	0	2	440	450
									VAVEEVDEEGKFVR	95.0	87.2	25.0	1605.81	0	10	1	0	2	440	453
									QNGDDPLLTYR	95.0	62.5	25.0	1291.63	0	10	0	0	2	472	482
									TALINSTGEEVAMR	95.0	89.2	25.0	1507.74	0	26	0	0	2	528	541
									ASASGSGAQVGGPISSGSSASSVTVTR	95.0	61.0	25.0	2365.16	0	0	4	0	2	598	624
Lamin-B1	LMNB1_HUMAN	LMNB1	66.39	100.0	5	5	13	11.30	ALYETELADAR	95.0	29.4	25.0	1251.62	0	1	0	0	2	80	90
									LQIELGK	95.0	28.2	25.0	800.49	0	2	0	0	2	103	109
									DAALATALGDKK	95.0	55.3	25.0	1173.65	0	2	0	0	2	146	157
									QLADETLLK	95.0	46.7	25.0	1030.58	0	2	0	0	2	183	191
									IQELEDLLAK	95.0	28.0	25.0	1171.66	0	1	0	0	2	321	330
									LLEGEEER	95.0	28.3	25.0	974.48	0	1	0	0	2	380	387
									IGDTSVSYK	95.0	45.9	25.0	969.49	0	7	0	0	2	475	483
Lamin-B2	LMNB2_HUMAN	LMNB2	67.67	100.0	11	11	32	19.00	ISEKEEVTTR	95.0	40.7	25.0	1191.62	0	3	0	0	2	58	67
									ALYESELADAR	95.0	52.3	25.0	1237.61	0	2	0	0	2	74	84
									LQIEIGK	95.0	28.2	25.0	800.49	0	2	0	0	2	97	103
									AELDEVNK	95.0	28.3	25.0	917.46	0	2	0	0	2	106	113
									EGELTVAQGR	95.0	34.7	25.0	1059.54	0	4	0	0	2	119	128
									VKDLESLFHR	95.0	51.7	25.0	1243.68	0	0	2	0	2	129	138
									DLESLFHR	95.0	38.6	25.0	1016.52	0	4	0	0	2	131	138
									SEVELAAALSDKR	95.0	53.2	25.0	1388.74	0	2	0	0	2	139	151
									GLESDVAELR	95.0	87.9	25.0	1088.56	0	6	0	0	2	152	161
									LESLSYQLSGLQK	95.0	87.8	25.0	1465.79	0	1	0	0	2	294	306
									LLEGEEER	95.0	28.3	25.0	974.48	0	1	0	0	2	374	381
									TVLVNADGEEVAMR	95.0	####	25.0	1519.74	0	4	0	0	2	542	555
Laminin subunit alpha-3	LAMA3_HUMAN	LAMA3	366.62	100.0	41	49	611	12.40	NQLLNYR	95.0	35.7	25.0	920.49	0	2	0	0	2	1872	1878
									KAQTLNNNVNR	95.0	40.1	25.0	1271.68	0	3	3	0	2	1915	1925
									AQTLNNNVNR	95.0	40.4	25.0	1143.59	0	4	0	0	2	1916	1925
									NVHILLK	95.0	27.7	25.0	836.54	0	1	0	0	2	1943	1949
									QISGTDGEGNNVPSGDFSR	95.0	####	25.0	1936.86	0	15	1	0	2	1950	1968
									ESQLLLNR	95.0	67.2	25.0	972.55	0	16	0	0	2	1998	2005
									THQGENNGLANSIR	95.0	84.6	25.0	1510.74	0	6	0	0	2	2012	2025
									DSLNEYEAK	95.0	32.1	25.0	1068.48	0	1	0	0	2	2026	2034
									ALGAIQR	95.0	54.0	25.0	728.44	0	15	0	0	2	2062	2068
									EINSLQSDFTK	95.0	53.6	25.0	1281.63	0	14	0	0	2	2072	2082
									LAASLNEAR	95.0	70.7	25.0	944.52	0	39	0	0	2	2111	2119
									TSLVEEAEK	95.0	40.3	25.0	1005.51	0	4	0	0	2	2136	2144
									SLQELAK	95.0	45.1	25.0	788.45	0	6	0	0	2	2148	2154
									AASASESALQTVIK	95.0	####	25.0	1375.74	0	35	0	0	2	2196	2209
									EVIDTNLTTLR	95.0	68.7	25.0	1274.70	0	6	0	0	2	2260	2270
									GDIDAMISSAK	95.0	80.3	25.0	1123.53	0	25	0	0	2	2279	2289
									ALTDADNSVNK	95.0	68.1	25.0	1147.56	0	50	0	0	2	2331	2341
									ELIQQAR	95.0	38.9	25.0	857.48	0	2	0	0	2	2375	2381
									ENGGTENMFVMYLGNK	95.0	58.2	25.0	1835.79	0	2	0	0	2	2427	2442
									EAELQVDQILTK	95.0	82.4	25.0	1386.75	0	39	0	0	2	2468	2479
									IYQFAR	95.0	33.7	25.0	797.43	0	8	0	0	2	2495	2500
									GATSSKPETPGVYDMDGR	95.0	57.1	25.0	1883.84	0	11	14	0	2	2506	2523
									LSFPPYK	95.0	31.7	25.0	851.47	0	5	0	0	2	2553	2559
									EESDKNYFEGTGYAR	95.0	64.9	25.0	1765.77	0	2	1	0	2	2596	2610
									NYFEGTGYAR	95.0	35.0	25.0	1177.53	0	2	0	0	2	2601	2610

									GLLFFAENGDR	95.0	67.9	25.0	1238.62	0	25	0	0	2	2633	2643
									FISLNIEDGK	95.0	57.3	25.0	1135.60	0	20	0	0	2	2644	2653
									LNSELPK	95.0	45.8	25.0	800.45	0	4	0	0	2	2660	2666
									GVGDAINNGR	95.0	52.7	25.0	972.49	0	4	0	0	2	2669	2678
									LLIDDQLLR	95.0	63.6	25.0	1098.65	0	29	0	0	2	2862	2870
									LPQELLKPR	95.0	66.7	25.0	1093.67	0	10	10	0	2	3001	3009
									SQFAVDMQTTSSR	95.0	93.9	25.0	1473.66	0	30	0	0	2	3010	3022
									GLVFHTGTK	95.0	28.4	25.0	959.53	0	1	0	0	2	3023	3031
									NSFMALYLSK	95.0	66.1	25.0	1189.59	0	6	0	0	2	3032	3041
									LVFALGTDGK	95.0	74.3	25.0	1020.57	0	36	0	0	2	3044	3053
									LVFALGTDGKK	95.0	49.8	25.0	1148.67	0	4	6	0	2	3044	3054
									LVVDGLR	95.0	43.6	25.0	771.47	0	6	0	0	2	3082	3088
									APVYLGSPPSGKPK	95.0	71.3	25.0	1397.78	0	7	9	0	2	3104	3117
									SLPTNSFVGCLK	95.0	59.7	25.0	1322.68	0	3	0	0	2	3118	3129
									SLTGILIHIGSQPGK	95.0	83.1	25.0	1520.88	0	24	9	0	2	3190	3204
									VTASMDSGAGGTSTSVTPK	95.0	####	25.0	1769.82	0	36	0	0	2	3215	3233
Laminin subunit alpha-5	LAMA5_HUMAN	LAMA5	399.77	100.0	22	24	95	6.68	LVGGPVAGGDPNQTIR	95.0	92.3	25.0	1550.83	0	6	0	0	2	84	99
									AHPASNAIDGTER	95.0	26.9	25.0	1338.64	0	0	1	0	2	114	126
									TNTLLGHLMGK	95.0	29.9	25.0	1200.64	0	1	0	0	2	266	276
									LELEEAATPEGHAVR	95.0	85.9	25.0	1621.82	0	4	2	0	2	876	890
									YALVVEYANEDAR	95.0	####	25.0	1512.73	0	4	0	0	2	1109	1121
									GQLQLVEGNFR	95.0	56.8	25.0	1260.67	0	2	0	0	2	1760	1770
									AGALLPAIHEQLR	95.0	38.0	25.0	1388.80	0	2	1	0	2	2181	2193
									TLLAAIR	95.0	39.7	25.0	757.49	0	6	0	0	2	2277	2283
									TLAEVER	95.0	28.6	25.0	817.44	0	1	0	0	2	2315	2321
									DTLASVFR	95.0	31.4	25.0	908.48	0	2	0	0	2	2435	2442
									TPLLQR	95.0	46.8	25.0	727.45	0	7	0	0	2	2466	2471
									AIEASNAYSR	95.0	61.4	25.0	1081.53	0	3	0	0	2	2518	2527
									AVAAEAQDTATR	95.0	70.1	25.0	1203.60	0	18	0	0	2	2634	2645
									VQSQLQAMQENVER	95.0	85.6	25.0	1675.81	0	4	0	0	2	2646	2659
									FVMYMGSR	94.6	26.4	25.0	1022.44	0	1	0	0	2	2781	2788
									QATGDYMGVSLR	95.0	43.7	25.0	1313.62	0	3	0	0	2	2789	2800
									TLQFGHMSVTVER	95.0	31.1	25.0	1520.75	0	0	3	0	2	2836	2848
									ISFDSQISTTK	95.0	81.5	25.0	1226.63	0	6	0	0	2	2954	2964
									AIQVFLLGGSR	95.0	28.0	25.0	1160.68	0	1	0	0	2	3026	3036
									GPPPELQPQPEGPPR	95.0	64.5	25.0	1595.82	0	10	0	0	2	3229	3243
									ILLVTDGAR	95.0	45.8	25.0	957.57	0	6	0	0	2	3437	3445
									TPPYLQLQVTEK	95.0	37.7	25.0	1416.77	0	1	0	0	2	3566	3577
Laminin subunit beta-1	LAMB1_HUMAN	LAMB1	198.05	100.0	10	11	30	5.94	TFRPAAMLIER	95.0	41.5	25.0	1320.71	0	0	2	0	2	142	152
									IQNLLK	95.0	35.4	25.0	728.47	0	3	0	0	2	224	229
									LHTLGDNLLDSR	95.0	46.9	25.0	1353.71	0	2	2	0	2	240	251
									ISGVIGPYR	95.0	41.6	25.0	961.55	0	6	0	0	2	1209	1217
									ETVDSVER	95.0	28.9	25.0	934.45	0	1	0	0	2	1218	1225
									DILAQSPAAEPLK	95.0	78.6	25.0	1352.74	0	2	0	0	2	1232	1244
									NIGNLFEEAEK	95.0	54.3	25.0	1263.62	0	7	0	0	2	1245	1255
									DVTEMMAQVEVK	95.0	33.9	25.0	1411.64	0	2	0	0	2	1259	1270
									YFQMSLEAEER	95.0	65.5	25.0	1418.63	0	1	0	0	2	1324	1334
									AAQNSGEAEYIEK	95.0	47.0	25.0	1409.65	0	2	0	0	2	1662	1674
Laminin subunit beta-2	LAMB2_HUMAN	LAMB2	195.96	100.0	6	6	13	4.34	IQNVVTSFAPQR	95.0	63.9	25.0	1359.74	0	2	0	0	2	108	119
									IQNLLK	95.0	35.4	25.0	728.47	0	3	0	0	2	236	241
									GQVLDVVER	95.0	38.2	25.0	1014.56	0	1	0	0	2	576	584

									AMDYDLLLR	95.0	42.3	25.0	1125.56	0	5	0	0	2	618	626
									LGIVQGIVGAR	95.0	62.4	25.0	1082.67	0	2	0	0	2	1238	1248
									AGNSLAASTAEETAGSAQGR	95.0	60.6	25.0	1848.87	0	1	0	0	2	1675	1694
									GPLGDQYQTVK	95.0	32.9	25.0	1205.62	0	2	0	0	2	1704	1714
Laminin subunit beta-3	LAMB3_HUMAN	LAMB3	129.55	100.0	26	33	612	24.50	VENVASSSGPMR	95.0	82.0	25.0	1249.58	0	75	0	0	2	82	93
									IQEVGEITNLR	95.0	69.1	25.0	1271.70	0	45	2	0	2	208	218
									LAPVPQR	95.0	30.4	25.0	780.47	0	1	0	0	2	224	230
									CLCLPNVVGPK	95.0	42.8	25.0	1256.65	0	2	0	0	2	451	461
									DLESLDR	95.0	36.1	25.0	847.42	0	2	0	0	2	681	687
									SFNGLLTMYQR	95.0	46.9	25.0	1345.66	0	3	0	0	2	688	698
									ISSADPSGAFR	95.0	58.9	25.0	1107.54	0	43	0	0	2	706	716
									MLSTAYEQSAQAAQQVSDSSR	95.0	####	25.0	2274.03	0	6	8	0	2	717	737
									LLDQLR	95.0	40.5	25.0	757.46	0	29	0	0	2	738	743
									LEMSSLPDLTPTFNK	95.0	46.0	25.0	1708.85	0	4	0	0	2	772	786
									AGGAFLMAGQVAEQLR	95.0	90.2	25.0	1634.83	0	4	0	0	2	825	840
									GFNAQLQR	95.0	51.3	25.0	933.49	0	25	0	0	2	841	848
									AAEESASQIQSSAQR	95.0	####	25.0	1562.74	0	45	2	0	2	855	869
									LETQVSASR	95.0	72.3	25.0	990.52	0	15	0	0	2	870	878
									MNEIQAIAAR	95.0	####	25.0	1132.58	0	49	0	0	2	932	941
									LPNVDLVLSQTK	95.0	77.5	25.0	1326.76	0	50	0	0	2	942	953
									RLQAEAEEAR	95.0	41.6	25.0	1172.60	0	11	0	0	2	961	970
									LQAEAEEAR	95.0	49.0	25.0	1016.50	0	24	0	0	2	962	970
									AHAVEGQVEDVVGNLR	95.0	89.6	25.0	1692.87	0	4	6	0	2	973	988
									QGTVALQEAQDTMQGTSR	95.0	####	25.0	1936.90	0	2	4	0	2	989	1006
									VAEVQQVLRPAEK	95.0	75.6	25.0	1466.83	0	10	24	0	2	1015	1027
									LGQSSMLGEQGAR	95.0	91.4	25.0	1349.65	0	78	0	0	2	1092	1104
									TEAEELFGETMEMMDR	95.0	####	25.0	1966.77	0	5	1	0	2	1110	1125
									MKDMELELLR	95.0	38.0	25.0	1309.65	0	2	0	0	2	1126	1135
									DMELELLR	95.0	43.5	25.0	1034.52	0	3	0	0	2	1128	1135
									SADLTGLEK	95.0	52.0	25.0	933.49	0	28	0	0	2	1144	1152
Laminin subunit gamma-1	LAMC1_HUMAN	LAMC1	177.58	100.0	7	7	31	5.28	AFDITYVR	95.0	49.3	25.0	984.51	0	7	0	0	2	142	149
									LNTFGDEVFNDPK	95.0	92.3	25.0	1495.71	0	7	0	0	2	256	268
									EAQDVKDVDQNLMDR	95.0	21.1	25.0	1791.82	0	0	1	0	2	1088	1102
									NTIEETGNLAEQAR	95.0	####	25.0	1545.75	0	10	0	0	2	1122	1135
									MEAENLEQLIDQK	95.0	93.2	25.0	1576.75	0	3	0	0	2	1291	1303
									TEQQTADQLLAR	95.0	56.8	25.0	1373.70	0	1	0	0	2	1330	1341
									KVSDLENEAK	95.0	33.6	25.0	1132.58	0	2	0	0	2	1557	1566
Laminin subunit gamma-2	LAMC2_HUMAN	LAMC2	130.96	100.0	30	33	629	25.60	HQDVFSSAQR	95.0	58.2	25.0	1174.56	0	83	0	0	2	236	245
									LDPVYFVAPAK	95.0	71.1	25.0	1219.67	0	24	0	0	2	246	256
									HPSAHDVILEGAGLR	95.0	86.8	25.0	1571.83	0	18	18	0	2	281	295
									ITAPLMPLGK	95.0	56.4	25.0	1056.61	0	34	0	0	2	296	305
									AGYFGDPLAPNPADK	95.0	61.6	25.0	1532.74	0	7	0	0	2	555	569
									IQMDQFMQQLQR	95.0	69.7	25.0	1597.75	0	41	0	0	2	618	629
									MEALISK	95.0	41.7	25.0	807.43	0	11	0	0	2	630	636
									AQGGDGVVPDTELEGR	95.0	68.3	25.0	1599.76	0	22	0	0	2	637	652
									MQQAEQALQDILR	95.0	####	25.0	1559.78	0	64	0	0	2	653	665
									DAQISEGASR	95.0	56.3	25.0	1033.49	0	6	0	0	2	666	675
									SLGLQLAK	95.0	44.4	25.0	829.51	0	8	0	0	2	676	683
									ALGSQYQNR	95.0	67.9	25.0	1036.52	0	15	0	0	2	707	715
									SLAQEATR	95.0	45.5	25.0	875.46	0	14	0	0	2	756	763
									LAESHVESASNMEQLTR	95.0	66.7	25.0	1917.90	0	9	39	0	2	764	780

								QALSLVR	95.0	51.2	25.0	786.48	0	8	0	0	2	788	794
								KALHEGVGSGSGSPDGAVVQGLVEK	95.0	81.2	25.0	2378.23	0	0	1	0	2	795	819
								ALHEGVGSGSGSPDGAVVQGLVEK	95.0	58.5	25.0	2250.14	0	0	8	0	2	796	819
								SLAQQLTR	95.0	48.2	25.0	916.52	0	9	0	0	2	825	832
								EATQAEIEADR	95.0	98.5	25.0	1232.58	0	43	0	0	2	833	843
								LLDSVSR	95.0	43.2	25.0	789.45	0	3	0	0	2	851	857
								LQGVSDQSFQVEEAK	95.0	####	25.0	1664.81	0	7	0	0	2	858	872
								LQGVSDQSFQVEEAKR	95.0	36.0	25.0	1820.91	0	0	7	0	2	858	873
								ADSLSSLVTR	95.0	65.7	25.0	1048.56	0	20	0	0	2	878	887
								EKSDQLLSR	95.0	29.9	25.0	1075.57	0	1	1	0	2	918	926
								SDQLLSR	95.0	49.8	25.0	818.44	0	6	0	0	2	920	926
								EFDLQVDNR	95.0	57.8	25.0	1135.54	0	13	0	0	2	957	965
								LSYISQK	95.0	31.5	25.0	838.47	0	5	0	0	2	976	982
								ALGSAAADAQR	95.0	81.7	25.0	1030.53	0	62	0	0	2	996	1006
								EVEGELER	95.0	41.0	25.0	960.46	0	13	0	0	2	1055	1062
								TQINSQLRPMMSELEER	95.0	30.5	25.0	2094.00	0	0	9	0	2	1132	1148
LanC-like protein 2	LANC2_HUMAN	LANCL2	50.84	99.5	2	2	4	6.67	LLQLQR	95.0	35.6	25.0	770.49	0	3	0	0	2	178	183
								SGNYPSSLSNETDR	95.0	58.9	25.0	1526.67	0	2	0	0	2	303	316
								FPAFELDSSK	95.0	48.4	25.0	1140.56	0	2	0	0	2	439	448
La-related protein 7	LARP7_HUMAN	LARP7	66.88	100.0	3	3	5	6.19	VNATGPQFVSGVIVK	95.0	64.6	25.0	1515.85	0	2	0	0	2	444	458
								IISTEPLPGR	95.0	51.0	25.0	1082.62	0	2	0	0	2	459	468
								LEILSGDHEQR	95.0	50.3	25.0	1296.65	0	1	0	0	2	521	531
Leucine zipper transcription factor-like protein 1	LZTL1_HUMAN	LZTFL1	34.58	100.0	3	3	7	13.70	ELLEQVAEFEK	95.0	82.9	25.0	1334.68	0	2	0	0	2	109	119
								LAPLNEGGTAELLNK	95.0	85.1	25.0	1539.84	0	2	0	0	2	138	152
								AQDLSNLENTVAALK	95.0	94.2	25.0	1586.84	0	3	0	0	2	205	219
Leucine-rich PPR motif-containing protein, mitochondrial	LPPRC_HUMAN	LRPPRC	157.89	100.0	3	3	3	2.22	SNTLPISLQSIR	95.0	26.9	25.0	1328.75	0	1	0	0	2	530	541
								SSLLLGFR	95.0	29.2	25.0	892.53	0	1	0	0	2	542	549
								GDVENIEVVQK	95.0	30.7	25.0	1229.64	0	1	0	0	2	1153	1163
Leucine-rich repeat-containing protein 47	LRC47_HUMAN	LRRC47	63.46	100.0	4	4	12	7.89	ELLLTGPGLEER	95.0	62.1	25.0	1326.73	0	3	0	0	2	23	34
								AAGGQLPPR	95.0	34.9	25.0	866.48	0	1	0	0	2	37	45
								ELSPDIAHLASLK	95.0	67.2	25.0	1393.77	0	4	0	0	2	193	205
								DGPSLLVVEQVR	95.0	55.5	25.0	1311.73	0	4	0	0	2	543	554
Leucine-rich repeat-containing protein 57	LRC57_HUMAN	LRRC57	26.74	100.0	3	3	4	13.00	TGVFQLK	95.0	32.9	25.0	792.46	0	1	0	0	2	16	22
								IESLPPLLIGK	95.0	27.2	25.0	1179.74	0	1	0	0	2	50	60
								ELPSTFGQLSALK	95.0	54.2	25.0	1390.76	0	2	0	0	2	99	111
Leucyl-tRNA synthetase, cytoplasmic	SYLC_HUMAN	LARS	134.45	100.0	3	3	5	2.98	SLGLSDEEIVK	95.0	54.4	25.0	1189.63	0	2	0	0	2	163	173
								STGNFLTLTQAIDK	95.0	39.1	25.0	1508.80	0	2	0	0	2	720	733
								TGFFEFQAAK	95.0	29.1	25.0	1145.56	0	1	0	0	2	823	832
Leukocyte elastase inhibitor	ILEU_HUMAN	SERPINB1	42.73	100.0	10	14	44	25.10	TFHFNTVEEVHSR	95.0	71.3	25.0	1602.77	0	2	2	2	2	57	69
								FQSLNADINK	95.0	52.4	25.0	1149.59	0	2	0	0	2	70	79
								FQSLNADINKR	95.0	50.8	25.0	1305.69	0	2	2	0	2	70	80
								IPELLASGMVDNMTK	95.0	####	25.0	1650.81	0	4	0	0	2	144	158
								LVLVNAIYFK	95.0	29.1	25.0	1179.71	0	1	0	0	2	159	168
								KIEEQLTLEK	95.0	53.8	25.0	1230.69	0	4	0	0	2	245	254
								IEEQLTLEK	95.0	62.7	25.0	1102.60	0	2	0	0	2	246	254
								LEESYTLNSDLAR	95.0	####	25.0	1510.74	0	4	0	0	2	278	290
								LGVQDLFNSSK	95.0	78.9	25.0	1207.63	0	12	0	0	2	291	301
								HNSSGSILFLGR	95.0	61.8	25.0	1287.68	0	3	2	0	2	364	375
Leukotriene A-4 hydrolase	LKHA4_HUMAN	LTA4H	69.27	100.0	9	9	32	15.70	GSPMEISLPIALSK	95.0	88.8	25.0	1458.79	0	13	0	0	2	84	97
								LTYTAEVSVPK	95.0	38.3	25.0	1207.66	0	1	0	0	2	155	165
								ELVALMSAIR	95.0	44.7	25.0	1118.62	0	1	0	0	2	166	175

									DGETPDPEDPSR	95.0	36.9	25.0	1314.54	0	6	0	0	2	176	187
									DGETPDPEDPSRK	95.0	33.8	25.0	1442.64	0	0	2	0	2	176	188
									SAYEFSETESMLK	95.0	97.8	25.0	1537.67	0	4	0	0	2	231	243
									EDDLNSFNATDLK	95.0	####	25.0	1481.68	0	1	0	0	2	481	493
									APLPLGHIK	95.0	48.1	25.0	945.59	0	2	0	0	2	511	519
									ASMHPVTAMLVGK	95.0	44.5	25.0	1373.69	0	2	0	0	2	594	606
Lipolysis-stimulated lipoprotein receptor	LSR_HUMAN	LSR	71.42	100.0	4	4	52	7.86	QGNAVTLGDYYQGR	95.0	58.5	25.0	1541.73	0	9	0	0	2	180	193
									SSSAGGQGSYVPLLR	95.0	####	25.0	1478.76	0	38	0	0	2	363	377
									DTDSSVASEVR	95.0	46.0	25.0	1165.53	0	3	0	0	2	378	388
									IQASQQDDSMR	95.0	37.1	25.0	1294.57	0	2	0	0	2	393	403
Liprin-alpha-1	LIPA1_HUMAN	PPFIA1	135.76	100.0	3	3	4	3.41	QAQSPAGVSSEVEVLK	95.0	81.5	25.0	1628.85	0	2	0	0	2	147	162
									VIELQEIISK	95.0	30.7	25.0	1171.69	0	1	0	0	2	252	261
									SGAIMSALSDTEIQR	95.0	82.7	25.0	1594.77	0	1	0	0	2	907	921
L-lactate dehydrogenase A chain	LDHA_HUMAN	LDHA	36.67	100.0	15	22	553	37.30	DQLIYNLLK	95.0	68.5	25.0	1119.64	0	72	0	0	2	6	14
									LKGEMMDLQHGSLFLR	95.0	65.4	25.0	1906.95	0	3	3	1	2	58	73
									GEMMDLQHGSLFLR	95.0	46.8	25.0	1665.77	0	9	21	0	2	60	73
									DYNVTANSK	95.0	62.8	25.0	1011.47	0	49	0	0	2	82	90
									LVIITAGAR	95.0	65.2	25.0	913.58	0	120	0	0	2	91	99
									LNLVQR	95.0	52.5	25.0	742.46	4	20	0	0	2	107	112
									NVNIFK	95.0	48.0	25.0	734.42	0	20	0	0	2	113	118
									FIIPNVVK	95.0	40.3	25.0	929.58	0	8	0	0	2	119	126
									VIGSGCNLDSAR	95.0	54.9	25.0	1248.60	0	7	0	0	2	158	169
									YLMGER	95.0	27.0	25.0	784.37	0	3	0	0	2	172	177
									TLHPDLGTDK	95.0	31.5	25.0	1096.56	0	3	2	0	2	213	222
									TLHPDLGTDKDK	95.0	39.2	25.0	1339.69	0	3	1	0	2	213	224
									QVVESAYEVIK	95.0	64.8	25.0	1264.68	0	29	0	0	2	233	243
									RVHPVSTMIK	95.0	27.0	25.0	1183.66	0	1	12	0	2	269	278
									VTLTSEEEAR	95.0	74.8	25.0	1134.56	0	162	0	0	2	306	315
L-lactate dehydrogenase B chain	LDHB_HUMAN	LDHB	36.62	100.0	10	13	164	35.30	LIAPVAEEEATVPNNK	95.0	87.8	25.0	1694.90	0	54	0	0	2	8	23
									GEMMDLQHGSLFLQTPK	95.0	60.0	25.0	1963.93	0	6	3	0	2	61	77
									IVADKDYSVTANSK	95.0	91.5	25.0	1510.77	0	19	5	0	2	78	91
									DYSVTANSK	95.0	37.7	25.0	984.46	0	5	0	0	2	83	91
									IVVVTAGVR	95.0	76.5	25.0	913.58	0	9	0	0	2	92	100
									LNLVQR	95.0	52.5	25.0	742.46	4	20	0	0	2	108	113
									NVNVFK	95.0	39.9	25.0	720.40	1	4	0	0	2	114	119
									FIIPQIVK	95.0	45.1	25.0	957.61	0	4	0	0	2	120	127
									VIGSGCNLDSAR	95.0	54.9	25.0	1248.60	0	7	0	0	2	159	170
									MVVESAYEVIK	95.0	69.4	25.0	1283.66	0	23	0	0	2	234	244
									GLTSVINQK	95.0	56.8	25.0	959.55	0	23	0	0	2	300	308
									LKDDEVAQLK	95.0	45.7	25.0	1158.64	0	8	0	0	2	309	318
Low molecular weight phosphotyrosine protein phosphatase	PPAC_HUMAN	ACP1	18.02	100.0	3	3	9	19.00	SPIAEAVFR	95.0	56.7	25.0	989.54	0	6	0	0	2	20	28
									HGIPMSHVAR	95.0	21.2	25.0	1120.57	0	0	1	0	2	67	76
									IELLGSYDPQK	95.0	51.9	25.0	1262.66	0	2	0	0	2	114	124
Lupus La protein	LA_HUMAN	SSB	46.82	100.0	5	6	19	14.70	SPSKPLPEVTDEYKNDVK	95.0	32.1	25.0	2046.04	0	0	6	1	2	92	109
									GFPTDATLDDIK	95.0	32.5	25.0	1292.64	0	2	0	0	2	117	128
									ETDLLILFK	95.0	36.8	25.0	1091.63	0	3	0	0	2	177	185
									DANNGNLQLR	95.0	39.9	25.0	1114.56	0	5	0	0	2	288	297
									IIEDQQESLNK	95.0	54.1	25.0	1316.67	0	2	0	0	2	318	328
L-xylulose reductase	DCXR_HUMAN	DCXR	25.89	100.0	3	3	12	11.90	GTVQALHATGAR	95.0	60.8	25.0	1181.64	0	5	0	0	2	22	33
									TQADLDSLVR	95.0	47.4	25.0	1117.58	0	5	0	0	2	40	49
									SFEVNLR	95.0	27.9	25.0	864.46	0	2	0	0	2	103	109

Lysophospholipase-like protein 1	LYPL1_HUMAN	LYPLAL1	26.30	100.0	3	4	10	16.50	HSASLIFLHGSGDSGQGLR	95.0	46.6	25.0	1938.98	0	0	3	0	2	20	38
									QVLNQDLTFQHIK	95.0	73.9	25.0	1583.85	0	2	2	0	2	43	55
									TELDILK	95.0	33.2	25.0	831.48	0	3	0	0	2	216	222
Lysosome-associated membrane glycoprotein 1	LAMP1_HUMAN	LAMP1	44.87	100.0	3	3	24	6.71	TVESITDIR	95.0	73.4	25.0	1033.55	0	17	0	0	2	138	146
									ALQATVGNSYK	95.0	36.6	25.0	1151.61	0	2	0	0	2	327	337
									AFSVNIFK	95.0	46.2	25.0	925.51	0	5	0	0	2	349	356
Lysyl oxidase homolog 2	LOXL2_HUMAN	LOXL2	86.71	100.0	3	3	13	3.36	ELGYVEAK	95.0	29.6	25.0	908.47	0	2	0	0	2	99	106
									TPVMEGYVEVK	95.0	40.2	25.0	1267.62	0	6	0	0	2	199	209
									VEVLVER	95.0	33.8	25.0	843.49	0	5	0	0	2	448	454
Lysyl-tRNA synthetase	SYK_HUMAN	KARS	68.03	100.0	15	16	56	25.30	VNGEDPYPHK	95.0	30.2	25.0	1155.54	0	1	0	0	2	89	98
									YSHLQPGDHLTDITLK	95.0	33.9	25.0	1837.94	0	0	2	0	2	112	127
									LIFYDLR	95.0	39.2	25.0	939.53	0	6	0	0	2	142	148
									SEEEFIHINNK	95.0	69.8	25.0	1359.65	0	2	0	0	2	165	175
									RGDIIGVQGNPGK	95.0	57.8	25.0	1310.72	0	2	0	0	2	178	190
									IITYIR	95.0	34.5	25.0	778.48	0	2	0	0	2	250	255
									VYEIGR	95.0	30.8	25.0	736.40	0	1	0	0	2	315	320
									INMVEELEK	95.0	30.3	25.0	1120.56	0	1	0	0	2	394	402
									LPETNLFETEETR	95.0	####	25.0	1578.76	0	6	0	0	2	408	420
									LPETNLFETEETRK	95.0	63.4	25.0	1706.86	0	2	13	0	2	408	421
									FELFVMK	95.0	32.4	25.0	929.48	0	4	0	0	2	486	492
									QLFEEQAK	94.8	26.5	25.0	992.50	0	1	0	0	2	510	517
									VAMFLTDSNNIK	95.0	47.5	25.0	1368.68	0	3	0	0	2	554	565
									EVLLFPAMKPEDK	95.0	40.9	25.0	1532.80	0	8	0	0	2	566	578
									KENVATTDTLESTTVGTSV	95.0	72.7	25.0	1952.97	0	2	0	0	2	579	597
Macrophage-capping protein	CAPG_HUMAN	CAPG	38.50	100.0	7	8	75	23.60	YQEGGVESAFHK	95.0	62.3	25.0	1351.63	0	6	0	0	2	116	127
									DLALAIR	95.0	45.1	25.0	771.47	0	4	0	0	2	192	198
									EGNPEEDLTADK	95.0	59.1	25.0	1317.58	0	9	0	0	2	232	243
									ANAQAAALYK	95.0	67.3	25.0	1020.55	0	11	0	0	2	244	253
									VSDATGQMNLTK	95.0	92.2	25.0	1280.62	0	24	0	0	2	254	265
									QAALQVAEGFISR	95.0	80.2	25.0	1389.75	0	15	2	0	2	307	319
									MQYAPNTQVEILPQGR	95.0	82.7	25.0	1860.93	0	4	0	0	2	320	335
Major vault protein	MVP_HUMAN	MVP	99.31	100.0	18	19	69	19.80	VLFAPMR	95.0	33.1	25.0	849.47	0	2	0	0	2	43	49
									MVTVPPR	95.0	36.0	25.0	815.44	0	4	0	0	2	50	56
									HADLEIR	95.0	42.2	25.0	853.45	0	8	0	0	2	85	91
									ALLDFEDKDGDK	95.0	52.7	25.0	1365.65	0	4	2	0	2	125	136
									ALQPLEEGEDEEK	95.0	69.9	25.0	1486.69	0	4	0	0	2	336	348
									GPLEYVPSAK	95.0	44.3	25.0	1060.57	0	3	0	0	2	361	370
									ELPPGVEELLNK	95.0	34.4	25.0	1337.73	0	2	0	0	2	418	429
									SLQPLAPR	95.0	38.4	25.0	881.52	0	1	0	0	2	445	452
									VPHNAAVQVYDYR	95.0	68.2	25.0	1531.77	0	2	0	0	2	462	474
									GAVASVTFDDFHK	95.0	26.7	25.0	1393.67	0	0	2	0	2	581	593
									TAVFGFETSEAK	95.0	73.2	25.0	1286.63	0	8	0	0	2	601	612
									IEGEGSVLQAK	95.0	59.5	25.0	1130.61	0	5	0	0	2	735	745
									ELELVYAR	95.0	60.2	25.0	992.54	0	5	0	0	2	767	774
									AQLELEVSK	95.0	41.2	25.0	1016.56	0	2	0	0	2	775	783
									AQQLAEVEVK	95.0	61.1	25.0	1114.61	0	3	0	0	2	784	793
									AQQLAEVEVKK	95.0	31.0	25.0	1242.71	0	2	0	0	2	784	794
									QMTEAIGPSTIR	95.0	44.7	25.0	1319.66	0	4	0	0	2	797	808
									DLAVAGPEMQVK	95.0	66.4	25.0	1273.65	0	6	0	0	2	809	820
Malate dehydrogenase, cytoplasmic	MDHC_HUMAN	MDH1	36.41	100.0	5	5	25	17.70	DVIATDKEDVAFK	95.0	80.8	25.0	1450.74	0	4	0	0	2	67	79
									VIVVGNPANTNCLTASK	95.0	99.3	25.0	1757.92	0	2	0	0	2	126	142

									LGVTANDVK	95.0	48.6	25.0	916.51	0	12	0	0	2	171	179
									GEFVTTVQQR	95.0	67.7	25.0	1164.60	0	6	0	0	2	221	230
									ESAFEFLSSA	95.0	36.6	25.0	1087.49	0	1	0	0	2	325	334
Malate dehydrogenase, mitochondrial	MDHM_HUMAN	MDH2	35.49	100.0	9	10	98	31.40	IFGVTTLDIVR	95.0	57.8	25.0	1233.72	0	15	0	0	2	166	176
									ANTFVAELK	95.0	53.8	25.0	992.54	0	9	0	0	2	177	185
									VNVPVIGGHAGK	95.0	40.5	25.0	1147.66	0	4	14	0	2	192	203
									TIIPLISQCTPK	95.0	51.6	25.0	1370.77	0	2	0	0	2	204	215
									VDFPQDQLTALTGR	95.0	47.2	25.0	1560.80	0	1	0	0	2	216	229
									IQEAGTEVVK	95.0	35.5	25.0	1073.58	0	6	0	0	2	230	239
									AGAGSATLSMAYAGAR	95.0	####	25.0	1470.70	0	16	0	0	2	242	257
									FVFSLVDAMNGK	95.0	64.7	25.0	1343.67	0	16	0	0	2	258	269
									MISDAIPELK	95.0	46.1	25.0	1132.59	0	15	0	0	2	315	324
Matrilin-2	MATN2_HUMAN	MATN2	106.82	100.0	4	4	7	6.07	VGLLQYGSTVK	95.0	69.2	25.0	1164.66	0	2	0	0	2	96	106
									VIMIVTDGRPQDSVAEVAAK	95.0	26.3	25.0	2115.11	0	0	2	0	2	164	183
									SLGEENFEVVK	95.0	41.5	25.0	1250.63	0	2	0	0	2	665	675
									AIEEELQEIASEPTNK	95.0	49.8	25.0	1800.89	0	1	0	0	2	797	812
Matrix metalloproteinase-14	MMP14_HUMAN	MMP14	65.87	100.0	3	3	9	4.98	VGEYATYEAIR	95.0	65.1	25.0	1271.63	0	3	0	0	2	135	145
									GLPASINTAYER	95.0	42.7	25.0	1291.66	0	2	0	0	2	363	374
									FNEELR	95.0	31.8	25.0	807.40	0	4	0	0	2	438	443
Mesothelin	MSLN_HUMAN	MSLN	68.97	100.0	3	3	14	6.35	FVAESAEVLLPR	95.0	30.0	25.0	1330.74	0	1	0	0	2	196	207
									IQSFLGGAPTEDLK	95.0	68.6	25.0	1475.77	0	7	0	0	2	504	517
									TDAVLPLTVAEVQK	95.0	63.9	25.0	1483.84	0	6	0	0	2	536	549
Metalloproteinase inhibitor 2	TIMP2_HUMAN	TIMP2	24.38	100.0	4	4	7	12.70	EVDSGNDIYGNPIK	95.0	74.3	25.0	1520.72	0	2	0	0	2	54	67
									EVDSGNDIYGNPIKR	95.0	82.8	25.0	1676.82	0	1	0	0	2	54	68
									IQYEIK	95.0	37.0	25.0	793.45	0	3	0	0	2	69	74
									EYLIAGK	95.0	27.0	25.0	793.45	0	1	0	0	2	109	115
Methionine adenosyltransferase 2 subunit beta	MAT2B_HUMAN	MAT2B	37.53	100.0	6	6	12	20.70	LVEEEVNIPNRR	95.0	20.5	25.0	1467.79	0	0	1	0	2	19	30
									VLVTGATGLLGR	95.0	94.5	25.0	1156.71	0	2	0	0	2	31	42
									EEDIPAPLNLYGK	95.0	55.1	25.0	1458.75	0	2	0	0	2	149	161
									AVLENNLGAAVLR	95.0	48.7	25.0	1339.77	0	3	0	0	2	169	181
									IPILYGEVEK	95.0	45.9	25.0	1160.66	0	2	0	0	2	182	191
									LETLGIGQR	95.0	65.8	25.0	986.56	0	2	0	0	2	300	308
Methionyl-tRNA synthetase, cytoplasmic	SYMC_HUMAN	MARS	101.10	100.0	4	4	10	5.11	ITQDIFQQLLK	95.0	69.6	25.0	1346.77	0	4	0	0	2	365	375
									GFVLQDTVEQLR	95.0	63.1	25.0	1404.75	0	2	0	0	2	377	388
									NPEQVDLYQFMAK	95.0	81.0	25.0	1598.75	0	2	0	0	2	542	554
									LENDQIESLR	95.0	33.5	25.0	1216.62	0	2	0	0	2	805	814
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1_HUMAN	MACF1	620.40	100.0	9	9	31	1.99	ENLEQAFEVAER	95.0	67.1	25.0	1434.69	0	2	0	0	2	253	264
									LQDELVTLR	95.0	49.5	25.0	1086.62	0	2	0	0	2	512	520
									SIQDAELLVK	95.0	35.1	25.0	1115.63	0	1	0	0	2	1165	1174
									DTDSLQSQIEDVR	95.0	74.4	25.0	1505.71	0	2	0	0	2	3089	3101
									AALLDQALSNAR	95.0	66.7	25.0	1242.68	0	5	0	0	2	3487	3498
									LVLDTVNEVSR	95.0	60.7	25.0	1244.68	0	2	0	0	2	3659	3669
									AGNELLESSAGDDASSLR	95.0	95.3	25.0	1791.84	0	5	0	0	2	4328	4345
									DQIIELDQTGNQLK	95.0	74.4	25.0	1614.83	0	1	0	0	2	4539	4552
									LDNFLGEVR	95.0	71.8	25.0	1062.56	0	11	0	0	2	4673	4681
Microtubule-associated protein RP/EB family member 1	MARE1_HUMAN	MAPRE1	29.98	100.0	4	5	20	17.20	LEHEYIQNFK	95.0	55.8	25.0	1320.66	0	6	4	0	2	67	76
									ILQAGFK	95.0	33.2	25.0	776.47	0	2	0	0	2	77	83
									FFDANYDGK	95.0	42.7	25.0	1076.47	0	4	0	0	2	114	122
									QGQETAVAPSLVAPALNKPK	95.0	50.3	25.0	2019.12	0	0	4	0	2	131	150
Mitochondrial import receptor subunit TOM70	TOM70_HUMAN	TOMM70A	67.44	100.0	5	5	9	9.05	ASPAPGSGHPEGPGAHLDMNSLDR	95.0	28.5	25.0	2386.08	0	0	2	0	2	90	113
									YMAEALLLR	95.0	59.5	25.0	1095.59	0	2	0	0	2	327	335

									GFEEVIK	95.0	29.1	25.0	821.44	0	1	0	0	2	464	470
									GLELISK	95.0	43.0	25.0	759.46	0	2	0	0	2	530	536
									YGLKPPTL	95.0	44.3	25.0	888.52	0	2	0	0	2	601	608
Mitogen-activated protein kinase 1	MK01_HUMAN	MAPK1	41.37	100.0	11	12	30	27.20	GQVFDVGPR	95.0	44.6	25.0	974.51	0	4	0	0	2	16	24
									FRHENIIGINDIIR	95.0	55.0	25.0	1709.94	0	0	2	0	2	78	91
									HENIIGINDIIR	95.0	69.8	25.0	1406.78	0	2	2	0	2	80	91
									YIHSANVLHR	95.0	32.7	25.0	1209.65	0	2	0	0	2	139	148
									VADPDHDHTGFLTEYVATR	95.0	69.7	25.0	2144.00	0	0	2	0	2	173	191
									APEIMLNSK	95.0	57.8	25.0	1018.52	0	2	0	0	2	195	203
									NYLLSLPHK	95.0	36.0	25.0	1084.62	0	2	0	0	2	262	270
									ALDLLDK	95.0	50.0	25.0	787.46	0	4	0	0	2	286	292
									FDMELDDLPK	95.0	82.0	25.0	1238.56	0	2	0	0	2	331	340
									LKELIFEETAR	95.0	34.9	25.0	1348.75	0	0	2	0	2	343	353
									ELIFEETAR	95.0	53.4	25.0	1107.57	0	4	0	0	2	345	353
Mitogen-activated protein kinase 14	MK14_HUMAN	MAPK14	41.28	100.0	3	3	17	8.61	YIHSADIIHR	95.0	25.7	25.0	1224.65	0	0	2	0	2	140	149
									ILDFGLAR	95.0	54.9	25.0	904.53	0	13	0	0	2	166	173
									TLFPGTDHIDQLK	95.0	59.4	25.0	1484.77	0	2	0	0	2	221	233
Mitotic checkpoint protein BUB3	BUB3_HUMAN	BUB3	37.14	100.0	4	4	13	17.70	LNQPPEDGISSVK	95.0	57.8	25.0	1383.71	0	2	0	0	2	9	21
									MHDLNTDQENLVGTHDAPIR	95.0	65.8	25.0	2292.07	0	0	4	0	2	81	100
									QGYVLSSIEGR	95.0	71.1	25.0	1208.63	0	2	0	0	2	192	202
									VAVEYLDPSPEVQK	95.0	59.8	25.0	1573.81	0	5	0	0	2	203	216
Moesin	MOES_HUMAN	MSN	67.80	100.0	23	31	338	26.90	QLFDQVVK	95.0	47.4	25.0	976.55	0	10	0	0	2	28	35
									KESPLLFK	95.0	32.5	25.0	961.57	0	2	0	0	2	72	79
									ESPLLFK	95.0	34.6	25.0	833.48	0	2	0	0	2	73	79
									LFFLQVK	95.0	46.6	25.0	894.54	0	7	0	0	2	101	107
									EDAVLEYLK	95.0	47.5	25.0	1079.56	0	12	0	0	2	185	193
									NISFNDKK	95.0	31.6	25.0	965.51	0	3	0	0	2	247	254
									FVIKPIDK	95.0	40.5	25.0	959.59	0	18	0	0	2	255	262
									FVIKPIDKK	95.0	29.4	25.0	1087.69	0	2	3	0	2	255	263
									KAPDFVFYAPR	95.0	55.3	25.0	1310.69	0	14	7	0	2	263	273
									APDFVFYAPR	95.0	75.6	25.0	1182.59	0	41	0	0	2	264	273
									RKPDTIEVQQMK	95.0	55.2	25.0	1488.78	0	21	54	0	2	295	306
									KPDTIEVQQMK	95.0	56.1	25.0	1332.68	0	17	2	0	2	296	306
									KAQQELEEQTR	95.0	84.6	25.0	1359.69	0	6	3	0	2	360	370
									AQQELEEQTR	95.0	63.3	25.0	1231.59	0	16	0	0	2	361	370
									ALELEQER	95.0	48.2	25.0	987.51	0	17	0	0	2	372	379
									EALLQASR	95.0	47.6	25.0	887.49	0	5	0	0	2	401	408
									KTQEQLALEMAELTAR	95.0	87.8	25.0	1847.95	0	2	2	0	2	412	427
									TQEQLALEMAELTAR	95.0	####	25.0	1719.86	0	4	2	0	2	413	427
									ISQLEMAR	95.0	50.7	25.0	963.49	0	20	0	0	2	428	435
									AQMVQEDLEK	95.0	61.0	25.0	1206.57	0	22	0	0	2	449	458
									ALTSELANAR	95.0	72.4	25.0	1045.56	0	13	0	0	2	524	533
									KTANDMIHAENMR	95.0	25.3	25.0	1562.71	0	0	1	0	2	538	550
									TANDMIHAENMR	95.0	43.3	25.0	1434.61	0	8	2	0	2	539	550
Mortality factor 4-like protein 2	MO4L2_HUMAN	MORF4L2	32.29	100.0	4	4	9	15.60	QLFQLPAK	95.0	27.6	25.0	944.56	0	2	0	0	2	145	152
									EYAVNEVVAGIK	95.0	50.2	25.0	1291.69	0	1	0	0	2	176	187
									IGAMLAYTPLDEK	95.0	71.6	25.0	1437.73	0	4	0	0	2	235	247
									NSASLFTASDYK	95.0	63.2	25.0	1303.62	0	2	0	0	2	266	277
mRNA turnover protein 4 homolog	MRT4_HUMAN	MRTO4	27.54	100.0	4	4	9	15.90	QNLIEELR	95.0	39.0	25.0	1014.56	0	1	0	0	2	24	31
									GEVGLLFTNR	95.0	64.4	25.0	1105.60	0	4	0	0	2	98	107
									QLGLPTALKR	95.0	27.9	25.0	1096.68	0	2	0	0	2	155	164

									LFGYEMAEFK	95.0	27.9	25.0	1250.58	0	2	0	0	2	192	201
Multifunctional protein ADE2	PUR6_HUMAN	PAICS	47.06	100.0	3	3	9	7.53	EVYELLDSPGK	95.0	63.4	25.0	1249.63	0	1	0	0	2	20	30
									DQITAGNAAR	95.0	51.3	25.0	1016.51	0	2	0	0	2	37	46
									EVTPEGLQMVK	95.0	48.8	25.0	1246.64	0	6	0	0	2	236	246
Myoferlin	MYOF_HUMAN	MYOF	234.70	100.0	16	16	45	8.44	VIVESASNIPK	95.0	39.9	25.0	1156.66	0	4	0	0	2	4	14
									DFETIGQNK	95.0	33.3	25.0	1051.51	0	1	0	0	2	71	79
									LIGTATVALK	95.0	36.4	25.0	986.62	0	1	0	0	2	80	89
									LISLLNEK	95.0	35.1	25.0	929.57	0	2	0	0	2	103	110
									GPVGTVSEAQLAR	95.0	86.0	25.0	1284.69	0	5	0	0	2	168	180
									AEDIPQMDDAFSQTVK	95.0	66.8	25.0	1810.82	0	6	0	0	2	367	382
									NDVVGTTYLHLSK	95.0	39.6	25.0	1446.76	0	1	0	0	2	451	463
									LQTNIEALK	95.0	37.1	25.0	1029.59	0	2	0	0	2	667	675
									YTLPLTEGK	95.0	32.8	25.0	1021.56	0	3	0	0	2	704	712
									ANVTVLDTQIR	95.0	67.7	25.0	1229.68	0	7	0	0	2	713	723
									EELYMPPLVIK	95.0	30.8	25.0	1347.72	0	3	0	0	2	1366	1376
									VGETIIDLENR	95.0	72.2	25.0	1258.66	0	2	0	0	2	1634	1644
									GFPQPILSEDGSR	95.0	48.4	25.0	1402.70	0	2	0	0	2	1685	1697
									DYSLDEFEANK	95.0	56.8	25.0	1330.58	0	2	0	0	2	1704	1714
									LDMIPDLK	95.0	34.4	25.0	960.51	0	2	0	0	2	1921	1928
									VEMTLEILNEK	95.0	78.8	25.0	1334.69	0	2	0	0	2	1966	1976
Myosin light polypeptide 6	MYL6_HUMAN	MYL6	16.91	100.0	3	4	20	24.50	EAFQLFDR	95.0	50.1	25.0	1025.51	0	12	0	0	2	14	21
									ALGQNPTNAEVLK	95.0	41.1	25.0	1354.73	0	5	0	0	2	38	50
									VFDKEGNGTVMGAEIR	95.0	45.7	25.0	1738.84	0	1	2	0	2	95	110
Myosin regulatory light chain 12A	ML12A_HUMAN	MYL12A	19.78	100.0	5	5	18	29.80	EAFNMIDQNR	95.0	33.8	25.0	1253.56	0	1	0	0	2	35	44
									LNGTDPEDVIR	95.0	73.2	25.0	1228.62	0	6	0	0	2	93	103
									ELLTTMGDR	95.0	36.7	25.0	1051.51	0	6	0	0	2	124	132
									FTDEEVDELYR	95.0	53.4	25.0	1415.63	0	4	0	0	2	133	143
									GNFNYIEFTR	95.0	65.3	25.0	1260.60	0	1	0	0	2	151	160
Myosin-9	MYH9_HUMAN	MYH9	226.52	100.0	45	52	387	20.60	KVIQYLAYVASSHK	95.0	22.7	25.0	1606.90	0	0	1	0	2	186	199
									VIQYLAYVASSHK	95.0	76.5	25.0	1478.80	0	3	0	0	2	187	199
									TDLLLEPYNK	95.0	70.4	25.0	1205.64	0	45	0	0	2	290	299
									IMGIPEEEQMGLLR	95.0	68.4	25.0	1647.81	0	16	0	0	2	328	341
									NTDQASMPDNTAAQK	95.0	56.6	25.0	1607.70	0	14	0	0	2	359	373
									EQADFAIEALAK	95.0	83.8	25.0	1305.67	0	23	0	0	2	408	419
									FVSELWK	95.0	28.0	25.0	908.49	0	1	0	0	2	607	613
									LDPHLVLDQLR	95.0	47.7	25.0	1318.75	0	9	9	0	2	683	693
									VVFQEFR	95.0	44.0	25.0	924.49	0	6	0	0	2	712	718
									YEILTPNSIPK	95.0	54.7	25.0	1274.70	0	5	0	0	2	721	731
									ALELDSNLYR	95.0	75.1	25.0	1193.62	0	17	0	0	2	746	755
									AGVLAHLEEER	95.0	48.0	25.0	1223.64	0	4	5	0	2	765	775
									IAEFTTNLTEEEEK	95.0	####	25.0	1653.79	0	31	0	0	2	1001	1014
									IAEFTTNLTEEEEKSK	95.0	93.4	25.0	1868.91	0	3	5	0	2	1001	1016
									NKHEAMITDLEER	95.0	47.8	25.0	1601.76	0	0	6	0	2	1023	1035
									HEAMITDLEER	95.0	66.8	25.0	1359.62	0	12	0	0	2	1025	1035
									KEEELQAALAR	95.0	59.2	25.0	1257.68	0	11	2	0	2	1081	1091
									DLGEELEALK	95.0	54.2	25.0	1116.58	0	2	0	0	2	1136	1145
									TLEEEAKTHEAQIQEMR	95.0	28.9	25.0	2058.98	0	0	2	0	2	1175	1191
									THEAQIQEMR	95.0	59.7	25.0	1258.58	0	10	1	0	2	1182	1191
									HSQAVEELAEQLEQTK	95.0	46.5	25.0	1839.91	0	0	2	0	2	1194	1209
									HSQAVEELAEQLEQTKR	95.0	64.0	25.0	1996.01	0	0	4	0	2	1194	1210
									QTLENERGELANEVK	95.0	48.3	25.0	1729.87	0	2	0	0	2	1220	1234

									KVEAQLQELQVK	95.0	83.6	25.0	1412.81	0	6	0	0	2	1249	1260
									VEAQLQELQVK	95.0	57.2	25.0	1284.72	0	5	0	0	2	1250	1260
									DLEGLSQR	95.0	33.2	25.0	917.47	0	2	0	0	2	1393	1400
									KFDQLLAEEK	95.0	60.5	25.0	1220.65	0	9	1	0	2	1445	1454
									FDQLLAEEK	95.0	49.1	25.0	1092.56	0	1	0	0	2	1446	1454
									TEMEDLMSSK	95.0	48.1	25.0	1202.49	0	4	0	0	2	1504	1513
									ALEQQVEEMK	95.0	38.3	25.0	1220.58	0	2	0	0	2	1529	1538
									LEVNLQAMK	95.0	38.5	25.0	1061.57	0	2	0	0	2	1558	1566
									DLQGRDEQSEEK	95.0	33.1	25.0	1433.65	0	1	0	0	2	1572	1583
									EMEAELEDER	95.0	65.5	25.0	1266.52	0	6	0	0	2	1593	1602
									EMEAELEDERK	95.0	28.9	25.0	1394.61	0	1	0	0	2	1593	1603
									DLEAHIDSANK	95.0	59.7	25.0	1212.59	0	8	0	0	2	1621	1631
									ASREEILAQAK	95.0	27.2	25.0	1215.67	0	1	0	0	2	1659	1669
									QAQQERDELADEIANSSGK	95.0	90.8	25.0	2088.98	0	0	9	0	2	1698	1716
									DELADEIANSSGK	95.0	77.2	25.0	1348.62	0	4	0	0	2	1704	1716
									ASITALEAK	95.0	47.6	25.0	903.51	0	5	0	0	2	1807	1815
									IAQLEEQLDNETK	95.0	####	25.0	1530.76	0	28	0	0	2	1816	1828
									IAQLEEQLDNETKER	95.0	43.5	25.0	1815.91	0	0	2	0	2	1816	1830
									QLEEAEEEAQR	95.0	74.4	25.0	1331.61	0	5	0	0	2	1878	1888
									ELEDATETADAMNR	95.0	94.8	25.0	1581.67	0	11	0	0	2	1899	1912
									RGDLPFVVPR	95.0	57.5	25.0	1155.66	0	6	11	0	2	1923	1932
									GDLPFVVPR	95.0	52.0	25.0	999.56	0	6	0	0	2	1924	1932
Myosin-Ib	MYO1B_HUMAN	MYO1B	131.97	100.0	4	4	9	3.96	YLGLLENVR	95.0	34.6	25.0	1076.61	0	4	0	0	2	618	626
									SSALVIQSYIR	95.0	44.9	25.0	1236.69	0	1	0	0	2	752	762
									IIIAEVVNK	95.0	56.0	25.0	998.62	0	3	0	0	2	987	995
									VSMSSQNDGFFAVHLK	95.0	23.6	25.0	1782.85	0	0	1	0	2	1037	1052
Myotrophin	MTPN_HUMAN	MTPN	12.88	100.0	3	3	5	18.60	NGDLDEVK	95.0	33.5	25.0	889.43	0	2	0	0	2	12	19
									NGDLDEVKDYVAK	95.0	63.3	25.0	1465.72	0	2	0	0	2	12	24
									GADINAPDK	95.0	29.5	25.0	900.44	0	1	0	0	2	58	66
Myristoylated alanine-rich C-kinase substrate	MARCS_HUMAN	MARCKS	31.54	100.0	3	3	11	12.70	GEPAAAAAPEAGASPVEK	95.0	71.4	25.0	1622.80	0	5	0	0	2	88	105
									LSGFSFK	95.0	33.9	25.0	785.42	0	4	0	0	2	166	172
									EAGEGGEAEAPAAEGGK	95.0	85.1	25.0	1529.67	0	2	0	0	2	177	193
N-acetyl-D-glucosamine kinase	NAGK_HUMAN	NAGK	37.36	100.0	6	6	16	18.60	SEVLLVSEDGK	95.0	91.6	25.0	1175.62	0	2	0	0	2	15	25
									AGVDPLVPLR	95.0	43.4	25.0	1036.62	0	1	0	0	2	60	69
									SLGLSLSGGDQEDAGR	95.0	81.4	25.0	1561.75	0	4	0	0	2	70	85
									ILIEELR	95.0	41.5	25.0	885.54	0	2	0	0	2	86	92
									LGILTHLYR	95.0	25.2	25.0	1085.65	0	0	2	0	2	198	206
									EGFLLALTQGR	95.0	67.8	25.0	1204.67	0	5	0	0	2	281	291
N-acetylglucosamine-6-sulfatase	GNS_HUMAN	GNS	62.07	100.0	3	3	43	6.16	IQEPNTFPAILR	95.0	63.9	25.0	1398.77	0	6	0	0	2	126	137
									AFQNVFAPR	95.0	54.8	25.0	1049.55	0	14	0	0	2	247	255
									TQMDGMSLLPILR	95.0	60.3	25.0	1506.77	0	23	0	0	2	389	401
NAD(P)H dehydrogenase [quinone] 1	NQO1_HUMAN	NQO1	30.85	100.0	3	4	23	12.40	ALIVLAHSER	95.0	44.4	25.0	1108.65	0	2	0	0	2	6	15
									EGHLSPDIVAEQK	95.0	67.5	25.0	1422.72	0	12	7	0	2	78	90
									FGLSVGHHLGK	95.0	61.5	25.0	1151.63	0	2	0	0	2	252	262
NAD-dependent deacetylase sirtuin-5	SIRT5_HUMAN	SIRT5	33.86	100.0	4	4	13	18.70	RVVVITQNIDELHR	95.0	52.5	25.0	1691.96	0	0	1	0	2	134	147
									NLLEIHGSLFK	95.0	54.4	25.0	1270.72	0	4	0	0	2	153	163
									GAPEPGTQDASIPVEK	95.0	79.2	25.0	1595.79	0	4	0	0	2	188	203
									GVPVAEFNTETTPATNR	95.0	####	25.0	1803.89	0	4	0	0	2	268	284
NADP-dependent malic enzyme	MAOX_HUMAN	ME1	64.13	100.0	4	4	13	7.17	DLAFTLEER	95.0	50.8	25.0	1093.55	0	4	0	0	2	27	35
									NFEHLNSDFDR	95.0	42.3	25.0	1393.61	0	1	0	0	2	61	71
									YLLLMDLQDR	95.0	41.8	25.0	1295.67	0	3	0	0	2	72	81

									TATVYPEPQNK	95.0	49.6	25.0	1247.63	0	5	0	0	2	526	536
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25_HUMAN	NAA25	112.28	100.0	4	4	9	3.70	TMFLPLAER	95.0	54.8	25.0	1093.57	0	2	0	0	2	171	179
									LTSEIQSR	95.0	36.0	25.0	933.50	0	2	0	0	2	224	231
									DTSEYIIQAYK	95.0	92.3	25.0	1330.65	0	2	0	0	2	576	586
									IPEFIAFR	95.0	39.2	25.0	992.56	0	3	0	0	2	593	600
N-alpha-acetyltransferase 50, NatE catalytic subunit	NAA50_HUMAN	NAA50	19.38	100.0	6	7	19	32.50	IELGDVTPHNIK	95.0	26.8	25.0	1335.73	0	0	4	0	2	6	17
									DVLEVGELAK	95.0	35.0	27.9	1072.59	0	2	0	0	2	38	47
									FGFEIIETK	95.0	61.5	25.0	1083.57	0	2	0	0	2	127	135
									FGFEIIETKK	95.0	43.9	25.0	1211.67	0	2	0	0	2	127	136
									RIEPADAHVLQK	95.0	34.5	25.0	1376.76	0	2	3	0	2	141	152
									VPSGQNADVQK	95.0	40.9	25.0	1142.58	0	4	0	0	2	156	166
Nardilysin	NRDC_HUMAN	NRD1	131.56	100.0	9	9	27	7.91	LGADESEEEGR	95.0	63.1	25.0	1191.51	0	4	0	0	2	81	91
									LGADESEEEGRR	95.0	22.8	25.0	1347.61	0	0	1	0	2	81	92
									GSLSNAGDPEIVK	95.0	39.3	25.0	1286.66	0	1	0	0	2	93	105
									TVFQFDVQR	95.0	56.8	25.0	1139.58	0	3	0	0	2	271	279
									ANLVLLSGANEGK	95.0	####	25.0	1285.71	0	7	0	0	2	606	618
									LVAGEHGLIIR	95.0	73.6	25.0	1177.71	0	2	0	0	2	751	761
									LLILEYAR	95.0	37.4	25.0	990.60	0	4	0	0	2	817	824
									GDANSEVTVYYQSGTR	95.0	64.4	25.0	1746.79	0	3	0	0	2	913	928
									LAHEIEALK	95.0	45.5	25.0	1023.58	0	2	0	0	2	1052	1060
Nck-associated protein 1	NCKP1_HUMAN	NCKAP1	128.78	100.0	4	4	7	4.17	AAEDLFVNIR	95.0	36.6	25.0	1147.61	0	1	0	0	2	306	315
									ELATVLSDQPGLLGPK	95.0	67.9	25.0	1637.91	0	2	0	0	2	352	367
									ASLGLADHR	95.0	30.8	25.0	939.50	0	2	0	0	2	502	510
									SLSELLGPYGMK	95.0	42.5	25.0	1310.67	0	2	0	0	2	838	849
NEDD8-activating enzyme E1 catalytic subunit	UBA3_HUMAN	UBA3	51.84	100.0	3	3	7	6.26	NLALSGFR	95.0	30.9	25.0	877.49	0	3	0	0	2	87	94
									AEVAAEFLNDR	95.0	51.6	25.0	1234.61	0	2	0	0	2	125	135
									IQDFNDTFYR	95.0	81.3	25.0	1318.61	0	2	0	0	2	148	157
NEDD8-activating enzyme E1 regulatory subunit	ULA1_HUMAN	NAE1	60.23	100.0	8	8	14	16.50	TYGLVGYMR	95.0	27.6	25.0	1075.52	0	1	0	0	2	155	163
									LDKPFPELR	95.0	28.2	25.0	1114.63	0	0	2	0	2	185	193
									EHFQSYDLDHMEK	95.0	31.5	25.0	1694.71	0	0	2	0	2	194	206
									GTIPDMIADSGK	95.0	49.0	25.0	1220.58	0	2	0	0	2	327	338
									LQNVYR	95.0	31.0	25.0	792.44	0	2	0	0	2	342	347
									DAAAVGNHVAK	95.0	38.3	25.0	1052.55	0	2	0	0	2	353	363
									LLQSIGQAPESISEK	95.0	66.0	25.0	1599.86	0	2	0	0	2	364	378
									SLAEEYGLDTINK	95.0	39.6	25.0	1452.72	0	1	0	0	2	397	409
NEDD8-conjugating enzyme Ubc12	UBC12_HUMAN	UBE2M	20.88	100.0	4	4	20	20.80	DINELNLPK	95.0	51.5	25.0	1055.57	0	6	0	0	2	37	45
									EAAEVLQNNR	95.0	36.2	25.0	1143.58	0	3	0	0	2	148	157
									LFEQNVQR	95.0	46.9	25.0	1033.54	0	9	0	0	2	159	166
									GGYIGSTYFER	95.0	37.0	25.0	1249.58	0	2	0	0	2	170	180
Nesprin-2	SYNE2_HUMAN	SYNE2	796.44	100.0	3	3	4	0.48	LLEPEDVDVVDPDEK	95.0	59.6	25.0	1711.83	0	2	0	0	2	258	272
									FSLYQTR	95.0	26.9	25.0	914.47	0	1	0	0	2	5732	5738
									DMEPQLAEMIK	95.0	37.0	25.0	1336.61	0	1	0	0	2	5793	5803
Neural cell adhesion molecule L1	L1CAM_HUMAN	L1CAM	139.99	100.0	6	6	17	4.53	TIIQKEPIDLR	95.0	21.6	25.0	1325.78	0	0	1	0	2	218	228
									TLQLLK	95.0	34.8	25.0	715.47	0	3	0	0	2	296	301
									VGEEDDGEYR	95.0	45.9	25.0	1168.48	0	4	0	0	2	302	311
									DATQITQGPR	95.0	43.4	25.0	1086.55	0	3	0	0	2	516	525
									AQLLVVGSPGPVPR	95.0	76.9	25.0	1389.82	0	5	0	0	2	604	617
									FHILFK	94.9	26.6	25.0	804.48	0	1	0	0	2	1047	1052
Neurolysin, mitochondrial	NEUL_HUMAN	NLN	80.64	100.0	6	6	15	8.10	TEELIVQTK	95.0	36.0	25.0	1060.59	0	2	0	0	2	61	69
									FDIEMSMR	95.0	34.4	25.0	1060.44	0	2	0	0	2	132	139
									VTAFLDDLSQK	95.0	48.1	25.0	1236.65	0	2	0	0	2	315	325

									EFILNLK	95.0	31.9	25.0	876.52	0	1	0	0	2	335	341
									DGSPIADDLLEK	95.0	38.3	25.0	1272.63	0	4	0	0	2	551	562
									LVNTGLLTLR	95.0	93.2	25.0	1099.68	0	4	0	0	2	568	577
Neutral alpha-glucosidase AB	GANAB_HUMAN	GANAB	106.86	100.0	13	15	70	13.20	FRIDELEPR	95.0	34.3	25.0	1174.62	0	1	0	0	2	101	109
									IDELEPR	95.0	42.5	25.0	871.45	0	6	0	0	2	103	109
									VPDVLVADPPIAR	95.0	38.0	25.0	1361.78	0	4	0	0	2	115	127
									DENSVELTMAEGPYK	95.0	####	25.0	1698.75	0	8	0	0	2	134	148
									GLLEFEHQR	95.0	34.3	25.0	1128.58	0	3	4	0	2	174	182
									VSQGSKDPAEGDGAQPEETPR	95.0	40.1	25.0	2154.99	0	0	10	0	2	186	206
									DPAEGDGAQPEETPR	95.0	65.6	25.0	1568.68	0	4	0	0	2	192	206
									VTEGGEPYR	95.0	39.6	25.0	1007.48	0	6	0	0	2	270	278
									MMDYLQGSGETPQTDVR	95.0	####	25.0	1959.84	0	8	0	0	2	338	354
									KLVAIVDPHIK	95.0	28.1	25.0	1232.77	0	0	2	0	2	462	472
									LVAIVDPHIK	95.0	67.7	25.0	1104.68	0	2	2	0	2	463	472
									SGGMERPFVLAR	95.0	30.5	25.0	1335.68	0	0	1	0	2	591	602
									NPEPELLVR	95.0	55.6	25.0	1066.59	0	9	0	0	2	654	662
Neutral amino acid transporter B(0)	AAAT_HUMAN	SLC1A5	56.58	100.0	3	3	34	5.91	LGPEGELLIR	95.0	73.5	25.0	1096.64	0	23	0	0	2	248	257
									STEPELIQVK	95.0	40.8	25.0	1143.63	0	5	0	0	2	493	502
									GPAGDATVASEK	95.0	63.5	25.0	1102.54	0	6	0	0	2	526	537
Neutrophil gelatinase-associated lipocalin	NGAL_HUMAN	LCN2	22.57	100.0	9	13	163	36.90	VPLQQNFQDNQFQGK	95.0	88.6	25.0	1790.88	0	51	6	0	2	36	50
									MYATIYELK	95.0	60.4	25.0	1147.57	0	45	0	0	2	71	79
									MYATIYELKEDK	95.0	64.7	25.0	1519.74	0	8	2	0	2	71	82
									SYPGLTSYLVR	95.0	44.0	25.0	1255.67	0	10	0	0	2	119	129
									VVSTNYNQHAMVFFK	95.0	56.5	25.0	1800.87	0	6	0	0	2	130	144
									ITLYGR	95.0	29.8	25.0	722.42	0	8	0	0	2	155	160
									TKELTSELK	95.0	36.0	25.0	1048.59	0	2	1	0	2	161	169
									ELTSELK	95.0	35.4	25.0	819.45	0	10	0	0	2	163	169
									ELTSELKENFIR	95.0	75.4	25.0	1478.79	0	12	2	0	2	163	174
NHL repeat-containing protein 2	NHLC2_HUMAN	NHLRC2	79.43	100.0	3	3	7	3.99	DSLVYQYLQK	95.0	59.0	25.0	1256.65	0	3	0	0	2	35	44
									MVSVLPIFR	95.0	32.1	25.0	1077.61	0	2	0	0	2	565	573
									LRLDLPSGSK	95.0	38.8	25.0	1085.63	0	2	0	0	2	618	627
Niban-like protein 1	NIBL1_HUMAN	FAM129B	82.67	100.0	12	12	46	14.70	IVFSGNLFQHQEDSK	95.0	65.8	25.0	1748.86	0	2	0	0	2	56	70
									IVFSGNLFQHQEDSKK	95.0	54.7	25.0	1876.96	0	1	0	0	2	56	71
									VEGPAFTDAIR	95.0	94.3	25.0	1175.61	0	4	0	0	2	191	201
									FEEVLSK	95.0	46.3	25.0	851.45	0	4	0	0	2	274	280
									VQQVQPAMQAVIR	95.0	36.2	25.0	1483.81	0	3	0	0	2	281	293
									TDMDQIITSK	95.0	68.0	25.0	1167.56	0	9	0	0	2	294	303
									EVTDMNLNVINEGGIDK	95.0	####	25.0	1876.90	0	8	0	0	2	355	371
									LDGLQQR	95.0	36.3	25.0	829.45	0	3	0	0	2	401	407
									FDVSSTSVFK	95.0	43.9	25.0	1116.56	0	8	0	0	2	408	417
									KYDYDSSSVR	95.0	34.2	25.0	1219.56	0	2	0	0	2	466	475
									YDYDSSSVR	95.0	28.8	25.0	1091.46	0	1	0	0	2	467	475
									DILQAVK	95.0	28.2	25.0	786.47	0	1	0	0	2	535	541
Nicotinamide phosphoribosyltransferase	NAMPT_HUMAN	NAMPT	55.50	100.0	8	8	39	18.70	EHFQDDVFNEK	95.0	59.8	25.0	1407.62	0	2	0	0	2	89	99
									YDGHLPIEIK	95.0	32.8	25.0	1184.63	0	0	5	0	2	108	117
									AVPEGFVIPR	95.0	58.6	25.0	1084.62	0	4	0	0	2	118	127
									GVSSQETAGIGASAHLVNFK	95.0	27.5	25.0	1973.01	0	0	2	0	2	197	216
									GTDTVAGLALIK	95.0	71.6	25.0	1158.67	0	12	0	0	2	217	228
									VLEILGK	95.0	52.0	25.0	771.50	0	8	0	0	2	324	330
									TPAGNFVTLEEGK	95.0	78.7	25.0	1362.69	0	3	0	0	2	435	447
									SYSFDEIRK	95.0	27.8	25.0	1144.56	0	3	0	0	2	470	478

Nicotinate phosphoribosyltransferase	PNCB_HUMAN	NAPRT1	57.56	100.0	4	4	12	7.25	LLEMGLR	95.0	43.8	25.0	847.47	0	2	0	0	2	165	171
									LDSGDLLQQAQEIR	95.0	79.0	25.0	1585.82	0	5	0	0	2	319	332
									LVAVGGQPR	95.0	28.4	25.0	896.53	0	1	0	0	2	397	405
									ALAQLSLSR	95.0	75.8	25.0	958.57	0	4	0	0	2	495	503
Nitrilase homolog 1	NIT1_HUMAN	NIT1	35.88	100.0	3	3	6	11.60	DPAETLHLSEPLGGK	95.0	73.5	25.0	1563.80	0	2	0	0	2	94	108
									LLEEYTQLAR	95.0	63.3	25.0	1235.66	0	2	0	0	2	109	118
									RPDLYGNLGHPLS	95.0	32.3	25.0	1438.74	0	0	2	0	2	315	327
Non-specific lipid-transfer protein	NLTP_HUMAN	SCP2	58.98	100.0	3	3	6	5.48	KLEEEGEQFVK	95.0	59.3	25.0	1335.68	0	2	0	0	2	443	453
									IGGIFAFK	95.0	38.4	25.0	852.50	0	2	0	0	2	455	462
									MNPQSAFFQGK	95.0	53.9	25.0	1270.59	0	2	0	0	2	512	522
NSFL1 cofactor p47	NSF1C_HUMAN	NSFL1C	40.56	100.0	8	8	43	23.80	EFVAVTGAEEDR	95.0	63.3	25.0	1322.62	0	2	0	0	2	11	22
									DLIHDQDEDEEEEEGQR	95.0	50.4	25.0	2085.85	0	0	2	0	2	77	93
									KSPNELVDDLFK	95.0	31.8	25.0	1404.74	0	1	0	0	2	113	124
									SPNELVDDLFK	95.0	65.5	25.0	1276.64	0	11	0	0	2	114	124
									LGAAPEEESAYVAGEK	95.0	98.0	25.0	1620.78	0	4	0	0	2	157	172
									RGEVPAELR	95.0	38.5	25.0	1026.57	0	3	0	0	2	215	223
									ELADESQTLK	95.0	28.9	25.0	1133.57	0	2	0	0	2	347	356
									EANLLNAVIVQR	95.0	69.0	25.0	1339.77	0	18	0	0	2	357	368
Nuclear autoantigenic sperm protein	NASP_HUMAN	NASP	85.22	100.0	3	3	9	4.44	EVSEEQPVVTLEK	95.0	51.9	25.0	1486.76	0	2	0	0	2	276	288
									EAQLYAAQAHLK	95.0	48.4	25.0	1342.71	0	2	0	0	2	536	547
									SGNVAELALK	95.0	49.3	25.0	1001.56	0	5	0	0	2	662	671
Nuclear cap-binding protein subunit 1	NCBP1_HUMAN	NCBP1	91.82	100.0	4	5	19	5.44	ATNDEIFSILK	95.0	58.5	25.0	1250.66	0	13	0	0	2	512	522
									SFSHSFSALAK	95.0	54.8	25.0	1181.59	0	2	0	0	2	558	568
									DGVLEEQIER	95.0	49.4	25.0	1187.59	0	2	0	0	2	685	694
									FIMILTEHLVR	95.0	45.8	25.0	1387.78	0	1	1	0	2	717	727
Nuclear migration protein nudC	NUDC_HUMAN	NUDC	38.23	100.0	9	9	41	30.20	TDFFIGGEEGMAEK	95.0	81.0	25.0	1546.67	0	4	0	0	2	40	53
									LITQTFSHHNQLAQK	95.0	71.2	25.0	1765.93	0	2	0	0	2	54	68
									ELTDEEAER	95.0	43.3	25.0	1091.49	0	1	0	0	2	106	114
									DMVVDIQR	95.0	41.7	25.0	991.49	0	4	0	0	2	197	204
									GQPAIIDGELYNEVK	95.0	####	25.0	1645.84	0	7	0	0	2	213	227
									VVTVHLEK	95.0	35.4	25.0	924.55	0	1	0	0	2	240	247
									LVSSDPEINTK	95.0	44.4	25.0	1202.63	0	9	0	0	2	257	267
									LSDLDSETR	95.0	41.1	25.0	1035.50	0	5	0	0	2	276	284
									SMGLPTSDEQK	95.0	47.1	25.0	1208.55	0	8	0	0	2	298	308
Nuclear mitotic apparatus protein 1	NUMA1_HUMAN	NUMA1	238.24	100.0	33	37	157	16.90	IHGTEEGQQILK	95.0	36.6	25.0	1352.72	0	1	2	0	2	43	54
									VLEGSELELAK	95.0	84.7	25.0	1187.65	0	8	0	0	2	87	97
									MTMLLLYHSTMSSK	95.0	44.6	25.0	1690.79	0	2	0	0	2	98	111
									LALLNEK	95.0	34.5	25.0	800.49	0	2	0	0	2	261	267
									ELEELR	95.0	30.7	25.0	788.41	0	2	0	0	2	277	282
									ELSAALQDK	95.0	39.7	25.0	974.52	0	1	0	0	2	365	373
									ELSAALQDKK	95.0	40.1	25.0	1102.61	0	3	0	0	2	365	374
									QEAATLAANNTQLQAR	95.0	####	25.0	1699.87	0	3	0	0	2	420	435
									VEMLETER	95.0	54.6	25.0	1022.48	0	11	0	0	2	436	443
									EELEQASQAHGAR	95.0	44.4	25.0	1425.67	0	4	5	0	2	483	495
									HQVEQLSSSLK	95.0	34.9	25.0	1255.66	0	5	0	0	2	551	561
									DSAQTSVTQAQR	95.0	74.3	25.0	1291.62	0	18	0	0	2	632	643
									DQLQEQLQALK	95.0	67.4	25.0	1313.71	0	4	0	0	2	698	708
									AADALEEQQR	95.0	66.4	25.0	1130.54	0	7	0	0	2	725	734
									LADDLSTLQEK	95.0	49.4	25.0	1232.64	0	2	0	0	2	898	908
									EAEQMGNELER	95.0	37.3	25.0	1321.57	0	10	0	0	2	973	983
									AALMESQGQQQEER	95.0	62.6	25.0	1620.73	0	9	0	0	2	986	999

								AQADLALEK	95.0	36.1	25.0	958.52	0	2	0	0	2	1016	1024
								QQEQADSLER	95.0	32.2	25.0	1203.56	0	1	0	0	2	1139	1148
								DSALETLQGQLEEK	95.0	95.0	25.0	1560.78	0	6	0	0	2	1161	1174
								AQELGHSQSALASAQR	95.0	81.5	25.0	1653.83	0	2	3	0	2	1175	1190
								LLQAETASNSAR	95.0	70.8	25.0	1260.65	0	19	0	0	2	1271	1282
								EEVQSLREEAEK	95.0	40.8	25.0	1446.71	0	2	0	0	2	1292	1303
								QELTSQAER	95.0	27.0	25.0	1061.52	0	1	0	0	2	1313	1321
								AEELGQELK	95.0	45.2	25.0	1016.53	0	5	0	0	2	1322	1330
								QFLEVELDQAR	95.0	29.1	25.0	1347.69	0	1	0	0	2	1463	1473
								YVQELAAVR	95.0	32.8	25.0	1048.58	0	2	0	0	2	1476	1484
								ELEVMTAK	95.0	28.0	25.0	936.47	0	1	0	0	2	1504	1511
								AVQAQGGESQQEAQR	95.0	72.8	25.0	1586.75	0	5	0	0	2	1574	1588
								KQQNQELQEQLR	95.0	40.1	25.0	1541.80	0	2	0	0	2	1625	1636
								LGHELQQAGLK	95.0	42.8	25.0	1193.66	0	3	1	0	2	1655	1665
								SLEAQVAHADQQLR	95.0	58.7	25.0	1565.80	0	1	0	0	2	1682	1695
								FQVATDALK	95.0	26.9	25.0	992.54	0	1	0	0	2	1700	1708
Nuclear pore complex protein Nup214	NU214_HUMAN	NUP214	213.60	99.5	2	2	3	1.29	IFDSPEELPK	95.0	39.9	25.0	1174.60	0	2	0	0	2	27	36
								DAGGMVIDMK	95.0	29.0	25.0	1068.47	0	1	0	0	2	147	156
								LSLEGER	95.0	28.8	25.0	803.43	0	1	0	0	2	420	426
Nuclear pore complex protein Nup93	NUP93_HUMAN	NUP93	93.47	100.0	6	6	10	7.57	SSLDNIEMAYAR	95.0	89.5	25.0	1385.64	0	2	0	0	2	176	187
								SFLNIK	95.0	27.1	25.0	721.42	0	1	0	0	2	295	300
								FESTDPR	95.0	28.5	25.0	851.39	0	1	0	0	2	539	545
								LLSPVVPQISAPQSNK	95.0	44.9	25.0	1677.95	0	2	0	0	2	645	660
								NMALSIAER	95.0	43.5	25.0	1020.51	0	2	0	0	2	665	673
								LVPLNQESVEER	95.0	45.0	25.0	1412.74	0	2	0	0	2	719	730
Nuclear receptor-binding protein	NRBP_HUMAN	NRBP1	59.83	100.0	3	3	11	7.48	NMDTSAVLAEIPAGPGR	95.0	####	25.0	1714.84	0	2	0	0	2	359	375
								TPTPEPAEVETR	95.0	47.0	25.0	1326.65	0	2	0	0	2	431	442
								LTSLLEETLNK	95.0	49.7	25.0	1260.70	0	7	0	0	2	507	517
Nuclease-sensitive element-binding protein 1	YBOX1_HUMAN	YBX1	35.91	100.0	5	5	19	20.40	NDTKEDVFVHQTAIK	95.0	28.8	25.0	1744.89	0	0	2	0	2	78	92
								EDVFVHQTAIK	95.0	45.4	25.0	1286.67	0	4	0	0	2	82	92
								SVGDGETVEFDVVEGEK	95.0	87.2	25.0	1795.82	0	1	0	0	2	102	118
								GAEAANVTGPGGVPVQGSK	95.0	####	25.0	1695.87	0	11	0	0	2	119	137
								NEGSESAPEGQAQQR	95.0	32.9	25.0	1587.70	0	1	0	0	2	171	185
Nucleobindin-1	NUCB1_HUMAN	NUCB1	53.86	100.0	5	5	14	12.40	MDAEQDPNVQVDHLNLLK	95.0	28.0	25.0	2095.01	0	0	1	0	2	119	136
								DLELLIQTATR	95.0	46.9	25.0	1272.72	0	3	0	0	2	153	163
								FEEELAAR	95.0	41.1	25.0	964.47	0	3	0	0	2	350	357
								LSQETEALGR	95.0	49.6	25.0	1103.57	0	2	0	0	2	368	377
								LPEVEVPQHL	95.0	45.2	25.0	1160.63	0	5	0	0	2	452	461
Nucleolin	NUCL_HUMAN	NCL	76.60	100.0	11	11	230	14.10	TGISDVFAK	95.0	61.9	25.0	937.50	0	40	0	0	2	325	333
								NDLAVVDVR	95.0	63.7	25.0	1000.54	0	25	0	0	2	334	342
								VTQDELK	95.0	35.9	25.0	832.44	0	5	0	0	2	404	410
								EVFEDAAEIR	95.0	68.7	25.0	1178.57	0	29	0	0	2	411	420
								GIAYIEFK	95.0	52.8	25.0	940.51	0	49	0	0	2	430	437
								QGTEIDGR	95.0	30.4	25.0	875.42	0	1	0	0	2	450	457
								SISLYYTGEK	95.0	45.9	25.0	1160.58	0	12	0	0	2	458	467
								LELQGPR	95.0	39.9	25.0	812.46	0	19	0	0	2	555	561
								GLSEDTTEETLK	95.0	76.4	25.0	1322.63	0	30	0	0	2	578	589
								ESFDGSVR	95.0	39.3	25.0	896.41	0	7	0	0	2	590	597
								EAMEDGEIDGNK	95.0	52.6	25.0	1323.54	0	13	0	0	2	628	639
Nucleophosmin	NPM_HUMAN	NPM1	32.56	100.0	6	6	44	18.00	ADKDYHFK	95.0	36.9	25.0	1023.49	0	1	0	0	2	25	32
								VDNDENEHQLSLR	95.0	75.4	25.0	1568.73	0	20	0	0	2	33	45

									TVSLGAGAK	95.0	33.9	25.0	803.46	1	0	0	0	2	46	54
									VTLATLK	95.0	42.8	25.0	745.48	0	4	0	0	2	74	80
									LLSISGK	95.0	31.7	25.0	717.45	0	2	0	0	2	135	141
									GPSSVEDIK	95.0	59.0	25.0	931.47	0	16	0	0	2	240	248
Nucleoprotein TPR	TPR_HUMAN	TPR	267.27	100.0	12	12	45	5.59	FLADQQSEIDGLK	95.0	61.4	25.0	1463.74	0	2	0	0	2	28	40
									NIAIQSQFTR	95.0	51.4	25.0	1177.63	0	2	0	0	2	106	115
									LDELQASDVSVK	95.0	90.3	25.0	1303.67	0	3	0	0	2	166	177
									TDELLALGR	95.0	69.9	25.0	987.55	0	3	0	0	2	205	213
									ELENANDLLSATK	95.0	96.3	25.0	1417.72	0	4	0	0	2	352	364
									VLLMELEEAR	95.0	37.5	25.0	1218.64	0	3	0	0	2	502	511
									ISTQLDFASK	95.0	33.9	25.0	1109.58	0	1	0	0	2	714	723
									EGVQGPLNVSLSEEGK	95.0	70.6	25.0	1642.83	0	8	0	0	2	1176	1191
									SQEQILEILR	95.0	63.4	25.0	1228.69	0	11	0	0	2	1192	1201
									FEVAQVESLR	95.0	67.2	25.0	1177.62	0	5	0	0	2	1214	1223
									VELLER	95.0	35.2	25.0	758.44	0	1	0	0	2	1228	1233
									ELQELQDSLNAER	95.0	57.0	25.0	1544.76	0	2	0	0	2	1234	1246
Nucleoside diphosphate kinase 3	NDK3_HUMAN	NME3	19.00	100.0	5	5	9	29.60	TFLAVKPDGVQR	95.0	49.1	25.0	1330.75	0	2	0	0	2	24	35
									RLVGEIVR	95.0	31.5	25.0	941.59	0	2	0	0	2	36	43
									LVGEIVR	95.0	37.2	25.0	785.49	0	2	0	0	2	37	43
									ALIGATNPADAPPGTIR	95.0	76.0	25.0	1634.89	0	2	0	0	2	106	122
									NLIHGSDSVESAR	95.0	36.3	25.0	1384.68	0	1	0	0	2	132	144
Nucleoside diphosphate kinase A	NDKA_HUMAN	NME1	17.13	100.0	9	12	152	57.90	TFIAIKPDGVQR	95.0	48.6	25.0	1344.76	0	24	3	0	2	7	18
									GLVGEIIK	95.0	47.0	25.0	828.52	0	18	0	0	2	19	26
									GLVGEIIKR	95.0	45.9	25.0	984.62	0	3	0	0	2	19	27
									FMQASEDLLK	95.0	56.3	25.0	1197.58	0	12	0	0	2	40	49
									EHYVDLK	95.0	37.5	25.0	903.46	0	2	0	0	2	50	56
									DRPFFAGLVK	95.0	52.6	25.0	1149.64	0	11	0	0	2	57	66
									VMLGETNPADSKPGTIR	95.0	98.7	25.0	1801.91	0	14	31	0	2	89	105
									GDFCIQVGR	95.0	69.7	25.0	1051.50	0	4	0	0	2	106	114
									NIIHGSDSVESAEK	95.0	67.4	25.0	1485.72	0	21	9	0	2	115	128
Nucleoside diphosphate kinase B	NDKB_HUMAN	NME2	17.28	100.0	4	5	40	53.30	TFIAIKPDGVQR	95.0	48.6	25.0	1344.76	0	24	3	0	2	7	18
									GLVGEIIK	95.0	47.0	25.0	828.52	0	18	0	0	2	19	26
									GLVGEIIKR	95.0	45.9	25.0	984.62	0	3	0	0	2	19	27
									ASEEHLK	94.7	26.5	25.0	813.41	0	1	0	0	2	43	49
									QHYIDLK	95.0	27.5	25.0	916.49	0	2	0	0	2	50	56
									DRPFFPGLVK	95.0	46.5	25.0	1175.66	0	13	0	0	2	57	66
									VMLGETNPADSKPGTIR	95.0	98.7	25.0	1801.91	0	14	31	0	2	89	105
									GDFCIQVGR	95.0	69.7	25.0	1051.50	0	4	0	0	2	106	114
									NIIHGSDSVK	95.0	55.7	25.0	1069.56	0	23	1	0	2	115	124
NudC domain-containing protein 1	NUDC1_HUMAN	NUDCD1	66.74	100.0	8	9	18	13.20	LYVIGTGER	95.0	32.8	25.0	1007.55	0	2	0	0	2	136	144
									IEKEELDMK	95.0	37.7	25.0	1150.57	0	1	0	0	2	187	195
									DHQFLEGK	95.0	26.8	25.0	973.47	0	1	0	0	2	317	324
									ESNSLEISLIK	95.0	72.4	25.0	1232.67	0	4	0	0	2	340	350
									LMHLTSEELNPNPDK	95.0	53.7	25.0	1753.84	0	1	1	0	2	383	397
									QPAPMSTVLYNR	95.0	34.5	25.0	1392.69	0	2	0	0	2	522	533
									LFVLTTK	95.0	37.7	25.0	821.51	0	2	0	0	2	566	572
									NLFLIK	95.0	29.9	25.0	747.48	0	4	0	0	2	573	578
Obg-like ATPase 1	OLA1_HUMAN	OLA1	44.73	100.0	8	11	41	19.40	KGGDGIKPPPIIGR	95.0	55.2	25.0	1404.83	0	2	1	0	2	5	18
									GGDGIKPPPIIGR	95.0	35.5	25.0	1276.74	0	2	1	0	2	6	18
									IGIVGLPNVGK	95.0	62.1	25.0	1066.66	0	11	0	0	2	25	35
									VPVPDER	95.0	47.0	25.0	811.43	0	8	0	0	2	64	70

									LQELSAEER	95.0	60.5	25.0	1074.54	0	7	0	0	2	271	279
									YLEANMTQSALPK	95.0	65.6	25.0	1481.73	0	2	0	0	2	282	294
									GFIMAEVMK	95.0	42.9	25.0	1057.51	0	1	0	0	2	341	349
									YEDFKEEGSENAVK	95.0	66.7	25.0	1644.74	0	4	2	0	2	350	363
Omega-amidase NIT2	NIT2_HUMAN	NIT2	30.59	100.0	3	3	10	13.80	KIHLFDIDVPGK	95.0	42.5	25.0	1381.78	0	0	2	0	2	112	123
									FAELAQIYAQR	95.0	55.6	25.0	1309.69	0	4	0	0	2	158	168
									AVDNQVYVATASPAR	95.0	89.5	25.0	1561.80	0	4	0	0	2	196	210
Ornithine aminotransferase, mitochondrial	OAT_HUMAN	OAT	48.52	100.0	4	4	10	10.90	TVQGPPTSDDIFER	95.0	78.7	25.0	1561.75	0	2	0	0	2	33	46
									YGAHNYHPLPVALER	95.0	40.0	25.0	1736.89	0	0	1	0	2	50	64
									LPSDVVTAVR	95.0	49.9	25.0	1056.60	0	1	0	0	2	363	372
									GLLNAIVIK	95.0	51.0	25.0	940.62	0	6	0	0	2	375	383
Oxysterol-binding protein 1	OSBP1_HUMAN	OSBP	89.40	100.0	4	4	7	5.95	DFLMLAQTHSK	95.0	41.7	25.0	1306.65	0	3	0	0	2	278	288
									IRLEETLEQLAK	95.0	40.6	25.0	1442.82	0	0	2	0	2	302	313
									LTEDLEYHELLDR	95.0	21.8	25.0	1645.81	0	0	1	0	2	450	462
									ATEDGTPYDPYK	95.0	34.0	25.0	1356.60	0	1	0	0	2	757	768
PCI domain-containing protein 2	PCID2_HUMAN	PCID2	46.01	100.0	3	4	12	6.77	AVSEGNLLLLHEALAK	95.0	66.8	25.0	1677.95	0	4	2	0	2	285	300
									CGIFLILEK	95.0	41.2	25.0	1092.61	0	4	0	0	2	308	316
									CGIFLILEKLK	95.0	41.0	25.0	1276.77	0	0	2	0	2	308	318
PCTP-like protein	PCTL_HUMAN	STARD10	33.03	100.0	3	3	5	13.70	LAASTEPQGPRPVLGR	95.0	23.0	25.0	1648.91	0	0	2	0	2	4	19
									AVSIQTGYLIQSTGPK	95.0	####	25.0	1662.91	0	2	0	0	2	164	179
									SSQFLAPK	95.0	33.1	25.0	877.48	0	1	0	0	2	203	210
PDZ and LIM domain protein 1	PDLI1_HUMAN	PDLIM1	36.05	100.0	5	5	41	20.10	DFEQPLAISR	95.0	58.1	25.0	1175.61	0	19	0	0	2	23	32
									MNLASEPQEVLHIGSAHNR	95.0	49.0	25.0	2119.04	0	0	6	0	2	104	122
									SAMPFTASPASSTTAR	95.0	68.3	25.0	1598.75	0	2	0	0	2	123	138
									VAASIGNAQK	95.0	41.7	25.0	958.53	0	8	0	0	2	247	256
									CGTGIVGVFVK	95.0	48.9	25.0	1136.61	0	6	0	0	2	263	273
PDZ and LIM domain protein 5	PDLI5_HUMAN	PDLIM5	63.98	100.0	4	4	14	7.38	EVVKPVPITSPAVSK	95.0	51.3	25.0	1550.92	0	4	0	0	2	102	116
									AEHIPAGK	94.8	26.6	25.0	822.45	0	1	0	0	2	408	415
									GPFLVALGK	95.0	50.1	25.0	901.55	0	3	0	0	2	429	437
									NTMAYIGFVEEK	95.0	63.4	25.0	1417.67	0	6	0	0	2	451	462
PDZ and LIM domain protein 7	PDLI7_HUMAN	PDLIM7	49.83	100.0	3	3	15	6.13	DFNVPLSISR	95.0	45.8	25.0	1147.61	0	4	0	0	2	23	32
									LSLGLSR	95.0	36.5	25.0	745.46	0	3	0	0	2	77	83
									VLEEGGFFEEK	95.0	75.1	25.0	1283.62	0	8	0	0	2	314	324
PDZ domain-containing protein GIPC1	GIPC1_HUMAN	GIPC1	36.03	100.0	3	3	5	11.10	VDDLLESYMGIR	95.0	63.0	25.0	1426.69	0	2	0	0	2	268	279
									DTELAATMVELGK	95.0	58.9	25.0	1393.69	0	2	0	0	2	280	292
									NPDELAEALDER	95.0	61.6	25.0	1371.64	0	1	0	0	2	296	307
Peptidyl-prolyl cis-trans isomerase A	PPIA_HUMAN	PPIA	17.99	100.0	6	7	371	33.30	VSFELFADK	95.0	66.5	25.0	1055.54	0	98	0	0	2	20	28
									TAENFR	95.0	27.5	25.0	737.36	0	1	0	0	2	32	37
									ALSTGEKGFGYK	95.0	50.1	25.0	1257.65	0	2	0	0	2	38	49
									FEDENFILK	95.0	68.3	25.0	1154.57	0	135	0	0	2	83	91
									HVVFGK	95.0	31.4	25.0	686.40	2	0	0	0	2	126	131
									VKEGMNIVEAMER	95.0	69.3	25.0	1537.74	0	18	13	0	2	132	144
									EGMNIVEAMER	95.0	48.0	25.0	1310.57	0	104	0	0	2	134	144
Peptidyl-prolyl cis-trans isomerase B	PPIB_HUMAN	PPIB	23.73	100.0	9	11	110	36.10	IGDEDVGR	95.0	75.0	25.0	860.41	0	17	0	0	2	52	59
									VIFGLFGK	95.0	44.4	25.0	880.53	0	2	0	0	2	60	67
									TVDNFVALATGEK	95.0	94.8	25.0	1364.71	0	32	0	0	2	72	84
									DFMIQGGDFTR	95.0	62.9	25.0	1302.58	0	8	0	0	2	99	109
									FPDENFK	95.0	36.4	25.0	896.41	0	2	0	0	2	123	129
									DTNGSQFFITTVK	95.0	90.7	25.0	1457.73	0	16	0	0	2	146	158
									HVVFGK	95.0	31.4	25.0	686.40	2	0	0	0	2	166	171
									IEVEKPFAIAK	95.0	50.7	25.0	1244.73	0	20	5	0	2	205	215

									IEVEKPFAIAKE	95.0	46.0	25.0	1373.77	0	2	4	0	2	205	216
Peptidyl-prolyl cis-trans isomerase C	PPIC_HUMAN	PPIC	22.75	99.5	2	2	9	12.70	IVIGLFGK	95.0	28.4	25.0	846.54	0	1	0	0	2	54	61
									TVENFVALATGEK	95.0	72.1	25.0	1378.72	0	8	0	0	2	66	78
									HVVFGK	95.0	31.4	25.0	686.40	2	0	0	0	2	160	165
Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF_HUMAN	PPIF	22.02	100.0	3	3	14	14.00	VVLELK	95.0	43.3	25.0	700.46	0	3	0	0	2	62	67
									TAENFR	95.0	27.5	25.0	737.36	0	1	0	0	2	74	79
									FPDENFTLK	95.0	55.1	25.0	1110.55	0	7	0	0	2	125	133
									KIESFGSK	95.0	44.5	25.0	895.49	0	4	0	0	2	183	190
Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4_HUMAN	FKBP4	51.79	100.0	15	19	80	30.10	ATESGAQSAPLPMEGVDISPK	95.0	89.0	25.0	2101.01	0	9	2	0	2	8	28
									EGTGTEMPMIGDR	95.0	47.2	25.0	1425.60	0	10	0	0	2	40	52
									FDSSLDR	95.0	37.1	25.0	839.39	0	3	0	0	2	67	73
									FDSSLDRK	95.0	31.2	25.0	967.48	0	1	0	0	2	67	74
									DKFSFDLGK	95.0	48.0	25.0	1056.54	0	4	0	0	2	75	83
									FSFDLGK	95.0	34.6	25.0	813.41	0	6	0	0	2	77	83
									GEDLTEEEDGGIIR	95.0	87.3	25.0	1532.71	0	10	0	0	2	139	152
									FQIPPNAELK	95.0	29.3	25.0	1156.64	0	2	0	0	2	235	244
									QALLQYK	95.0	36.2	25.0	863.50	0	1	0	0	2	288	294
									ALELDSNNEK	95.0	35.5	25.0	1132.55	0	7	0	0	2	345	354
									RGEAHLAVNDFELAR	95.0	87.7	25.0	1697.87	0	4	3	3	2	359	373
									GEAHLAVNDFELAR	95.0	41.9	25.0	1541.77	0	2	2	0	2	360	373
									VLQLYPNNK	95.0	47.1	25.0	1088.61	0	3	0	0	2	379	387
									LYANMFER	95.0	47.4	25.0	1059.49	0	4	0	0	2	410	417
									SNTAGSQSQVETEA	95.0	46.5	25.0	1408.62	0	4	0	0	2	446	459
Peptidyl-prolyl cis-trans isomerase H	PPIH_HUMAN	PPIH	19.19	100.0	4	5	18	30.50	IELFADVVPK	95.0	46.5	25.0	1130.65	0	4	0	0	2	29	38
									TAENFR	95.0	27.5	25.0	737.36	0	1	0	0	2	39	44
									GPFADENFK	95.0	40.6	25.0	1024.47	0	5	0	0	2	93	101
									HVVFGK	95.0	31.4	25.0	686.40	2	0	0	0	2	138	143
									IIDGLLVMR	95.0	59.9	25.0	1045.61	0	2	0	0	2	144	152
									KIENVPTGPNNKPK	95.0	44.8	25.0	1535.85	0	2	5	0	2	153	166
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1_HUMAN	PPIL1	18.22	100.0	4	5	9	29.50	NFAELAR	95.0	43.9	25.0	820.43	0	3	0	0	2	38	44
									DFMIQGGDPTGTGR	95.0	63.3	25.0	1467.65	0	2	0	0	2	59	72
									QFEDELHPDLK	95.0	37.0	25.0	1370.66	0	2	1	0	2	81	91
									VGMVETNSQDRPVDDVK	95.0	33.0	25.0	1904.90	0	1	0	0	2	142	158
Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3_HUMAN	PPIL3	18.14	100.0	3	3	6	23.60	GFMVQTGDPTGTGR	95.0	70.7	25.0	1439.66	0	3	0	0	2	48	61
									KFEDEYSEYLK	95.0	65.5	25.0	1450.67	0	2	0	0	2	70	80
									VIDGLETLDELEK	95.0	28.9	25.0	1473.77	0	1	0	0	2	121	133
Perilipin-3	PLIN3_HUMAN	PLIN3	47.03	100.0	4	4	8	11.50	VSGAQEMVSSAK	95.0	49.6	25.0	1209.58	0	1	0	0	2	129	140
									DTVATQLSEAVDATR	95.0	####	25.0	1576.78	0	2	0	0	2	141	155
									LGQMVLSGVDTVLGK	95.0	80.5	25.0	1532.84	0	2	0	0	2	181	195
									QEQSYFVR	95.0	48.1	25.0	1056.51	0	3	0	0	2	231	238
Peripheral plasma membrane protein CASK	CSKP_HUMAN	CASK	105.11	100.0	4	4	9	4.43	FTSSPGLSTEDLK	95.0	43.3	25.0	1381.68	0	2	0	0	2	48	60
									LFEGIIK	95.0	36.6	25.0	819.50	0	4	0	0	2	226	232
									NTDEPMGITLK	95.0	41.2	25.0	1234.60	0	2	0	0	2	496	506
									VGDIIQIISK	95.0	38.0	25.0	1085.66	0	1	0	0	2	642	651
Periplakin	PEPL_HUMAN	PPL	204.66	100.0	8	8	33	4.90	ELSELIEQLQK	95.0	63.8	25.0	1329.73	0	8	0	0	2	26	36
									LLAASQAR	95.0	32.9	25.0	829.49	0	3	0	0	2	201	208
									TENPGDASDLQGR	95.0	47.6	25.0	1359.61	0	3	0	0	2	493	505
									AITGILRPPLEQGR	95.0	28.9	25.0	1520.89	0	0	1	0	2	524	537
									NITNELLR	95.0	40.1	25.0	972.55	0	5	0	0	2	551	558
									SLLGEVEQNLQAAK	95.0	35.9	25.0	1499.81	0	1	0	0	2	667	680
									NLLDEIASR	95.0	55.3	25.0	1030.55	0	8	0	0	2	772	780

								FTEVYAINR	95.0	63.7	25.0	1112.57	0	4	0	0	2	846	854
Peroxidasin homolog	PXDN_HUMAN	PXDN	165.26	100.0	6	6	13	3.65	VVAHLTVQPR	95.0	22.0	25.0	1119.66	0	0	1	0	2	513	522
									SPNDLLALFR	95.0	65.5	25.0	1145.63	0	3	0	0	2	653	662
									AGEIFER	95.0	51.7	25.0	821.42	0	4	0	0	2	675	681
									AFFSPFR	95.0	27.4	25.0	871.45	0	1	0	0	2	1101	1107
									IVNEGGIDPLLR	95.0	69.0	25.0	1295.73	0	3	0	0	2	1108	1119
									GLFGVAGK	95.0	28.4	25.0	748.44	0	1	0	0	2	1120	1127
Peroxiredoxin-1	PRDX1_HUMAN	PRDX1	22.09	100.0	13	14	375	52.30	IGHPAPNFK	95.0	39.2	25.0	980.53	0	10	0	0	2	8	16
									ATAVMPDGQFK	95.0	48.8	25.0	1180.57	0	18	0	0	2	17	27
									DISLSDYK	95.0	40.5	25.0	940.46	0	3	0	0	2	28	35
									KQGGLGPMNIPLVSDPK	95.0	37.5	25.0	1766.95	0	3	4	0	2	93	109
									QGGLGPMNIPLVSDPK	95.0	96.1	25.0	1638.85	0	21	0	0	2	94	109
									RTIAQDYGVLK	95.0	44.6	25.0	1263.71	0	2	0	0	2	110	120
									TIAQDYGVLK	95.0	62.8	25.0	1107.60	0	51	0	0	2	111	120
									ADEGISFR	95.0	58.2	25.0	894.43	0	18	0	0	2	121	128
									GLFIIDDK	95.0	53.1	25.0	920.51	0	58	0	0	2	129	136
									GLFIIDDKGILR	95.0	35.8	25.0	1359.80	0	0	2	0	2	129	140
									QITVNDLPVGR	95.0	72.9	25.0	1211.67	0	65	0	0	2	141	151
									SVDETLR	95.0	56.0	25.0	819.42	0	14	0	0	2	152	158
									LVQAFQFTDK	95.0	67.5	25.0	1196.63	0	106	0	0	2	159	168
Peroxiredoxin-2	PRDX2_HUMAN	PRDX2	21.87	100.0	5	5	21	23.20	ATAVVDGAFK	95.0	62.9	25.0	978.53	0	2	0	0	2	17	26
									RLSEDYGVLK	95.0	44.1	25.0	1179.64	0	1	0	0	2	110	119
									LSEDYGVLK	95.0	53.3	25.0	1023.54	0	10	0	0	2	111	119
									GLFIIDGK	95.0	32.2	25.0	862.50	0	5	0	0	2	128	135
									QITVNDLPVGR	95.0	72.9	25.0	1211.67	0	65	0	0	2	140	150
									SVDEALR	95.0	39.0	25.1	789.41	0	3	0	0	2	151	157
Peroxiredoxin-4	PRDX4_HUMAN	PRDX4	30.52	99.5	2	2	4	15.90	IPLLSDLTHQISK	95.0	56.2	25.0	1464.84	0	2	0	0	2	174	186
									GLFIIDDK	95.0	53.1	25.0	920.51	0	58	0	0	2	201	208
									GLFIIDDKGILR	95.0	35.8	25.0	1359.80	0	0	2	0	2	201	212
									QITLNDLPVGR	95.0	63.4	25.0	1225.69	0	2	0	0	2	213	223
									SVDETLR	95.0	56.0	25.0	819.42	0	14	0	0	2	224	230
Peroxiredoxin-5, mitochondrial	PRDX5_HUMAN	PRDX5	22.01	100.0	4	4	67	20.60	VNLAELFK	95.0	47.8	25.0	933.54	0	19	0	0	2	76	83
									THLPGFVEQAEALK	95.0	53.0	25.0	1539.82	0	2	0	0	2	103	116
									LLADPTGAFGK	95.0	68.8	25.0	1089.59	0	37	0	0	2	149	159
									FSMVVQDGIVK	95.0	70.2	25.0	1238.65	0	9	0	0	2	181	191
Peroxiredoxin-6	PRDX6_HUMAN	PRDX6	25.02	100.0	9	11	98	30.80	DFTPVCTTELGR	95.0	75.7	25.0	1395.66	0	2	0	0	2	42	53
									LAPEFAK	95.0	40.9	25.0	775.43	0	2	0	0	2	57	63
									LPFPIIDDR	95.0	59.4	25.0	1085.60	0	46	0	0	2	98	106
									LPFPIIDDRNR	95.0	23.9	25.0	1355.74	0	0	1	0	2	98	108
									VVFVFGPDK	95.0	46.7	25.0	1007.56	0	15	0	0	2	133	141
									VVFVFGPDKK	95.0	47.7	25.0	1135.65	0	4	7	0	2	133	142
									LSILYPATTGR	95.0	63.5	25.0	1191.67	0	14	0	0	2	145	155
									DGDSVMVLPTIPEEEAK	95.0	56.8	25.0	1845.88	0	3	0	0	2	183	199
									DGDSVMVLPTIPEEEAKK	95.0	44.8	25.0	1973.97	0	2	2	0	2	183	200
Phenylalanyl-tRNA synthetase beta chain	SYFB_HUMAN	FARSB	66.10	100.0	6	6	15	11.00	AAGASDVVLYK	95.0	71.5	25.0	1093.59	0	2	0	0	2	54	64
									IRPFAVAAVLR	95.0	32.1	25.0	1212.76	0	0	1	0	2	117	127
									TYTIANQFPLNK	95.0	67.8	25.0	1409.74	0	5	0	0	2	384	395
									TTLLPGLLK	95.0	29.7	25.0	955.62	0	1	0	0	2	452	460
									ASEGPAFFPGR	95.0	61.6	25.0	1135.55	0	4	0	0	2	537	547
									LGVLHPDVITK	95.0	31.1	25.0	1191.71	0	2	0	0	2	561	571
Phosphatidylethanolamine-	PEBP1_HUMAN	PEBP1	21.04	100.0	4	4	19	21.40	VLTPTQVK	95.0	29.7	25.0	885.54	0	2	0	0	2	40	47

binding protein 1									LYTLVLTDPDAPSRK	95.0	59.7	25.0	1688.92	0	0	2	0	2	63	77
									CDEPILSNR	95.0	32.2	25.0	1103.52	0	2	0	0	2	133	141
									LYEQLSGK	95.0	50.5	25.0	937.50	0	13	0	0	2	180	187
Phosphatidylinositol transfer protein alpha isoform	PIPNA_HUMAN	PITPNA	31.79	100.0	3	3	4	13.30	MLAPEGALNIHEK	95.0	67.7	25.0	1438.74	0	2	0	0	2	74	86
									TVITNEYMK	95.0	38.1	25.0	1114.55	0	1	0	0	2	96	104
									VENFIHK	95.0	27.2	25.0	886.48	0	1	0	0	2	209	215
									LFTNFHR	95.0	40.0	25.0	934.49	0	6	0	0	2	220	226
Phosphatidylinositol transfer protein beta isoform	PIPNB_HUMAN	PITPNB	31.52	100.0	6	7	22	21.40	NETGGGEGIEVLK	95.0	56.7	25.0	1302.65	0	3	0	0	2	32	44
									MIAPEGSLVFHEK	95.0	63.2	25.0	1473.74	0	4	4	0	2	74	86
									TIVTNEYMK	95.0	32.7	25.0	1114.55	0	1	0	0	2	96	104
									SQVEPADYK	95.0	44.3	25.0	1036.49	0	3	0	0	2	147	155
									VENFIQK	95.0	27.9	25.0	877.48	0	1	0	0	2	209	215
									IFTNFHR	95.0	40.0	25.0	934.49	0	6	0	0	2	220	226
Phosphoacetylglucosamine mutase	AGM1_HUMAN	PGM3	59.83	100.0	4	4	14	7.38	MGLLAVLR	95.0	59.1	25.0	888.53	0	4	0	0	2	42	49
									ATIEGYYQK	95.0	35.3	25.0	1072.53	0	2	0	0	2	178	186
									IATLISSFLK	95.0	35.6	25.0	1092.67	0	4	0	0	2	301	310
									AFVRPSGTEDVVR	95.0	49.2	25.0	1432.75	0	4	0	0	2	493	505
Phosphoglucomutase-1	PGM1_HUMAN	PGM1	61.43	100.0	12	15	50	24.60	TQAYQDQKPGTSGLR	95.0	54.2	25.0	1649.82	0	2	7	0	2	9	23
									QEATLVVGGDGR	95.0	70.9	25.0	1201.62	0	4	0	0	2	53	64
									EAIQLIAR	95.0	40.9	25.0	913.55	0	2	0	0	2	69	76
									FNISNGGPAPEAITDK	95.0	####	25.0	1630.81	0	2	0	0	2	131	146
									VDLGVLGK	95.0	54.2	25.0	800.49	0	2	0	0	2	165	172
									SIFDFSALK	95.0	49.6	25.0	1027.55	0	2	0	0	2	201	209
									ELLSGPNR	94.6	26.4	25.0	885.48	0	1	0	0	2	210	217
									IDAMHGVVGPYVK	95.0	36.4	25.0	1401.72	0	2	4	0	2	222	234
									SGEHDFGAAFDGDGDR	95.0	80.1	25.0	1652.66	0	4	2	0	2	278	293
									YDYEEVEAEGANK	95.0	####	25.0	1516.64	0	4	0	0	2	428	440
									LSGTGSAGATIR	95.0	85.0	25.0	1090.59	0	11	0	0	2	504	515
									LYIDSYEK	95.0	28.3	25.0	1030.51	0	1	0	0	2	516	523
Phosphoglucomutase-2	PGM2_HUMAN	PGM2	68.27	100.0	9	9	17	14.40	MEFGTAGLR	95.0	35.0	25.0	997.48	0	2	0	0	2	55	63
									AAMGPGISR	95.0	29.8	25.0	875.44	0	1	0	0	2	64	72
									YPNPEEGK	95.0	33.4	25.0	933.43	0	2	0	0	2	293	300
									IVLANDPDADRLAVAEK	95.0	62.4	25.0	1809.97	0	2	0	0	2	317	333
									SALKDTYMLSSTVSSK	95.0	86.6	25.0	1733.86	0	2	0	0	2	367	382
									DTYMLSSTVSSK	95.0	59.2	25.0	1334.61	0	2	0	0	2	371	382
									NLSLSQQLK	95.0	28.8	25.0	1030.59	0	1	0	0	2	458	466
									DLTTGYDDSQPDKK	95.0	73.7	25.0	1582.72	0	4	0	0	2	520	533
									YNLQPK	95.0	27.5	25.0	762.41	0	1	0	0	2	605	610
Phosphoglycerate kinase 1	PGK1_HUMAN	PGK1	44.60	100.0	19	23	198	47.50	LTLDKLDVK	95.0	48.0	25.0	1044.63	0	4	0	0	2	7	15
									VDFNVPMK	95.0	41.3	25.0	965.48	0	8	0	0	2	23	30
									SVVLMSHLGRPDGVPMPDK	95.0	30.0	25.0	2067.04	0	1	5	0	2	57	75
									YSLEPVAVELK	95.0	57.4	25.0	1247.69	0	6	0	0	2	76	86
									DVLFLK	95.0	48.8	25.0	734.44	0	5	0	0	2	92	97
									DCVGPEVEK	95.0	46.6	25.0	1032.47	0	3	0	0	2	98	106
									FHVEEEGK	95.0	33.1	25.0	974.46	0	3	0	0	2	124	131
									FHVEEEGKGK	95.0	46.7	25.0	1159.57	0	9	11	0	2	124	133
									LGDVYVNDAFGTAHR	95.0	####	25.0	1634.79	0	9	20	0	2	157	171
									AHSSMVGVNLPQK	95.0	54.7	25.0	1383.71	0	10	1	0	2	172	184
									AGGFLMK	95.0	51.8	25.0	739.38	0	8	0	0	2	185	191
									ELNYFAK	95.0	36.3	25.0	884.45	0	3	0	0	2	193	199
									IQLINNMLDK	95.0	29.4	25.0	1217.66	0	1	0	0	2	221	230

									VLNNMEIGTSLFDEEGAK	95.0	83.3	25.0	1982.94	0	4	0	0	2	247	264
									ITLPVDFVTADK	95.0	57.5	25.0	1318.73	0	2	0	0	2	280	291
									YAEAVTR	95.0	48.5	25.0	809.42	0	19	0	0	2	324	330
									ALMDEVVK	95.0	50.6	25.0	920.48	0	7	0	0	2	354	361
									VSHVSTGGGASLELLEGK	95.0	####	25.0	1740.91	0	4	0	0	2	389	406
									VLPGVDALSNI	95.0	56.0	25.0	1097.62	0	55	0	0	2	407	417
Phosphoglycerate mutase 1	PGAM1_HUMAN	PGAM1	28.79	100.0	3	4	52	15.40	HYGGLTGLNK	95.0	53.5	25.0	1059.56	0	12	0	0	2	91	100
									VLIAAHGNSLR	95.0	58.8	25.0	1150.67	0	19	19	0	2	181	191
									NLKPIKPMQFLGDEETVR	95.0	38.0	25.0	2131.12	0	0	2	0	2	223	240
Phosphoglycolate phosphatase	PGP_HUMAN	PGP	33.99	100.0	3	3	5	11.80	GETAVPGAPEALR	95.0	27.7	25.0	1267.66	0	1	0	0	2	42	54
									LGFITNNSSK	95.0	39.0	25.0	1080.57	0	2	0	0	2	63	72
									TILTLTGVSTLGDVK	95.0	54.2	25.0	1517.88	0	2	0	0	2	276	290
Phospholipid transfer protein	PLTP_HUMAN	PLTP	54.72	100.0	7	7	38	16.20	MHAAFGGTFK	95.0	36.2	25.0	1082.51	0	4	0	0	2	153	162
									DPVASTSNLDMDFR	95.0	79.5	25.0	1583.70	0	3	0	0	2	222	235
									GAFFPLTER	94.8	26.6	25.0	1037.54	0	1	0	0	2	236	244
									AVEPQLQEEER	95.0	58.6	25.0	1327.65	0	7	0	0	2	252	262
									AGALQLLLVGDK	95.0	75.5	25.0	1197.72	0	20	0	0	2	283	294
									VPHDLDMLLR	95.0	39.1	25.0	1224.64	0	0	1	0	2	295	304
									TMLQIGVMPMLNER	95.0	81.5	25.0	1680.81	0	2	0	0	2	416	429
Phosphomannomutase 2	PMM2_HUMAN	PMM2	28.07	100.0	3	3	6	13.00	IGVVGGSDFEK	95.0	34.9	25.0	1107.57	0	2	0	0	2	41	51
									VQEQLGNDVVEK	95.0	78.3	25.0	1357.70	0	2	0	0	2	52	63
									IEFYELDKK	95.0	50.4	25.0	1184.62	0	2	0	0	2	142	150
Phosphopantothenate--cysteine ligase	PPCS_HUMAN	PPCS	33.99	100.0	4	4	10	13.20	RVVLVTSGGTK	95.0	45.8	25.0	1116.67	0	2	0	0	2	36	46
									FLDNFSSGR	95.0	56.0	25.0	1042.50	0	2	0	0	2	56	64
									LETDPAIVINR	95.0	50.0	25.0	1240.69	0	2	0	0	2	232	242
									LLLSEEEIEK	95.0	42.9	25.0	1202.65	0	4	0	0	2	278	287
Phosphoribosyl pyrophosphate synthase-associated protein 2	KPRB_HUMAN	PRPSAP2	40.91	100.0	5	7	19	13.80	VQVYQEPNR	95.0	42.5	25.0	1132.57	0	4	0	0	2	49	57
									GKDVFIIQTVSK	95.0	57.1	25.0	1334.77	0	2	0	0	2	69	80
									DVFIIQTVSK	95.0	53.2	25.0	1149.65	0	6	0	0	2	71	80
									EKPPITVVGDVGGR	95.0	64.7	25.0	1423.79	0	2	2	0	2	250	263
									IFVMATHGLLSSDAPR	95.0	76.4	25.0	1730.89	0	2	1	0	2	293	308
Phosphoribosylformylglycinamidine synthase	PUR4_HUMAN	PFAS	144.71	100.0	5	6	10	4.11	ATGLGPVDR	95.0	33.1	25.0	885.48	0	2	0	0	2	110	118
									FGEPVLAGFAR	95.0	57.4	25.0	1163.62	0	2	0	0	2	396	406
									SLGLQLPDGQR	95.0	40.8	25.0	1183.64	0	1	0	0	2	407	417
									ELSDPAGAIIYTSR	95.0	93.6	25.0	1492.76	0	2	1	0	2	528	541
									VGPGPALMLR	95.0	57.2	25.0	1026.58	0	2	0	0	2	1211	1220
Phosphoserine aminotransferase	SERC_HUMAN	PSAT1	40.41	100.0	14	17	76	36.20	QVVNFGPGPAK	95.0	38.4	25.0	1113.61	0	4	0	0	2	6	16
									LPHSVLLEIQK	95.0	51.1	25.0	1276.76	0	6	2	0	2	17	27
									GVGISVLEMSHR	95.0	53.1	25.0	1300.67	0	4	2	0	2	34	45
									IINNTENLVR	95.0	79.3	25.0	1185.66	0	4	0	0	2	52	61
									ELLAVPDNYK	95.0	32.0	25.0	1161.62	0	1	0	0	2	62	71
									KFGTINIVHPK	95.0	41.5	25.0	1253.74	0	0	3	0	2	117	127
									FGTINIVHPK	95.0	56.5	25.0	1125.64	0	5	4	0	2	118	127
									FGVIFAGAQK	95.0	62.6	25.0	1037.58	0	2	0	0	2	191	200
									NVGSAGVTVVIVR	95.0	88.8	25.0	1270.75	0	2	0	0	2	201	213
									DDLLGFALR	95.0	55.9	25.0	1019.55	0	21	0	0	2	214	222
									MNIPFR	95.0	36.3	25.0	793.40	0	3	0	0	2	301	306
									ALELNMLSLK	95.0	48.7	25.0	1147.64	0	8	0	0	2	324	333
									ASLYNAVTIEDVQK	95.0	90.3	25.0	1550.81	0	4	0	0	2	343	356
									FLEMHQL	95.0	27.8	25.0	933.45	0	1	0	0	2	364	370
Phosphoserine phosphatase	SERB_HUMAN	PSPH	24.99	100.0	4	4	12	19.10	LALIQPSR	95.0	46.3	25.0	897.55	0	4	0	0	2	66	73

									LIAEQPPHLTPGIR	95.0	73.2	25.0	1541.88	0	2	0	0	2	79	92
									SIVEHVASK	95.0	44.0	25.0	969.54	0	3	0	0	2	114	122
									LNIPATNVFANR	95.0	70.9	25.0	1329.73	0	3	0	0	2	123	134
Pigment epithelium-derived factor	PEDF_HUMAN	SERPINF1	46.33	100.0	5	6	35	13.40	SSFVAPLEK	95.0	31.3	25.0	977.53	0	4	0	0	2	152	160
									KTSLEDFYLDEER	95.0	79.9	25.0	1644.78	0	2	2	0	2	225	237
									TVQAVLTVPK	95.0	71.1	25.0	1055.65	0	8	0	0	2	307	316
									LQSLFDSPDFSK	95.0	80.1	25.0	1383.68	0	8	0	0	2	334	345
									DTDTGALLFIGK	95.0	93.6	25.0	1250.66	0	11	0	0	2	400	411
Plakophilin-2	PKP2_HUMAN	PKP2	97.40	100.0	3	3	6	2.61	LLQLLK	95.0	28.4	25.0	727.51	0	2	0	0	2	400	405
									TAISLLR	95.0	38.7	25.0	773.49	0	2	0	0	2	748	754
									NLSLQNEIAK	95.0	33.5	25.0	1129.62	0	2	0	0	2	759	768
Plakophilin-3	PKP3_HUMAN	PKP3	87.07	100.0	3	3	4	2.89	ILNPLLDR	95.0	28.0	25.0	953.58	0	2	0	0	2	656	663
									SLTGLIR	95.0	27.0	25.0	759.47	0	1	0	0	2	674	680
									LPGSVGEK	95.0	27.1	25.0	786.44	0	1	0	0	2	704	711
Plasminogen activator inhibitor 1	PAI1_HUMAN	SERPINE1	45.04	100.0	9	11	56	25.40	VFQQVAQASK	95.0	67.9	25.0	1105.60	0	20	0	0	2	42	51
									LVQGFMPHFFR	95.0	44.6	25.0	1394.70	0	2	1	0	2	128	138
									QVDFSEVER	95.0	61.0	25.0	1108.53	0	10	0	0	2	146	154
									GMISNLLGK	95.0	46.2	25.0	948.52	0	5	0	0	2	169	177
									GAVDQLTR	95.0	36.5	25.0	859.46	0	3	0	0	2	178	185
									TPFPDSSTHR	95.0	35.7	25.0	1144.54	0	1	0	0	2	200	209
									SDGSTVSVPMMAQTNK	95.0	31.2	25.0	1684.75	0	1	0	0	2	215	230
									KPLENLGMTDMFR	95.0	53.3	25.0	1583.76	0	6	4	0	2	311	323
									HNPTGTVLFMGQVMEP	95.0	98.7	25.0	1789.83	0	3	0	0	2	387	402
Plasminogen activator inhibitor 2	PAI2_HUMAN	SERPINB2	46.58	100.0	4	5	12	8.92	GSYPDAILQAQAADK	95.0	####	25.0	1547.77	0	4	0	0	2	88	102
									EKLNIGYIEDLK	95.0	67.1	25.0	1434.78	0	2	2	0	2	239	250
									LNIGYIEDLK	95.0	73.4	25.0	1177.65	0	2	0	0	2	241	250
									SMGMEDAFNK	95.0	45.7	25.0	1161.46	0	2	0	0	2	326	335
Plastin-1	PLSI_HUMAN	PLS1	70.24	100.0	3	3	5	11.10	EELEELQEAFNK	95.0	61.0	25.0	1478.70	0	2	0	0	2	11	22
									MINLSEPDTIDER	95.0	69.1	25.0	1548.72	0	2	0	0	2	168	180
									LSPEELLLR	95.0	71.8	25.0	1069.63	0	21	0	0	2	266	274
									AYFHLLNQIAPK	95.0	41.5	25.0	1414.78	0	3	4	0	2	300	311
									AGLMLQEADK	95.0	57.0	25.0	1091.54	0	1	0	0	2	335	344
									QFVTPADVVSGNPK	95.0	####	25.0	1458.76	0	18	0	0	2	349	362
Plastin-2	PLSL_HUMAN	LCP1	70.27	100.0	11	13	46	24.90	GSVSDEEMMELR	95.0	54.3	25.0	1414.58	0	8	0	0	2	4	15
									EITENLMATGDLDQDGR	95.0	82.5	25.0	1893.85	0	1	0	0	2	52	68
									ISFDEFIK	95.0	34.8	25.0	998.52	0	3	0	0	2	69	76
									MINLSVPDTIDER	95.0	72.4	25.0	1518.75	0	36	0	0	2	166	178
									NEALIALLR	95.0	68.6	25.0	1012.62	0	17	0	0	2	245	253
									EGESLEDLMK	95.0	31.6	25.0	1166.52	0	1	0	0	2	254	263
									LSPEELLLR	95.0	71.8	25.0	1069.63	0	21	0	0	2	264	272
									IGNFSTDIK	95.0	60.0	25.0	994.52	0	3	0	0	2	286	294
									AYYHLLEQVAPK	95.0	48.6	25.0	1431.76	0	1	5	0	2	298	309
									GDEEGVPAVVIDMSGLR	95.0	41.4	25.0	1759.85	0	1	0	0	2	310	326
									VNKPPYPK	95.0	30.6	25.0	942.54	0	6	0	0	2	442	449
									SSSISSFKDPK	95.0	27.2	25.0	1182.60	0	1	0	0	2	535	545
									TENLNDDEKLNNAK	95.0	64.4	25.0	1617.77	0	2	2	0	2	571	584
									YAISMAR	95.0	27.2	25.0	827.41	0	1	0	0	2	585	591
Plastin-3	PLST_HUMAN	PLS3	70.80	100.0	19	24	271	29.40	DELDELKEAFAK	95.0	49.0	25.0	1407.70	0	2	0	0	2	12	23
									EANMPLPGYK	95.0	39.1	25.0	1135.55	0	6	0	0	2	43	52
									LMLDGDR	95.0	36.9	25.0	835.40	0	7	0	0	2	60	66
									HVIPMNPNTDDLFK	95.0	54.4	25.0	1656.81	0	10	4	0	2	145	158

									MINLSVPDTIDER	95.0	72.4	25.0	1518.75	0	36	0	0	2	169	181
									NEALAALLR	95.0	81.9	25.0	970.57	0	85	0	0	2	248	256
									DGETLEELMK	95.0	60.2	25.0	1180.54	0	17	0	0	2	257	266
									LSPEELLLR	95.0	71.8	25.0	1069.63	0	21	0	0	2	267	275
									INNFSADIK	95.0	54.4	25.0	1021.53	0	15	0	0	2	289	297
									INNFSADIKDSK	95.0	54.0	25.0	1351.69	0	2	1	0	2	289	300
									AYFHLLNQIAPK	95.0	41.5	25.0	1414.78	0	3	4	0	2	301	312
									IDINMSGFNETDDLK	95.0	83.3	25.0	1727.78	0	2	0	0	2	321	335
									IDINMSGFNETDDLKR	95.0	96.7	25.0	1883.88	0	4	3	0	2	321	336
									AESMLQQADK	95.0	56.9	25.0	1136.53	0	7	0	0	2	337	346
									QFVTPADVVSGNPK	95.0	####	25.0	1458.76	0	18	0	0	2	351	364
									VNKPPYPK	95.0	30.6	25.0	942.54	0	6	0	0	2	445	452
									STSIQSFK	95.0	37.8	25.0	897.47	0	5	0	0	2	538	545
									YAVSMAR	95.0	43.1	25.0	813.39	0	4	0	0	2	588	594
									VYALPEDLVEVKPK	95.0	65.4	25.0	1599.90	0	6	3	0	2	600	613
Platelet-activating factor acetylhydrolase IB subunit alpha	LIS1_HUMAN	PAFAH1B1	46.62	100.0	8	9	36	21.20	AIADYLR	95.0	47.3	25.0	821.45	0	4	0	0	2	14	20
									SNGYEEAYSVFK	95.0	85.3	25.0	1393.63	0	2	0	0	2	21	32
									EAELDVNEELDKK	95.0	52.5	25.0	1531.75	0	2	0	0	2	34	46
									LNEAKEEFTSGGPLGQK	95.0	40.9	25.0	1804.91	0	0	2	0	2	72	88
									EEFTSGGPLGQK	95.0	46.4	25.0	1249.61	0	2	0	0	2	77	88
									YALSGHR	95.0	39.9	25.0	803.42	0	2	0	0	2	102	108
									GHTDSVQDISFDHSGK	95.0	85.7	25.0	1729.78	0	1	4	0	2	148	163
									TAPYVVTGSVDQTVK	95.0	78.5	25.0	1564.82	0	17	0	0	2	391	405
Platelet-activating factor acetylhydrolase IB subunit gamma	PA1B3_HUMAN	PAFAH1B3	25.72	100.0	3	3	14	11.30	AIVQLVNER	95.0	47.3	25.0	1041.61	0	4	0	0	2	119	127
									VVVLGLLPR	95.0	68.2	25.0	965.65	0	9	0	0	2	133	141
									GQHPNPLR	95.0	29.6	25.0	918.49	0	1	0	0	2	142	149
Plectin-1	PLEC1_HUMAN	PLEC1	531.77	100.0	158	178	1328	31.60	HISDLYEDLR	95.0	55.3	25.0	1260.62	0	3	0	0	2	199	208
									LQNVQIALDYLR	95.0	37.0	25.0	1445.81	0	1	0	0	2	237	248
									NDDIADGNPK	95.0	47.0	25.0	1058.48	0	13	0	0	2	259	268
									MVEGYQGLR	95.0	48.9	25.0	1068.51	0	2	0	0	2	308	316
									LFNAIIHR	95.0	56.4	25.0	983.58	0	2	0	0	2	329	336
									HKPLLIDMNK	95.0	19.2	25.0	1224.68	0	0	1	0	2	337	346
									LLDPEDVDVPQPDEK	95.0	71.5	25.0	1708.83	0	7	0	0	2	372	386
									ANELQLR	95.0	38.0	25.0	843.47	0	7	0	0	2	411	417
									HHTAAFEER	95.0	31.9	25.0	1097.51	0	1	9	0	2	434	442
									VPPGYHPLDVEK	95.0	50.5	25.0	1350.71	0	2	0	0	2	494	505
									LHVAILER	95.0	38.6	25.0	950.58	0	2	0	0	2	510	517
									LLFNDVQTLK	95.0	64.2	25.0	1190.68	0	14	0	0	2	588	597
									RPELEDSTLR	95.0	48.2	25.0	1215.63	0	18	0	0	2	651	660
									GLHQSIEEFR	95.0	57.7	25.0	1215.61	0	2	4	0	2	697	706
									ARSDEGQLSPATR	95.0	29.8	25.0	1387.69	0	1	0	0	2	712	724
									SDEGQLSPATR	95.0	49.3	25.0	1160.55	0	4	0	0	2	714	724
									LDLQYAK	95.0	34.3	25.0	850.47	0	1	0	0	2	734	740
									SLESLHSFVAAATK	95.0	70.8	25.0	1460.77	0	4	4	0	2	751	764
									KESYSALMR	95.0	32.6	25.0	1100.54	0	1	1	0	2	792	800
									ESYSALMR	95.0	32.2	25.0	972.45	0	5	0	0	2	793	800
									IKELQNAGDR	95.0	38.5	25.0	1143.61	0	2	6	0	2	809	818
									LQEALR	95.0	32.5	25.0	729.43	0	2	0	0	2	878	883
									LEDLLQDAQDEK	95.0	57.7	25.0	1416.69	0	3	0	0	2	897	908
									AVVQLKPR	95.0	44.0	25.0	910.58	0	8	0	0	2	927	934
									DSQDAGGFGPEDR	95.0	69.9	25.0	1350.56	0	34	0	0	2	1076	1088

AQAEVEGLGK	95.0	52.3	25.0	1001.53	0	16	0	0	2	1166	1175
VLALPEPSPAAPTLR	95.0	61.7	25.0	1531.88	0	7	0	0	2	1187	1201
SELELTLGK	95.0	48.4	25.0	989.55	0	9	0	0	2	1202	1210
SLSAIYLEK	95.0	61.4	25.0	1023.57	0	11	0	0	2	1216	1224
GTQGAEEVLR	95.0	65.3	25.0	1059.54	0	21	0	0	2	1234	1243
EAQAVPATLPELEATK	95.0	50.7	25.0	1667.89	0	28	0	0	2	1251	1266
AQAEAQQPTFDALR	95.0	77.9	25.0	1545.77	0	4	0	0	2	1274	1287
HGERDVEVER	95.0	28.2	25.0	1225.59	0	0	5	0	2	1304	1313
VAQLLER	95.0	38.5	25.0	828.49	0	8	0	0	2	1318	1324
ELEQLGR	95.0	27.8	25.0	844.45	0	2	0	0	2	1338	1344
RQEQIQAMPLADSQAVR	95.0	48.0	25.0	1956.99	0	2	10	0	2	1366	1382
QEQIQAMPLADSQAVR	95.0	####	25.0	1800.89	0	6	1	0	2	1367	1382
QEQALLEEIER	95.0	44.6	25.0	1357.70	0	11	0	0	2	1387	1397
DYELQLVTYK	95.0	55.7	25.0	1271.65	0	11	0	0	2	1418	1427
AQLEPVASPAK	95.0	47.5	25.0	1110.62	0	15	0	0	2	1428	1438
FISETLR	95.0	47.5	25.0	865.48	0	3	0	0	2	1473	1479
LAEVEAALEK	95.0	72.8	27.2	1072.59	0	4	0	0	2	1499	1508
SIQEELQQLR	95.0	60.0	25.0	1243.66	0	7	0	0	2	1554	1563
LRIEEEIR	95.0	34.1	25.0	1057.60	0	2	2	0	2	1585	1592
IEEEIR	95.0	33.5	25.0	788.41	0	2	0	0	2	1587	1592
LQLEATER	95.0	32.8	25.0	959.52	0	3	0	0	2	1596	1603
GGAEGELQALR	95.0	60.7	25.0	1100.57	0	2	0	0	2	1606	1616
QAEVELASR	95.0	46.4	25.0	1002.52	0	2	0	0	2	1649	1657
ALQALEELR	95.0	54.9	25.0	1042.59	0	5	0	0	2	1671	1679
QVQVALETAQR	95.0	73.4	25.0	1242.68	0	3	0	0	2	1699	1709
SAEAELQSK	95.0	66.4	25.0	962.48	0	18	0	0	2	1710	1718
SAEAELQSKR	95.0	52.5	25.0	1118.58	0	2	0	0	2	1710	1719
SLQEEHVAVAQLR	95.0	69.2	25.0	1479.79	0	13	16	0	2	1732	1744
LQAEEVAQQK	95.0	57.2	25.0	1143.60	0	13	0	0	2	1783	1792
SLAQAEAEK	95.0	39.4	25.0	946.48	0	3	0	0	2	1793	1801
QRELAEQELEK	94.6	26.4	25.0	1372.71	0	1	0	0	2	1823	1833
ELAEQELEK	95.0	48.4	25.0	1088.55	0	5	0	0	2	1825	1833
QLAEGTAQQR	95.0	34.9	25.0	1101.56	0	1	0	0	2	1836	1845
LAAEQELIR	95.0	55.2	25.0	1042.59	0	2	0	0	2	1846	1854
LRAETEQGEQQR	95.0	58.9	25.0	1444.71	0	8	2	0	2	1855	1866
QLLEEELAR	95.0	69.2	25.0	1100.59	0	8	0	0	2	1867	1875
AEMEVLLASK	95.0	72.1	25.0	1106.58	0	7	0	0	2	1899	1908
FRELAEEAAR	95.0	39.6	25.0	1191.61	0	3	2	0	2	1933	1942
ELAEEAAR	95.0	30.4	25.0	888.44	0	1	0	0	2	1935	1942
QLAEEDAAR	95.0	27.2	25.0	1002.49	0	1	0	0	2	1955	1963
LAAIGEATR	95.0	63.6	25.0	901.51	0	20	0	0	2	1976	1984
TEAEIALK	95.0	29.4	25.0	874.49	0	1	0	0	2	1987	1994
LAEDEAFQR	95.0	71.7	25.0	1078.52	0	21	0	0	2	2006	2014
GLVEDTLR	95.0	36.0	25.0	902.49	0	2	0	0	2	2048	2055
RQVEEEILALK	95.0	37.0	25.0	1327.76	0	1	0	0	2	2058	2068
QVEEEILALK	95.0	47.0	25.0	1171.66	0	6	0	0	2	2059	2068
AELELELGR	95.0	44.5	25.0	1029.56	0	1	0	0	2	2079	2087
SKEQAELEAAR	95.0	56.6	25.0	1231.63	0	9	18	0	2	2098	2108
EQAELEAAR	95.0	58.5	25.0	1016.50	0	10	0	0	2	2100	2108
QLAAEEERR	95.0	42.9	25.0	1101.56	0	0	3	0	2	2111	2119
SLAAEEEAAR	95.0	70.3	25.0	1046.51	0	17	0	0	2	2130	2139

KAALEEVER	94.9	26.6	25.0	1044.57	0	1	0	0	2	2142	2150
AALEEVER	95.0	58.9	25.0	916.47	0	13	0	0	2	2143	2150
QLQLAQEAAQK	95.0	69.2	25.0	1227.67	0	5	0	0	2	2172	2182
AHAFAVQQK	95.0	30.8	25.0	999.54	0	2	0	0	2	2190	2198
LKQSAEEQAQAR	95.0	26.7	25.0	1358.70	0	0	1	0	2	2254	2265
AQAEQAALR	95.0	41.6	25.0	957.51	0	6	0	0	2	2287	2295
FAEQTLR	95.0	44.8	25.0	864.46	0	2	0	0	2	2310	2316
AQVEQELTTLR	95.0	78.5	25.0	1287.69	0	29	0	0	2	2319	2329
LQLEETDHQK	95.0	37.8	25.0	1240.62	0	10	2	0	2	2330	2339
NLLDEELQR	95.0	70.9	25.0	1129.58	0	15	0	0	2	2340	2348
LKAEATEAAR	95.0	50.3	25.0	1059.58	0	4	8	0	2	2349	2358
SQVEEELFSVR	95.0	86.8	25.0	1322.66	0	16	0	0	2	2361	2371
VQMEELSK	95.0	35.6	25.0	979.48	0	3	0	0	2	2372	2379
FLQEEAEK	95.0	41.2	25.0	993.49	0	6	0	0	2	2402	2409
LSVAAQEAAR	95.0	90.2	25.0	1015.55	0	42	0	0	2	2420	2429
QLAEEDLAQQR	95.0	60.6	25.0	1300.65	0	19	0	0	2	2432	2442
LKAEAELLQQQK	95.0	76.6	25.0	1398.80	0	6	0	0	2	2462	2473
AEAELLQQQK	95.0	52.1	25.0	1157.62	0	7	0	0	2	2464	2473
QLEMSAEAER	95.0	49.3	25.0	1179.53	0	17	0	0	2	2512	2521
LREAIAELER	95.0	26.3	25.0	1199.67	0	0	2	0	2	2585	2594
EAIAELER	95.0	56.6	25.0	930.49	0	17	0	0	2	2587	2594
AKLEQLFQDEVAK	95.0	32.0	25.0	1518.82	0	0	2	0	2	2651	2663
LEQLFQDEVAK	95.0	84.2	25.0	1319.68	0	14	0	0	2	2653	2663
LVASMEEAR	95.0	40.8	25.0	1021.50	0	13	0	0	2	2685	2693
KQEELQQLEQQR	95.0	81.8	25.0	1556.80	0	2	0	0	2	2706	2717
RQQEELLAEENQR	95.0	63.2	25.0	1642.81	0	2	2	0	2	2718	2730
QQEELLAEENQR	95.0	72.8	25.0	1486.71	0	5	0	0	2	2719	2730
LREQLQLLEEQHR	95.0	42.1	25.0	1691.92	0	0	2	0	2	2731	2743
EQLQLLEEQHR	95.0	70.8	25.0	1422.73	0	3	1	0	2	2733	2743
AALAHSEEVTASQVAATK	95.0	####	25.0	1783.92	0	2	0	0	2	2744	2761
LQEAGILSAEELQR	95.0	####	25.0	1556.83	0	12	0	0	2	2795	2808
LAQGHTTVDELAR	95.0	46.6	25.0	1410.73	0	1	3	0	2	2809	2821
SSIAGLLLK	95.0	60.8	25.0	901.57	0	65	0	0	2	2833	2841
LSVYAALQR	95.0	35.9	25.0	1020.58	0	1	0	0	2	2847	2855
EGVVGPELHHK	95.0	27.2	25.0	1201.63	0	1	0	0	2	2893	2903
LLEAQIATGGVIDPVHSHR	95.0	43.9	25.0	2013.09	0	0	1	0	2	2942	2960
VPVDVAYR	95.0	47.6	25.0	918.50	0	6	0	0	2	2961	2968
GYFDEEMNR	95.0	32.4	25.0	1176.46	0	2	0	0	2	2970	2978
VLADPSDDTK	95.0	47.3	25.0	1060.52	0	14	0	0	2	2979	2988
GGELVYTDSEAR	95.0	61.1	25.0	1296.61	0	26	0	0	2	3028	3039
IIITVVEEQEQK	95.0	81.4	25.0	1428.79	0	7	0	0	2	3095	3106
SLVPAAELLESR	95.0	49.3	25.0	1284.72	0	27	0	0	2	3116	3127
ELYQQLQR	95.0	33.4	25.0	1077.57	0	3	0	0	2	3132	3139
LSIYNALK	95.0	36.3	25.0	921.54	0	5	0	0	2	3175	3182
LTVDEAVR	95.0	36.8	25.0	902.49	0	4	0	0	2	3213	3220
AGLVGPEFHEK	95.0	41.9	25.0	1183.61	0	0	1	0	2	3221	3231
LLDAQLSTGGIVDPSK	95.0	85.7	25.0	1613.87	0	3	0	0	2	3270	3285
ARQEELYSELQAR	95.0	22.6	25.0	1592.80	0	0	2	0	2	3356	3368
QEELYSELQAR	95.0	42.8	25.0	1365.66	0	2	0	0	2	3358	3368
TPVEVPVGGFK	95.0	38.8	25.0	1129.63	0	9	0	0	2	3374	3384
LSFSGLR	95.0	49.0	25.0	779.44	0	16	0	0	2	3440	3446

									APVPASELLASGVLSR	95.0	####	25.0	1566.89	0	30	0	0	2	3447	3462
									DLSELGSVR	95.0	68.9	25.0	975.51	0	3	0	0	2	3477	3485
									VSIYEAMR	95.0	30.3	25.0	984.48	0	1	0	0	2	3506	3513
									LYVHEAVK	95.0	30.3	25.0	958.54	0	2	0	0	2	3544	3551
									AGVVGPELHEQLLSAEK	95.0	98.1	25.0	1776.95	0	5	2	0	2	3552	3568
									DPYSGSTISLFQAMQK	95.0	61.6	25.0	1788.85	0	1	0	0	2	3575	3590
									GYFSEEMNR	95.0	39.5	25.0	1148.47	0	6	0	0	2	3629	3637
									AEVVETTQVYTEEETRR	95.0	32.9	25.0	2039.99	0	2	1	0	2	3686	3702
									QQGLASYDYVR	95.0	46.9	25.0	1299.63	0	5	0	0	2	3771	3781
									LTAEDLFEAR	95.0	74.0	25.0	1164.59	0	37	0	0	2	3784	3793
									QTLSIYQALK	95.0	48.2	25.0	1164.66	0	2	0	0	2	3839	3848
									GLLSAEVAR	95.0	61.0	25.0	915.53	0	7	0	0	2	3850	3858
									GLVGPELHDR	95.0	50.7	25.0	1092.58	0	4	1	0	2	3888	3897
									ELIPTEEALR	95.0	40.2	25.0	1170.64	0	12	0	0	2	3926	3935
									LLDAQLATGGIVDPR	95.0	79.6	25.0	1538.85	0	8	0	0	2	3936	3950
									DTHDQLSEPSEVR	95.0	51.7	25.0	1512.69	0	5	0	0	2	3969	3981
									SYVDPSTDER	95.0	26.9	25.0	1168.51	0	1	0	0	2	3982	3991
									LSYTQLLR	95.0	76.2	25.0	993.57	0	39	0	0	2	3992	3999
									RDDGTGQLLLPLSDAR	95.0	59.0	25.0	1726.91	0	2	0	0	2	4003	4018
									DDGTGQLLLPLSDAR	95.0	73.2	25.0	1570.81	0	36	0	0	2	4004	4018
									SQVMDEATALQLR	95.0	59.4	25.0	1477.73	0	1	0	0	2	4037	4049
									EGLTSIEEVTK	95.0	52.1	25.0	1205.63	0	6	0	0	2	4050	4060
									LSVYQAMK	95.0	28.5	25.0	955.49	0	1	0	0	2	4084	4091
									MGIVGPEFK	95.0	44.1	25.0	993.51	0	5	0	0	2	4130	4138
									LISLFQAMK	95.0	51.0	25.0	1066.60	0	12	0	0	2	4159	4167
									LPVEVAYK	95.0	35.6	25.0	918.53	0	1	0	0	2	4198	4205
									NLVDNITGQR	95.0	52.2	25.0	1129.60	0	4	0	0	2	4438	4447
									FPVTDAVNK	95.0	34.4	25.0	990.53	0	3	0	0	2	4467	4475
									VPLDEALQR	95.0	62.0	25.0	1040.57	0	6	0	0	2	4543	4551
									SMVEEGTGLR	95.0	36.8	25.0	1094.51	0	2	0	0	2	4590	4599
									LLEAAAQSTK	95.0	30.5	25.0	1031.57	0	2	0	0	2	4600	4609
Poly [ADP-ribose] polymerase 1	PARP1_HUMAN	PARP1	113.07	100.0	19	21	61	21.80	MAIMVQSPMFDGK	95.0	68.7	25.0	1502.67	0	4	0	0	2	35	47
									HPDVEVDGFSELR	95.0	86.3	25.0	1499.71	0	6	0	0	2	66	78
									TLGDFAAEYAK	95.0	56.4	25.0	1185.58	0	4	0	0	2	109	119
									MVDPEKPQLGMIDR	95.0	20.3	25.0	1660.80	0	0	1	0	2	143	156
									GFSLLATEDK	95.0	60.2	25.0	1080.56	0	1	0	0	2	183	192
									GFSLLATEDKEALK	95.0	46.9	25.0	1521.82	0	2	0	0	2	183	196
									ELLIFNK	95.0	31.9	25.0	876.52	0	1	0	0	2	263	269
									VVSEDFLQDVSASTK	95.0	####	25.0	1624.81	0	10	0	0	2	453	467
									AEPVEVVAPR	95.0	32.8	25.0	1066.59	0	2	0	0	2	487	496
									GGAAVDPDSGLEHSAHVLEK	95.0	75.5	25.0	1988.97	0	2	0	1	2	529	548
									LQLLEDDKENR	95.0	61.8	25.0	1372.71	0	2	0	0	2	572	582
									LEQMPSKEDAIEHFMK	95.0	38.7	25.0	1964.91	0	0	2	0	2	601	616
									LPKPVQDLIK	95.0	27.3	25.0	1150.72	0	0	2	0	2	665	674
									MIFDVESMK	95.0	47.8	25.0	1131.51	0	2	0	0	2	675	683
									MIFDVESMKK	95.0	19.4	25.0	1259.60	0	0	2	0	2	675	684
									KPPLLNNADSVQAK	95.0	68.9	25.0	1494.83	0	2	0	0	2	748	761
									GGSDDSSKDPIDVNYEK	95.0	65.8	25.0	1825.81	0	2	0	0	2	780	796
									VVDRDSEEAEIIR	95.0	45.4	25.0	1530.78	0	2	0	0	2	803	815
									TTNFAGILSQGLR	95.0	86.4	25.0	1377.75	0	9	2	0	2	866	878
Poly(ADP-ribose)	ARHL2_HUMAN	ADPRHL2	38.93	100.0	3	3	5	11.30	TEALYYTDDTAMAR	95.0	82.6	25.0	1636.72	0	2	0	0	2	70	83

glycohydrolase ARH3									EAFDEVDMAHR	95.0	29.6	25.0	1335.56	0	1	0	0	2	93	103
									VAGISLAYSSVQDVQK	95.0	99.7	25.0	1664.89	0	2	0	0	2	157	172
Poly(rC)-binding protein 1	PCBP1_HUMAN	PCBP1	37.48	100.0	5	6	59	20.80	IITLTGPTNAIFK	95.0	65.9	25.0	1388.82	0	21	0	0	2	58	70
									LVVPATQCGSLIGK	95.0	52.5	25.0	1442.80	0	2	0	0	2	102	115
									ESTGAQVQVAGDMLPNSTER	95.0	####	25.0	2105.98	0	17	13	0	2	125	144
									AITIAGVPQSVTECVK	95.0	91.2	25.0	1672.89	0	2	0	0	2	145	160
									IANPVEGSSGR	95.0	44.2	25.0	1086.55	0	4	0	0	2	315	325
Polyadenylate-binding protein 1	PABP1_HUMAN	PABPC1	70.65	100.0	11	12	61	16.70	FSPAGPILSIR	95.0	56.9	25.0	1157.67	0	7	0	0	2	31	41
									ALDTMNFDVIK	95.0	74.6	25.0	1282.64	0	14	0	0	2	68	78
									KSGVGNIFIK	95.0	28.4	25.0	1062.63	0	1	0	0	2	95	104
									SGVGNIFIK	95.0	64.1	25.0	934.54	0	11	0	0	2	96	104
									NFGEDMDDER	95.0	41.8	25.0	1243.45	0	3	0	0	2	197	206
									FGPALSVK	95.0	49.0	25.0	818.48	0	3	0	0	2	214	221
									GFGFVSFER	95.0	38.2	25.0	1045.51	0	1	0	0	2	232	240
									YQGVNLYVK	95.0	49.8	25.0	1083.58	0	2	0	0	2	291	299
									NLDDGIDDERLR	95.0	47.2	25.0	1430.69	0	2	0	0	2	300	311
									EFSPFGTITSAK	95.0	57.2	25.0	1284.65	0	6	0	0	2	313	324
									IVATKPLYVALAQR	95.0	91.9	25.0	1542.94	0	5	6	0	2	357	370
Polyadenylate-binding protein 4	PABP4_HUMAN	PABPC4	70.77	99.5	2	2	4	4.97	ALDTMNFDVIK	95.0	74.6	25.0	1282.64	0	14	0	0	2	68	78
									GFGFVSYEK	95.0	31.0	25.0	1033.50	0	2	0	0	2	232	240
									EFSPFGSITSAK	95.0	32.0	25.0	1270.63	0	2	0	0	2	313	324
Polymerase I and transcript release factor	PTRF_HUMAN	PTRF	43.46	100.0	3	4	9	9.49	QAEMEGAVQSIQGELSK	95.0	98.9	25.0	1820.87	0	5	0	0	2	79	95
									KLEVNEAELLR	95.0	67.1	25.0	1313.74	0	2	1	0	2	137	147
									VMIYQDEVK	95.0	27.4	25.0	1140.56	0	1	0	0	2	153	161
Polypeptide N-acetylgalactosaminyltransferase 2	GALT2_HUMAN	GALNT2	64.72	100.0	3	3	12	5.95	FNQVESDKLR	95.0	19.4	25.0	1235.64	0	0	2	0	2	104	113
									TPMIAGGLFVMDK	95.0	93.0	25.0	1411.70	0	8	0	0	2	303	315
									NFYYAAVPSAR	95.0	41.6	25.0	1258.62	0	2	0	0	2	394	404
Polypeptide N-acetylgalactosaminyltransferase 5	GALT5_HUMAN	GALNT5	106.25	100.0	4	4	11	5.00	ALLPEDSGTHQVLR	95.0	57.8	25.0	1535.82	0	5	0	0	2	412	425
									EILLVDDFSTK	95.0	27.7	25.0	1279.68	0	3	0	0	2	530	540
									CPVMAGGLFSIDK	95.0	36.4	25.0	1410.68	0	2	0	0	2	667	679
									NDNPYSFPK	94.5	26.4	25.0	1081.49	0	1	0	0	2	727	735
Polypyrimidine tract-binding protein 1	PTBP1_HUMAN	PTBP1	57.20	100.0	5	5	31	9.23	VTNLLMLK	95.0	51.6	25.0	947.56	0	14	0	0	2	85	92
									GQPIYIQFSNHK	95.0	62.7	25.0	1431.74	0	6	0	0	2	123	134
									HQNVQLPR	95.0	39.3	25.0	991.54	0	6	0	0	2	411	418
									EGQEDQGLTK	95.0	33.7	25.0	1104.52	0	1	0	0	2	419	428
									VLFSSNGGVVK	95.0	40.8	25.0	1106.62	0	4	0	0	2	472	482
Prefoldin subunit 2	PFD2_HUMAN	PFDN2	16.63	100.0	3	4	13	22.70	GAVSAEQVIAGFNR	95.0	82.6	25.0	1418.74	0	6	2	0	2	19	32
									MVGGVLVER	95.0	36.9	25.0	975.53	0	2	0	0	2	73	81
									IIETLTQQLQAK	95.0	80.6	25.0	1385.80	0	3	0	0	2	100	111
Prefoldin subunit 3	PFD3_HUMAN	VBP1	22.64	100.0	6	6	10	30.50	QPGNETADTVLK	95.0	29.9	25.0	1272.64	0	1	0	0	2	40	51
									KLDEQYQK	95.0	51.5	25.0	1051.54	0	1	0	0	2	52	59
									FMELNLAQK	95.0	31.9	25.0	1109.57	0	1	0	0	2	62	70
									LKGQIPEIK	95.0	30.3	25.0	1025.64	0	1	0	0	2	74	82
									FLLADNLYCK	95.0	54.5	25.0	1256.63	0	2	0	0	2	105	114
									DQFTTTEVNMAR	95.0	79.5	25.0	1428.64	0	4	0	0	2	167	178
Pre-mRNA-processing factor 19	PRP19_HUMAN	PRPF19	55.16	100.0	4	4	19	8.73	TVPEELVKPEELSK	95.0	70.3	25.0	1597.87	0	8	0	0	2	193	206
									SSEQILATLK	95.0	50.4	25.0	1089.62	0	4	0	0	2	252	261
									TLQLDNNFEVK	95.0	54.3	25.0	1320.68	0	6	0	0	2	429	439
									FIASTGMDR	95.0	29.8	25.0	1013.47	0	1	0	0	2	489	497
Pre-mRNA-processing-splicing factor 8	PRP8_HUMAN	PRPF8	273.59	100.0	7	7	30	2.78	ALNMAIPGGPK	95.0	29.6	25.0	1084.58	0	1	0	0	2	268	278
									YYVLNALK	95.0	32.1	25.0	983.56	0	1	0	0	2	453	460

									LLILALER	95.0	28.4	25.0	940.62	0	1	0	0	2	838	845
									IDLTLLNR	95.0	45.7	25.0	957.57	0	10	0	0	2	988	995
									ANPALYVLR	95.0	43.4	25.0	1016.59	0	5	0	0	2	1736	1744
									FGDLILK	95.0	41.7	25.0	805.48	0	11	0	0	2	1902	1908
									NNVNVASLTQSEIR	95.0	77.2	25.0	1544.80	0	1	0	0	2	1995	2008
Presequence protease, mitochondrial	PREP_HUMAN	PITRM1	117.44	100.0	4	4	7	4.24	AVEDFLR	95.0	32.5	25.0	849.45	0	2	0	0	2	795	801
									DPNTIETLQSFGK	95.0	39.4	25.0	1449.72	0	2	0	0	2	925	937
									FTQQDIDEAK	95.0	28.7	25.0	1194.56	0	1	0	0	2	947	956
									STHGLAILGPENPK	95.0	21.6	25.0	1433.77	0	0	2	0	2	1014	1027
Proactivator polypeptide	SAP_HUMAN	PSAP	58.09	100.0	8	8	43	11.60	DVVTAAGDMLK	95.0	38.4	25.0	1135.57	0	3	0	0	2	68	78
									NVIPALELVEPIK	95.0	37.9	25.0	1434.86	0	2	0	0	2	291	303
									NVIPALELVEPIKK	95.0	61.8	25.0	1562.95	0	10	0	0	2	291	304
									EILDAFDK	95.0	33.0	25.0	950.48	0	5	0	0	2	337	344
									KLVGYLDR	95.0	38.1	25.0	963.56	0	2	0	0	2	414	421
									LVGYLDR	95.0	44.9	25.0	835.47	0	4	0	0	2	415	421
									QEILAALEK	95.0	49.2	25.0	1014.58	0	15	0	0	2	430	438
									GCSFLPDPYQK	95.0	35.4	25.0	1311.60	0	2	0	0	2	439	449
Probable aminopeptidase NPEPL1	PEPL1_HUMAN	NPEPL1	55.84	100.0	3	3	4	6.50	ELGIIPTIIR	95.0	30.3	25.0	1124.70	0	1	0	0	2	207	216
									GIVYDTGGLSIK	95.0	43.7	25.0	1222.67	0	1	0	0	2	261	272
									TVEINNTDAEGR	95.0	74.5	25.0	1318.62	0	2	0	0	2	335	346
Probable ATP-dependent RNA helicase DDX17	DDX17_HUMAN	DDX17	72.35	100.0	12	12	92	18.00	NFYVEHPEVAR	95.0	44.7	25.0	1360.66	0	3	0	0	2	54	64
									LTPYEVDELR	95.0	31.0	25.0	1234.63	0	1	0	0	2	65	74
									LTPYEVDELRR	95.0	26.9	25.0	1390.73	0	1	0	0	2	65	75
									DMVGIAQTGSGK	95.0	45.9	25.0	1179.57	0	10	0	0	2	131	142
									ELAQQVQQVADDYGK	95.0	99.5	25.0	1691.82	0	10	0	0	2	176	190
									LIDFLESGK	95.0	50.8	25.0	1021.56	0	8	0	0	2	226	234
									MLDMGFEPQIR	95.0	55.4	25.0	1368.63	0	18	0	0	2	251	261
									QLAEDFLR	95.0	56.5	25.0	991.52	0	6	0	0	2	286	293
									TIIFVETK	95.0	33.6	25.0	950.56	0	2	0	0	2	342	349
									APILIATDVASR	95.0	78.2	25.0	1226.71	0	26	0	0	2	390	401
									VLEEANQAINPK	95.0	54.1	25.0	1325.71	0	5	0	0	2	457	468
									LMQLVDHR	95.0	31.3	25.0	1027.54	0	2	0	0	2	469	476
Probable ATP-dependent RNA helicase DDX5	DDX5_HUMAN	DDX5	69.13	100.0	7	7	20	14.80	TAQEVETYR	95.0	56.2	25.0	1096.53	0	3	0	0	2	69	77
									TTYLVLDEADR	95.0	68.0	25.0	1295.65	0	6	0	0	2	242	252
									MLDMGFEPQIR	95.0	55.4	25.0	1368.63	0	18	0	0	2	253	263
									QLAEDFLK	95.0	30.7	25.0	963.51	0	2	0	0	2	288	295
									TIVFVETK	95.0	34.6	25.0	936.54	0	2	0	0	2	344	351
									APILIATDVASR	95.0	78.2	25.0	1226.71	0	26	0	0	2	392	403
									TGTAYTFFTPNNIK	95.0	61.2	25.0	1574.79	0	2	0	0	2	438	451
									QVSDLISVLR	95.0	79.5	25.0	1129.66	0	4	0	0	2	452	461
									LLQLVEDR	95.0	33.1	25.0	985.57	0	1	0	0	2	471	478
Probable ATP-dependent RNA helicase DDX6	DDX6_HUMAN	DDX6	54.40	100.0	7	7	16	15.90	SGAYLIPLLER	95.0	43.2	25.0	1231.70	0	2	0	0	2	147	157
									DNIQAMVIVPTR	95.0	30.8	25.0	1372.73	0	1	0	0	2	163	174
									VMATTGGTNLR	95.0	49.3	25.0	1136.57	0	4	0	0	2	196	206
									GVTQYYAYVTER	95.0	69.0	25.0	1449.70	0	4	0	0	2	308	319
									VFHDFR	95.0	30.2	25.0	820.41	0	1	0	0	2	376	381
									LAETYLHR	95.0	46.1	25.0	1002.54	0	2	0	0	2	414	421
									SLYVAEYHSEPVEDEKP	95.0	28.8	25.0	1991.92	0	0	2	0	2	467	483
Probable O-sialoglycoprotein endopeptidase	OSGEP_HUMAN	OSGEP	36.41	100.0	3	3	8	9.55	PAVLGFEGSANK	95.0	71.8	25.0	1189.62	0	3	0	0	1	2	13
									LVELPYTVK	95.0	34.1	25.0	1061.62	0	3	0	0	2	190	198
									TPLSDSGVTQR	95.0	34.4	25.0	1160.59	0	2	0	0	2	313	323

Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X_HUMAN	USP9X	289.53	100.0	3	3	4	0.86	NDALSMIIK	95.0	48.6	25.0	1020.54	0	2	0	0	2	297	305
									NLEIFR	95.0	34.7	25.0	791.44	0	1	0	0	2	323	328
									AVLNLLR	95.0	29.1	25.0	798.52	0	1	0	0	2	2152	2158
Probable Xaa-Pro aminopeptidase 3	XPP3_HUMAN	XPNPEP3	57.02	100.0	3	3	5	8.28	AILFVPR	95.0	47.2	25.0	815.51	0	100	0	0	2	149	155
									GVQQLIQR	95.0	27.9	25.0	941.55	0	1	0	0	2	235	242
									APVEEAFLYAK	95.0	49.2	25.0	1237.65	0	2	0	0	2	275	285
									GADILAYPPVVAGGNR	95.0	53.3	25.0	1569.84	0	2	0	0	2	294	309
Procollagen C-endopeptidase enhancer 1	PCOC1_HUMAN	PCOLCE	47.95	100.0	4	4	25	13.80	YDALEVFAGSGTSGQR	95.0	####	25.0	1657.78	0	16	0	0	2	92	107
									YDSVSVFNGAVSDDSR	95.0	87.3	25.0	1717.77	0	2	0	0	2	215	230
									TGGLDLPSPPTGASLK	95.0	38.0	25.0	1510.81	0	4	0	0	2	366	381
									GVSYLLMGQVEENR	95.0	57.8	25.0	1610.78	0	3	0	0	2	395	408
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3_HUMAN	PLOD3	84.77	100.0	11	12	75	16.50	SAEFFNYTVR	95.0	68.2	25.0	1233.59	0	1	0	0	2	58	67
									YKDDDDDQLFYTR	95.0	80.9	25.0	1693.73	0	4	0	0	2	185	197
									LYLDPGLR	95.0	46.0	25.0	946.54	0	5	0	0	2	198	205
									LSLNLDHK	95.0	52.5	25.0	939.53	0	5	0	0	2	208	215
									NVAYDTLPIVVHGNGPTK	95.0	####	25.0	1895.00	0	2	0	0	2	242	259
									LLLLDYPPDR	95.0	62.1	25.0	1214.68	0	9	0	0	2	318	327
									LVGPEEALSPGEAR	95.0	87.0	25.0	1424.74	0	26	0	0	2	359	372
									ILIEENR	95.0	30.9	25.0	886.50	0	1	0	0	2	405	411
									SEDYVELVQR	95.0	66.8	25.0	1237.61	0	12	0	0	2	441	450
									LAGGYENVPTVDIHMK	95.0	73.3	25.0	1759.87	0	2	4	0	2	600	615
									AVMNFVVR	95.0	64.5	25.0	951.51	0	4	0	0	2	648	655
Profilin-1	PROF1_HUMAN	PFN1	15.04	100.0	8	8	130	52.10	SSFYVNGLTLGGQK	95.0	40.0	25.0	1470.76	0	1	0	0	2	57	70
									DSLLQDGEFSMDLR	95.0	71.1	25.0	1641.74	0	2	0	0	2	76	89
									STGGAPTFNVTVTK	95.0	81.3	25.0	1379.72	0	82	0	0	2	92	105
									TDKTLVLLMGK	95.0	37.5	25.0	1234.71	0	1	0	0	2	106	116
									TLVLLMGK	95.0	59.5	25.0	890.54	0	10	0	0	2	109	116
									EGVHGGLINK	95.0	54.0	25.0	1023.56	0	27	0	0	2	117	126
									EGVHGGLINKK	95.0	39.9	25.0	1151.65	0	4	0	0	2	117	127
									CYEMASHLR	95.0	33.6	25.0	1182.50	0	3	0	0	2	128	136
Programmed cell death 6-interacting protein	PDC6I_HUMAN	PDCD6IP	96.01	100.0	20	23	69	22.70	TSEVDLAKPLVK	95.0	71.2	25.0	1299.75	0	2	0	0	2	12	23
									HEGALETLLR	95.0	46.0	25.0	1138.62	0	1	0	0	2	61	70
									LALASLGYEK	95.0	44.8	25.0	1064.60	0	4	0	0	2	111	120
									ETVLSALSR	95.0	58.1	25.0	975.55	0	3	0	0	2	165	173
									EVFPVLAAK	95.0	43.9	25.0	973.57	0	4	0	0	2	240	248
									FGEEIAR	95.0	31.4	25.0	821.42	0	3	0	0	2	270	276
									YDEYVNVK	95.0	31.9	25.0	1029.49	0	3	0	0	2	291	298
									VPDLKDLDPIGK	95.0	44.2	25.0	1309.74	0	2	0	0	2	323	334
									STPVNVPISQK	95.0	42.7	25.0	1169.65	0	2	0	0	2	340	350
									FTDLFEK	95.0	35.2	25.0	899.45	0	2	0	0	2	351	357
									MVPVSVQQSLAAYNQR	95.0	90.3	25.0	1806.92	0	2	2	0	2	358	373
									SVIEQGGIQTVDQLIK	95.0	91.3	25.0	1727.95	0	4	0	0	2	423	438
									ELPELLQR	95.0	53.1	25.0	997.57	0	4	0	0	2	439	446
									EILDESLR	95.0	38.6	25.0	974.52	0	2	0	0	2	449	456
									LLDEEEATDNDLR	95.0	####	25.0	1532.71	0	9	0	0	2	457	469
									TPSNELYKPLR	95.0	38.4	25.0	1317.72	0	2	2	0	2	479	489
									SLLSNLDEVK	95.0	51.6	25.0	1117.61	0	2	0	0	2	554	563
									SLLSNLDEVKK	95.0	49.0	25.0	1245.71	0	6	2	0	2	554	564
									NIQVSHQEFSK	95.0	52.2	25.0	1316.66	0	4	0	0	2	628	638
									DLQQSIAR	94.9	26.6	25.0	930.50	0	2	0	0	2	708	715
Programmed cell death	PDC10_HUMAN	PDCD10	24.68	100.0	3	4	9	16.00	ELLDTVNNVFK	95.0	44.4	25.0	1291.69	0	2	0	0	2	140	150

protein 10									AINVFVSANR	95.0	44.0	25.0	1090.60	0	2	0	0	2	187	196
									LIHQTNLILQTFK	95.0	79.2	25.0	1568.92	0	4	1	0	2	197	209
Programmed cell death protein 6	PDCD6_HUMAN	PDCD6	21.85	100.0	4	5	18	17.80	SIISMFDR	95.0	41.4	25.0	984.48	0	3	0	0	2	67	74
									QALSGFGYR	95.0	77.0	25.0	998.51	0	7	0	0	2	117	125
									LSDQFHDILIR	95.0	44.7	25.0	1356.73	0	2	2	0	2	126	136
									LTDIFR	95.0	32.5	25.0	764.43	0	4	0	0	2	161	166
Proliferating cell nuclear antigen	PCNA_HUMAN	PCNA	28.75	100.0	7	7	38	26.10	SEGFDTYR	95.0	49.9	25.0	974.42	0	4	0	0	2	54	61
									NLAMGVNLTSMSK	95.0	27.8	25.0	1397.68	0	1	0	0	2	65	77
									CAGNEDIITLR	95.0	60.2	25.0	1261.62	0	2	0	0	2	81	91
									MPSGEFAR	95.0	43.2	25.0	910.41	0	18	0	0	2	139	146
									DLSHIGDAVVISCAK	95.0	59.3	25.0	1584.81	0	2	0	0	2	150	164
									YLNFFTK	95.0	40.2	25.0	932.49	0	8	0	0	2	211	217
									YYLAPK	95.0	31.8	25.0	754.41	0	3	0	0	2	249	254
Proliferation-associated protein 2G4	PA2G4_HUMAN	PA2G4	43.77	100.0	12	12	121	28.90	GDAMIMEETGK	95.0	45.6	25.0	1213.51	0	16	0	0	2	52	62
									SDQDYILK	95.0	40.3	25.0	981.49	0	8	0	0	2	94	101
									TIIQNPTDQQK	95.0	56.1	25.0	1285.67	0	19	0	0	2	200	210
									AFFSEVER	95.0	52.5	25.0	984.48	0	6	0	0	2	264	271
									RFDAMPFTLR	95.0	32.0	25.0	1269.64	0	1	0	0	2	272	281
									FDAMPFTLR	95.0	41.2	25.0	1113.54	0	4	0	0	2	273	281
									HELLQPFNVLYEK	95.0	47.7	25.0	1629.86	0	2	0	0	2	299	311
									EGEFVAQFK	95.0	48.4	25.0	1054.52	0	9	0	0	2	312	320
									FTVLLMPNGPMR	95.0	59.8	25.0	1407.71	0	2	0	0	2	321	332
									ITSGPFEPDLYK	95.0	80.1	25.0	1366.69	0	10	0	0	2	333	344
									SEMEVQDAELK	95.0	71.3	25.0	1294.58	0	26	0	0	2	345	355
									ALLQSSASR	95.0	75.6	25.0	932.52	0	18	0	0	2	356	364
Prolyl endopeptidase	PPCE_HUMAN	PREP	80.68	100.0	5	6	9	8.45	ELPDVLER	95.0	27.4	25.0	970.52	0	1	0	0	2	163	170
									GMFYNSYPQQDGK	95.0	61.9	25.0	1550.66	0	2	0	0	2	184	196
									SDGTETSTNLHQK	95.0	44.7	25.0	1417.66	0	2	0	0	2	197	209
									VINIDFRDPEESK	95.0	38.2	25.0	1561.79	0	2	1	0	2	313	325
									KQSNPLLIHVDTK	95.0	21.4	25.0	1492.85	0	0	1	0	2	665	677
Proprotein convertase subtilisin/kexin type 9	PCSK9_HUMAN	PCSK9	74.35	100.0	5	6	27	8.96	LPGTYVVVLK	95.0	60.5	25.0	1088.67	0	5	0	0	2	74	83
									EETHLSQSER	95.0	32.5	25.0	1215.56	0	1	0	0	2	84	93
									MSGDLLELALK	95.0	74.0	25.0	1205.64	0	9	0	0	2	126	136
									VMVTDFENVPEEDGTR	95.0	86.7	25.0	1853.82	0	2	0	0	2	200	215
									AHNAFGGEGVYAIAR	95.0	89.2	25.0	1532.76	0	8	2	0	2	511	525
Prostaglandin F2 receptor negative regulator	FPRP_HUMAN	PTGFRN	98.54	100.0	9	9	17	9.90	VPTATLVR	95.0	28.8	25.0	856.53	0	1	0	0	2	26	33
									EGEPFELR	95.0	34.7	25.0	976.47	0	1	0	0	2	161	168
									SVLALTHEGR	95.0	50.0	25.0	1082.60	0	2	0	0	2	195	204
									ALSADQGSYR	95.0	40.2	25.0	1067.51	0	1	0	0	2	237	246
									MPDSTLPGSR	95.0	32.3	25.0	1076.50	0	1	0	0	2	320	329
									AQDGDFIFSK	95.0	37.1	25.0	1127.54	0	5	0	0	2	483	492
									MYQTQVSDAGLYR	95.0	75.4	25.0	1547.72	0	3	0	0	2	642	654
									APVLLSSLDR	95.0	41.4	25.0	1070.62	0	1	0	0	2	742	751
									MDVLNAFK	95.0	39.4	25.0	953.48	0	2	0	0	2	823	830
Prostaglandin reductase 1	PTGR1_HUMAN	PTGR1	35.85	100.0	4	5	14	8.81	VVGAVGSDEK	95.0	31.8	25.0	960.50	0	3	0	0	2	169	178
									TVESLEETLK	95.0	46.1	25.0	1148.60	0	2	0	0	2	195	204
									TVESLEETLKK	95.0	54.8	25.0	1276.70	0	2	3	0	2	195	205
									MEAFVVYR	95.0	52.0	25.0	1030.50	0	4	0	0	2	267	274
Proteasome activator complex subunit 1	PSME1_HUMAN	PSME1	28.71	100.0	9	11	51	36.90	TENLLGSYFPK	95.0	55.6	25.0	1268.65	0	3	0	0	2	25	35
									KISELDAFLK	95.0	61.6	25.0	1163.67	0	2	0	0	2	36	45
									EPALNEANLSNLK	95.0	71.5	25.0	1412.74	0	6	0	0	2	46	58

									APLDIPVPDPVK	95.0	47.4	25.0	1260.72	0	8	0	0	2	59	70
									APLDIPVPDPVKEK	95.0	50.5	25.0	1517.86	0	4	7	0	2	59	72
									IEDGNNFGVAVQEK	95.0	72.4	25.0	1519.74	0	11	0	0	2	142	155
									VFELMTSLHTK	95.0	29.0	25.0	1321.68	0	0	2	0	2	156	166
									QLVHELDEAEYR	95.0	74.2	25.0	1501.73	0	4	2	0	2	199	210
									LMVMEIR	95.0	47.5	25.0	923.47	0	2	0	0	2	214	220
Proteasome activator complex subunit 2	PSME2_HUMAN	PSME2	27.38	100.0	9	12	50	26.40	KQVEVFR	95.0	39.8	25.0	905.52	0	5	0	0	2	15	21
									QVEVFR	95.0	30.6	25.0	777.43	0	2	0	0	2	16	21
									IEDGNDFGVAIQEK	95.0	####	25.0	1534.74	0	10	0	0	2	132	145
									TKVEAFQTTISK	95.0	76.8	25.0	1352.74	0	5	2	0	2	155	166
									VEAFQTTISK	95.0	40.4	25.0	1123.60	0	4	0	0	2	157	166
									ALVHERDEAAYGELR	95.0	73.0	25.0	1728.87	0	2	3	2	2	189	203
									DEAAYGELR	95.0	43.6	25.0	1023.47	0	5	0	0	2	195	203
									AMVLDLR	95.0	41.0	25.0	833.46	0	6	0	0	2	204	210
									GEEKPSMY	95.0	31.5	25.0	956.40	0	4	0	0	2	232	239
Proteasome activator complex subunit 3	PSME3_HUMAN	PSME3	29.49	100.0	4	4	23	16.90	KLLELDSFLK	95.0	34.0	25.0	1205.71	0	1	0	0	2	37	46
									VFVMPNGMLK	95.0	44.8	25.0	1167.59	0	4	0	0	2	101	110
									SNQQLVDIIEK	95.0	66.7	25.0	1286.70	0	11	0	0	2	111	121
									NQYVTLHDMILK	95.0	49.7	25.0	1490.77	0	7	0	0	2	226	237
Proteasome assembly chaperone 2	PSMG2_HUMAN	PSMG2	29.38	100.0	3	3	7	7.58	KLVALQLR	95.0	37.6	25.0	940.63	0	2	0	0	2	84	91
									LVALQLR	95.0	39.2	25.0	812.54	0	2	0	0	2	85	91
									VIVLSSSHSYQR	95.0	52.6	25.0	1375.73	0	3	0	0	2	118	129
Proteasome subunit alpha type-1	PSA1_HUMAN	PSMA1	29.54	100.0	7	8	29	24.70	IHQIEYAMEAVK	95.0	59.6	25.0	1447.73	0	4	3	0	2	19	30
									THAVLVALK	95.0	45.2	25.0	951.60	0	2	0	0	2	42	50
									AQSELAAHQK	95.0	27.5	25.0	1082.56	0	1	0	0	2	52	61
									LVSLIGSK	95.0	37.6	25.0	816.52	0	1	0	0	2	108	115
									ETLPAEQDLTTK	95.0	29.6	25.0	1345.68	0	1	0	0	2	197	208
									KAQPAQPADEPAEK	95.0	35.3	25.0	1479.74	0	2	0	0	2	243	256
									AQPAQPADEPAEK	95.0	54.8	25.0	1351.65	0	15	0	0	2	244	256
Proteasome subunit alpha type-3	PSA3_HUMAN	PSMA3	28.42	100.0	9	12	33	34.90	VFQVEYAMK	95.0	53.0	25.0	1130.56	0	2	0	0	2	21	29
									AVENSSTAIGIR	95.0	70.2	25.0	1217.65	0	6	0	0	2	30	41
									DGVVFGVEK	95.0	39.5	25.0	949.50	0	4	0	0	2	44	52
									LYEEGSNKR	95.0	33.3	25.0	1095.54	0	1	0	0	2	58	66
									HVGMAVAGLLADAR	95.0	83.3	25.0	1396.74	0	4	4	0	2	73	86
									SNFGYNIPLK	95.0	33.9	25.0	1152.60	0	1	0	0	2	101	110
									IIYIVHDEVK	95.0	44.0	25.0	1228.69	0	3	1	0	2	197	206
									IIYIVHDEVKDK	95.0	65.0	25.0	1471.82	0	4	1	0	2	197	208
									ESLKEEDESDDDNM	95.0	67.0	25.0	1671.62	0	2	0	0	2	242	255
Proteasome subunit alpha type-4	PSA4_HUMAN	PSMA4	29.47	100.0	5	5	21	16.90	TTIFSPEGR	95.0	48.2	25.0	1007.52	0	2	0	0	2	9	17
									LLDEVFFSEK	95.0	73.8	25.0	1226.63	0	13	0	0	2	55	64
									QAYTQFGGK	95.0	41.5	25.0	999.49	0	2	0	0	2	119	127
									SALALAIK	95.0	37.7	25.0	786.51	0	2	0	0	2	188	195
									VEIATLTR	95.0	51.1	25.0	902.53	0	2	0	0	2	211	218
Proteasome subunit alpha type-5	PSA5_HUMAN	PSMA5	26.39	100.0	6	7	28	24.50	GVNTFSPEGR	95.0	47.3	25.0	1063.52	0	7	0	0	2	11	20
									ITSPLMEPSSIEK	95.0	69.3	25.0	1447.74	0	3	0	0	2	54	66
									AIGSASEGAQSSLQEVYHK	95.0	####	25.0	1961.96	0	4	3	0	2	169	187
									SSLIILK	95.0	72.9	25.0	773.51	0	7	0	0	2	197	203
									EELEEVIK	95.0	37.4	25.0	988.52	0	2	0	0	2	232	239
									EELEEVIKDI	95.0	48.7	25.0	1216.63	0	2	0	0	2	232	241
Proteasome subunit alpha type-6	PSA6_HUMAN	PSMA6	27.38	100.0	5	6	32	22.00	HITIFSPEGR	95.0	54.9	25.0	1156.61	0	2	0	0	2	12	21
									LYQVEYAFK	95.0	56.9	25.0	1160.60	0	2	0	0	2	22	30

									AINQGGLTSVAVR	95.0	96.5	25.0	1285.72	0	10	0	0	2	31	43
									LLDSSTVTHLFK	95.0	78.4	25.0	1360.75	0	13	2	0	2	60	71
									QTESTSFLEK	95.0	31.6	25.0	1169.57	0	3	0	0	2	172	181
Proteasome subunit alpha type-7	PSA7_HUMAN	PSMA7	27.87	100.0	6	6	22	21.80	GRDIVVLGVEK	95.0	33.8	25.0	1184.70	0	0	2	0	2	37	47
									DIVVLGVEK	95.0	40.7	25.0	971.58	0	5	0	0	2	39	47
									NYTDEAIETDDLTIK	95.0	####	25.0	1740.82	0	2	0	0	2	175	189
									ALLEVVQSGGK	95.0	73.9	25.0	1100.63	0	8	0	0	2	194	204
									NIELAVMR	95.0	45.5	25.0	961.51	0	2	0	0	2	205	212
									ILNPEEIEK	95.0	45.9	25.0	1084.59	0	3	0	0	2	219	227
Proteasome subunit beta type-1	PSB1_HUMAN	PSMB1	26.47	100.0	3	4	8	12.40	LSEGFSIHTR	95.0	60.4	25.0	1146.59	0	2	2	0	2	57	66
									DVFISAAER	95.0	43.9	25.0	1007.52	0	2	0	0	2	205	213
									EGIREETVSLR	95.0	54.6	25.0	1288.69	0	2	0	0	2	229	239
Proteasome subunit beta type-2	PSB2_HUMAN	PSMB2	22.82	100.0	5	6	15	24.40	VAASNIVQMK	95.0	75.4	25.0	1076.58	0	7	0	0	2	20	29
									NVQLYK	95.0	27.1	25.0	764.43	0	1	0	0	2	63	68
									NLADCLR	95.0	33.6	25.0	861.42	0	2	0	0	2	87	93
									AVELLR	95.0	42.2	25.0	700.44	0	6	0	0	2	156	161
									CLEELQK	95.0	34.7	25.0	919.46	0	2	0	0	2	163	169
									NGIHDLDNISFPK	95.0	68.1	25.0	1469.74	0	2	1	0	2	186	198
Proteasome subunit beta type-3	PSB3_HUMAN	PSMB3	22.93	100.0	3	3	8	17.60	FGIQAQMVTTDFQK	95.0	87.7	25.0	1629.79	0	3	0	0	2	28	41
									LNLYELK	95.0	45.5	25.0	892.51	0	4	0	0	2	71	77
									DAVSGMGVIVHIIEK	95.0	57.6	25.0	1583.85	0	1	0	0	2	178	192
Proteasome subunit beta type-4	PSB4_HUMAN	PSMB4	29.19	100.0	3	3	15	12.90	TQNPMVTGTSVLGVK	95.0	81.1	25.0	1547.81	0	3	0	0	2	46	60
									QPVLSQTEAR	95.0	55.8	25.0	1128.60	0	10	0	0	2	202	211
									FQIATVTEK	95.0	38.1	25.0	1036.57	0	2	0	0	2	232	240
Proteasome subunit beta type-5	PSB5_HUMAN	PSMB5	28.46	100.0	7	9	50	25.50	HGVIVAADSR	95.0	51.5	25.0	1024.55	0	13	0	0	2	69	78
									ATAGAYIASQTVK	95.0	97.5	25.0	1280.68	0	6	0	0	2	79	91
									LLANMVYQYK	95.0	73.5	25.0	1258.65	0	2	0	0	2	141	150
									RGPGLYYVDSEGNR	95.0	76.7	25.0	1582.76	0	4	2	0	2	166	179
									GPGLYYVDSEGNR	95.0	77.1	25.0	1426.66	0	2	0	0	2	167	179
									AIYQATYR	95.0	43.8	25.0	985.51	0	4	0	0	2	218	225
									VSSDNVADLHEK	95.0	76.5	25.0	1313.63	0	14	3	0	2	246	257
Proteasome subunit beta type-6	PSB6_HUMAN	PSMB6	25.34	100.0	3	3	20	13.00	TTTGSYIANR	95.0	68.5	25.0	1083.54	0	11	0	0	2	54	63
									LAAIAESGVER	95.0	68.4	25.0	1115.61	0	4	0	0	2	210	220
									QVLLGDQIPK	95.0	69.4	25.0	1110.65	0	5	0	0	2	221	230
Proteasome subunit beta type-7	PSB7_HUMAN	PSMB7	29.95	100.0	6	7	17	19.10	DGIVLGADTR	95.0	43.1	25.0	1016.54	0	2	0	0	2	53	62
									ATEGMVVADK	95.0	40.8	25.0	1036.50	0	2	0	0	2	63	72
									FRPDMEEEEAK	95.0	47.5	25.0	1396.61	0	8	0	0	2	185	195
									LDFLRPYTVPNK	95.0	34.8	25.0	1462.81	0	2	0	0	2	226	237
									LDFLRPYTVPNKK	95.0	39.0	25.0	1590.90	0	1	1	0	2	226	238
									GTTAVLTEK	95.0	30.1	25.0	919.51	0	1	0	0	2	250	258
Proteasome subunit beta type-8	PSB8_HUMAN	PSMB8	30.34	100.0	8	11	29	29.30	FQHGVIAAVDSR	95.0	64.9	25.0	1299.68	0	2	4	0	2	80	91
									ASAGSYISALR	95.0	####	25.0	1095.58	0	4	0	0	2	92	102
									ISVSAASK	95.0	35.5	25.0	762.44	0	3	0	0	2	146	153
									KGPGLYYVDEHGTR	95.0	65.3	25.0	1591.79	0	4	3	0	2	179	192
									GPGLYYVDEHGTR	95.0	47.8	25.0	1463.69	0	2	0	0	2	180	192
									AIAYATHR	95.0	36.1	25.0	902.48	0	3	0	0	2	231	238
									DSYSGGVVNMYHMK	95.0	27.0	25.0	1619.68	0	1	0	0	2	239	252
									VESTDVSDLLHQYR	95.0	68.9	25.0	1661.81	0	1	2	0	2	259	272
Proteasome subunit beta type-9	PSB9_HUMAN	PSMB9	23.25	100.0	5	6	24	25.60	AGAPTGDLPR	95.0	30.7	25.0	954.50	0	2	0	0	2	4	13
									VSAGEAVVNR	95.0	69.8	25.0	1001.54	0	11	0	0	2	40	49
									EGGQVYGTLGGMLTR	95.0	83.6	25.0	1554.76	0	4	0	0	2	127	141

									FTTDAIALAMSR	95.0	64.7	25.0	1312.66	0	2	1	0	2	174	185
									VILGNELPK	95.0	38.7	25.0	982.59	0	4	0	0	2	207	215
Proteasome-associated protein ECM29 homolog	ECM29_HUMAN	ECM29	204.28	100.0	8	8	27	4.72	VYLGDIPLK	95.0	44.9	25.0	1017.60	0	6	0	0	2	305	313
									YLLLLAAGDPR	95.0	48.5	25.0	1201.69	0	6	0	0	2	517	527
									TLMSSGQMAPSSSNK	95.0	37.7	25.0	1557.69	0	3	0	0	2	632	646
									MSEQQDLER	95.0	28.5	25.0	1151.50	0	1	0	0	2	771	779
									GMMSTVTEVR	95.0	65.5	25.0	1142.52	0	3	0	0	2	1262	1271
									ALSINTLVK	95.0	41.7	25.0	958.59	0	4	0	0	2	1272	1280
									LMSALLSGLTDR	95.0	43.6	25.0	1292.69	0	1	0	0	2	1401	1412
									AQGAIAMASIAK	95.0	38.0	25.0	1147.61	0	3	0	0	2	1545	1556
Protein arginine N-methyltransferase 1	ANM1_HUMAN	PRMT1	41.50	100.0	8	10	39	20.50	ANKLDHVVTIIK	95.0	41.3	25.0	1350.81	0	0	5	0	2	122	133
									LDHVVTIIK	95.0	46.6	25.0	1037.64	0	4	0	0	2	125	133
									GKVEEVELPVEK	95.0	61.8	25.0	1355.74	0	6	2	0	2	134	145
									ATLYVTAIEDR	95.0	67.8	25.0	1251.66	0	4	0	0	2	186	196
									DVAIKEPLVDVVDPK	95.0	68.5	25.0	1636.92	0	12	2	0	2	219	233
									EPLVDVVDPK	95.0	37.6	25.0	1110.60	0	1	0	0	2	224	233
									EVDIYTVK	95.0	27.1	25.0	966.51	0	1	0	0	2	244	251
									TGEEIFGTIGMRPNAK	95.0	42.0	25.0	1736.86	0	2	0	0	2	317	332
Protein arginine N-methyltransferase 5	ANM5_HUMAN	PRMT5	72.67	100.0	6	6	13	11.00	SDLLLSGR	95.0	30.0	25.0	860.48	0	1	0	0	2	69	76
									VPLVAPEDLR	95.0	52.4	25.0	1108.64	0	3	0	0	2	155	164
									DDIIENAPTTHTEEYSGEEK	95.0	46.1	25.0	2278.00	0	0	2	0	2	165	184
									AAILPTSIFLTNK	95.0	53.9	25.0	1388.81	0	3	0	0	2	228	240
									YSQYQQAIYK	95.0	45.5	25.0	1291.63	0	2	0	0	2	334	343
									GPLVNASLR	95.0	36.5	25.0	926.54	0	2	0	0	2	369	377
Protein argonaute-2	AGO2_HUMAN	EIF2C2	97.19	100.0	5	5	10	7.10	LQANFFEMDIPK	95.0	34.3	25.0	1468.71	0	1	0	0	2	40	51
									NLYTAMPLPIGR	95.0	61.7	25.0	1361.72	0	2	0	0	2	99	110
									VLQPPSILYGGR	95.0	43.8	25.0	1299.74	0	4	0	0	2	412	423
									YAQGADSVEPMFR	95.0	34.6	25.0	1486.66	0	1	0	0	2	494	506
									QEIIQDLAAMVR	95.0	66.1	25.0	1402.74	0	2	0	0	2	636	647
Protein diaphanous homolog 1	DIAP1_HUMAN	DIAPH1	141.33	100.0	7	7	18	5.58	EMVSQYLYTSK	95.0	73.0	25.0	1364.64	0	4	0	0	2	123	133
									SAMMYIQELR	95.0	35.5	25.0	1273.59	0	2	0	0	2	144	153
									AMDPAVPNMMIDAAK	95.0	32.8	25.0	1622.72	0	2	0	0	2	247	261
									LYKPEVQLR	95.0	22.7	25.0	1145.67	0	0	2	0	2	772	780
									FENNELFAK	95.0	48.0	25.0	1111.54	0	4	0	0	2	806	814
									LNAILFK	95.0	35.0	25.0	818.51	0	2	0	0	2	937	943
									FPDELAHVEK	95.0	39.8	25.0	1184.59	0	0	2	0	2	1037	1046
Protein disulfide-isomerase	PDIA1_HUMAN	P4HB	57.10	100.0	12	17	95	24.00	VDATEESDLAQQYGVR	95.0	####	25.0	1780.83	0	7	3	0	2	82	97
									YQLDKDGVVLFK	95.0	66.5	25.0	1424.78	0	3	10	0	2	196	207
									DGVVLFK	95.0	62.5	25.0	777.45	0	6	0	0	2	201	207
									NNFEGEVTK	95.0	31.5	25.0	1037.49	0	2	0	0	2	214	222
									ENLLDFIK	95.0	48.1	25.0	991.55	0	9	0	0	2	223	230
									THILLFLPK	95.0	55.0	25.0	1081.68	0	19	3	0	2	255	263
									ILEFFGLK	95.0	37.2	25.0	966.57	0	1	0	0	2	301	308
									LITLEEEMTK	95.0	59.1	25.0	1222.62	0	5	0	0	2	317	326
									YKPESEELTAER	95.0	57.7	25.0	1451.70	0	6	3	0	2	327	338
									NFEDVAFDEKK	95.0	58.8	25.0	1341.63	0	2	1	0	2	376	386
									LGETYKDHENIVIAK	95.0	67.6	25.0	1729.91	0	2	0	0	2	410	424
									MDSTANEVEAVK	95.0	74.1	25.0	1309.59	0	13	0	0	2	425	436
Protein disulfide-isomerase A3	PDIA3_HUMAN	PDIA3	56.77	100.0	18	20	101	33.30	RLAPEYEAAATR	95.0	50.6	25.0	1347.70	0	3	0	0	2	62	73
									LAPEYEAAATR	95.0	84.1	25.0	1191.60	0	8	0	0	2	63	73
									YGVSGYPTLK	95.0	45.6	25.0	1084.57	0	13	0	0	2	95	104

								IFRDGEEAGAYDGPR	95.0	49.3	25.0	1652.77	0	2	0	0	2	105	119
								DGEEAGAYDGPR	95.0	69.8	25.0	1236.51	0	16	0	0	2	108	119
								TADGIVSHLK	95.0	49.5	25.0	1040.57	0	8	0	0	2	120	129
								TADGIVSHLKK	95.0	27.2	25.0	1168.67	0	2	0	0	2	120	130
								QAGPASVPLR	95.0	44.8	25.0	995.56	0	2	0	0	2	131	140
								LNFAVASR	95.0	52.8	25.0	877.49	0	7	0	0	2	297	304
								FVMQEEFSR	95.0	53.6	25.0	1188.54	0	8	0	0	2	336	344
								FLQDYFDGNLKR	95.0	59.1	25.0	1515.76	0	2	0	0	2	352	363
								SEPIPESNDGPVK	95.0	61.0	25.0	1368.66	0	2	0	0	2	367	379
								VVVAENFDEIVNNENK	95.0	####	25.0	1832.90	0	2	0	0	2	380	395
								LSKDPNIVIAK	95.0	62.1	25.0	1197.72	0	2	2	0	2	423	433
								DPNIVIAK	95.0	39.3	25.0	869.51	0	3	0	0	2	426	433
								MDATANDVPSPYEVR	95.0	89.4	25.0	1680.75	0	7	0	0	2	434	448
								GFPTIYFSPANK	95.0	41.9	25.0	1341.68	0	3	0	0	2	449	460
								EATNPPVIQEEKPK	95.0	67.2	25.0	1579.83	0	8	1	0	2	483	496
Protein disulfide-isomerase A4	PDIA4_HUMAN	PDIA4	72.92	100.0	15	16	68	23.90	DKDPPIPVAK	95.0	27.7	25.0	1079.61	0	1	0	0	2	110	119
								IDATSASVLASR	95.0	####	25.0	1190.64	0	6	0	0	2	120	131
								KGQAVDYEGSR	95.0	46.2	25.0	1209.59	0	2	4	0	2	145	155
								GQAVDYEGSR	95.0	46.0	25.0	1081.49	0	6	0	0	2	146	155
								TQEEIVAK	95.0	37.3	25.0	917.49	0	2	0	0	2	156	163
								VDATAETDLAK	95.0	46.9	25.0	1133.57	0	9	0	0	2	235	245
								RFDVSGYPTLK	95.0	35.7	25.0	1282.68	0	1	0	0	2	246	256
								FDVSGYPTLK	95.0	55.2	25.0	1126.58	0	9	0	0	2	247	256
								FHHTFSTEIAK	95.0	32.9	25.0	1317.66	0	0	2	0	2	336	346
								SHMMDVQGSTQDSAIK	95.0	20.3	25.0	1766.77	0	0	1	0	2	371	386
								TFDSIVMDPK	95.0	63.4	25.0	1168.56	0	2	0	0	2	534	543
								QLEPVYNSLAK	95.0	43.8	25.0	1261.68	0	5	0	0	2	560	570
								MDATANDVPSDR	95.0	56.0	25.0	1307.55	0	13	0	0	2	583	594
								FEGGDRDLEHLSK	95.0	46.7	25.0	1502.72	0	4	0	0	2	617	629
								FIEEHATK	95.0	32.5	25.0	974.49	0	1	0	0	2	630	637
Protein disulfide-isomerase A6	PDIA6_HUMAN	PDIA6	48.10	100.0	6	7	53	18.20	NRPEDYQGGR	95.0	40.3	25.0	1191.55	0	2	0	0	2	109	118
								TGEAIVDAALSALR	95.0	90.6	25.0	1386.76	0	12	0	0	2	119	132
								KDVIELTDDSFDK	95.0	96.0	25.0	1524.74	0	2	2	0	2	160	172
								LAAVDATVNQVLASR	95.0	####	25.0	1527.85	0	21	0	0	2	217	231
								GESPVDYDGGR	95.0	61.8	25.0	1151.50	0	10	0	0	2	246	256
								GSTAPVGGGAFPTIVER	95.0	81.9	25.0	1615.84	0	4	0	0	2	393	409
Protein DJ-1	PARK7_HUMAN	PARK7	19.87	100.0	6	6	24	28.60	ALVILAK	95.0	53.2	25.0	727.51	0	9	0	0	2	6	12
								GAEEMETVIPVDVMR	95.0	59.9	25.0	1707.79	0	2	0	0	2	13	27
								VTVAGLAGK	95.0	35.2	25.0	815.50	0	2	0	0	2	33	41
								VTTHPLAK	95.0	34.8	25.0	866.51	0	2	0	0	2	123	130
								DGLILTSR	95.0	37.1	25.0	874.50	0	4	0	0	2	149	156
								APLVLKD	95.0	34.1	25.0	755.47	0	5	0	0	2	183	189
Protein FADD	FADD_HUMAN	FADD	23.26	100.0	3	3	7	11.50	ELLASLR	95.0	32.8	25.0	801.48	0	2	0	0	2	65	71
								NTEKENATVAHLVGALR	95.0	55.3	25.0	1822.98	0	0	4	0	2	150	166
								ENATVAHLVGALR	95.0	49.9	25.0	1350.75	0	1	0	0	2	154	166
Protein FAM49B	FA49B_HUMAN	FAM49B	36.73	100.0	6	7	19	18.80	EIYNQVNVVLK	95.0	37.0	25.0	1318.74	0	1	0	0	2	34	44
								EAIQHPADEK	95.0	37.9	25.0	1137.55	0	4	0	0	2	65	74
								KFYEFSQR	95.0	28.1	25.0	1104.55	0	1	0	0	2	92	99
								FYEFSQR	95.0	47.3	25.0	976.45	0	2	0	0	2	93	99
								INNVPAEGENEVNNELANR	95.0	####	25.0	2096.00	0	4	3	0	2	168	186
								MSLFYAEATPMLK	95.0	85.7	25.0	1533.73	0	4	0	0	2	187	199

Protein FAM50A	FA50A_HUMAN	FAM50A	40.22	100.0	4	4	8	13.00	NPDVDTSFLPDR	95.0	58.8	25.0	1375.65	0	2	0	0	2	159	170
									GNTMQQFLQK	95.0	35.4	25.0	1210.59	0	2	0	0	2	220	229
									ALEILR	95.0	34.3	25.0	714.45	0	2	0	0	2	230	235
									LLSDATVEKDESHAGK	95.0	41.1	25.0	1699.85	0	2	0	0	2	290	305
Protein KIAA0664	K0664_HUMAN	KIAA0664	146.65	100.0	3	3	5	2.52	AVGSISSTAFDIR	95.0	71.0	25.0	1323.69	0	2	0	0	2	704	716
									IGIGELITR	95.0	42.3	25.0	971.59	0	1	0	0	2	811	819
									FLENALAVSTK	95.0	52.3	25.0	1192.66	0	2	0	0	2	1126	1136
Protein KIAA1967	K1967_HUMAN	KIAA1967	102.89	100.0	3	3	4	2.60	MLLSLPEK	95.0	27.9	25.0	946.53	0	1	0	0	2	559	566
									TLAAEMQELR	95.0	57.3	25.0	1177.59	0	2	0	0	2	856	865
									LLQELR	95.0	27.4	25.0	771.47	0	1	0	0	2	888	893
Protein kinase C and casein kinase substrate in neurons protein 2	PACN2_HUMAN	PACSIN2	55.72	100.0	3	3	8	6.38	VSELHLEVK	95.0	56.7	25.0	1053.59	0	3	0	0	2	93	101
									ADPSLNPEQLK	95.0	44.9	25.0	1211.63	0	2	0	0	2	178	188
									HLDLSNVAGYK	95.0	44.9	25.0	1216.63	0	3	0	0	2	254	264
Protein NDRG1	NDRG1_HUMAN	NDRG1	42.82	100.0	3	4	9	12.20	EMQDVDLAEVKPLVEK	95.0	78.7	25.0	1858.95	0	2	3	0	2	4	19
									SIIGMGTGAGAYILTR	95.0	64.5	25.0	1596.84	0	2	0	0	2	133	148
									YFVQGMGYMPSASMTR	95.0	81.0	25.0	1873.79	0	2	0	0	2	307	322
Protein Niban	NIBAN_HUMAN	FAM129A	103.12	100.0	4	5	24	4.85	NDYAVESYENK	95.0	55.8	25.0	1331.57	0	7	0	0	2	95	105
									ENTQPFVVLPK	95.0	66.1	25.0	1271.70	0	9	0	0	2	150	160
									EVNEVSQNFQTTK	95.0	79.4	25.0	1523.73	0	6	0	0	2	372	384
									LMNLPLHSVK	95.0	30.0	25.0	1167.66	0	1	1	0	2	396	405
Protein phosphatase 1 regulatory subunit 7	PP1R7_HUMAN	PPP1R7	41.55	100.0	9	10	40	24.20	HSSGIVADLSEQSLK	95.0	94.0	25.0	1570.81	0	2	2	0	2	35	49
									IEGFEVLK	95.0	29.7	25.0	934.52	0	2	0	0	2	91	98
									ELDLYDNQIK	95.0	47.2	25.0	1250.63	0	4	0	0	2	124	133
									LFLVNNK	95.0	38.8	25.0	847.50	0	6	0	0	2	169	175
									IEGLQNLVNLR	95.0	68.6	25.0	1268.73	0	9	0	0	2	245	255
									LTMLDIASNR	95.0	56.6	25.0	1149.59	0	4	0	0	2	276	285
									SLETVYLER	95.0	53.2	25.0	1109.58	0	4	0	0	2	322	330
									VMLALPSVR	95.0	35.9	25.0	1001.58	0	5	0	0	2	343	351
									QIDATFVR	95.0	38.4	25.0	949.51	0	2	0	0	2	352	359
Protein phosphatase methylesterase 1	PPME1_HUMAN	PPME1	42.30	100.0	6	7	23	14.00	IVALDLR	95.0	35.0	25.0	799.50	0	3	0	0	2	107	113
									VKNPEDLSAETMAK	95.0	43.1	25.0	1548.76	0	1	2	0	2	120	133
									LLLLAGVDR	95.0	68.7	25.0	969.61	0	10	0	0	2	317	325
									LDKDLTIGQMQGK	95.0	51.2	25.0	1462.76	0	3	0	0	2	326	338
									DLTIGQMQGK	95.0	38.1	25.0	1106.55	0	1	0	0	2	329	338
									VAEAVATFLIR	95.0	80.3	25.0	1189.69	0	3	0	0	2	359	369
Protein RCC2	RCC2_HUMAN	RCC2	56.07	100.0	4	4	30	5.56	VAIFIEK	95.0	45.1	25.0	819.50	0	2	0	0	2	312	318
									TKDGQILPVPNVVVR	95.0	48.9	25.0	1634.96	0	2	0	0	2	319	333
									DGQILPVPNVVVR	95.0	60.2	25.0	1405.82	0	11	0	0	2	321	333
									LFDFPGR	95.0	44.7	25.0	851.44	0	15	0	0	2	378	384
Protein S100-A11	S10AB_HUMAN	S100A11	11.72	100.0	3	3	63	23.80	ISSPTETER	95.0	66.6	25.0	1019.50	0	34	0	0	2	4	12
									DGYNYTLSK	95.0	64.4	25.0	1060.49	0	11	0	0	2	28	36
									DPGVLDR	95.0	50.2	25.0	771.40	0	18	0	0	2	56	62
Protein S100-A14	S10AE_HUMAN	S100A14	11.64	100.0	3	3	4	31.70	SANAEDAQEFSDVER	95.0	####	25.0	1667.71	0	2	0	0	2	6	20
									AIETLIK	95.0	33.2	25.0	787.49	0	1	0	0	2	21	27
									NFHQYSVEGGK	95.0	30.5	25.0	1265.59	0	1	0	0	2	28	38
Protein SET	SET_HUMAN	SET	33.47	100.0	6	7	54	27.90	KPRPPPALGPEETSASAGLPK	95.0	83.5	25.0	2100.15	0	0	4	0	2	15	35
									EQQEAIEHIDEVQNEIDR	95.0	70.9	25.0	2195.02	0	1	6	0	2	40	57
									LNEQASEEILK	95.0	61.7	25.0	1273.66	0	16	0	0	2	58	68
									LRQPFFQK	95.0	19.5	25.0	1063.60	0	0	2	0	2	76	83
									VEVTEFEDIK	95.0	70.0	25.0	1208.60	0	11	0	0	2	123	132
									EFHLNESGDPSSK	95.0	63.1	25.0	1446.65	0	14	0	0	2	155	167

Protein TFG	TFG_HUMAN	TFG	43.43	100.0	4	4	14	6.50	AQLGEDIR	95.0	30.8	25.0	901.47	0	1	0	0	2	15	22
									AQLGEDIRR	95.0	26.7	25.0	1057.58	0	1	0	0	2	15	23
									LLSNDEVTIK	95.0	58.5	25.0	1131.63	0	10	0	0	2	48	57
									RELIELR	95.0	36.8	25.0	928.56	0	2	0	0	2	107	113
Protein transport protein Sec23A	SC23A_HUMAN	SEC23A	86.14	100.0	7	7	19	11.00	VPLTQATR	95.0	37.9	25.0	885.52	0	3	0	0	2	209	216
									GPQVQQPPPSNR	95.0	49.4	25.0	1304.67	0	7	0	0	2	217	228
									HFEALANR	95.0	35.5	25.0	957.49	0	2	0	0	2	330	337
									MGFGGTLEIK	95.0	61.0	25.0	1068.54	0	2	0	0	2	400	409
									GAIQFVTQYQHSSGQR	95.0	86.5	25.0	1806.89	0	2	0	0	2	477	492
									SGYQDMPEYENFR	95.0	72.6	25.0	1651.67	0	1	0	0	2	670	682
									HLLQAPVDDAQEILHSR	95.0	57.0	25.0	1942.01	0	0	2	0	2	683	699
Protein transport protein Sec24A	SC24A_HUMAN	SEC24A	119.73	100.0	5	5	8	4.76	VVNLLQER	95.0	51.3	25.0	970.57	0	1	0	0	2	350	357
									ELVQDLLK	95.0	32.0	25.0	957.56	0	3	0	0	2	593	600
									SMTASLSDAR	95.0	29.2	25.0	1054.48	0	1	0	0	2	855	864
									VDNLSDEGALNISDR	95.0	79.6	25.0	1617.77	0	1	0	0	2	949	963
									ANFLQNMIEDR	95.0	44.2	25.0	1366.64	0	2	0	0	2	1063	1073
Protein transport protein Sec24C	SC24C_HUMAN	SEC24C	118.31	100.0	8	8	26	8.23	GTEPFVTGVR	95.0	30.2	25.0	1062.56	0	2	0	0	2	341	350
									QAQVPLAAVIKPLAR	95.0	36.2	25.0	1574.97	0	0	4	0	2	390	404
									SLLDFLPR	95.0	36.7	25.0	960.55	0	7	0	0	2	529	536
									VGFVTYNK	95.0	38.8	25.0	927.49	0	2	0	0	2	547	554
									YASFQVENDQER	95.0	96.0	25.0	1485.66	0	2	0	0	2	723	734
									VVGFDAVMR	95.0	49.3	25.0	1009.51	0	6	0	0	2	746	754
									SDVLQPGAEVTTDDR	95.0	37.3	25.0	1602.76	0	1	0	0	2	914	928
									SPVESTTEPPAVR	95.0	28.9	25.0	1369.70	0	2	0	0	2	957	969
Protein transport protein Sec31A	SC31A_HUMAN	SEC31A	133.00	100.0	4	4	14	3.36	LVTFENVR	95.0	40.1	25.0	977.54	0	4	0	0	2	404	411
									YLELLGYR	95.0	48.7	25.0	1026.56	0	6	0	0	2	489	496
									AQDGSHPLSLQDLIEK	95.0	58.6	25.0	1750.90	0	1	0	0	2	708	723
									TTFEDLIQR	95.0	42.3	25.0	1122.58	0	3	0	0	2	1121	1129
Protein unc-45 homolog A	UN45A_HUMAN	UNC45A	103.06	100.0	3	3	12	4.24	TVATLSILGTR	95.0	76.0	25.0	1131.67	0	5	0	0	2	230	240
									ALIPLALEGTDVGQTK	95.0	91.9	25.0	1625.91	0	5	0	0	2	692	707
									GAVVVLNMVEASR	95.0	58.7	25.0	1360.73	0	2	0	0	2	882	894
Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PIMT_HUMAN	PCMT1	24.63	100.0	8	10	28	31.70	SGGASHSELIHNLR	95.0	71.8	25.0	1477.75	0	4	4	0	2	5	18
									VFEVMLATDR	95.0	57.9	25.0	1196.60	0	2	0	0	2	28	37
									ELVDDSINNVR	95.0	68.3	25.0	1273.64	0	3	0	0	2	114	124
									KDDPTLLSSGR	95.0	34.5	25.0	1188.62	0	3	0	0	2	125	135
									DDPTLLSSGR	95.0	38.1	25.0	1060.53	0	1	0	0	2	126	135
									VQLVVGDGR	95.0	43.5	25.0	942.54	0	4	0	0	2	136	144
									MKPLMGVIYVPLTDK	95.0	47.2	25.0	1736.93	0	2	0	0	2	205	219
									MKPLMGVIYVPLTDKEK	95.0	57.2	25.0	1994.07	0	0	4	1	2	205	221
Protocadherin Fat 2	FAT2_HUMAN	FAT2	479.29	100.0	13	13	83	3.36	SNEFSLVSVK	95.0	44.0	25.0	1109.58	0	2	0	0	2	309	318
									SGSGPYFYSQIR	95.0	47.2	25.0	1361.65	0	2	0	0	2	337	348
									YTLLSPTEK	95.0	37.0	25.0	1051.57	0	7	0	0	2	857	865
									ATDSGQPPLSASVR	95.0	54.7	25.0	1385.70	0	7	0	0	2	1318	1331
									VPQDTVPGVELLR	95.0	49.0	25.0	1422.80	0	10	0	0	2	1457	1469
									ASDEDSEVNYSIK	95.0	57.9	25.0	1456.64	0	5	0	0	2	1896	1908
									ISLTQVLDK	95.0	45.6	25.0	1016.60	0	8	0	0	2	1956	1964
									VSIEDVNDNPPK	95.0	87.4	25.0	1326.65	0	2	0	0	2	2058	2069
									VGASDGVFR	95.0	41.4	25.0	907.46	0	2	0	0	2	2454	2462
									DVIEINPVTGVVK	95.0	63.0	25.0	1382.79	0	17	0	0	2	2632	2644
									AVAAQDPVIYSLVR	95.0	59.0	25.0	1501.84	0	4	0	0	2	2715	2728
									TPVAVVFAR	95.0	72.5	25.0	959.57	0	16	0	0	2	3130	3138

									IIAAQGLPR	95.0	28.7	25.0	938.58	0	1	0	0	2	3587	3595
Purine nucleoside phosphorylase	PNPH_HUMAN	PNP	32.10	100.0	7	8	36	27.00	LVFGFLNGR	95.0	40.6	25.0	1022.58	0	1	0	0	2	68	76
									FEVGDIMLIR	95.0	65.5	25.0	1208.63	0	2	0	0	2	124	133
									FPAMSDAYDR	95.0	46.6	25.0	1188.50	0	6	0	0	2	159	168
									LGADAVGMSTVPEVIVAR	95.0	73.9	25.0	1800.95	0	6	0	0	2	212	229
									VFGFSLITNK	95.0	46.3	25.0	1125.63	0	6	0	0	2	235	244
									VIMDYESLEK	95.0	52.9	25.0	1242.59	0	5	0	0	2	245	254
									ANHEEVLAAGK	95.0	74.9	25.0	1138.59	0	9	1	0	2	255	265
Puromycin-sensitive aminopeptidase	PSA_HUMAN	NPEPPS	103.26	100.0	19	20	73	22.40	IDFVGELNDK	95.0	31.0	25.0	1149.58	0	1	0	0	2	146	155
									YAAVTQFEATDAR	95.0	####	25.0	1442.69	0	1	0	0	2	173	185
									VALSNMNVIDR	95.0	75.6	25.0	1247.64	0	3	0	0	2	211	221
									KPYPDDENLVEVK	95.0	71.0	25.0	1545.78	0	4	2	0	2	222	234
									ETALLIDPK	95.0	43.3	25.0	999.57	0	3	0	0	2	328	336
									ILMDKPEMNVVLK	95.0	42.0	25.0	1561.83	0	4	0	0	2	559	571
									LNLGTVGFYR	95.0	63.9	25.0	1139.62	0	6	0	0	2	581	590
									DLSLPPVDR	95.0	30.8	25.0	1011.55	0	1	0	0	2	607	615
									LGLQNDLFSLAR	95.0	50.1	25.0	1346.74	0	1	0	0	2	616	627
									AGIISTVEVLK	95.0	65.3	25.0	1129.68	0	5	0	0	2	628	638
									DVFSPIGER	95.0	49.4	25.0	1019.52	0	3	0	0	2	681	689
									QILSADLR	95.0	57.5	25.0	915.53	0	2	0	0	2	737	744
									SPVYLTVLK	95.0	59.9	25.0	1019.61	0	16	0	0	2	745	753
									HGDGTTLDIMLK	95.0	61.9	25.0	1316.65	0	2	0	0	2	754	765
									VLGATLLPDLIQK	95.0	57.0	25.0	1380.85	0	2	0	0	2	782	794
									YQGGFLISR	95.0	68.4	25.0	1040.55	0	7	0	0	2	842	850
									LSVEGFAVDK	95.0	55.9	25.0	1064.56	0	5	0	0	2	854	863
									AFFESHPAPSAER	95.0	51.8	25.0	1445.68	0	4	0	0	2	870	882
									DAESIHQYLLQR	95.0	45.9	25.0	1472.75	0	0	1	0	2	901	912
Putative deoxyribonuclease TATDN1	TATD1_HUMAN	TATDN1	33.58	100.0	3	3	7	9.43	HQDDLQDVIGR	95.0	72.4	25.0	1295.63	0	4	0	0	2	28	38
									AVEIGVK	95.0	30.8	25.0	715.43	0	1	0	0	2	39	45
									ELLNLAENNK	95.0	44.0	25.0	1157.62	0	2	0	0	2	95	104
Putative elongation factor 1-alpha-like 3	EF1A3_HUMAN	EEF1AL3	50.12	100.0	10	12	426	23.60	THINIVVIGHVDSGK	95.0	65.4	25.0	1588.88	0	0	3	0	2	6	20
									STTTGHLIYK	95.0	47.0	25.0	1120.60	0	77	0	0	2	21	30
									YYVTIIDAPGHR	95.0	73.4	25.0	1404.73	0	79	33	0	2	85	96
									EHALLAYTLGVK	95.0	69.6	25.0	1314.74	0	26	16	0	2	135	146
									QLIVGVNK	95.0	40.6	25.0	870.54	0	3	0	0	2	147	154
									MDSTEPPYSQK	95.0	37.9	25.0	1298.56	0	2	0	0	2	155	165
									YEEIVK	95.0	38.6	25.0	780.41	0	8	0	0	2	167	172
									EVSTYIK	95.0	29.8	25.0	839.45	0	1	0	0	2	173	179
									LPLQDVYK	95.0	58.3	25.0	975.55	0	58	0	0	2	248	255
									IGGIGTVPVGR	95.0	92.9	25.0	1025.61	0	117	0	0	2	256	266
									QTVAVGVIK	95.0	61.6	25.0	914.57	0	4	0	0	2	431	439
Putative GTP-binding protein RAY-like	RAYL_HUMAN	RABL4	20.46	100.0	3	3	11	19.90	TALAQIFR	95.0	43.1	25.0	919.54	0	6	0	0	2	19	26
									SYTLTTGMDLVVK	95.0	40.1	25.0	1443.74	0	1	0	0	2	35	47
									SQAPGISLPGVLVGNK	95.0	74.5	25.0	1536.87	0	4	0	0	2	109	124
Putative heat shock protein HSP 90-beta 4	H90B4_HUMAN	HSP90AB4P	58.25	100.0	3	3	13	11.70	MSLIINTFYSNK	95.0	51.3	25.0	1446.73	0	1	0	0	2	1	12
									SLIINTFYSNK	95.0	61.4	25.0	1299.69	0	10	0	0	1	2	12
									IRYESLTDPSK	95.0	38.1	25.0	1308.68	0	1	6	0	2	30	40
									YESLTDPSK	95.0	58.4	25.0	1039.49	0	31	0	0	2	32	40
									VILHLK	95.0	42.5	25.0	722.49	0	19	0	0	2	156	161
									VILHLKEDQTEYLEER	95.0	74.5	25.0	2015.04	0	2	2	1	2	156	171
									EDQTEYLEER	95.0	69.7	25.0	1311.57	0	83	0	0	2	162	171

									LDEVFSK	95.0	29.5	25.0	837.44	0	2	0	0	2	337	343
									EGLELPEDEEEK	95.0	60.0	25.0	1416.64	0	60	0	0	2	447	458
									EGLELPEDEEEKK	95.0	48.9	25.0	1544.73	0	10	0	0	2	447	459
Putative heterogeneous nuclear ribonucleoprotein A1-like 3	RA1L3_HUMAN	HNRPA1L3	34.21	100.0	4	6	96	18.40	SESPKEPEQLR	95.0	36.9	25.0	1299.65	0	6	1	0	2	4	14
									EDSQRPGAHLTVK	95.0	59.0	25.0	1437.74	0	41	6	0	2	93	105
									KIFVGGIK	95.0	28.2	25.0	861.56	0	2	0	0	2	106	113
									IFVGGIK	95.0	30.1	25.0	733.46	0	1	0	0	2	107	113
									IFVGGIKEDTEEHHLR	95.0	66.9	25.0	1879.97	0	2	9	3	2	107	122
									EDTEEHHLR	95.0	33.4	25.0	1165.52	0	1	0	0	2	114	122
									DYFEQYGK	95.0	33.2	25.0	1049.46	0	1	0	0	2	123	130
									IEVIEIMTDR	95.0	79.6	25.0	1234.64	0	41	0	0	2	131	140
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15_HUMAN	DHX15	90.92	100.0	13	15	49	17.60	FTDILVR	95.0	41.3	25.0	863.50	0	1	0	0	2	146	152
									HQSFVLVGETGSGK	95.0	70.7	25.0	1445.74	0	4	2	0	2	153	166
									VAAMSVAQR	95.0	62.8	25.0	948.49	0	2	0	0	2	196	204
									YMTDGMLLR	95.0	29.1	25.0	1131.52	0	1	0	0	2	235	243
									EAMNDPLLER	95.0	39.2	25.0	1203.57	0	2	0	0	2	244	253
									YGVIILDEAHER	95.0	60.5	25.0	1414.73	0	2	4	0	2	254	265
									TLATDILMGVLK	95.0	45.6	25.0	1290.73	0	5	0	0	2	266	277
									VIVMSATLDAGK	95.0	50.7	25.0	1220.66	0	2	0	0	2	288	299
									EVDDLGPEVGDIK	95.0	82.5	25.0	1385.68	0	9	0	0	2	372	384
									VESLLVTAISK	95.0	96.4	25.0	1159.69	0	4	0	0	2	453	463
									TEMQDNTYPEILR	95.0	35.0	25.0	1625.75	0	1	0	0	2	492	504
									SNLGSVVLQLK	95.0	72.9	25.0	1157.69	0	8	0	0	2	505	515
									DYYINIR	95.0	30.4	25.0	956.48	0	2	0	0	2	684	690
Putative RNA-binding protein Luc7-like 2	LC7L2_HUMAN	LUC7L2	46.50	100.0	4	4	6	11.70	VHELNEEIGK	95.0	35.0	25.0	1167.60	0	2	0	0	2	126	135
									VEQLGAEGNVEESQK	95.0	84.0	25.0	1616.78	0	2	0	0	2	140	154
									NSMPASSFQQQK	95.0	37.1	25.0	1368.62	0	1	0	0	2	175	186
									LHLGFIEIR	95.0	32.2	25.0	1097.65	0	1	0	0	2	214	222
Pyridoxal kinase	PDXK_HUMAN	PDXK	35.08	100.0	3	4	9	11.90	YDYVLTGYTR	95.0	55.1	25.0	1250.61	0	4	0	0	2	77	86
									KIHSQEEALR	95.0	22.6	25.0	1210.65	0	0	1	0	2	161	170
									AQAGEGVRPSPMQLELR	95.0	30.1	25.0	1854.95	0	2	2	0	2	276	292
Pyridoxal phosphate phosphatase	PLPP_HUMAN	PDXP	31.68	100.0	3	3	6	11.50	LGFGGLR	95.0	35.1	25.0	719.42	0	2	0	0	2	75	81
									TPGTGSLAAAVETASGR	95.0	26.0	25.0	1545.79	0	0	2	0	2	190	206
									LETDILFGHR	95.0	71.5	25.0	1200.64	0	2	0	0	2	240	249
Pyruvate kinase isozymes M1/M2	KPYM_HUMAN	PKM2	57.92	100.0	21	26	837	39.40	LDIDSPPITAR	95.0	79.3	25.0	1197.65	0	118	0	0	2	33	43
									NTGIICTIGPASR	95.0	65.8	25.0	1359.71	0	2	0	0	2	44	56
									SVETLKEMIK	95.0	34.7	25.0	1193.64	0	3	0	0	2	57	66
									LNFSHGTHEYHAETIK	95.0	91.8	25.0	1883.90	0	8	26	1	2	74	89
									GSGTAEVELK	95.0	79.0	25.0	990.51	0	40	0	0	2	126	135
									GSGTAEVELKK	95.0	63.2	25.0	1118.61	0	92	11	0	2	126	136
									ITLDNAYMEK	95.0	66.4	25.0	1213.58	0	60	0	0	2	142	151
									IYVDDGLISLQVK	95.0	72.5	25.0	1462.82	0	4	0	0	2	174	186
									GADFLVTEVENGGSLGSK	95.0	####	25.0	1779.88	0	17	0	0	2	189	206
									KGVNLPGAAVDLPAVSEK	95.0	####	25.0	1764.99	0	34	19	0	2	207	224
									GVNLPGAAVDLPAVSEK	95.0	####	25.0	1636.89	0	33	0	0	2	208	224
									DIQDLK	95.0	45.2	25.0	731.39	0	9	0	0	2	225	230
									ASDVHEVR	95.0	36.1	25.0	912.45	0	2	0	0	2	248	255
									IENHEGVR	95.0	44.4	25.0	953.48	0	2	0	0	2	271	278
									GDLGIEIPAEK	95.0	65.2	25.0	1141.61	0	111	0	0	2	295	305
									VFLAQK	95.0	41.2	25.0	705.43	2	38	0	0	2	306	311
									AGKPVICATQMLESMIK	95.0	29.6	25.0	1908.96	0	0	1	0	2	320	336

									GDYPLEAVR	95.0	68.2	25.0	1019.52	0	82	0	0	2	368	376
									MQHLIAR	95.0	37.6	25.0	884.48	0	31	0	0	2	377	383
									APIIAVTR	95.0	70.7	25.0	840.53	0	41	0	0	2	448	455
									VNFAMNVGK	95.0	60.2	25.0	995.50	0	50	0	0	2	490	498
Quinone oxidoreductase	QOR_HUMAN	CRYZ	35.19	100.0	7	7	18	21.60	VFEFGGPEVLK	95.0	38.7	25.0	1221.65	0	1	0	0	2	13	23
									SDIAVPIPK	95.0	55.2	25.0	939.55	0	4	0	0	2	26	34
									ILGTAGTEEGQK	95.0	32.5	25.0	1203.62	0	3	0	0	2	176	187
									EVNYIDK	95.0	27.4	25.0	880.44	0	1	0	0	2	202	208
									DLSLLSHGGR	95.0	62.9	25.0	1054.56	0	4	0	0	2	233	242
									GTIEINPR	95.0	48.0	25.0	899.49	0	3	0	0	2	250	257
									ESSIIGVTLFSSTK	95.0	59.5	25.0	1468.79	0	2	0	0	2	263	276
Rab GDP dissociation inhibitor alpha	GDIA_HUMAN	GDI1	50.57	100.0	8	8	57	22.80	FQLLEGPPESMGR	95.0	58.5	25.0	1476.72	0	25	0	0	2	56	68
									FLMANGQLVK	95.0	32.9	25.0	1136.61	0	3	0	0	2	80	89
									MLLYTEVTR	95.0	44.5	25.0	1141.59	0	27	0	0	2	90	98
									VVEGSFVYK	95.0	63.8	25.0	1027.55	0	5	0	0	2	104	112
									TFEGVDPQTTSMR	95.0	64.1	25.0	1484.67	0	10	0	0	2	157	169
									LYSESLAR	95.0	48.0	25.0	938.49	0	10	0	0	2	211	218
									YIAIASTTVETTDPEK	95.0	####	25.0	1738.87	0	3	0	0	2	349	364
									MAGTAFDFENMK	95.0	37.8	25.0	1393.58	0	2	0	0	2	424	435
									MAGTAFDFENMKR	95.0	57.9	25.0	1549.68	0	4	0	0	2	424	436
									KQNDVFGEAEQ	95.0	48.5	25.0	1264.58	0	6	0	0	2	437	447
									QNDVFGEAEQ	95.0	27.7	25.0	1136.49	0	2	0	0	2	438	447
Rab GDP dissociation inhibitor beta	GDIB_HUMAN	GDI2	50.65	100.0	13	14	80	27.90	FKIPGSPPESMGR	95.0	20.7	25.0	1418.71	0	0	2	0	2	56	68
									FLMANGQLVK	95.0	32.9	25.0	1136.61	0	3	0	0	2	80	89
									MLLYTEVTR	95.0	44.5	25.0	1141.59	0	27	0	0	2	90	98
									VTEGSFVYK	95.0	63.5	25.0	1029.53	0	7	0	0	2	104	112
									TFEGIDPK	95.0	44.7	25.0	906.46	0	4	0	0	2	157	164
									LYSESLAR	95.0	48.0	25.0	938.49	0	10	0	0	2	211	218
									YIAIVSTTVETK	95.0	86.7	25.0	1324.74	0	4	0	0	2	349	360
									YIAIVSTTVETKEPEK	95.0	85.9	25.0	1807.97	0	2	2	0	2	349	364
									EIRPALELLEPIEQK	95.0	34.4	25.0	1778.01	0	4	0	0	2	365	379
									FVSISDLLVPK	95.0	61.4	25.0	1217.71	0	4	0	0	2	380	390
									DLGTESQIFISR	95.0	66.8	25.0	1365.70	0	5	0	0	2	391	402
									MTGSEFDFEEMK	95.0	93.0	25.0	1482.58	0	2	0	0	2	424	435
									MTGSEFDFEEMKR	95.0	66.6	25.0	1638.68	0	4	0	0	2	424	436
Rab3 GTPase-activating protein non-catalytic subunit	RBGPR_HUMAN	RAB3GAP2	155.97	100.0	8	8	13	5.17	EEILSGALR	95.0	50.8	25.0	987.55	0	2	0	0	2	27	35
									VILLDVAR	95.0	38.0	25.0	898.57	0	2	0	0	2	408	415
									SPNLDLVETEIK	95.0	32.0	25.0	1357.72	0	1	0	0	2	568	579
									LQALLEK	95.0	30.0	25.0	814.50	0	1	0	0	2	682	688
									DGVLPVK	95.0	45.6	25.0	727.44	0	2	0	0	2	705	711
									VSSLQAEPLPR	95.0	67.8	25.0	1196.66	0	2	0	0	2	914	924
									FSAATYLMDK	95.0	54.9	25.0	1162.55	0	2	0	0	2	1066	1075
									VIELLPEK	95.0	34.0	25.0	940.57	0	1	0	0	2	1364	1371
Radixin	RADI_HUMAN	RDX	68.55	100.0	6	6	12	20.80	PKPINVR	95.0	37.8	25.0	823.51	0	1	0	0	1	2	8
									QLFDQVVK	95.0	47.4	25.0	976.55	0	10	0	0	2	28	35
									KENPLQFK	94.6	26.4	25.0	1003.56	0	1	0	0	2	72	79
									ENPLQFK	95.0	46.2	25.0	875.46	0	2	0	0	2	73	79
									LFFLQVK	95.0	46.6	25.0	894.54	0	7	0	0	2	101	107
									NISFNDKK	95.0	31.6	25.0	965.51	0	3	0	0	2	247	254
									FVIKPIDK	95.0	40.5	25.0	959.59	0	18	0	0	2	255	262
									FVIKPIDKK	95.0	29.4	25.0	1087.69	0	2	3	0	2	255	263

									KAPDFVFYAPR	95.0	55.3	25.0	1310.69	0	14	7	0	2	263	273
									APDFVFYAPR	95.0	75.6	25.0	1182.59	0	41	0	0	2	264	273
									RKPDTIEVQQMK	95.0	55.2	25.0	1488.78	0	21	54	0	2	295	306
									KPDTIEVQQMK	95.0	56.1	25.0	1332.68	0	17	2	0	2	296	306
									KALELDQER	95.0	47.8	25.0	1101.59	0	4	0	0	2	371	379
									ALELDQER	95.0	34.4	25.0	973.50	0	1	0	0	2	372	379
									IALLEEAK	95.0	37.0	25.0	886.52	0	2	0	0	2	428	435
									AFAAQEDLEK	95.0	28.6	25.0	1121.55	0	2	0	0	2	449	458
									QLQALSSELAQAR	95.0	90.1	25.0	1414.76	0	2	0	0	2	527	539
									TQNDVLHAENVK	95.0	38.5	25.0	1367.69	0	1	0	0	2	545	556
Ran GTPase-activating protein 1	RAGP1_HUMAN	RANGAP1	63.53	100.0	11	11	83	22.00	TQVAGGQLSFK	95.0	37.8	25.0	1135.61	0	2	0	0	2	16	26
									LEGNTVGVEAAR	95.0	65.4	25.0	1215.63	0	12	0	0	2	56	67
									LENDGATALAEAFR	95.0	95.6	25.0	1477.73	0	12	0	0	2	192	205
									VINLNDNTFTEK	95.0	67.3	25.0	1407.71	0	16	0	0	2	240	251
									GAVAMAETLK	95.0	34.0	25.0	1006.52	0	1	0	0	2	252	261
									GAVAIADAIR	95.0	68.8	25.0	956.55	0	14	0	0	2	280	289
									DAALAVAEAMADK	95.0	85.3	25.0	1291.62	0	6	0	0	2	308	320
									SSVLIAQQTDTSDPEK	95.0	####	25.0	1718.84	0	10	0	0	2	453	468
									MAVQDAVDALMQK	95.0	73.5	25.0	1451.69	0	7	0	0	2	488	500
									LLVHMGLLK	95.0	33.9	25.0	1039.63	0	2	0	0	2	516	524
									HSLLQTLYK	95.0	31.5	25.0	1102.63	0	1	0	0	2	578	586
Rap1 GTPase-GDP dissociation stimulator 1	GDS1_HUMAN	RAP1GDS1	66.30	100.0	8	8	23	17.10	VANIIAEVAK	95.0	65.6	25.0	1027.61	0	6	0	0	2	68	77
									DQEVLLQTGR	95.0	60.6	25.0	1158.61	0	2	0	0	2	102	111
									EQFASTNIAEELVK	95.0	62.8	25.0	1578.80	0	2	0	0	2	217	230
									VDSDKEDDITELK	95.0	60.1	25.0	1506.72	0	1	0	0	2	278	290
									HVEDGNVTVQHAALSALR	95.0	65.2	25.0	1916.99	0	0	2	0	2	369	386
									MLSAGVTEAVLK	95.0	64.2	25.0	1234.67	0	4	0	0	2	398	409
									MLIDAQAEAAEQLGK	95.0	####	25.0	1603.80	0	2	0	0	2	428	442
									SVAQQASLTEQR	95.0	57.5	25.0	1317.68	0	4	0	0	2	591	602
Ras GTPase-activating protein-binding protein 1	G3BP1_HUMAN	G3BP1	52.14	100.0	5	5	13	16.70	VMEKPSPLLVGR	95.0	27.5	25.0	1341.76	0	0	2	0	1	2	13
									NSSYVHGGLDSNGKPADAVYGQK	95.0	49.5	25.0	2364.12	0	0	2	0	2	37	59
									FMQTFVLAPEGSVANK	95.0	86.7	25.0	1754.88	0	2	0	0	2	108	123
									FYVHNDIFR	95.0	45.0	25.0	1210.60	0	0	5	0	2	124	132
									SSSPAPADIAQTVQEDLR	95.0	####	25.0	1884.93	0	2	0	0	2	230	247
Ras GTPase-activating-like protein IQGAP1	IQGA1_HUMAN	IQGAP1	189.24	100.0	45	51	253	24.90	LTAEEMDER	95.0	62.1	25.0	1109.48	0	17	0	0	2	26	34
									LGNFFSPK	95.0	57.4	25.0	909.48	0	10	0	0	2	81	88
									ATGLHFR	95.0	38.3	25.0	801.44	0	3	0	0	2	105	111
									IFYPETTDIYDR	95.0	47.3	25.0	1532.73	0	1	0	0	2	131	142
									IFYPETTDIYDRK	95.0	81.2	25.0	1660.82	0	2	0	0	2	131	143
									LGLAPQIQDLYGK	95.0	49.9	25.0	1415.79	0	2	0	0	2	162	174
									VDFTEEEINNMK	95.0	62.7	25.0	1484.66	0	8	0	0	2	175	186
									VDFTEEEINNMKTELEK	95.0	39.1	25.0	2084.97	0	0	2	0	2	175	191
									YGIQMPAFSK	95.0	55.7	25.0	1157.57	0	4	0	0	2	192	201
									RIPADTFAALK	95.0	46.8	25.0	1202.69	0	3	0	0	2	231	241
									IPADTFAALK	95.0	34.2	25.0	1046.59	0	2	0	0	2	232	241
									ALQSPALGLR	95.0	55.4	25.0	1025.61	0	17	0	0	2	327	336
									EELQSGVDAANSAAQQYQR	95.0	####	25.0	2064.96	0	2	1	0	2	369	387
									RLAAVALINAAIQK	95.0	70.5	25.0	1451.91	0	1	2	0	2	388	401
									LAAVALINAAIQK	95.0	74.6	25.0	1295.80	0	4	0	0	2	389	401
									YLDELMK	95.0	37.5	25.0	927.45	0	3	0	0	2	497	503
									TLQALQIPAAK	95.0	65.3	25.0	1153.69	0	16	0	0	2	557	567

									EEIQSSISGVTAAYNR	95.0	####	25.0	1724.84	0	5	0	0	2	723	738
									DHINDIIK	95.0	36.0	25.0	967.52	0	1	0	0	2	834	841
									IQAFIR	95.0	30.5	25.0	747.45	0	4	0	0	2	842	847
									TLINAEDPPMVVVR	95.0	64.6	25.0	1569.83	0	2	0	0	2	857	870
									MREEVITLIR	95.0	41.2	25.0	1275.71	0	3	4	0	2	892	901
									SNQQLENDLNLMDIK	95.0	####	25.0	1790.86	0	9	0	0	2	902	916
									ITLQDVVSHSK	95.0	67.3	25.0	1226.67	0	5	2	0	2	925	935
									EQLSDMMMINK	95.0	42.5	25.0	1387.59	0	4	0	0	2	943	953
									EEYLLLR	95.0	37.8	25.0	935.52	0	5	0	0	2	1018	1024
									SKVDQIQEIVTGNPTVIK	95.0	####	25.0	1969.10	0	2	0	0	2	1036	1053
									VDQIQEIVTGNPTVIK	95.0	####	25.0	1753.97	0	9	0	0	2	1038	1053
									LPYDVTPEQALAHEEVK	95.0	74.6	25.0	1938.98	0	2	2	0	2	1112	1128
									AVTDKFLSAIVSSVDK	95.0	90.3	25.0	1679.92	0	2	1	0	2	1140	1155
									FLSAIVSSVDK	95.0	60.5	25.0	1165.65	0	5	0	0	2	1145	1155
									DSLHEKFPDAGEDELLK	95.0	37.4	25.0	1942.94	0	0	0	2	2	1169	1185
									FPDAGEDELLK	95.0	55.5	25.0	1233.60	0	7	0	0	2	1175	1185
									IIGNLLYYR	95.0	63.5	25.0	1124.65	0	15	0	0	2	1186	1194
									TEVSLTLTNK	95.0	58.8	25.0	1105.61	0	1	0	0	2	1359	1368
									FDVPGDENAEMDAR	95.0	88.5	25.0	1581.65	0	20	0	0	2	1369	1382
									RLIVDVIR	95.0	37.4	25.0	983.64	0	2	0	0	2	1390	1397
									LIVDVIR	95.0	45.2	25.0	827.54	0	9	0	0	2	1391	1397
									SVKEDSNLTLQEK	95.0	65.0	25.0	1490.77	0	2	0	0	2	1443	1455
									EDSNLTLQEK	95.0	42.1	25.0	1176.57	0	4	0	0	2	1446	1455
									KLTELGTVDPK	95.0	32.5	25.0	1200.68	0	1	0	0	2	1465	1475
									LTELGTVDPK	95.0	62.4	27.2	1072.59	0	4	0	0	2	1466	1475
									YQELINDIAR	95.0	49.2	25.0	1234.64	0	7	0	0	2	1478	1487
									LQQTYAALNSK	95.0	55.1	25.0	1236.66	0	10	0	0	2	1506	1516
									ATFYGEQVDYYK	95.0	88.2	25.0	1483.67	0	2	0	0	2	1517	1528
Ras suppressor protein 1	RSU1_HUMAN	RSU1	31.52	100.0	4	4	9	13.70	LTMVPPNIAELK	95.0	44.4	25.0	1341.74	0	4	0	0	2	52	63
									LQILSLR	95.0	47.2	25.0	842.55	0	2	0	0	2	159	165
									EIGELTQLK	95.0	33.7	25.0	1030.58	0	2	0	0	2	175	183
									HMQANPEPPK	95.0	42.6	25.0	1164.55	0	1	0	0	2	249	258
Ras-related C3 botulinum toxin substrate 1	RAC1_HUMAN	RAC1	21.43	100.0	3	3	14	16.70	LTPITYPQGLAMAK	95.0	62.4	25.0	1519.82	0	6	0	0	2	134	147
									YLECSALTQR	95.0	38.0	25.0	1240.60	0	1	0	0	2	154	163
									TVFDEAIR	95.0	45.4	25.0	950.49	0	7	0	0	2	167	174
Ras-related protein Rab-11B	RB11B_HUMAN	RAB11B	24.47	100.0	8	9	46	38.10	DDEYDYLFK	95.0	43.2	25.0	1207.52	0	2	0	0	2	5	13
									VVLIGDSGVGK	95.0	75.8	25.0	1043.61	0	6	0	0	2	14	24
									NEFNLESK	95.0	34.7	25.0	980.47	0	1	0	0	2	34	41
									STIGVEFATR	95.0	70.4	25.0	1080.57	0	12	0	0	2	42	51
									GAVGALLVYDIAK	95.0	69.2	25.0	1289.75	0	7	0	0	2	83	95
									HLTYENVER	95.0	38.1	25.0	1160.57	0	1	0	0	2	96	104
									DHADSNIVIMLVGNK	95.0	76.8	25.0	1641.83	0	5	1	0	2	111	125
									NILTEIYR	95.0	57.0	25.0	1021.57	0	11	0	0	2	167	174
Ras-related protein Rab-14	RAB14_HUMAN	RAB14	23.88	100.0	4	4	22	24.70	YIIIGDMGVGK	95.0	56.2	25.0	1181.62	0	2	0	0	2	14	24
									GAAGALMVYDITR	95.0	78.2	25.0	1353.68	0	5	0	0	2	83	95
									NLTNPNTVIILIGNK	95.0	52.6	25.0	1623.94	0	2	0	0	2	111	125
									TGENVEDAFLEAAK	95.0	85.3	25.0	1493.71	0	13	0	0	2	157	170
Ras-related protein Rab-2A	RAB2A_HUMAN	RAB2A	23.53	100.0	5	6	29	27.80	YIIIGDTGVGK	95.0	59.5	25.0	1135.64	0	7	0	0	2	9	19
									GAAGALLVYDITR	95.0	57.0	25.0	1319.73	0	4	0	0	2	78	90
									KEEGEAFAR	95.0	40.7	25.0	1036.51	0	1	0	0	2	131	139
									EHGLIFMETSAK	95.0	40.0	25.0	1378.67	0	3	1	0	2	140	151

								TASNVEEAFINTAK	95.0	####	25.0	1494.74	0	13	0	0	2	152	165
Ras-related protein Rab-5C	RAB5C_HUMAN	RAB5C	23.46	100.0	4	4	17	23.60	LVLLGESAVGK	95.0	57.0	25.0	1085.66	0	2	0	0	2	24	34
									QASPNIVIALAGNK	95.0	61.6	25.0	1395.80	0	7	0	0	2	122	135
									TAMNVNEIFMAIAK	95.0	49.5	25.0	1584.78	0	4	0	0	2	167	180
									GVDLQENNPASR	95.0	49.3	25.0	1299.63	0	4	0	0	2	199	210
Ras-related protein Rab-6A	RAB6A_HUMAN	RAB6A	23.58	100.0	5	5	46	26.90	LVFLGEQSVGK	95.0	66.0	25.0	1176.66	0	20	0	0	2	16	26
									TMYLEDR	95.0	31.1	25.0	943.42	0	1	0	0	2	54	60
									GSDVIIMLVGNK	95.0	97.6	25.0	1261.68	0	14	0	0	2	116	127
									ELNVMFIETSAK	95.0	90.9	25.0	1397.70	0	8	0	0	2	147	158
									VAAALPGMESTQDR	95.0	29.8	25.0	1461.70	0	3	0	0	2	170	183
Ras-related protein Rab-7a	RAB7A_HUMAN	RAB7A	23.47	100.0	3	3	21	15.00	VIILGDSGVGK	95.0	46.8	25.0	1057.63	0	5	0	0	2	11	21
									ATIGADFLTK	95.0	65.6	25.0	1036.57	0	8	0	0	2	39	48
									DEFLIQASPR	95.0	59.5	25.0	1175.61	0	8	0	0	2	104	113
Receptor-type tyrosine-protein phosphatase F	PTPRF_HUMAN	PTPRF	212.86	100.0	11	12	46	6.66	DFLPVDPATSNGR	95.0	43.7	25.0	1388.68	0	7	0	0	2	171	183
									YSAPANLYVR	95.0	66.9	25.0	1153.60	0	6	0	0	2	217	226
									NVLELSNVVR	95.0	53.8	25.0	1142.65	0	5	0	0	2	283	292
									AAGTEGPFQEVDGVATTR	95.0	99.1	25.0	1805.87	0	2	0	0	2	356	373
									VLAVNSIGR	95.0	59.1	25.0	928.56	0	5	0	0	2	389	397
									VYYTPDSR	95.0	26.9	25.0	1000.47	0	1	0	0	2	449	456
									SDMGVGVFTPTIEAR	95.0	75.5	25.0	1595.77	0	8	0	0	2	586	600
									HVVDGISR	95.0	26.8	25.0	882.48	0	1	0	0	2	657	664
									AHTDVGPGPESSPVLVR	95.0	76.6	25.0	1717.89	0	3	4	0	2	686	702
									IISYTVVFR	95.0	35.9	25.0	1097.64	0	3	0	0	2	948	956
									TMPVEQVFAK	94.7	26.5	25.0	1165.59	0	1	0	0	2	1007	1016
Receptor-type tyrosine-protein phosphatase kappa	PTPRK_HUMAN	PTPRK	162.09	100.0	5	5	11	3.34	GLNPGTLNILVR	95.0	64.1	25.0	1266.75	0	2	0	0	2	117	128
									SPHFLR	95.0	32.5	25.0	756.42	0	1	0	0	2	195	200
									GSGVSNFAQLIVR	95.0	51.7	25.0	1347.74	0	3	0	0	2	277	289
									IAEIQAR	95.0	27.7	25.0	800.46	0	1	0	0	2	398	404
									SLQGTSFENK	95.0	36.0	25.0	1110.54	0	4	0	0	2	497	506
Regulator of chromosome condensation	RCC1_HUMAN	RCC1	44.95	100.0	3	3	12	8.55	DTSVEGSEMVPGK	95.0	33.0	25.0	1351.60	0	1	0	0	2	102	114
									SMVPVQVQLDVPVVK	95.0	90.6	25.0	1653.92	0	6	0	0	2	162	176
									VPELFANR	95.0	53.1	25.0	945.52	0	5	0	0	2	207	214
Regulator of microtubule dynamics protein 1	RMD1_HUMAN	FAM82B	35.79	100.0	3	3	5	9.87	MLFATPPSSTYEK	95.0	38.7	25.0	1487.71	0	2	0	0	2	231	243
									AEQVDPNFYSK	95.0	42.6	25.0	1297.61	0	1	0	0	2	251	261
									NLLLLGK	95.0	35.2	25.0	770.51	0	2	0	0	2	262	268
Renin receptor	RENR_HUMAN	ATP6AP2	38.99	100.0	3	3	5	6.86	SPGSVVFR	95.0	35.3	25.0	848.46	0	1	0	0	2	24	31
									ILVDALQK	95.0	29.7	25.0	899.56	0	1	0	0	2	239	246
									SFDTSLIR	95.0	43.8	25.0	938.49	0	3	0	0	2	268	275
Retinol-binding protein 1	RET1_HUMAN	RBP1	15.83	100.0	8	10	36	44.40	ALDVNVALR	95.0	52.1	25.0	970.57	0	2	0	0	2	23	31
									KIANLLKPDK	95.0	44.1	25.0	1139.71	0	2	2	0	2	32	41
									IANLLKPDK	95.0	57.6	25.0	1011.62	0	5	0	0	2	33	41
									EIVQDGDHMIIR	95.0	66.4	25.0	1441.71	0	6	3	0	2	42	53
									TLSTFR	95.0	31.1	25.0	724.40	0	1	0	0	2	54	59
									NYIMDFQVGK	95.0	51.2	25.0	1230.58	0	5	0	0	2	60	69
									EFEEDLTGIDDR	95.0	77.4	25.0	1438.63	0	6	0	0	2	70	81
									EFEEDLTGIDDRK	95.0	75.8	25.0	1566.73	0	4	0	0	2	70	82
Rho GDP-dissociation inhibitor 1	GDIR1_HUMAN	ARHGDIA	23.19	100.0	3	4	17	14.70	SIQEIQELDKDDESLR	95.0	94.1	25.0	1917.94	0	4	0	0	2	34	49
									IDKTDYMVGSYGPR	95.0	81.7	25.0	1617.76	0	5	6	0	2	139	152
									TDYMVGSYGPR	95.0	47.9	25.0	1261.55	0	2	0	0	2	142	152
Rho GDP-dissociation inhibitor 2	GDIR2_HUMAN	ARHGDIB	22.97	100.0	6	7	26	26.40	APEPHVEEDDDDELDSK	95.0	43.5	25.0	1939.80	0	0	2	0	2	5	21
									KTLLGDGPVVTDPK	95.0	35.3	25.0	1439.81	0	2	1	0	2	50	63

									TLLGDGPVVTDPK	95.0	64.4	25.0	1311.72	0	8	0	0	2	51	63
									APNVVVTR	95.0	46.2	25.0	855.50	0	11	0	0	2	64	71
									DIVSGLK	95.0	34.5	25.0	731.43	0	1	0	0	2	118	124
									YVQHTYR	95.0	27.1	25.0	966.48	0	1	0	0	2	125	131
Rho GTPase-activating protein 1	RHG01_HUMAN	ARHGAP1	50.42	100.0	4	4	12	10.00	SSSPELVTHLK	95.0	49.2	25.0	1197.65	0	4	0	0	2	49	59
									HQIVEVAGDDK	95.0	29.9	25.0	1210.61	0	2	0	0	2	70	80
									NPEQEPIPIVLR	95.0	56.2	25.0	1404.78	0	4	0	0	2	253	264
									AINPINTFTK	95.0	41.4	25.0	1118.62	0	2	0	0	2	412	421
Rho guanine nucleotide exchange factor 1	ARHG1_HUMAN	ARHGEF1	102.42	100.0	3	3	6	5.04	FVQEVVQSQQVAVGR	95.0	30.2	25.0	1673.90	0	0	2	0	2	138	152
									LLMHLEEMQHTISTDEEK	95.0	23.9	25.0	2216.02	0	0	2	0	2	197	214
									SAAVVNAIGLYMR	95.0	68.9	25.0	1380.73	0	2	0	0	2	215	227
Rho guanine nucleotide exchange factor 16	ARHGG_HUMAN	ARHGEF16	80.09	100.0	3	3	6	4.37	SLPLISASR	94.9	26.7	25.0	943.56	0	1	0	0	2	492	500
									IEPSELPLPGGGNR	95.0	60.4	25.0	1435.75	0	4	0	0	2	562	575
									VAVEGNVR	95.0	28.6	25.0	843.47	0	1	0	0	2	691	698
Rho-associated protein kinase 1	ROCK1_HUMAN	ROCK1	158.16	100.0	5	5	8	4.51	NIDNFLSR	95.0	32.3	25.0	978.50	0	1	0	0	2	51	58
									GAFGEVQLVR	95.0	44.2	25.0	1075.59	0	1	0	0	2	85	94
									NSLTFPDDNDISK	95.0	43.4	25.0	1465.68	0	2	0	0	2	295	307
									SISQLESLNR	95.0	58.6	25.0	1146.61	0	2	0	0	2	574	583
									TQAFEADNLK	95.0	43.7	25.0	1136.56	0	2	0	0	2	792	801
									QEINTLLEAK	95.0	35.2	25.0	1158.64	0	1	0	0	2	809	818
Rho-associated protein kinase 2	ROCK2_HUMAN	ROCK2	160.89	100.0	12	12	17	8.86	MPGAPETAPGDGAGASR	95.0	33.4	25.0	1557.70	0	1	0	0	2	10	26
									NIDNFLNR	95.0	37.9	25.0	1005.51	0	2	0	0	2	67	74
									GAFGEVQLVR	95.0	44.2	25.0	1075.59	0	1	0	0	2	101	110
									SNMEIDMTYQLK	95.0	64.3	25.0	1504.67	0	2	0	0	2	684	695
									IYESIEEAK	95.0	27.4	25.0	1081.54	0	1	0	0	2	721	729
									KLLEER	95.0	32.1	25.0	787.47	0	1	0	0	2	739	744
									VENLLLEAEK	95.0	37.0	25.0	1157.64	0	1	0	0	2	750	759
									VENLLLEAEKR	95.0	25.3	25.0	1313.74	0	0	2	0	2	750	760
									SIAEEQYSDLEK	95.0	80.2	25.0	1411.66	0	1	0	0	2	930	941
									DATIASLEETNR	95.0	61.5	25.0	1319.64	0	2	0	0	2	965	976
									LKDEEISAAAIK	95.0	41.7	25.0	1287.72	0	2	0	0	2	1006	1017
									NLLLLANSTEEQQK	95.0	80.7	25.0	1600.85	0	1	0	0	2	1326	1339
Rho-related GTP-binding protein RhoG	RHOG_HUMAN	RHOG	21.29	100.0	3	3	6	14.70	LKEQGQAPITPQQGQALAK	95.0	35.8	25.0	2006.10	0	0	2	0	2	129	147
									EQGQAPITPQQGQALAK	95.0	43.6	25.0	1764.92	0	2	0	0	2	131	147
									AVLNPTPIK	95.0	51.9	25.0	952.58	0	2	0	0	2	175	183
Ribonuclease inhibitor	RINI_HUMAN	RNH1	49.96	100.0	3	3	54	8.89	VNPALAELNLR	95.0	55.4	25.0	1209.70	0	16	0	0	2	54	64
									ELTVSNNDINEAGVR	95.0	####	25.0	1630.80	0	7	0	0	2	174	188
									ELSLAGNELGDEGAR	95.0	####	25.0	1530.74	0	31	0	0	2	288	302
Ribose-phosphate pyrophosphokinase 2	PRPS2_HUMAN	PRPS2	34.75	100.0	3	3	10	12.30	PNIVLFSGSSHQDLSQR	95.0	41.8	25.0	1884.96	0	0	2	0	1	2	18
									LGLELGK	95.0	48.4	25.0	729.45	0	6	0	0	2	23	29
									FSNQETSVEIGESVR	95.0	####	25.0	1681.80	0	2	0	0	2	35	49
Ribosome maturation protein SBDS	SBDS_HUMAN	SBDS	28.75	100.0	8	9	25	28.40	LTNVAVVR	95.0	38.3	25.0	871.54	0	2	0	0	2	12	19
									GEVQVSDKER	95.0	51.1	25.0	1146.58	0	7	2	0	2	91	100
									DIATIVADK	95.0	36.1	25.0	945.53	0	3	0	0	2	110	118
									QQALEVIK	95.0	38.9	25.0	928.55	0	2	0	0	2	152	159
									FILPVNEGKK	94.6	19.0	25.0	1144.67	0	0	1	0	2	176	185
									EIDELIK	95.0	27.0	25.0	859.48	0	1	0	0	2	219	225
									GSLEVLNLK	95.0	49.2	25.0	972.57	0	4	0	0	2	232	240
									DVEEGDEKFE	95.0	33.6	25.0	1196.50	0	3	0	0	2	241	250
Ribosome-binding protein 1	RRBP1_HUMAN	RRBP1	152.45	100.0	6	6	16	4.96	DALNQATSQVESK	95.0	79.3	25.0	1390.68	0	1	0	0	2	807	819
									LQSSEAEVR	95.0	30.2	25.0	1018.52	0	1	0	0	2	922	930

									SIEALLEAGQAR	95.0	45.7	25.0	1257.68	0	7	0	0	2	959	970
									SILAETEGMLR	95.0	57.2	25.0	1235.63	0	2	0	0	2	1133	1143
									HLEEIVEK	95.0	30.6	25.0	996.54	0	2	0	0	2	1176	1183
									TAGPLESSETEEASQLK	95.0	####	25.0	1776.85	0	3	0	0	2	1334	1350
Ribosome-recycling factor, mitochondrial	RRFM_HUMAN	MRRF	29.26	100.0	4	4	11	20.60	LALNQISQISMK	95.0	65.7	25.0	1361.75	0	5	0	0	2	128	139
									ESGMNLNPEVEGTLIR	95.0	75.4	25.0	1774.86	0	2	0	0	2	164	179
									SKDTVSEDTIR	95.0	41.4	25.0	1250.62	0	2	0	0	2	222	232
									QISQMADDTVAELDR	95.0	####	25.0	1707.79	0	2	0	0	2	237	251
RNA polymerase-associated protein RTF1 homolog	RTF1_HUMAN	RTF1	76.56	100.0	3	3	9	5.22	SQPVSLPEELNR	95.0	35.4	25.0	1368.71	0	3	0	0	2	310	321
									VAEITGVVETAK	95.0	61.5	25.0	1216.68	0	2	0	0	2	362	373
									FNDQDIEEIVK	95.0	76.2	25.0	1349.66	0	4	0	0	2	447	457
RNA-binding protein 12	RBM12_HUMAN	RBM12	97.38	100.0	3	3	6	3.33	LQGLPIVAGTMDIR	95.0	44.0	25.0	1499.83	0	2	0	0	2	7	20
									HVIDFFK	95.0	45.3	25.0	905.49	0	3	0	0	2	445	451
									ATGEGFVEFR	95.0	30.0	25.0	1112.54	0	1	0	0	2	470	479
RNA-binding protein FUS	FUS_HUMAN	FUS	53.41	100.0	3	3	12	5.32	TGQPMINLYTDR	95.0	32.3	25.0	1424.68	0	4	0	0	2	317	328
									LKGEATVSFDDPPSAK	95.0	41.3	25.0	1661.84	0	0	5	0	2	333	348
									GEATVSFDDPPSAK	95.0	68.5	25.0	1420.66	0	3	0	0	2	335	348
RNA-binding protein Raly	RALY_HUMAN	RALY	32.45	100.0	4	4	20	13.70	VFIGNLNTALVK	95.0	81.5	25.0	1288.76	0	10	0	0	2	23	34
									KSDVETIFSK	95.0	48.3	25.0	1153.61	0	5	0	0	2	35	44
									GYAFVQYSNER	95.0	56.3	25.0	1333.62	0	2	0	0	2	56	66
									SNIDALLSR	95.0	54.2	25.0	988.54	0	3	0	0	2	199	207
RuvB-like 1	RUVB1_HUMAN	RUVBL1	50.21	100.0	6	6	19	16.40	QAASGLVGQENAR	95.0	57.2	25.0	1300.66	0	2	0	0	2	34	46
									TALALAIAQELGSK	95.0	79.4	25.0	1385.80	0	6	0	0	2	77	90
									KTEVLMENFR	95.0	38.5	25.0	1282.65	0	2	0	0	2	108	117
									LDPSIFESLQK	95.0	45.1	25.0	1276.68	0	6	0	0	2	172	182
									VEAGDVIYIEANSGAVK	95.0	####	25.0	1734.89	0	2	0	0	2	185	201
									TMLYTPQEMK	95.0	31.5	25.0	1273.58	0	1	0	0	2	363	372
RuvB-like 2	RUVB2_HUMAN	RUVBL2	51.14	100.0	10	11	29	25.30	GLGLDDALEPR	95.0	66.8	25.0	1155.60	0	2	0	0	2	30	40
									AAGVVLEMIR	95.0	65.9	25.0	1074.60	0	2	0	0	2	55	64
									AVLIAGQPGTGK	95.0	59.6	25.0	1111.65	0	4	0	0	2	72	83
									TEALTQAFR	95.0	28.0	25.0	1036.54	0	1	0	0	2	116	124
									TTEMETIYDLGTK	95.0	78.9	25.0	1517.70	0	2	0	0	2	165	177
									DKVQAGDVITIDK	95.0	53.0	25.0	1401.76	0	3	0	0	2	185	197
									ALESDMAPVLIMATNR	95.0	####	25.0	1763.87	0	4	2	0	2	315	330
									LLIVSTTPYSEK	95.0	61.6	25.0	1350.75	0	3	0	0	2	354	365
									GTEVQVDDIKR	95.0	31.1	25.0	1259.66	0	1	0	0	2	418	428
									VYSLFLDESR	95.0	60.8	25.0	1228.62	0	5	0	0	2	429	438
S-adenosylmethionine synthase isoform type-2	METK2_HUMAN	MAT2A	43.64	100.0	7	7	31	19.20	TQVTVQYMQDR	95.0	64.1	25.0	1384.65	0	7	0	0	2	182	192
									GAVLPIR	95.0	40.7	25.0	725.47	0	3	0	0	2	193	199
									YLDEDTIYHLQPSGR	95.0	46.6	25.0	1806.87	0	0	2	0	2	235	249
									FVIGGPQGDAGLTGR	95.0	####	25.0	1444.75	0	13	0	0	2	250	264
									ELLEIVKK	95.0	46.5	25.0	971.61	0	2	0	0	2	344	351
									NFDLRPGVIVR	95.0	25.5	25.0	1285.74	0	0	3	0	2	352	362
									TAAYGHFGR	95.0	27.4	25.0	979.47	0	1	0	0	2	374	382
Scavenger mRNA-decapping enzyme DcpS	DCPS_HUMAN	DCPS	38.59	100.0	3	3	5	11.60	VNEASGDGDGEDAVVILEK	95.0	####	25.0	1916.91	0	2	0	0	2	68	86
									NILHQGQEAILQR	95.0	62.4	25.0	1519.83	0	1	0	0	2	243	255
									TLTFALR	95.0	36.1	25.0	821.49	0	2	0	0	2	316	322
Sec1 family domain-containing protein 1	SCFD1_HUMAN	SCFD1	72.36	100.0	4	4	14	7.48	MLNFNVPHIK	95.0	36.2	25.0	1228.65	0	2	0	0	2	26	35
									GTAAEMVAVK	95.0	47.5	25.0	992.51	0	2	0	0	2	215	224
									LTSAVSSLPELLEK	95.0	82.1	25.0	1486.84	0	6	0	0	2	382	395
									VMNTGSQFVMEGVK	95.0	81.0	25.0	1558.72	0	4	0	0	2	523	536

Semaphorin-3A	SEM3A_HUMAN	SEMA3A	88.87	100.0	4	4	7	4.54	DFAIFR	95.0	30.4	25.0	768.40	0	3	0	0	2	198	203
									VFLGPYAHR	95.0	22.9	25.0	1059.57	0	0	2	0	2	351	359
									TFGGFDSTK	95.0	27.2	25.0	959.45	0	1	0	0	2	385	393
									DLPDDVITFAR	95.0	27.9	25.0	1261.64	0	1	0	0	2	394	404
Semaphorin-3C	SEM3C_HUMAN	SEMA3C	85.19	100.0	5	5	15	7.46	ILLMDEDQDR	95.0	37.4	25.0	1263.59	0	1	0	0	2	56	65
									SEDQVFMIDSK	95.0	68.1	25.0	1314.59	0	3	0	0	2	148	158
									NHPLMYNSIYPIHK	95.0	38.7	25.0	1742.87	0	0	5	0	2	403	416
									YHVLFLGTDR	95.0	41.9	25.0	1220.64	0	2	0	0	2	444	453
									IIATSQGLLIR	95.0	64.6	25.0	1184.74	0	4	0	0	2	621	631
Septin-11	SEP11_HUMAN	SEPT11	49.38	100.0	3	3	42	6.76	SYELQESNVR	95.0	40.8	25.0	1224.59	0	2	0	0	2	84	93
									VNIIPIIAK	95.0	39.9	25.0	980.65	0	38	0	0	2	176	184
									RNEFLGELQK	95.0	44.3	25.0	1233.66	0	2	0	0	2	327	336
Septin-2	SEPT2_HUMAN	SEPT2	41.47	100.0	3	3	23	9.42	TVQIEASTVEIEER	95.0	99.2	25.0	1603.82	0	6	0	0	2	78	91
									VNIVPVIAK	95.0	43.5	25.0	952.62	0	11	0	0	2	175	183
									ILDEIEEHNIK	95.0	63.1	25.0	1352.71	0	6	0	0	2	199	209
Septin-7	SEPT7_HUMAN	SEPT7	50.66	100.0	6	7	16	18.10	FEDYLNAESR	95.0	66.2	25.0	1243.56	0	4	0	0	2	138	147
									VNIIPLIAK	95.0	39.9	25.0	980.65	0	38	0	0	2	187	195
									IYEFPETDDEEENK	95.0	67.6	25.0	1757.74	0	4	0	0	2	222	235
									DVTNNVHYENYR	95.0	73.5	25.0	1523.69	0	2	0	0	2	299	310
									LAAVTYNGVDNNK	95.0	31.8	25.0	1378.70	0	1	0	0	2	314	326
									SPLAQMEEERR	95.0	20.7	25.0	1361.65	0	0	1	0	2	334	344
									LKDSEAELQR	95.0	42.2	25.0	1188.62	0	2	2	0	2	372	381
Septin-8	SEPT8_HUMAN	SEPT8	55.74	99.5	2	2	4	5.80	VNIIPIIAK	95.0	39.9	25.0	980.65	0	38	0	0	2	179	187
									EFLSELQR	95.0	40.3	25.0	1021.53	0	2	0	0	2	332	339
									ELEEETNAFNR	95.0	46.9	25.0	1351.61	0	2	0	0	2	390	400
Serine hydroxymethyltransferase, cytosolic	GLYC_HUMAN	SHMT1	53.07	100.0	4	4	8	8.49	DSDVEVYNIIK	95.0	39.6	25.0	1294.65	0	1	0	0	2	28	38
									YSEGYPGQR	95.0	31.3	25.0	1056.47	0	2	0	0	2	73	81
									ALSEALTELGYK	95.0	65.5	25.0	1294.69	0	3	0	0	2	337	348
									YQAAVQALR	95.0	36.5	25.0	1019.56	0	2	0	0	2	457	465
Serine hydroxymethyltransferase, mitochondrial	GLYM_HUMAN	SHMT2	55.98	100.0	7	7	15	15.30	YSEGYPGKR	95.0	40.7	25.0	1056.51	0	2	0	0	2	96	104
									TGLIDYNQLALTAR	95.0	64.1	25.0	1548.84	0	2	0	0	2	201	214
									AHLLADMAHISGLVAAK	95.0	54.8	25.0	1733.94	0	1	0	0	2	246	262
									SGLIFYR	95.0	44.6	25.0	855.47	0	4	0	0	2	287	293
									VLELVSITANK	95.0	83.1	25.0	1186.70	0	2	0	0	2	399	409
									LGAPALTSR	95.0	42.3	25.0	885.52	0	2	0	0	2	426	434
									AFPMPGFDEH	95.0	37.7	25.0	1163.48	0	2	0	0	2	495	504
Serine/threonine-protein kinase 24	STK24_HUMAN	STK24	49.29	100.0	5	5	8	14.20	AANVLLSEHGEVK	95.0	27.3	25.0	1366.73	0	0	2	0	2	159	171
									LADFGVAGQLTDTQIKR	95.0	30.0	25.0	1832.99	0	0	1	0	2	172	188
									VLFLIPK	95.0	55.0	25.0	829.55	0	3	0	0	2	239	245
									NNPPTLEGNYSKPLK	95.0	35.2	25.0	1671.87	0	1	0	0	2	246	260
									KTSYLTELIDR	95.0	65.5	25.0	1338.73	0	1	0	0	2	292	302
Serine/threonine-protein kinase 3	STK3_HUMAN	STK3	56.28	100.0	5	5	11	14.70	QPEEVFDVLEK	95.0	43.5	25.0	1332.67	0	3	0	0	2	22	32
									QVPVESDLQEIIK	95.0	29.9	25.0	1497.82	0	3	0	0	2	57	69
									AGNILLNTEGHAK	95.0	42.4	25.0	1337.72	0	2	0	0	2	149	161
									LADFGVAGQLTDTMAK	95.0	96.8	25.0	1653.82	0	1	0	0	2	162	177
									ATATQLLQHPFIK	95.0	24.5	25.0	1467.83	0	0	2	0	2	267	279
									EIEELR	95.0	30.7	25.0	788.41	0	2	0	0	2	462	467
Serine/threonine-protein kinase Nek9	NEK9_HUMAN	NEK9	107.15	100.0	3	3	11	4.60	AGGGAAEQEELHYIPIR	95.0	32.2	25.0	1810.91	0	0	2	0	2	40	56
									SSTVTEAPIAVVTSR	95.0	79.7	25.0	1517.82	0	2	0	0	2	331	345
									LGINLLGGPLGGK	95.0	51.4	25.0	1208.74	0	7	0	0	2	638	650
Serine/threonine-protein	OXSR1_HUMAN	OXSR1	58.01	100.0	4	4	9	8.54	LLSGGSVLDIIK	95.0	33.6	25.0	1214.74	0	1	0	0	2	94	105

kinase OSR1									SGVLDESTIATILR	95.0	50.5	25.0	1474.81	0	2	0	0	2	115	128
									EVLEGLEYLHK	95.0	44.5	25.0	1329.71	0	1	0	0	2	129	139
									IPISLVLR	95.0	37.2	25.0	910.61	0	5	0	0	2	432	439
Serine/threonine-protein kinase PAK 1	PAK1_HUMAN	PAK1	60.63	100.0	3	3	6	7.34	SVIEPLPVTPTR	95.0	46.9	25.0	1308.75	0	2	0	0	2	204	215
									KELIINEILVMR	95.0	24.2	25.0	1486.87	0	0	1	0	2	309	320
									IAKPLSSLTPLIAAAK	95.0	28.7	25.0	1593.99	0	0	3	0	2	523	538
Serine/threonine-protein kinase PAK 2	PAK2_HUMAN	PAK2	58.03	100.0	3	4	13	7.82	KELIINEILVMK	95.0	70.5	25.0	1458.86	0	8	1	0	2	288	299
									SDNVLLGMEGSVK	95.0	71.1	25.0	1364.67	0	3	0	0	2	371	383
									LAKPLSSLTPLIMAAK	95.0	27.1	25.0	1669.99	0	1	0	0	2	502	517
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha	2ABA_HUMAN	PPP2R2A	51.68	100.0	3	3	7	7.83	NAAQFLLSTNDK	95.0	66.7	25.0	1321.67	0	3	0	0	2	106	117
									LFEEPEDPSNR	95.0	53.6	25.0	1332.61	0	3	0	0	2	268	278
									DEISVDSLDFNK	95.0	44.4	25.0	1381.65	0	1	0	0	2	406	417
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	2A5E_HUMAN	PPP2R5E	54.68	100.0	4	5	14	10.30	SQGKPIELTPLPLLK	95.0	30.1	25.0	1633.99	0	1	2	0	2	38	52
									DVPSSEQPELFLK	95.0	36.8	25.0	1488.76	0	4	0	0	2	53	65
									FLESQEFQPSIAK	95.0	85.3	25.0	1523.77	0	5	0	0	2	161	173
									IQEPLFK	95.0	36.0	25.0	874.50	0	2	0	0	2	340	346
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	2AAA_HUMAN	PPP2R1A	65.29	100.0	7	8	61	12.90	LSTIALALGVER	95.0	53.1	25.0	1242.74	0	5	0	0	2	35	46
									VLELDNVK	95.0	50.8	25.0	929.53	0	2	0	0	2	195	202
									TDLVPAFQNLMK	95.0	60.2	25.0	1392.72	0	18	0	0	2	281	292
									ELVSDANQHVK	95.0	36.2	25.0	1239.63	0	7	0	0	2	332	342
									VLAMSGDPNYLHR	95.0	65.6	25.0	1488.73	0	4	6	0	2	486	498
									MAGDPVANVR	95.0	72.4	25.0	1045.51	0	6	0	0	2	528	537
									LTQDQDVDVK	95.0	51.6	25.0	1160.58	0	13	0	0	2	567	576
Serine/threonine-protein phosphatase 2A activator	PTPA_HUMAN	PPP2R4	40.65	100.0	6	7	29	16.50	KEIHTVPDMGK	95.0	36.0	25.0	1270.65	0	1	2	0	2	28	38
									LVALLNTLDR	95.0	75.2	25.0	1127.68	0	15	0	0	2	112	121
									VDDQIAIVFK	95.0	58.6	25.0	1147.64	0	4	0	0	2	209	218
									VNQGLIR	94.7	26.5	25.0	799.48	0	1	0	0	2	322	328
									FPVIQHFK	95.0	46.5	25.0	1015.57	0	3	0	0	2	338	345
									FGSLLPIHPVTSG	95.0	53.0	25.0	1324.73	0	3	0	0	2	346	358
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	PP2BA_HUMAN	PPP3CA	58.67	100.0	10	10	40	19.60	EVFDNDGKPR	95.0	34.5	25.0	1176.56	0	4	0	0	2	33	42
									LEESVALR	95.0	37.0	25.0	916.51	0	3	0	0	2	56	63
									IITEGASILR	95.0	55.1	25.0	1072.64	0	4	0	0	2	64	73
									LFEVGGSPANTR	95.0	79.3	25.0	1247.64	0	7	0	0	2	101	112
									TLFLLR	95.0	31.9	25.0	762.49	0	2	0	0	2	143	148
									HLTEYFTFK	95.0	45.4	25.0	1185.59	0	3	0	0	2	155	163
									VFSVLR	95.0	34.0	25.0	720.44	0	2	0	0	2	409	414
									EESESVLTLK	95.0	35.6	25.0	1134.59	0	2	0	0	2	415	424
									GLTPTGMLPSGVLSGGK	95.0	80.0	25.0	1587.84	0	9	0	0	2	425	441
									DAMPSDANLNSINK	95.0	68.4	25.0	1505.69	0	4	0	0	2	488	501
Serine/threonine-protein phosphatase 4 regulatory subunit 3A	P4R3A_HUMAN	SMEK1	95.35	100.0	6	6	13	7.92	AESDGSLLLESK	95.0	78.0	25.0	1248.63	0	2	0	0	2	44	55
									EVIPISDPELK	95.0	48.9	25.0	1239.68	0	3	0	0	2	248	258
									TLVDPENMLATANK	95.0	76.5	25.0	1532.76	0	4	0	0	2	454	467
									VLVLMASK	95.0	30.0	25.0	876.52	0	1	0	0	2	540	547
									SFLFEPVVK	95.0	27.6	25.0	1065.60	0	1	0	0	2	577	585
									ALEDVDYVQTFK	95.0	71.5	25.0	1427.71	0	2	0	0	2	627	638
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6_HUMAN	PPP6C	35.13	100.0	3	4	7	11.50	APLDLDKYVEIAR	95.0	40.9	25.0	1502.82	0	1	0	0	1	2	14
									VTNEFVHINNLK	95.0	59.8	25.0	1427.76	0	4	1	0	2	220	231
									AHQLVHEGYK	95.0	30.4	25.0	1181.61	0	1	0	0	2	236	245
Serine/threonine-protein phosphatase 6 regulatory subunit 3	SAPS3_HUMAN	SAPS3	97.65	100.0	5	6	18	5.73	LIEFLLK	95.0	28.8	25.0	875.56	0	1	0	0	2	44	50
									VLSILISR	95.0	43.0	25.0	900.59	0	4	0	0	2	127	134
									KPEQIVDFLK	95.0	44.8	25.0	1216.69	0	3	0	0	2	135	144

									HIGTSAIMDLLLR	95.0	50.2	25.0	1455.80	0	2	2	0	2	156	168
									GPNSALVQQLIK	95.0	72.3	25.0	1267.74	0	6	0	0	2	475	486
Serine-threonine kinase receptor-associated protein	STRAP_HUMAN	STRAP	38.42	100.0	5	6	17	18.30	AATAAADFTAK	95.0	54.6	25.0	1037.53	0	2	0	0	2	74	84
									IYDLNKPEAEPK	95.0	30.0	25.0	1416.74	0	1	0	0	2	126	137
									SFEAPATINSASLHPEK	95.0	89.4	25.0	1798.90	0	2	3	0	2	219	235
									EFLVAGGEDFK	95.0	48.2	25.0	1211.59	0	6	0	0	2	236	246
									YDYNSGEELESYK	95.0	78.7	25.0	1596.67	0	3	0	0	2	250	262
Serpin B13	SPB13_HUMAN	SERPINB13	44.26	100.0	3	4	8	9.97	GATASQLEEVFHSEK	95.0	75.1	25.0	1632.79	0	2	0	0	2	47	61
									LTNDYELNITNR	95.0	58.8	25.0	1465.73	0	2	0	0	2	96	107
									HNESNSILFFGR	95.0	74.2	25.0	1420.70	0	3	1	0	2	376	387
Serpin B4	SPB4_HUMAN	SERPINB4	44.84	100.0	4	4	6	10.30	VLHFDQVTENTTEK	95.0	41.8	25.0	1660.82	0	0	2	0	2	56	69
									STDAYELK	95.0	43.5	25.0	926.45	0	2	0	0	2	95	102
									LEEKLTAEK	95.0	20.1	25.0	1060.59	0	0	1	0	2	257	265
									TNSILFYGR	94.8	26.6	25.0	1070.56	0	1	0	0	2	378	386
Serpin B5	SPB5_HUMAN	SERPINB5	42.08	100.0	11	13	117	34.70	GDTANEIGQVLHFENVK	95.0	64.4	25.0	1870.93	0	4	0	0	2	48	64
									DVPFGFQTVTSDVNK	95.0	95.3	25.0	1653.81	0	5	0	0	2	65	79
									LSSFYSLK	95.0	42.8	25.0	944.51	0	2	0	0	2	80	87
									SLNLSTEFISSTK	95.0	79.8	25.0	1426.74	0	16	0	0	2	97	109
									ELETVDFKDK	95.0	32.7	25.0	1223.62	0	2	0	0	2	115	124
									GQINNSIK	95.0	40.8	25.0	873.48	0	2	0	0	2	130	137
									ILVVNAAYFVGK	95.0	69.5	25.0	1293.76	0	2	0	0	2	159	170
									IIELPFQNK	95.0	49.1	25.0	1101.63	0	54	0	0	2	216	224
									HLSMFILLPK	95.0	37.0	25.0	1214.70	0	10	2	0	2	225	234
									DVEDESTGLEK	95.0	62.1	25.0	1221.55	0	10	0	0	2	235	245
									HIFSEDTSDFSGMSETK	95.0	82.9	25.0	1933.81	0	4	4	0	2	295	311
Serpin B6	SPB6_HUMAN	SERPINB6	42.60	100.0	10	11	34	35.40	GNTAAQMAQILSFNK	95.0	93.7	25.0	1609.80	0	4	0	0	2	47	61
									SGGGGDIHQGFQSLLTEVNK	95.0	90.2	25.0	2044.01	0	2	2	0	2	62	81
									TGTQYLLR	95.0	62.8	25.0	951.53	0	3	0	0	2	82	89
									IAELLSPGSVDPLTR	95.0	55.1	25.0	1567.87	0	6	0	0	2	146	160
									LVLVNAVYFR	95.0	39.9	25.0	1193.70	0	2	0	0	2	161	170
									NEEKPVQMMFK	95.0	31.1	25.0	1412.66	0	2	0	0	2	192	202
									LDMMDEEEVEVSLPR	95.0	57.2	25.0	1823.80	0	1	0	0	2	259	273
									LEESYDMESVLR	95.0	48.4	25.0	1486.67	0	2	0	0	2	276	287
									NLGMTDAFELGK	95.0	59.1	25.0	1311.63	0	8	0	0	2	288	299
									ADFSGMSQTDLSLSK	95.0	####	25.0	1602.73	0	2	0	0	2	300	314
Serpin B8	SPB8_HUMAN	SERPINB8	42.75	99.9	2	2	4	11.80	TGTQYLLR	95.0	62.8	25.0	951.53	0	3	0	0	2	80	87
									ISEVLDAGTVDPLTK	95.0	####	25.0	1557.84	0	2	0	0	2	144	158
									LVLVNAIYFK	95.0	29.1	25.0	1179.71	0	1	0	0	2	159	168
									LGMIDAFDEAK	95.0	41.7	25.0	1225.58	0	2	0	0	2	286	296
Serpin B9	SPB9_HUMAN	SERPINB9	42.39	100.0	6	6	12	23.10	AFQSLLTEVNK	95.0	74.4	25.0	1249.68	0	3	0	0	2	69	79
									IEELLPGSSIDAETR	95.0	91.7	25.0	1629.83	0	1	0	0	2	144	158
									LVLVNAIYFK	95.0	29.1	25.0	1179.71	0	1	0	0	2	159	168
									INQEEQRPVQMMYQEATFK	95.0	23.1	25.0	2402.11	0	0	2	0	2	187	205
									AQLLELPYAR	95.0	46.0	25.0	1173.66	0	2	0	0	2	214	223
									STEVEVLLPK	95.0	44.1	25.0	1114.64	0	2	0	0	2	262	271
									HLGIVDAFQQGK	95.0	24.6	25.0	1312.70	0	0	2	0	2	286	297
Serpin H1	SERPH_HUMAN	SERPINH1	46.42	100.0	12	16	161	25.40	KPAAAAAPGTAEK	95.0	58.7	25.0	1182.65	0	4	0	0	2	23	35
									AVLSAEQLR	95.0	48.2	25.0	986.56	0	5	0	0	2	95	103
									DEEVHAGLGELLR	95.0	82.6	25.0	1437.73	0	5	2	0	2	104	116
									TGLYNYYDDEK	95.0	63.8	25.0	1380.60	0	2	0	0	2	240	250
									TGLYNYYDDEKEK	95.0	75.2	25.0	1637.73	0	17	5	0	2	240	252

									LQIVEMPLAHK	95.0	56.3	25.0	1294.72	0	17	12	0	2	253	263
									KAVAISLPK	95.0	43.4	25.0	926.60	0	9	0	0	2	300	308
									AVAISLPK	95.0	45.3	25.0	798.51	0	8	0	0	2	301	308
									GVVEVTHDLQK	95.0	61.4	25.0	1224.66	0	21	0	0	2	309	319
									HLAGLGLTEAIDK	95.0	84.9	25.0	1337.74	0	18	5	0	2	320	332
									HLAGLGLTEAIDKNK	95.0	62.1	25.0	1579.88	0	0	3	0	2	320	334
									DTQSGSLLFIGR	95.0	76.5	25.0	1293.68	0	28	0	0	2	394	405
Serum albumin	ALBU_HUMAN	ALB	69.35	100.0	5	6	153	6.08	YLYEIAR	95.0	42.0	25.0	927.49	0	55	0	0	2	162	168
									LVTDLTK	95.0	26.7	25.0	789.47	0	1	0	0	2	258	264
									FQNALLVR	95.0	40.8	25.0	960.56	0	2	0	0	2	427	434
									KVPQVSTPTLVEVSR	95.0	####	25.0	1639.94	0	54	20	0	2	438	452
									VPQVSTPTLVEVSR	95.0	84.1	25.0	1511.84	0	21	0	0	2	439	452
Seryl-tRNA synthetase, cytoplasmic	SYSC_HUMAN	SARS	58.76	100.0	4	5	23	8.56	VLDLDLFR	95.0	55.7	25.0	990.56	0	11	0	0	1	2	9
									FKDPGLVDQLVK	95.0	46.0	25.0	1358.77	0	2	4	0	2	27	38
									LLIDEAILK	95.0	52.5	25.0	1027.64	0	1	0	0	2	108	116
									YLIATSEQPIAALHR	95.0	27.0	25.0	1682.92	0	0	5	0	2	267	281
S-formylglutathione hydrolase	ESTD_HUMAN	ESD	31.45	100.0	5	5	24	12.80	FAVYLPPK	95.0	49.9	25.0	934.54	0	11	0	0	2	32	39
									AFSGYLGTDQSK	95.0	71.4	25.0	1273.61	0	7	0	0	2	187	198
									AYDATHLVK	95.0	36.3	25.0	1017.54	0	2	0	0	2	201	209
									KIPVVFR	95.0	31.4	25.0	858.56	0	1	0	0	2	247	253
									IPVVFR	95.0	31.9	25.0	730.46	0	3	0	0	2	248	253
SH3 domain-binding glutamic acid-rich-like protein	SH3L1_HUMAN	SH3BGRL	12.76	100.0	4	5	7	34.20	KQQDVLGFLEANK	95.0	53.9	25.0	1489.80	0	1	2	0	2	19	31
									IGFEEK	95.0	41.6	25.0	722.37	0	1	0	0	2	32	37
									DIAANEENRK	95.0	29.2	25.0	1159.57	0	1	0	0	2	38	47
									GDYDAFFEAR	95.0	69.6	25.0	1190.51	0	2	0	0	2	77	86
SH3 domain-binding protein 1	3BP1_HUMAN	SH3BP1	75.70	100.0	3	3	11	4.56	SLSSLDTALAELR	95.0	80.4	25.0	1375.74	0	3	0	0	2	241	253
									LPPENLSNLR	95.0	35.3	25.0	1152.64	0	2	0	0	2	391	400
									LAEEQEVNK	95.0	54.3	25.0	1059.53	0	6	0	0	2	409	417
Sialic acid synthase	SIAS_HUMAN	NANS	40.29	100.0	4	5	12	15.60	ALERPYTSK	95.0	28.4	25.0	1064.57	0	1	0	0	2	66	74
									VGSGDTNNFPYLEK	95.0	74.1	25.0	1540.73	0	4	0	0	2	132	145
									GSDHSASLEPGELAELVR	95.0	70.5	25.0	1866.92	0	2	3	0	2	247	264
									IPEGTILTMDMLTVK	95.0	60.5	25.0	1693.88	0	2	0	0	2	301	315
Signal peptidase complex subunit 2	SPCS2_HUMAN	SPCS2	24.99	100.0	3	3	5	11.50	YVENFGLIDGR	95.0	62.0	25.0	1282.64	0	2	0	0	2	74	84
									SIFLVAHR	95.0	29.5	25.0	942.55	0	2	0	0	2	138	145
									LTFISGR	95.0	30.3	25.0	793.46	0	1	0	0	2	174	180
Signal recognition particle 14 kDa protein	SRP14_HUMAN	SRP14	14.55	100.0	3	3	16	16.90	KGTVEGFEPADNK	95.0	44.5	25.0	1391.68	0	7	0	0	2	43	55
									GTVEGFEPADNK	95.0	37.2	25.0	1263.59	0	4	0	0	2	44	55
									FQMAYSNLLR	95.0	56.3	25.0	1258.62	0	5	0	0	2	79	88
Signal transducer and activator of transcription 1-alpha/beta	STAT1_HUMAN	STAT1	87.32	100.0	4	4	16	5.60	MYLMLDNK	95.0	31.6	25.0	1059.49	0	1	0	0	2	202	209
									TGVQFTVK	94.7	26.5	25.0	879.49	0	1	0	0	2	337	344
									GLNVDQLNMLGEK	95.0	80.2	25.0	1446.73	0	7	0	0	2	513	525
									VMAAENIPENPLK	95.0	84.3	25.0	1441.74	0	7	0	0	2	653	665
Signal transducer and activator of transcription 3	STAT3_HUMAN	STAT3	88.05	100.0	5	5	8	11.00	FLQESNVLYQHNLR	95.0	28.5	25.0	1760.91	0	0	1	0	2	71	84
									LLQTAATAAQQGGQANHPTAAVVTEK	95.0	86.7	25.0	2576.34	0	0	3	0	2	115	140
									MQQLEQMLTALDQMR	95.0	19.8	25.0	1883.87	0	0	1	0	2	200	214
									VMNMEESNNGSLSAEFK	95.0	33.2	25.0	1918.82	0	1	0	0	2	393	409
									GLSIEQLTTLAEK	95.0	89.1	25.0	1402.78	0	2	0	0	2	519	531
SLIT and NTRK-like protein 6	SLIK6_HUMAN	SLITRK6	95.10	100.0	3	3	5	4.16	FVPLTHLDLR	95.0	21.7	25.0	1210.69	0	0	1	0	2	182	191
									LILAGNIIHSLMK	95.0	31.7	25.0	1438.85	0	1	0	0	2	368	380
									EILPGTFNPMPK	95.0	47.0	25.0	1359.70	0	3	0	0	2	449	460
Small nuclear	SMD1_HUMAN	SNRPD1	13.26	100.0	3	5	14	20.20	LSHETVTIELK	95.0	50.2	25.0	1269.71	0	4	2	0	2	10	20

ribonucleoprotein Sm D1									NREPVQLETLSIR	95.0	68.2	25.0	1554.86	0	3	2	0	2	49	61
									EPVQLETLSIR	95.0	35.3	25.0	1284.72	0	3	0	0	2	51	61
Small nuclear ribonucleoprotein-associated proteins B and B'	RSMB_HUMAN	SNRPB	24.59	100.0	3	3	14	12.50	IFIGTFK	95.0	42.4	25.0	825.49	0	4	0	0	2	26	32
									VLGLVLLR	95.0	61.7	25.0	882.61	0	2	0	0	2	66	73
									GENLVSMTVEGPPPK	95.0	####	25.0	1570.78	0	8	0	0	2	74	88
Sodium/potassium-transporting ATPase subunit alpha-1	AT1A1_HUMAN	ATP1A1	112.88	100.0	15	15	149	18.20	LSLDELHR	95.0	40.0	25.0	982.53	0	1	0	0	2	46	53
									NMVPQQALVIR	95.0	43.0	25.0	1284.71	0	2	0	0	2	163	173
									VDNSSLTGESEPQTR	95.0	43.2	25.0	1619.75	0	3	0	0	2	213	227
									SPDFTNENPLETR	95.0	96.5	25.0	1519.70	0	32	0	0	2	228	240
									GIVVYTGDR	95.0	50.3	25.0	979.52	0	13	0	0	2	256	264
									AVFQANQENLPILK	95.0	56.1	25.0	1584.87	0	3	0	0	2	431	444
									AVAGDASESALLK	95.0	80.4	25.0	1231.65	0	27	0	0	2	446	458
									IVEIPFNSTNK	95.0	50.4	25.0	1261.68	0	7	0	0	2	477	487
									NPNTSEPQHLLVMK	95.0	28.4	25.0	1623.82	0	0	3	0	2	495	508
									VIMVTGDHPITAK	95.0	52.7	25.0	1397.75	0	1	0	0	2	613	625
									GVGIISEGNETVEDIAAR	95.0	####	25.0	1829.92	0	2	0	0	2	630	647
									LNIPVSQVNPR	95.0	61.3	25.0	1236.71	0	22	0	0	2	648	658
									DMTSEQLDDILK	95.0	77.6	25.0	1423.66	0	29	0	0	2	672	683
									ADIGVAMGIAGSDVSK	95.0	82.2	25.0	1506.75	0	3	0	0	2	728	743
									LIFDNLKK	94.8	26.6	25.0	990.60	0	1	0	0	2	767	774
Solute carrier family 2, facilitated glucose transporter member 1	GTR1_HUMAN	SLC2A1	54.07	100.0	3	3	28	4.88	FLLINR	95.0	33.5	25.0	775.48	0	6	0	0	2	213	218
									VTILELFR	95.0	58.6	25.0	990.60	0	20	0	0	2	257	264
									TFDEIASGFR	95.0	56.9	25.0	1142.55	0	2	0	0	2	459	468
Sorbitol dehydrogenase	DHSO_HUMAN	SORD	38.31	100.0	4	5	11	13.20	VAIEPGAPR	95.0	29.3	25.0	909.52	0	2	0	0	2	92	100
									AMGAAQVVVTDLSATR	95.0	####	25.0	1605.83	0	4	2	0	2	194	209
									EIGADLVLQISK	95.0	42.3	25.0	1285.74	0	1	0	0	2	215	226
									ALEAFETFKK	95.0	49.1	25.0	1183.64	0	2	0	0	2	331	340
Sorcin	SORCN_HUMAN	SRI	21.66	100.0	6	6	32	28.80	LMVSMLDR	95.0	34.9	25.0	996.49	0	4	0	0	2	77	84
									DMSGTMGFNEFK	95.0	80.4	25.0	1395.56	0	12	0	0	2	85	96
									SGTVDPQELQK	95.0	34.4	25.0	1201.61	0	5	0	0	2	117	127
									ALTTMGFR	95.0	43.1	25.0	912.46	0	5	0	0	2	128	135
									LSPQAVNSIAK	95.0	55.1	25.0	1127.64	0	4	0	0	2	136	146
									ALTDSFR	95.0	33.2	25.0	809.42	0	2	0	0	2	168	174
Sorting nexin-2	SNX2_HUMAN	SNX2	58.45	100.0	8	8	16	16.60	SMSAPVIFDR	95.0	28.4	25.0	1138.56	0	2	0	0	2	117	126
									FSDFLGLHSK	95.0	59.8	25.0	1150.59	0	2	0	0	2	184	193
									EDSSSTEFVEK	95.0	34.7	25.0	1257.55	0	2	0	0	2	224	234
									HPTLLQDPDLR	95.0	39.1	25.0	1304.70	0	2	0	0	2	249	259
									QFLESSELPR	95.0	68.4	25.0	1205.62	0	2	0	0	2	260	269
									QQQFENLDQQLR	95.0	50.7	25.0	1546.76	0	2	0	0	2	310	321
									ELSANTAAFAK	95.0	53.9	25.0	1122.58	0	2	0	0	2	336	346
									ALSQLAEVEEK	95.0	58.3	25.0	1216.64	0	2	0	0	2	363	373
Sorting nexin-6	SNX6_HUMAN	SNX6	46.63	100.0	3	3	5	7.14	EKLEDFFK	95.0	26.8	25.0	1055.54	0	1	0	0	2	182	189
									DVDDFFEHER	95.0	49.3	25.0	1308.55	0	2	0	0	2	205	214
									NLVELAELELK	95.0	41.6	25.0	1270.73	0	2	0	0	2	376	386
Sorting nexin-9	SNX9_HUMAN	SNX9	66.57	100.0	3	3	4	5.88	SYIEYQLTPTNTNR	95.0	58.2	25.0	1699.83	0	1	0	0	2	268	281
									FEEEFIK	95.0	31.9	25.0	941.46	0	2	0	0	2	319	325
									TYEEIASLVAEQPK	95.0	59.1	25.0	1577.81	0	1	0	0	2	470	483
SPARC	SPRC_HUMAN	SPARC	34.61	100.0	3	6	38	7.92	DEDNNLLTEK	95.0	49.7	25.0	1190.55	0	10	0	0	2	182	191
									RLEAGDHPVELLAR	95.0	58.0	25.0	1575.86	0	4	7	1	2	205	218
									LEAGDHPVELLAR	95.0	86.4	25.0	1419.76	0	12	4	0	2	206	218
Spectrin alpha chain, brain	SPTA2_HUMAN	SPTAN1	284.52	100.0	50	58	231	21.90	LQIASDENYKDPTNLQGK	95.0	76.9	25.0	2034.01	0	2	0	0	2	64	81

									LMELHR	94.9	26.6	25.0	814.42	0	1	0	0	2	124	129
									KFEEFQTDMAAHEER	95.0	37.2	25.0	1883.82	0	0	8	0	2	190	204
									VNEVNQFAAK	95.0	51.3	25.0	1119.58	0	6	0	0	2	205	214
									LIQEQHPEEELIK	95.0	67.5	25.0	1605.85	0	4	0	0	2	215	227
									LFGAAEVQR	95.0	65.8	25.0	990.54	0	11	0	0	2	251	259
									EKEQLMASDDFGR	95.0	59.0	25.0	1541.69	0	2	5	0	2	273	285
									EQLMASDDFGR	95.0	45.0	25.0	1284.55	0	4	0	0	2	275	285
									DLASVQALLR	95.0	71.9	25.0	1085.63	0	6	0	0	2	286	295
									DLAALEDK	95.0	38.0	25.0	874.45	0	2	0	0	2	303	310
									LQQSHPLSATQIQVK	95.0	56.4	25.0	1677.93	0	1	2	0	2	321	335
									FLADFR	95.0	35.0	25.0	768.40	0	2	0	0	2	366	371
									GEIDAHEDSFK	95.0	29.2	25.0	1247.55	0	3	0	0	2	408	418
									LTVLSEER	95.0	40.4	25.0	946.52	0	4	0	0	2	442	449
									LIQNNHYAMEDVATR	95.0	44.3	25.0	1790.85	0	0	8	0	2	533	547
									TATDEAYKDPSNLQGK	95.0	45.3	25.0	1737.83	0	3	2	0	2	595	610
									HQAFEAELSANQSR	95.0	98.1	25.0	1587.75	0	2	1	0	2	614	627
									LIDVNHYAK	95.0	25.9	27.3	1072.58	0	0	1	0	2	638	646
									LLEATELK	95.0	33.4	25.0	916.54	0	2	0	0	2	663	670
									EANQQQQFNR	95.0	40.6	25.0	1262.59	0	3	0	0	2	676	685
									DLTNVQNLQK	95.0	63.8	25.0	1172.63	0	8	0	0	2	709	718
									IDGITIQAR	95.0	63.1	25.0	986.56	0	6	0	0	2	734	742
									YEALKEPMVAR	95.0	32.7	25.0	1322.68	0	2	0	0	2	766	776
									LQQLFR	95.0	32.5	25.0	804.47	0	6	0	0	2	786	791
									EKEPIAASTNR	95.0	23.4	25.0	1215.63	0	0	1	0	2	802	812
									DLIGVQNLLK	95.0	47.8	25.0	1112.67	0	3	0	0	2	815	824
									KHQALQAEIAGHEPR	95.0	23.5	25.0	1684.89	0	0	0	1	2	825	839
									HQALQAEIAGHEPR	95.0	58.4	25.0	1556.79	0	0	3	0	2	826	839
									GNAMVEEGHFAAEDVK	95.0	77.3	25.0	1719.76	0	6	6	0	2	847	862
									KGDILTLLNSTNK	95.0	91.1	25.0	1416.81	0	3	0	0	2	990	1002
									QGFVPAAYVK	95.0	40.9	25.0	1079.59	0	4	0	0	2	1013	1022
									KFDDFQK	95.0	31.5	25.0	927.46	0	3	0	0	2	1132	1138
									SQLLGSAHEVQR	95.0	61.9	25.0	1324.70	0	5	1	0	2	1226	1237
									VNSLGETAER	95.0	55.8	25.0	1075.54	0	2	0	0	2	1289	1298
									LIQSHPESAEDLQEK	95.0	52.6	25.0	1723.85	0	2	0	0	2	1299	1313
									LGDSHDLQR	95.0	33.5	25.0	1040.51	0	3	0	0	2	1335	1343
									DVTGAEALLER	95.0	87.0	25.0	1173.61	0	13	0	0	2	1370	1380
									LGESQTLQQFSR	95.0	76.5	25.0	1393.71	0	5	0	0	2	1547	1558
									LQTASDESYKDPTNIQSK	95.0	31.0	25.0	2024.98	0	0	1	0	2	1571	1588
									GVIDMGNSLIER	95.0	72.1	25.0	1319.66	0	11	0	0	2	1608	1619
									LLVGSEDYGR	95.0	42.2	25.0	1108.56	0	3	0	0	2	1785	1794
									DLTGVQNLR	95.0	42.5	25.0	1015.55	0	2	0	0	2	1795	1803
									LSDDNTIGKEEIQQR	95.0	49.6	25.0	1745.87	0	1	4	0	2	1830	1844
									DLSSVQTLLTK	95.0	75.6	25.0	1204.68	0	13	0	0	2	2007	2017
									KVEDLFLTFAK	95.0	58.9	25.0	1310.74	0	3	0	0	2	2088	2098
									MQHNLEQQIQAR	95.0	53.8	25.0	1511.74	0	2	0	0	2	2304	2315
									NTTGVTEEALK	95.0	58.9	25.0	1162.60	0	6	0	0	2	2316	2326
									SSEEIESAFR	95.0	88.1	25.0	1154.53	0	9	0	0	2	2405	2414
									ALSSEGKPYVTK	95.0	56.0	25.0	1279.69	0	4	1	0	2	2415	2426
									EELYQNLTR	95.0	60.8	25.0	1165.58	0	3	0	0	2	2427	2435
Spectrin beta chain, brain 1	SPTB2_HUMAN	SPTBN1	274.60	100.0	52	58	267	26.30	ITDLYTDLR	95.0	71.1	25.0	1109.58	0	15	0	0	2	75	83
									LLEVLSGER	95.0	65.3	25.0	1015.58	0	2	0	0	2	91	99

								ALQFLK	95.0	32.6	25.0	719.45	0	3	0	0	2	119	124
								FQIQDISVETEDNK	95.0	75.2	25.0	1665.80	0	2	0	0	2	157	170
								FQIQDISVETEDNKEK	95.0	21.7	25.0	1922.93	0	0	1	0	2	157	172
								DGMAFNALIHK	95.0	43.8	25.0	1232.61	0	2	3	0	2	204	214
								HRPDLIDFDK	95.0	50.5	25.0	1255.64	0	0	3	0	2	215	224
								LLDPEDISVDHPDEK	95.0	77.4	25.0	1721.82	0	4	2	0	2	250	264
								VLDNAIETEK	95.0	63.3	25.0	1131.59	0	8	0	0	2	293	302
								LEQLAR	95.0	29.1	25.0	729.43	0	1	0	0	2	420	425
								KHEAIETDIAAYEER	95.0	43.4	25.0	1774.86	0	0	2	0	2	463	477
								ELEAENYHDIKR	95.0	20.8	25.0	1516.74	0	0	1	0	2	487	498
								LEMNLGLQK	95.0	30.8	25.0	1061.57	0	2	0	0	2	524	532
								VLVLSQDYGK	95.0	64.7	25.0	1121.62	0	2	0	0	2	549	558
								HLLGVEDLLQK	95.0	45.6	25.0	1264.73	0	5	0	0	2	559	569
								EGEDMIAEEHFGSEK	95.0	60.8	25.0	1723.71	0	2	0	0	2	700	714
								IVSSSDVGHDEYSTQSLVK	95.0	94.0	25.0	2050.99	0	2	2	0	2	766	784
								LSGIEER	95.0	31.4	25.0	803.43	0	9	0	0	2	824	830
								QALQDTLALYK	95.0	66.0	25.0	1263.69	0	8	0	0	2	843	853
								FESLEPEMNNQASR	95.0	48.8	25.0	1667.73	0	8	0	0	2	891	904
								VAVVNQIAR	95.0	56.5	25.0	969.58	0	9	0	0	2	905	913
								EAEKLESEHPDQAQAILSR	95.0	58.4	25.0	2151.07	0	0	5	0	2	1018	1036
								LQQFLR	95.0	35.5	25.0	804.47	0	15	0	0	2	1064	1069
								TQTAIASEDMPNTLTEAEK	95.0	####	25.0	2065.96	0	10	0	0	2	1081	1099
								NEIDNYEEDYQK	95.0	81.3	25.0	1559.65	0	3	0	0	2	1109	1120
								INAVVETGR	95.0	60.5	25.0	958.53	0	10	0	0	2	1225	1233
								LVSDGNINSDR	95.0	61.3	25.0	1189.58	0	11	0	0	2	1235	1245
								ETASELLMR	95.0	57.6	25.0	1065.52	0	7	0	0	2	1262	1270
								MLTAQDMSYDEAR	95.0	65.0	25.0	1562.65	0	13	0	0	2	1295	1307
								EGMQLISEKPETEAVVK	95.0	70.3	25.0	1903.97	0	2	9	0	2	1336	1352
								DLTSVNILLK	95.0	42.3	25.0	1115.67	0	2	0	0	2	1411	1420
								EIEELQSQAQALSQEGK	95.0	####	25.0	1887.93	0	4	0	0	2	1435	1451
								FMELLEPLNER	95.0	46.4	25.0	1406.70	0	2	0	0	2	1467	1477
								MPLATSTDHGHNLQTVQLLIK	95.0	52.8	25.0	2333.23	0	0	1	0	2	1505	1525
								IDDIFER	95.0	34.8	25.0	907.45	0	10	0	0	2	1541	1547
								SQNIVTDSSSLSAEAIR	95.0	####	25.0	1777.89	0	5	0	0	2	1548	1564
								ALVADSHPESER	95.0	52.6	25.0	1310.63	0	4	0	0	2	1657	1668
								TQILAASYELHK	95.0	60.9	25.0	1373.74	0	2	1	0	2	1798	1809
								DQNTVETLQR	95.0	50.1	25.0	1203.60	0	9	0	0	2	1835	1844
								MHTTFEHDIQALGTQVR	95.0	55.8	25.0	1999.97	0	0	2	0	2	1845	1861
								LVDTGDKFR	95.0	42.9	25.0	1050.56	0	3	0	0	2	1907	1915
								DVSSVELLMNNHQGIK	95.0	60.3	25.0	1799.90	0	3	1	0	2	1942	1957
								HYASEEIKEK	95.0	28.0	25.0	1233.61	0	0	2	0	2	1982	1991
								LILEVHQFSR	95.0	38.6	25.0	1241.70	0	1	0	0	2	2015	2024
								EIGQSVDEVEK	95.0	33.1	25.0	1232.60	0	1	0	0	2	2044	2054
								FSALER	95.0	26.9	25.0	722.38	0	1	0	0	2	2073	2078
								LTTLELLEVR	95.0	76.9	25.0	1186.70	0	2	0	0	2	2079	2088
								TALPAQSAATLPAR	95.0	74.2	25.0	1367.76	0	9	0	0	2	2178	2191
								TQETPSAQMEGFLNR	95.0	97.6	25.0	1724.79	0	7	0	0	2	2192	2206
								TAASGIPYHSEVPVSLK	95.0	51.2	25.0	1755.93	0	1	0	0	2	2242	2258
								LNDGNEYLFQAK	95.0	70.2	25.0	1411.69	0	9	0	0	2	2279	2290
								AQTLPTSVVTITSESSPGK	95.0	94.6	25.0	1903.00	0	2	0	0	2	2326	2344
Spectrin beta chain, brain 2	SPTN2_HUMAN	SPTBN2	271.28	100.0	3	3	49	2.85	ALQFLK	95.0	32.6	25.0	719.45	0	3	0	0	2	122	127

									FQIQDISVETEDNK	95.0	75.2	25.0	1665.80	0	2	0	0	2	160	173
									FQIQDISVETEDNKEK	95.0	21.7	25.0	1922.93	0	0	1	0	2	160	175
									LLDPEDVNVDQPDEK	95.0	59.3	25.0	1725.82	0	2	0	0	2	253	267
									GEMSGRLGPLK	95.0	32.3	25.0	1144.61	0	45	0	0	2	688	698
									DLTSVNILLK	95.0	42.3	25.0	1115.67	0	2	0	0	2	1414	1423
									DLPSVQLLMK	95.0	27.7	25.0	1159.64	0	2	0	0	2	1519	1528
Spermidine synthase	SPEE_HUMAN	SRM	33.81	100.0	5	5	15	13.20	YQDILVFR	95.0	46.9	25.0	1053.57	0	4	0	0	2	48	55
									KVLIIGGGDGGVLR	95.0	39.0	25.0	1353.82	0	0	1	0	2	96	109
									VLIIGGGDGGVLR	95.0	51.9	25.0	1225.73	0	6	0	0	2	97	109
									YYNSDVHR	95.0	30.8	25.0	1053.47	0	3	0	0	2	278	285
									AAFVLPEFAR	95.0	39.6	25.0	1120.61	0	1	0	0	2	286	295
Spermine synthase	SPSY_HUMAN	SMS	41.25	100.0	5	5	9	12.30	HSTLDFMLGAK	95.0	59.2	25.0	1235.61	0	2	0	0	2	6	16
									NGSFANLR	95.0	43.8	25.0	878.45	0	2	0	0	2	55	62
									MKELSQDSTGR	95.0	27.8	25.0	1267.59	0	1	0	0	2	97	107
									RLPPIVR	95.0	28.7	25.0	850.56	0	1	0	0	2	110	116
									LILDLSMK	95.0	41.4	25.0	948.54	0	3	0	0	2	297	304
Spliceosome RNA helicase BAT1	UAP56_HUMAN	BAT1	48.97	100.0	13	16	136	29.70	GSYVSIHSSGFR	95.0	58.8	25.0	1296.63	0	6	0	0	2	37	48
									DFLLKPELLR	95.0	30.1	25.0	1243.74	0	2	9	0	2	49	58
									ELAFQISK	95.0	47.5	25.0	935.52	0	17	0	0	2	124	131
									VAVFFGGLSIK	95.0	35.6	25.0	1137.67	0	8	0	0	2	145	155
									MLEQLDMR	95.0	31.0	25.0	1067.49	0	2	0	0	2	201	208
									DVQEIFR	95.0	41.3	25.0	906.47	1	15	0	0	2	210	216
									QVMMFSATLSK	95.0	59.0	25.0	1274.61	0	5	0	0	2	223	233
									FMQDPMEIFVDDETK	95.0	70.5	25.0	1876.80	0	2	0	0	2	242	256
									LTLHGLQQYYVK	95.0	65.0	25.0	1462.81	0	7	1	0	2	257	268
									RILVATNLFGR	95.0	38.1	25.0	1259.76	0	1	0	0	2	339	349
									ILVATNLFGR	95.0	73.6	25.0	1103.66	0	35	0	0	2	340	349
									GLAITFVSDENDAK	95.0	####	25.0	1479.73	0	20	0	0	2	385	398
									ILNDVQDR	95.0	38.1	25.0	972.51	0	5	0	0	2	399	406
Splicing factor 3A subunit 1	SF3A1_HUMAN	SF3A1	88.87	100.0	3	3	13	3.78	VQAQVIQETIVPK	95.0	35.2	25.0	1452.84	0	1	0	0	2	132	144
									LTAQFVAR	95.0	37.7	25.0	905.52	0	2	0	0	2	169	176
									LQYEGIFIK	95.0	45.3	25.0	1110.62	0	10	0	0	2	757	765
Splicing factor 3A subunit 3	SF3A3_HUMAN	SF3A3	58.83	100.0	3	3	18	6.79	VKPLQDQNELFGK	95.0	39.2	25.0	1515.82	0	2	0	0	2	200	212
									SALLALGLK	95.0	61.3	25.0	885.58	0	7	0	0	2	265	273
									SLESLDTSLFAK	95.0	54.6	25.0	1310.68	0	9	0	0	2	292	303
Splicing factor 3B subunit 1	SF3B1_HUMAN	SF3B1	145.82	100.0	4	4	8	3.68	SLVEIIEHGLVDEQQK	95.0	52.7	25.0	1836.97	0	2	0	0	2	685	700
									TEILPPFFK	95.0	33.0	25.0	1091.61	0	2	0	0	2	808	816
									ATVNTFGYIAK	95.0	62.0	25.0	1184.63	0	2	0	0	2	1076	1086
									VPELNVQNGVLK	95.0	53.2	25.0	1309.75	0	2	0	0	2	1138	1149
Splicing factor 3B subunit 3	SF3B3_HUMAN	SF3B3	135.56	100.0	11	11	63	10.90	ILELLRPDPNTGK	95.0	32.7	25.0	1465.84	0	3	0	0	2	37	49
									DYIVVGSDSGR	95.0	70.5	25.0	1167.56	0	3	0	0	2	76	86
									IVILEYQPSK	95.0	58.4	25.0	1189.68	0	2	0	0	2	87	96
									IVPGQFLAVDPK	95.0	27.6	25.0	1283.74	0	1	0	0	2	115	126
									AVMISAIEK	95.0	27.0	25.0	977.53	0	1	0	0	2	129	137
									FLAVGLVDNTVR	95.0	83.1	25.0	1303.74	0	15	0	0	2	604	615
									TVLDPVTGDLSDTR	95.0	94.2	25.0	1488.75	0	25	0	0	2	677	690
									MQGQEAVLAMSSR	95.0	89.8	25.0	1439.66	0	6	0	0	2	706	718
									HIANYISGIQTIGHR	95.0	49.7	25.0	1679.90	0	0	2	0	2	985	999
									LPPNTNDEVDEDPTGNK	95.0	69.0	25.0	1854.84	0	4	0	0	2	1058	1074
									SYYFPVK	95.0	26.8	25.0	903.46	0	1	0	0	2	1165	1171
Splicing factor,	SFRS1_HUMAN	SFRS1	27.73	100.0	4	4	16	15.30	IYVGNLPPDIR	95.0	41.9	25.0	1256.70	0	1	0	0	2	18	28

arginine/serine-rich 1									DIEDVFYK	95.0	28.3	25.0	1028.49	0	1	0	0	2	31	38
									DAEDAVYGR	95.0	42.6	25.0	995.44	0	2	0	0	2	66	74
									DGTGVVEFVR	95.0	54.0	25.0	1078.55	0	12	0	0	2	155	164
Splicing factor, proline- and glutamine-rich	SFPQ_HUMAN	SFPQ	76.13	100.0	3	3	19	5.23	YGEPGEVFINK	95.0	59.9	25.0	1252.62	0	12	0	0	2	320	330
									FATHAAALSVR	95.0	35.7	25.0	1143.63	0	0	6	0	2	366	376
									FGQGGAGPVGGQGPR	95.0	30.2	25.0	1341.67	0	1	0	0	2	667	681
SPRY domain-containing protein 4	SPRY4_HUMAN	SPRYD4	23.11	100.0	5	5	7	23.70	TAHSSLALFR	95.0	29.9	25.0	1102.60	0	1	0	0	2	38	47
									YGLVGLEPTK	95.0	38.7	25.0	1076.60	0	2	0	0	2	54	63
									VALNVER	95.0	31.1	25.0	800.46	0	2	0	0	2	64	70
									APVEGIGQPEK	95.0	26.9	25.0	1124.59	0	1	0	0	2	140	150
									VGLLLEYEAQK	95.0	41.8	25.0	1262.70	0	1	0	0	2	151	161
Squamous cell carcinoma antigen recognized by T-cells 3	SART3_HUMAN	SART3	109.92	99.9	2	2	3	2.49	EFESAIVEAAR	95.0	43.2	25.0	1221.61	0	1	0	0	2	233	243
									IQLIFER	95.0	33.2	25.0	918.54	0	2	0	0	2	329	335
									ELEELR	95.0	30.7	25.0	788.41	0	2	0	0	2	441	446
Src substrate cortactin	SRC8_HUMAN	CTTN	61.57	100.0	5	5	43	10.20	ENVFQEHQTLK	95.0	35.5	25.0	1372.69	0	3	0	0	2	60	70
									FGVEQDR	95.0	39.8	25.0	850.41	0	2	0	0	2	88	94
									ANFENLAK	95.0	42.6	25.0	906.47	0	14	0	0	2	352	359
									TQTPPVSPAPQPTEER	95.0	75.5	25.0	1734.87	0	8	0	0	2	399	414
									LPSSPVYEDAASFK	95.0	94.6	25.0	1510.74	0	16	0	0	2	415	428
Staphylococcal nuclease domain-containing protein 1	SND1_HUMAN	SND1	101.98	100.0	19	20	107	22.60	QINLSNIR	95.0	43.0	25.0	957.55	0	6	0	0	2	48	55
									EYGMIYLGK	95.0	45.8	25.0	1089.53	0	3	0	0	2	108	116
									YTIENPR	95.0	39.2	25.0	892.45	0	6	0	0	2	178	184
									EADGSETPEPFAAEAK	95.0	89.7	25.0	1648.73	0	16	0	0	2	234	249
									DYVAPTANLDQK	95.0	44.8	25.0	1334.66	0	5	0	0	2	328	339
									VMQVLNADAIVVK	95.0	76.8	25.0	1415.79	0	4	0	0	2	347	359
									TIHLSSIRPPR	95.0	27.0	25.0	1276.75	0	0	3	0	2	367	377
									SSHYDELLAAEAR	95.0	91.3	25.0	1461.70	0	4	0	0	2	473	485
									QFLPFLQR	95.0	38.9	25.0	1048.59	0	4	0	0	2	516	523
									SEAVVEYVFSGSR	95.0	####	25.0	1429.70	0	14	0	0	2	527	539
									ELVLQR	95.0	32.1	25.0	757.46	0	2	0	0	2	587	592
									EVEVEVESMDK	95.0	69.8	25.0	1309.58	0	7	0	0	2	593	603
									SLLSAEEAAK	95.0	64.3	25.0	1018.54	0	2	0	0	2	642	651
									NDIASHPPVEGSYAPR	95.0	80.0	25.0	1709.82	0	5	4	0	2	716	731
									LGTLSPAFSTR	95.0	65.4	25.0	1149.63	0	8	0	0	2	777	787
									TDAVDSVVR	95.0	45.3	25.0	961.49	0	7	0	0	2	811	819
									GDVGLGLVK	95.0	44.2	25.0	857.51	0	3	0	0	2	849	857
									VITEYLNAQESAK	95.0	89.4	25.0	1465.75	0	3	0	0	2	874	886
									ADDADEFGYSR	95.0	34.5	25.0	1245.50	0	1	0	0	2	900	910
Sterile alpha motif domain-containing protein 9	SAMD9_HUMAN	SAMD9	184.27	100.0	6	6	8	3.90	EILTEQDVNGAVLK	95.0	62.4	25.0	1528.82	0	1	0	0	2	34	47
									AFTNTATATEEDVK	95.0	87.7	25.0	1497.71	0	2	0	0	2	199	212
									FSLFVR	95.0	31.8	25.0	768.44	0	1	0	0	2	339	344
									HLDFLK	95.0	28.9	25.0	772.44	0	1	0	0	2	427	432
									MGTYSTILIK	95.0	51.8	25.0	1142.61	0	2	0	0	2	960	969
									FLQDMHTLLLTR	95.0	21.2	25.0	1503.80	0	0	1	0	2	1027	1038
Stress-70 protein, mitochondrial	GRP75_HUMAN	HSPA9	73.66	100.0	13	13	64	23.90	VLENAEGAR	95.0	37.7	25.0	958.50	0	2	0	0	2	77	85
									TTPSVVAFTADGER	95.0	59.2	25.0	1450.72	0	5	0	0	2	86	99
									QAVTNPNNTFYATK	95.0	83.5	25.0	1568.77	0	3	0	0	2	108	121
									RYDDPEVQK	95.0	44.0	25.0	1149.55	0	4	0	0	2	127	135
									DAGQISGLNVLR	95.0	79.3	25.0	1242.68	0	13	0	0	2	207	218
									VINEPTAAALAYGLDK	95.0	93.6	25.0	1645.88	0	4	0	0	2	219	234
									AQFEGIVTDLIR	95.0	60.9	25.0	1361.74	0	6	0	0	2	349	360

									SDIGEVILVGGMTR	95.0	76.4	25.0	1462.76	0	14	0	0	2	378	391
									VQQTVQDLFGR	95.0	81.9	25.0	1290.68	0	3	0	0	2	395	405
									EQQIVIQSSGGLSK	95.0	99.1	25.0	1473.79	0	3	0	0	2	542	555
									DDIENMVK	95.0	39.7	25.0	979.44	0	2	0	0	2	556	563
									VEAVNMAEGIIHDTETK	95.0	20.9	25.0	1872.90	0	0	1	0	2	579	595
									QAASSLQQASLK	95.0	35.8	25.0	1231.66	0	4	0	0	2	635	646
Stress-induced-phosphoprotein 1	STIP1_HUMAN	STIP1	62.62	100.0	19	25	172	32.00	LDPHNHVLYSNR	95.0	33.3	25.0	1464.73	0	2	0	0	2	33	44
									KAAALEFLNR	95.0	66.9	25.0	1132.65	0	3	2	0	2	78	87
									AAALEFLNR	95.0	63.2	25.0	1004.55	0	26	0	0	2	79	87
									TYEEGLKHEANNPQLK	95.0	58.8	25.0	1870.93	0	2	11	1	2	94	109
									EGLQNMEAR	95.0	38.9	25.0	1063.48	0	7	0	0	2	110	118
									TLLSDPTYR	95.0	30.6	25.0	1065.56	0	3	0	0	2	145	153
									ELIEQLR	95.0	41.7	25.0	900.52	0	7	0	0	2	154	160
									ETKPEPMEEDLPENKK	95.0	37.9	25.0	1929.91	0	0	2	0	2	208	223
									EKELGNDAYK	94.6	19.0	25.0	1166.57	0	0	1	0	2	228	237
									DFDTALK	95.0	30.9	25.0	809.40	0	1	0	0	2	240	246
									IGNSYFK	95.0	56.9	25.0	828.43	0	5	0	0	2	306	312
									IGNSYFKEEK	95.0	43.0	25.0	1214.61	0	6	0	0	2	306	315
									YKDAIHFYNK	95.0	47.5	25.0	1298.65	0	1	1	0	2	316	325
									DAIHFYNK	95.0	36.4	25.0	1007.49	0	6	0	0	2	318	325
									LAYINPDLALEEK	95.0	72.0	25.0	1488.79	0	26	0	0	2	352	364
									AMADPEVQQIMSDPAMR	95.0	95.3	25.0	1937.84	0	7	5	0	2	489	505
									LILEQMQK	95.0	38.8	25.0	1018.56	0	3	0	0	2	506	513
									DPQALSEHLK	95.0	39.5	25.0	1137.59	0	9	2	0	2	514	523
									LMDVGLIAIR	95.0	72.4	25.0	1116.64	0	33	0	0	2	534	543
Stromelysin-2	MMP10_HUMAN	MMP10	54.14	100.0	5	5	12	10.10	FLGLEVTGK	95.0	61.3	25.0	963.55	0	4	0	0	2	69	77
									LDTDTLEVMR	95.0	58.0	25.0	1208.58	0	1	0	0	2	78	87
									IVNYTPDLPR	95.0	28.9	25.0	1187.64	0	1	0	0	2	117	126
									GEYLFFK	95.0	34.4	25.0	903.46	0	4	0	0	2	303	309
									LIADDFPGVEPK	95.0	34.9	25.0	1300.68	0	2	0	0	2	424	435
Structural maintenance of chromosomes protein 1A	SMC1A_HUMAN	SMC1A	143.22	100.0	7	7	16	6.33	AFVSMVYSEEGAEDR	95.0	99.3	25.0	1705.74	0	2	0	0	2	78	92
									TALFEEISR	95.0	60.0	25.0	1065.56	0	8	0	0	2	152	160
									SGELAQEYDKR	95.0	28.8	25.0	1295.62	0	1	0	0	2	161	171
									INDIKR	95.0	30.9	25.0	758.45	0	2	0	0	2	748	753
									IIDETMAQLQDLK	95.0	49.4	25.0	1533.78	0	1	0	0	2	862	874
									LNEQQSVLQR	95.0	31.8	25.0	1214.65	0	1	0	0	2	1010	1019
									DKFQETSDEFEAAR	95.0	26.3	25.0	1672.75	0	0	1	0	2	1036	1049
Structural maintenance of chromosomes protein 2	SMC2_HUMAN	SMC2	135.64	100.0	6	6	11	5.60	TILEEEITPTIQK	95.0	51.1	25.0	1514.83	0	4	0	0	2	197	209
									ALNHEIEELEK	95.0	34.5	25.0	1324.67	0	1	0	0	2	276	286
									SLEDALAEAQR	95.0	78.6	25.0	1202.60	0	2	0	0	2	298	308
									GLVASLISVK	95.0	31.1	25.0	986.62	0	1	0	0	2	524	533
									EVITAQDTVIK	95.0	34.4	25.0	1216.68	0	1	0	0	2	880	890
									AMNVLTEAEER	95.0	54.4	25.0	1278.60	0	2	0	0	2	987	997
Structural maintenance of chromosomes protein 3	SMC3_HUMAN	SMC3	141.53	100.0	10	10	18	9.29	QVIIQGFR	95.0	34.7	25.0	960.56	0	2	0	0	2	5	12
									DQTIVDPFSSK	95.0	47.1	25.0	1236.61	0	2	0	0	2	16	26
									LALLHEGTGPR	95.0	40.0	25.0	1163.65	0	1	0	0	2	62	72
									DLQDELAGNSEQR	95.0	60.4	25.0	1474.68	0	1	0	0	2	311	323
									EENAEQQALAAK	95.0	40.0	25.0	1301.63	0	1	0	0	2	475	486
									DTAYPETNDAIPMISK	95.0	49.4	25.0	1781.83	0	2	0	0	2	597	612
									GALTGGYYDTR	95.0	49.8	25.0	1173.55	0	2	0	0	2	662	672
									KAEEELGELEAK	95.0	76.2	25.0	1345.68	0	2	0	0	2	684	695

									ELGSLPQEAFEK	95.0	56.9	25.0	1347.68	0	4	0	0	2	945	956
									ATLVMKK	95.0	32.3	25.0	806.48	0	1	0	0	2	1053	1059
Structural maintenance of chromosomes protein 4	SMC4_HUMAN	SMC4	147.17	100.0	3	3	11	2.48	SNNIINETTTR	95.0	27.6	25.0	1262.63	0	1	0	0	2	435	445
									LFDLVKVK	95.0	29.4	25.0	961.61	0	1	0	0	2	693	700
									DTLVADNLDQATR	95.0	74.0	25.0	1431.71	0	9	0	0	2	714	726
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCB2_HUMAN	SUCLG2	46.49	100.0	4	4	8	9.72	FFVADTANEALEAAK	95.0	####	25.0	1596.79	0	3	0	0	2	59	73
									ETYLAILMDR	95.0	41.9	25.0	1240.62	0	2	0	0	2	151	160
									LYNLFLK	95.0	32.3	25.0	910.54	0	1	0	0	2	228	234
									INFDDNAEFR	95.0	53.5	25.0	1240.56	0	2	0	0	2	260	269
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_HUMAN	OXCT1	56.14	100.0	8	9	28	18.10	FYTDPVEAVK	95.0	39.5	25.0	1168.59	0	2	0	0	2	42	51
									MVSSYVGENAEFER	95.0	95.6	25.0	1633.72	0	4	0	0	2	111	124
									DGSVAIASKPR	95.0	51.5	25.0	1100.61	0	5	0	0	2	177	187
									AGNVIFR	95.0	39.7	25.0	776.44	0	2	0	0	2	218	224
									QHEADADLINAGK	95.0	37.8	25.0	1381.67	0	1	0	0	2	356	368
									GGHVDLTMLGAMQVSK	95.0	87.6	25.0	1675.81	0	3	2	0	2	391	406
									GMGGAMDLVSSAK	95.0	53.5	25.0	1255.57	0	7	0	0	2	422	434
									VVVTMEHSAK	95.0	30.9	25.0	1116.57	0	2	0	0	2	437	446
Sulfhydryl oxidase 1	QSOX1_HUMAN	QSOX1	82.56	100.0	10	10	35	13.40	NGSGAVFPVAGADVQTLR	95.0	73.0	25.0	1758.91	0	2	0	0	2	130	147
									LEEIDGFFAR	95.0	53.4	25.0	1196.59	0	4	0	0	2	173	182
									EVALDLSQHK	95.0	41.3	25.0	1139.61	0	8	0	0	2	202	211
									VLNTEANVVR	95.0	48.1	25.0	1114.62	0	8	0	0	2	218	227
									VPVLMESR	95.0	42.3	25.0	946.50	0	4	0	0	2	249	256
									SFYTAYLQR	95.0	33.0	25.0	1148.57	0	1	0	0	2	257	265
									FPVLEGQR	94.6	26.4	25.0	945.52	0	1	0	0	2	319	326
									IPYSFFK	95.0	37.6	25.0	901.48	0	1	0	0	2	366	372
									EVLPAIR	95.0	33.3	25.0	797.49	0	2	0	0	2	434	440
									LAGAPSEDPQFPK	95.0	62.2	25.0	1356.68	0	4	0	0	2	488	500
SUMO-activating enzyme subunit 1	SAE1_HUMAN	SAE1	38.43	100.0	6	6	12	17.60	VEKEEAGGGISEEEAAQYDR	95.0	31.6	25.0	2166.98	0	0	2	0	1	2	21
									EEAGGGISEEEAAQYDR	95.0	####	25.0	1810.77	0	2	0	0	2	5	21
									VLLVGLK	95.0	37.7	25.0	741.52	0	2	0	0	2	39	45
									AQNLNPMVDVK	95.0	59.6	25.0	1244.63	0	3	0	0	2	99	109
									VSQGVEDGPDTKR	95.0	30.6	25.0	1387.68	0	1	0	0	2	184	196
									LDSSETTMVK	95.0	44.7	25.0	1126.53	0	2	0	0	2	199	208
SUMO-activating enzyme subunit 2	SAE2_HUMAN	UBA2	71.21	100.0	5	5	10	8.59	QFILVMNALDNR	95.0	65.8	25.0	1449.75	0	2	0	0	2	108	119
									VTVLTLQDK	95.0	43.7	25.0	1016.60	0	2	0	0	2	459	467
									FAMVAPDVQIEDGK	95.0	55.2	25.0	1535.74	0	3	0	0	2	473	486
									LSEFGIR	95.0	44.4	25.0	821.45	0	2	0	0	2	506	512
									DVEFEVVGDAPEK	95.0	40.3	25.0	1433.68	0	1	0	0	2	541	553
SUMO-conjugating enzyme UBC9	UBC9_HUMAN	UBE2I	17.99	100.0	4	6	23	16.50	KDHPFGFVAVPTK	95.0	79.0	25.0	1442.78	0	4	7	0	2	18	30
									DHPFGFVAVPTK	95.0	38.4	25.0	1314.68	0	2	5	0	2	19	30
									MLFKDDYPSSPPK	95.0	34.5	25.0	1540.74	0	3	0	0	2	62	74
									DDYPSSPPK	95.0	32.2	25.0	1005.45	0	2	0	0	2	66	74
Superkiller viralicidic activity 2-like 2	SK2L2_HUMAN	SKIV2L2	117.79	100.0	5	5	12	4.32	VIFTSPIK	95.0	32.1	25.0	904.55	0	1	0	0	2	185	192
									GIVILMVDEK	95.0	51.7	25.0	1132.63	0	1	0	0	2	533	542
									TVLQMDELK	95.0	28.3	25.0	1092.56	0	2	0	0	2	844	852
									MTDVFEGSIIR	95.0	55.2	25.0	1283.63	0	5	0	0	2	985	995
									RLEELLR	95.0	31.7	25.0	928.56	0	3	0	0	2	999	1005
Superoxide dismutase [Mn], mitochondrial	SODM_HUMAN	SOD2	24.70	100.0	6	7	17	27.90	HHAAYVNNLNVTEEK	95.0	75.7	25.0	1738.85	0	4	2	0	2	54	68
									YQEALAK	95.0	41.1	25.0	822.44	0	2	0	0	2	69	75
									GDVTAQIALQPALK	95.0	94.7	25.0	1424.81	0	4	0	0	2	76	89
									GELLEAIKR	95.0	51.8	25.0	1028.61	0	2	0	0	2	115	123

									DFGSFDKFK	95.0	45.2	25.0	1090.52	0	2	0	0	2	124	132
									NVRPDYLK	95.0	27.3	25.0	1004.55	0	1	0	0	2	195	202
Suppressor of G2 allele of SKP1 homolog	SUGT1_HUMAN	SUGT1	41.01	100.0	5	5	14	14.50	SLELNPNNSTAMLR	95.0	71.2	25.0	1575.78	0	4	0	0	2	71	84
									NYAAALETFTEGQK	95.0	70.1	25.0	1542.74	0	3	0	0	2	94	107
									ELSALVK	95.0	38.8	25.0	759.46	0	2	0	0	2	205	211
									LEGQGDVPTPK	95.0	46.2	25.0	1140.59	0	4	0	0	2	257	267
									QFVADVK	95.0	28.1	25.0	806.44	0	1	0	0	2	268	274
Switch-associated protein 70	SWP70_HUMAN	SWAP70	68.98	100.0	3	3	6	4.96	VQDNFDKIEFNR	95.0	27.7	25.0	1524.74	0	0	3	0	2	81	92
									FSTELER	95.0	29.4	25.0	881.44	0	1	0	0	2	387	393
									SSELEQYLQR	95.0	53.4	25.0	1252.62	0	2	0	0	2	409	418
Symplekin	SYMPK_HUMAN	SYMPK	141.14	100.0	3	3	11	2.67	VVDLLNQAALITNDSK	95.0	66.1	25.0	1713.94	0	6	0	0	2	36	51
									LIANLNMLLR	95.0	45.8	25.0	1186.70	0	1	0	0	2	110	119
									AALEQLLK	95.0	49.4	25.0	885.54	0	4	0	0	2	234	241
Synaptic vesicle membrane protein VAT-1 homolog	VAT1_HUMAN	VAT1	41.90	100.0	5	5	14	18.10	EVAEAATGEDASSPPPK	95.0	76.1	25.0	1655.78	0	4	0	0	2	6	22
									TVENVTVFGTASASK	95.0	26.9	25.0	1510.77	0	1	0	0	2	211	225
									GVDIVMDPLGGSDTAK	95.0	99.9	25.0	1590.77	0	4	0	0	2	256	271
									VVTYGMANLLTGPK	95.0	61.8	25.0	1479.79	0	2	0	0	2	282	295
									VLLVPGPEK	95.0	35.5	25.0	951.59	0	3	0	0	2	383	391
Synaptobrevin homolog YKT6	YKT6_HUMAN	YKT6	22.40	100.0	6	7	23	24.70	LYSLSVLYK	95.0	34.1	25.0	1085.62	0	1	0	0	2	3	11
									VAFTLLEK	95.0	46.0	25.0	920.55	0	2	0	0	2	89	96
									VQAELDETK	95.0	34.8	25.0	1032.52	0	4	0	0	2	142	150
									IILHNTMESLLER	95.0	53.7	25.0	1584.84	0	7	2	0	2	151	163
									GEKLDDLVSK	95.0	56.3	25.0	1103.59	0	4	0	0	2	164	173
									LDDLVSK	95.0	35.5	25.0	789.44	0	3	0	0	2	167	173
Syndecan-4	SDC4_HUMAN	SDC4	21.62	100.0	6	8	140	25.30	ETEVIDPQDLLEGR	95.0	70.7	25.0	1613.80	0	7	0	0	2	23	36
									AGSGSQVPTEPK	95.0	50.3	25.0	1157.58	0	29	0	0	2	93	104
									KLEENEVIPK	95.0	49.9	25.0	1198.67	0	30	14	0	2	105	114
									LEENEVIPK	95.0	49.0	25.0	1070.57	0	2	0	0	2	106	114
									RISPVEESEDVSNK	95.0	73.4	25.0	1588.78	0	20	2	0	2	115	128
									ISPVEESEDVSNK	95.0	97.5	25.0	1432.68	0	36	0	0	2	116	128
Talin-1	TLN1_HUMAN	TLN1	269.75	100.0	25	26	124	12.30	IGITNHDEYSLVR	95.0	55.6	25.0	1516.78	0	0	2	0	2	119	131
									AGFLDLK	95.0	43.4	25.0	763.44	0	12	0	0	2	257	263
									GLAGAVSELLR	95.0	53.9	25.0	1085.63	0	3	0	0	2	614	624
									ILAQATSDLVNAIK	95.0	27.9	25.0	1456.84	0	1	0	0	2	828	841
									ADAEGESDLENSR	95.0	74.0	25.0	1392.59	0	6	0	0	2	842	854
									QAAASATQTIAAAQHAASTPK	95.0	42.3	25.0	1995.03	0	0	4	0	2	923	943
									AVAEQIPLLVQGVR	95.0	55.0	25.0	1492.88	0	4	0	0	2	958	971
									NLGTALAELR	95.0	51.2	25.0	1057.60	0	6	0	0	2	1026	1035
									ALSTDPAAPNLK	95.0	48.4	25.0	1197.65	0	7	0	0	2	1321	1332
									VLGEAMTGISQNAK	95.0	64.4	25.0	1434.73	0	4	0	0	2	1402	1415
									NGNLPEFGDAISTASK	95.0	29.8	25.0	1620.79	0	1	0	0	2	1416	1431
									EVANSTANLVK	95.0	38.1	25.0	1145.62	0	1	0	0	2	1531	1541
									ALDGAFTEENR	95.0	53.2	25.0	1222.57	0	5	0	0	2	1545	1555
									AAMEPIVISAK	95.0	43.8	25.0	1145.62	0	5	0	0	2	1594	1604
									TMLESAGGLIQTAR	95.0	####	25.0	1463.75	0	8	0	0	2	1605	1618
									TLSHPQQMALLDQTK	95.0	42.1	25.0	1726.88	0	0	2	0	2	1752	1766
									VLVQNAAGSQEK	95.0	52.5	25.0	1243.66	0	16	0	0	2	2032	2043
									LAQAAQSSVATITR	95.0	92.8	25.0	1416.78	0	7	0	0	2	2044	2057
									ALGDLISATK	95.0	66.7	25.0	988.57	0	14	0	0	2	2090	2099
									ALEATTEHIR	95.0	40.7	25.0	1140.60	0	3	0	0	2	2145	2154
									TSTPEDFIR	95.0	46.3	25.0	1065.52	0	2	0	0	2	2169	2177

									QEDVIATANLSR	95.0	63.5	25.0	1316.68	0	2	0	0	2	2198	2209
									EAAYHPEVAPDVR	95.0	32.9	25.0	1453.71	0	1	1	0	2	2221	2233
									SIAAATSALVK	95.0	70.3	25.0	1031.61	0	6	0	0	2	2351	2361
									AAAFEEQENETVVVK	95.0	45.2	25.0	1663.82	0	1	0	0	2	2477	2491
T-complex protein 1 subunit alpha	TCPA_HUMAN	TCP1	60.33	100.0	11	12	61	19.20	LLEVEHPAAK	95.0	36.2	25.0	1106.62	0	5	0	0	2	64	73
									IHPTSVISGYR	95.0	27.4	25.0	1229.66	0	2	0	0	2	112	122
									YPVNSVNILK	95.0	40.3	25.0	1146.65	0	2	0	0	2	190	199
									TSASIILR	95.0	43.2	25.0	860.52	0	2	0	0	2	371	378
									EQLAIAEFAR	95.0	66.1	25.0	1147.61	0	29	0	0	2	434	443
									AFHNEAQVNPER	95.0	59.1	25.0	1411.67	0	4	6	0	2	469	480
									QAGVFEPTIVK	95.0	34.3	25.0	1188.66	0	1	0	0	2	500	510
									FATEAAITILR	95.0	71.8	25.0	1205.69	0	2	0	0	2	516	526
									IDDLIK	95.0	33.2	25.0	716.42	0	2	0	0	2	527	532
									DDKHGSYEDAVHSGALND	95.0	46.8	25.0	1929.82	0	0	2	0	2	539	556
									HGSYEDAVHSGALND	95.0	88.6	25.0	1571.67	0	4	0	0	2	542	556
T-complex protein 1 subunit beta	TCPB_HUMAN	CCT2	57.47	100.0	17	20	55	32.30	ILLSSGR	95.0	29.0	25.0	745.46	0	1	0	0	2	51	57
									DASLMVTNDGATILK	95.0	99.5	25.0	1564.79	0	2	0	0	2	58	72
									NIGVDNPAAK	95.0	32.1	25.0	998.53	0	1	0	0	2	73	82
									VLVDMSR	95.0	39.4	25.0	835.43	0	2	0	0	2	83	89
									EALLSSAVDHGSDEVK	95.0	84.9	25.0	1656.81	0	9	3	0	2	139	154
									QDLMNIAGTTLSSK	95.0	88.0	25.0	1494.75	0	2	0	0	2	157	170
									LAVEAVLR	95.0	36.0	25.0	870.54	0	2	0	0	2	182	189
									GSGNLEAIHIIK	95.0	53.8	25.0	1251.71	0	5	3	0	2	192	203
									IGVNQPK	95.0	32.5	25.0	755.44	0	4	0	0	2	224	230
									ILIANTGMDTDK	95.0	40.4	25.0	1307.65	0	2	0	0	2	237	248
									ILIANTGMDTDKIK	95.0	81.1	25.0	1548.83	0	4	1	0	2	237	250
									VAEIEHAEK	95.0	45.4	25.0	1025.53	0	2	0	0	2	264	272
									LIEEVMIGEDK	95.0	53.7	25.0	1291.65	0	1	0	0	2	348	358
									GATQQILDEAER	95.0	70.8	25.0	1330.66	0	4	0	0	2	377	388
									EAVAMESYAK	95.0	44.0	25.0	1114.51	0	4	0	0	2	432	441
									AAHSEGNTTAGLDMR	95.0	44.4	25.0	1546.69	0	2	0	0	2	467	481
									VDNIIK	95.0	27.5	25.0	701.42	0	1	0	0	2	517	522
T-complex protein 1 subunit delta	TCPD_HUMAN	CCT4	57.91	100.0	10	11	45	19.30	MIQDGKGDVTITNDGATILK	95.0	67.3	25.0	2106.08	0	0	2	0	2	60	79
									GDVTITNDGATILK	95.0	92.0	25.0	1417.75	0	7	0	0	2	66	79
									MLVELSK	95.0	38.0	25.0	835.46	0	2	0	0	2	90	96
									GIHPTIISESFQK	95.0	50.3	25.0	1456.78	0	2	4	0	2	127	139
									ETLLNSATTSLNSK	95.0	####	25.0	1478.77	0	8	0	0	2	161	174
									VIDPATATSVDLR	95.0	88.0	25.0	1357.73	0	12	0	0	2	194	206
									TDMDNQIVVSDYAQMDR	95.0	####	25.0	2032.86	0	4	0	0	2	258	274
									TVTIVVR	95.0	29.7	25.0	787.50	0	1	0	0	2	385	391
									LTEYSR	95.0	32.3	25.0	768.39	0	1	0	0	2	436	441
									TAGINVR	95.0	36.6	25.0	730.42	0	2	0	0	2	490	496
T-complex protein 1 subunit epsilon	TCPE_HUMAN	CCT5	59.65	100.0	14	16	57	18.30	LMVELSK	95.0	27.9	25.0	835.46	0	2	0	0	2	90	96
									IADGYEQAAR	95.0	78.9	25.0	1093.53	0	12	0	0	2	133	142
									VAIEHLDK	95.0	50.7	25.0	924.52	0	2	0	0	2	143	150
									RDVDFELIK	95.0	45.0	25.0	1134.62	0	2	0	0	2	202	210
									DVDFELIK	95.0	35.3	25.0	978.51	0	3	0	0	2	203	210
									GVIVDKDFSHPQMPK	95.0	46.2	25.0	1713.86	0	2	2	0	2	227	241
									HKLDVTSVEDYK	95.0	65.7	25.0	1433.73	0	2	0	0	2	264	275
									LDVTSVEDYK	95.0	73.7	25.0	1168.57	0	4	0	0	2	266	275
									EKFEEMIQQIK	95.0	47.8	25.0	1438.72	0	7	0	0	2	283	293

									FEEMIQQIK	95.0	31.0	25.0	1181.59	0	2	0	0	2	285	293
									FSELTAEK	95.0	45.0	25.0	924.47	0	4	0	0	2	345	352
									AVTIFIR	95.0	58.2	25.0	819.51	0	7	0	0	2	382	388
									KQQISLATQMVR	95.0	63.6	25.0	1418.78	0	2	2	0	2	514	525
									QQISLATQMVR	95.0	56.7	25.0	1290.68	0	2	0	0	2	515	525
T-complex protein 1 subunit eta	TCPH_HUMAN	CCT7	59.35	100.0	13	14	43	23.40	ATISNDGATILK	95.0	71.3	25.0	1203.66	0	3	0	0	2	56	67
									LLDVVHPAAK	95.0	59.6	25.0	1062.63	0	4	2	0	2	68	77
									TLVDIAK	95.0	38.6	25.0	759.46	0	1	0	0	2	78	84
									TATQLAVNK	95.0	48.9	25.0	945.54	0	2	0	0	2	127	135
									IKEIAVTVK	95.0	28.8	25.0	1000.64	0	1	0	0	2	136	144
									EIAVTVK	95.0	36.6	25.0	759.46	0	2	0	0	2	138	144
									TFSYAGFEMQPK	95.0	57.4	25.0	1421.64	0	2	0	0	2	219	230
									LPIGDVATQYFADR	95.0	61.8	25.0	1565.80	0	1	0	0	2	293	306
									VPEEDLKR	95.0	35.8	25.0	985.53	0	4	0	0	2	314	321
									GGAEQFMEETER	95.0	66.4	25.0	1399.58	0	8	0	0	2	376	387
									SLHDAIMIVR	95.0	24.1	25.0	1170.63	0	0	2	0	2	388	397
									NDSVVAGGGAIEMELSK	95.0	####	25.0	1692.81	0	4	0	0	2	402	418
									ALEIIPR	95.0	43.0	25.0	811.50	0	7	0	0	2	441	447
T-complex protein 1 subunit gamma	TCPG_HUMAN	CCT3	60.52	100.0	11	12	92	18.70	EIQVQHPAAK	94.7	26.5	25.0	1120.61	0	1	0	0	2	69	78
									KALDDMISTLK	95.0	41.1	25.0	1250.67	0	2	0	0	2	128	138
									ALDDMISTLK	95.0	43.3	25.0	1122.57	0	6	0	0	2	129	138
									IVLLDSSLEYK	95.0	53.7	25.0	1279.71	0	4	0	0	2	238	248
									KGESQTDIEITR	95.0	79.3	25.0	1376.70	0	5	0	0	2	249	260
									GISDLAQHYLMR	95.0	63.7	25.0	1419.71	0	12	4	0	2	295	306
									ANITAIR	95.0	39.6	25.0	758.45	0	3	0	0	2	307	313
									EILSEVER	95.0	51.4	25.0	974.52	0	6	0	0	2	382	389
									AVAQALEVIPR	95.0	95.8	25.0	1166.69	0	39	0	0	2	439	449
									TAVETAVLLLR	95.0	68.2	25.0	1185.72	0	8	0	0	2	508	518
									IDDIVSGHK	95.0	36.6	25.0	983.52	0	2	0	0	2	519	527
T-complex protein 1 subunit theta	TCPQ_HUMAN	CCT8	59.60	100.0	20	21	104	37.00	APGFAQMLK	95.0	48.6	25.0	978.51	0	2	0	0	2	8	16
									LFVTNDAATILR	95.0	82.8	25.0	1333.75	0	8	0	0	2	63	74
									DIDEVSSLLR	95.0	66.8	25.0	1146.60	0	17	0	0	2	156	165
									ETEGDVTSVK	95.0	35.5	25.0	1064.51	0	3	0	0	2	226	235
									TAEELMNFSK	95.0	55.4	25.0	1185.55	0	3	0	0	2	261	270
									GEENLMDAQVK	95.0	67.5	25.0	1249.57	0	16	0	0	2	271	281
									AIADTGANVVVTGGK	95.0	99.1	25.0	1372.74	0	2	0	0	2	282	296
									YNIMLVR	95.0	41.1	25.0	924.50	0	1	0	0	2	308	314
									TVGATALPR	95.0	36.9	25.0	885.52	0	1	0	0	2	327	335
									HEKEDGAISTIVLR	95.0	64.1	25.0	1567.84	0	3	1	0	2	365	378
									EDGAISTIVLR	95.0	44.0	25.0	1173.65	0	2	0	0	2	368	378
									GSTDNLMDDIER	95.0	69.5	25.0	1381.59	0	4	0	0	2	379	390
									AVDDGVNTFK	95.0	68.6	25.0	1065.52	0	9	0	0	2	391	400
									LVPGGGATEIELAK	95.0	58.5	25.0	1354.76	0	4	0	0	2	408	421
									KFAEAFEAIPR	95.0	41.2	25.0	1278.68	0	0	2	0	2	440	450
									FAEAFEAIPR	95.0	73.9	25.0	1150.59	0	12	0	0	2	441	450
									LYAVHQEGNK	95.0	33.0	25.0	1158.59	0	5	0	0	2	467	476
									NVGLDIEAEVPAVK	95.0	66.3	25.0	1453.79	0	4	0	0	2	477	490
									DMLEAGILDTYLGK	95.0	75.3	25.0	1554.77	0	2	0	0	2	491	504
									LATNAAVTVLR	95.0	####	25.0	1128.67	0	3	0	0	2	510	520
T-complex protein 1 subunit zeta	TCPZ_HUMAN	CCT6A	58.01	100.0	9	10	40	16.60	MLVSGAGDIK	95.0	41.4	25.0	1006.52	0	2	0	0	2	46	55
									IITEGFEAAK	95.0	62.8	25.0	1078.58	0	6	0	0	2	118	127

									ALQFLEEVK	95.0	65.5	25.0	1076.60	0	12	0	0	2	130	138
									EMDRETLIDVAR	95.0	36.8	25.0	1463.72	0	2	2	0	2	142	153
									SETDTSLIR	95.0	60.6	25.0	1021.52	0	1	0	0	2	200	208
									GLVLDHGAR	95.0	45.4	25.0	937.52	0	5	0	0	2	209	217
									TEVNSGFFYK	95.0	57.5	25.0	1191.57	0	4	0	0	2	242	251
									GIDPFSLDALSK	95.0	53.8	25.0	1262.66	0	2	0	0	2	296	307
									SVTLLIK	95.0	45.2	25.0	773.51	0	4	0	0	2	371	377
Tenascin	TENA_HUMAN	TNC	240.83	100.0	28	34	275	12.80	LEELENLVSSLR	95.0	66.4	25.0	1401.76	0	2	0	0	2	126	137
									VFAILENKK	95.0	39.4	25.0	1061.64	0	6	0	0	2	692	700
									NMNKEDEGEITK	95.0	41.6	25.0	1423.64	0	3	1	0	2	748	759
									LDAPSQIEVK	95.0	76.4	25.0	1099.60	0	16	0	0	2	803	812
									ETFTTGLDAPR	95.0	83.7	25.0	1207.60	0	23	0	0	2	887	897
									AAIDSYR	95.0	36.3	25.0	795.40	0	4	0	0	2	918	924
									YAPISGGDHAEVDVPK	95.0	99.2	25.0	1654.81	0	10	1	0	2	927	942
									EDKESNPATINAATELDTPK	95.0	93.8	25.0	2144.04	0	6	16	0	2	970	989
									ESNPATINAATELDTPK	95.0	85.2	25.0	1771.87	0	10	0	0	2	973	989
									AVDIPGLK	95.0	35.3	25.0	812.49	0	3	0	0	2	1128	1135
									STDLPGLK	95.0	33.2	25.0	830.46	0	2	0	0	2	1219	1226
									AATHYTITIR	95.0	52.0	25.0	1146.63	0	4	4	0	2	1227	1236
									SMEIPGLR	95.0	32.8	25.0	918.47	0	7	0	0	2	1310	1317
									AGTPYTVTLHGEVR	95.0	71.8	25.0	1500.78	0	6	0	0	2	1318	1331
									VSIYGVIR	95.0	58.3	25.0	906.54	0	15	0	0	2	1415	1422
									TPVLSAEASTAK	95.0	76.5	25.0	1174.63	0	18	0	0	2	1426	1437
									RSQTVSAIATTAMGSPK	95.0	44.2	25.0	1721.89	0	2	8	0	2	1698	1714
									SQTVSAIATTAMGSPK	95.0	####	25.0	1565.78	0	17	0	0	2	1699	1714
									APTAQVESFR	95.0	60.5	25.0	1105.56	0	4	0	0	2	1732	1741
									FTTDLDSPR	95.0	49.5	25.0	1051.51	0	8	0	0	2	1883	1891
									IQALNGPLR	95.0	69.5	25.0	981.58	0	7	0	0	2	1955	1963
									AYAAGFGDR	95.0	66.7	25.0	927.43	0	15	0	0	2	2042	2050
									AYAAGFGDRR	95.0	23.2	25.0	1083.53	0	1	1	0	2	2042	2051
									ITAQGQYELR	95.0	88.0	25.0	1178.62	0	15	0	0	2	2064	2073
									DHGETAFAVYDK	95.0	82.3	25.0	1352.61	0	12	0	0	2	2078	2089
									FSVGDAK	95.0	34.8	25.0	723.37	0	9	0	0	2	2090	2096
									LKVEGYSGTAGDSMAYHNGR	95.0	20.1	25.0	2128.97	0	0	1	0	2	2101	2120
									GHEHSIQFAEMK	95.0	38.6	25.0	1429.65	0	0	18	0	2	2174	2185
Thimet oligopeptidase	THOP1_HUMAN	THOP1	78.82	100.0	9	9	26	14.20	NILDFPQHVSPSK	95.0	68.3	25.0	1481.77	0	4	0	0	2	80	92
									LSEFDVEMSMR	95.0	29.0	25.0	1375.59	0	2	0	0	2	105	115
									LKPLGEQER	95.0	34.6	25.0	1069.60	0	0	2	0	2	302	310
									YYMNQVEETR	95.0	37.2	25.0	1348.58	0	4	0	0	2	339	348
									FYLDLYPR	95.0	45.0	25.0	1086.56	0	2	0	0	2	411	418
									QANTGLFNLR	95.0	75.2	25.0	1133.61	0	4	0	0	2	544	553
									VDQALHTQTDADPAEEYAR	95.0	60.5	25.0	2129.97	0	0	5	0	2	560	578
									FKQEGVLNSK	95.0	27.5	25.0	1149.63	0	0	2	0	2	627	636
									QDAFLLSK	95.0	28.4	25.0	921.50	0	1	0	0	2	668	675
Thiopurine S-methyltransferase	TPMT_HUMAN	TPMT	28.16	100.0	3	3	5	10.20	GALVAINPGDR	95.0	30.0	25.0	1082.60	0	1	0	0	2	153	163
									VDAFEER	95.0	30.8	25.0	865.41	0	3	0	0	2	220	226
									LYLLTEK	95.0	29.2	25.0	879.52	0	1	0	0	2	239	245
Thioredoxin	THIO_HUMAN	TXN	11.72	100.0	5	6	140	42.90	TAFQEALDAAGDK	95.0	####	25.0	1336.64	0	71	0	0	2	9	21
									MIKPFFHSLSEK	95.0	44.5	25.0	1479.77	0	4	7	0	2	37	48
									VGEFSGANK	95.0	57.1	25.0	908.45	0	47	0	0	2	86	94
									EKLEATINELV	95.0	56.1	25.0	1258.69	0	5	0	0	2	95	105

									LEATINELV	95.0	64.9	25.0	1001.55	0	6	0	0	2	97	105
Thioredoxin reductase 1, cytoplasmic	TRXR1_HUMAN	TXNRD1	70.89	100.0	7	8	20	11.60	LMHQAALLGQALQDSR	95.0	####	25.0	1767.92	0	2	0	0	2	219	234
									FLIATGERPR	95.0	36.6	25.0	1159.66	0	2	0	0	2	307	316
									YLGIPGDK	94.7	26.5	25.0	862.47	0	1	0	0	2	317	324
									GFDQDMANK	95.0	37.2	25.0	1041.43	0	2	0	0	2	377	385
									IGEHMEEHGIK	95.0	32.8	25.0	1295.61	0	2	3	0	2	386	396
									VEQIEAGTPGR	95.0	65.2	25.0	1156.60	0	6	0	0	2	406	416
									KIGLETVGVK	95.0	38.8	25.0	1043.65	0	2	0	0	2	449	458
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3_HUMAN	PRDX3	27.67	100.0	4	5	14	14.10	GTAVVNGEFK	95.0	39.0	25.0	1021.53	0	3	0	0	2	74	83
									DLSLDDFK	95.0	31.5	25.0	952.46	0	2	0	0	2	84	91
									HLSVNDLPVGR	95.0	47.5	25.0	1206.66	0	7	1	0	2	197	207
									SVEETLR	94.7	26.5	25.0	833.44	0	1	0	0	2	208	214
Threonyl-tRNA synthetase, cytoplasmic	SYTC_HUMAN	TARS	83.42	100.0	20	25	200	23.70	MGGEEKPIGAGEEK	95.0	45.1	25.0	1447.67	0	11	8	0	2	13	26
									LEMYNILK	95.0	28.8	25.0	1039.55	0	1	0	0	2	58	65
									AEHDSILAEK	95.0	54.1	25.0	1112.56	0	13	2	0	2	66	75
									VTLPDGK	95.0	33.8	25.0	729.41	0	8	0	0	2	85	91
									KETLLAMFK	95.0	48.9	25.0	1096.61	0	2	1	0	2	223	231
									ETLLAMFK	95.0	29.2	25.0	968.51	0	3	0	0	2	224	231
									ADMETLQR	95.0	40.8	25.0	979.45	0	2	0	0	2	289	296
									IYGISFPDPK	95.0	62.4	25.0	1136.60	0	20	0	0	2	297	306
									LADFGVLHR	95.0	52.4	25.0	1027.57	0	2	0	0	2	434	442
									NELSGALTGLTR	95.0	98.4	25.0	1231.66	0	52	0	0	2	443	454
									LNLSTRPEK	94.6	26.4	25.0	1057.60	0	1	0	0	2	496	504
									QLENSLNEFGEK	95.0	62.5	25.0	1407.68	0	7	0	0	2	518	529
									IDIQIK	95.0	34.1	25.0	729.45	0	2	0	0	2	544	549
									FNLTYVSHDGDDK	95.0	80.8	25.0	1510.68	0	8	2	0	2	571	583
									FNLTYVSHDGDDKK	95.0	64.6	25.0	1638.78	0	3	1	0	2	571	584
									RPVIVHR	95.0	27.2	25.0	876.55	0	1	0	0	2	585	591
									AILGSVER	95.0	37.5	25.0	844.49	0	7	0	0	2	592	599
									MIAILTENYGGK	95.0	67.5	25.0	1325.68	0	38	0	0	2	600	611
									ISGTVNIR	95.0	30.5	25.0	859.50	0	1	0	0	2	682	689
									TISETIER	95.0	43.2	25.0	948.50	0	4	0	0	2	700	707
Thrombospondin-1	TSP1_HUMAN	THBS1	129.36	100.0	16	19	247	13.90	GPDPSSPAFR	95.0	39.9	25.0	1030.50	0	12	0	0	2	51	60
									IEDANLIPPVPDDK	95.0	42.5	25.0	1535.80	0	2	0	0	2	61	74
									FQDLVDAVR	95.0	57.8	25.0	1062.56	0	8	0	0	2	75	83
									GFLLLASLR	95.0	54.4	25.0	989.61	0	22	0	0	2	87	95
									GTLLALER	95.0	43.5	25.0	872.52	0	4	0	0	2	102	109
									SITLFVQEDR	95.0	64.3	25.0	1207.63	0	7	0	0	2	155	164
									DLASIAR	95.0	33.1	25.5	745.42	0	6	0	0	2	190	196
									GGVNDNFQGVLQNVR	95.0	88.2	25.0	1616.81	0	31	2	0	2	202	216
									TIVTTLQDSIR	95.0	39.4	25.0	1246.70	0	4	0	0	2	289	299
									VTEENKELANELR	95.0	95.4	25.0	1544.79	0	5	16	0	2	301	313
									FTGSQPFGQGVEHATANK	95.0	81.2	25.0	1875.90	0	20	31	0	2	624	641
									LVPNPDQK	95.0	27.3	25.0	910.50	0	1	0	0	2	912	919
									FQMIPLDPK	95.0	52.4	25.0	1104.58	0	42	0	0	2	960	968
									AQGYSGLSVK	95.0	38.5	25.0	1009.53	0	3	0	0	2	1055	1064
									KIMADSGPIYDK	95.0	51.8	25.0	1353.67	0	9	0	0	2	1130	1141
									IMADSGPIYDK	95.0	42.3	25.0	1225.58	0	22	0	0	2	1131	1141
THUMP domain-containing protein 1	THUM1_HUMAN	THUMPD1	39.30	100.0	3	3	7	8.78	FQSVESGANNVVFIR	95.0	58.4	25.0	1666.85	0	1	0	0	2	117	131
									GTFQIVYK	95.0	29.7	25.0	955.52	0	1	0	0	2	194	201
									YNLQEVVK	95.0	45.7	25.0	992.54	0	5	0	0	2	262	269

Thymidine phosphorylase	TYPH_HUMAN	TYMP	49.94	100.0	7	8	18	16.20	KLVEGLSALVVDVK	95.0	58.3	25.0	1469.89	0	2	2	0	2	222	235
									LVEGLSALVVDVK	95.0	82.1	25.0	1341.80	0	4	0	0	2	223	235
									FGGAAVFPNQEQAR	95.0	52.8	25.0	1491.73	0	2	0	0	2	236	249
									TLVGVGASLGLR	95.0	55.3	25.0	1142.69	0	2	0	0	2	254	265
									VAAALTAMDKPLGR	95.0	47.6	25.0	1429.78	0	2	0	0	2	266	279
									MLAAQGVDPGLAR	95.0	56.7	25.0	1314.68	0	2	0	0	2	346	358
									ALQEALVLSDR	95.0	58.5	25.0	1214.67	0	2	0	0	2	454	464
Thyroid receptor-interacting protein 13	TRP13_HUMAN	TRIP13	48.53	100.0	3	3	17	8.33	NVQSVSIIDTELK	95.0	66.2	25.0	1445.78	0	4	0	0	2	69	81
									VVNAVLTQIDQIK	95.0	80.2	25.0	1440.84	0	7	0	0	2	276	288
									LSLLLNDISR	95.0	61.7	25.0	1143.67	0	6	0	0	2	369	378
TIP41-like protein	TIPRL_HUMAN	TIPRL	31.43	100.0	4	4	10	14.00	GTLLGESLK	95.0	45.6	25.0	917.53	0	2	0	0	2	118	126
									VVPTTDHIDTEK	95.0	26.9	25.0	1354.69	0	1	0	0	2	129	140
									IDGVLIR	95.0	45.7	25.0	785.49	0	4	0	0	2	189	195
									IDPNPADSQK	95.0	29.4	25.0	1084.53	0	3	0	0	2	258	267
Trafficking protein particle complex subunit 3	TPPC3_HUMAN	TRAPPC3	20.26	100.0	5	5	12	27.80	DYENDEDVNK	95.0	33.8	25.0	1240.50	0	2	0	0	2	33	42
									MGFNIGVR	95.0	49.5	25.0	909.46	0	2	0	0	2	47	54
									LIEDFLAR	95.0	36.1	25.0	976.55	0	6	0	0	2	55	62
									GALEMVQMAVEAK	95.0	41.4	25.0	1408.68	0	1	0	0	2	137	149
									RIEDNLPAGEE	95.0	47.6	25.0	1242.60	0	1	0	0	2	170	180
Trafficking protein particle complex subunit 4	TPPC4_HUMAN	TRAPPC4	24.32	100.0	3	3	5	12.30	AIFSVYVVNK	95.0	62.6	25.0	1139.65	0	2	0	0	1	2	11
									FVVLADPR	95.0	37.9	25.0	916.53	0	2	0	0	2	155	162
									QAGIDSLLR	95.0	40.7	25.0	972.55	0	1	0	0	2	163	171
Transaldolase	TALDO_HUMAN	TALDO1	37.52	100.0	14	14	108	33.20	MESALDQLK	95.0	47.5	25.0	1050.51	0	4	0	0	2	11	19
									LGGSQEDQIK	95.0	83.2	25.0	1074.54	0	25	0	0	2	72	81
									VSTEVDAR	95.0	49.8	25.0	876.44	0	17	0	0	2	103	110
									LSFDKDAMVAR	95.0	37.8	25.0	1268.63	0	0	2	0	2	111	121
									RLIELYK	95.0	30.3	25.0	934.57	0	3	0	0	2	124	130
									LIELYK	95.0	44.0	25.0	778.47	0	4	0	0	2	125	130
									SYEPLEDPGVK	95.0	46.6	25.0	1233.60	0	4	0	0	2	205	215
									TIVMGASFR	95.0	59.8	25.0	997.51	0	10	0	0	2	231	239
									ALAGCDFLTISPK	95.0	64.2	25.0	1392.72	0	2	0	0	2	246	258
									LLGELLQDNAK	95.0	82.6	25.0	1213.68	0	20	0	0	2	259	269
									AAQASDLEK	95.0	40.3	25.0	932.47	0	4	0	0	2	278	286
									IHLDEK	95.0	29.6	25.0	754.41	0	2	0	0	2	287	292
									KFAADAVK	95.0	37.5	25.0	849.48	0	2	0	0	2	314	321
									FAADAVK	95.0	47.8	25.0	721.39	0	9	0	0	2	315	321
Transcription elongation factor B polypeptide 2	ELOB_HUMAN	TCEB2	13.12	100.0	3	4	9	24.60	ESSTVFELKR	95.0	60.6	25.0	1195.63	0	2	0	0	2	20	29
									RIVEGILK	95.0	26.9	25.0	927.60	0	1	0	0	2	29	36
									LYKDDQLLDDGK	95.0	71.8	25.0	1422.71	0	4	2	0	2	44	55
Transcription elongation factor SPT6	SPT6H_HUMAN	SUPT6H	199.06	100.0	6	6	15	3.42	IKEALGFMR	95.0	31.7	25.0	1080.59	0	3	0	0	2	359	367
									ALQQFLYVQMAK	95.0	65.9	25.0	1455.77	0	4	0	0	2	716	727
									VLGIAFSSAR	95.0	80.7	25.0	1020.58	0	5	0	0	2	781	790
									KPHVVTVAGENR	95.0	20.9	25.0	1306.72	0	0	1	0	2	844	855
									HITLYDIR	95.0	27.3	25.0	1030.57	0	1	0	0	2	1120	1127
									FLLGYQPR	95.0	26.9	25.0	993.55	0	1	0	0	2	1472	1479
Transcription initiation factor IIA subunit 2	T2AG_HUMAN	GTF2A2	12.44	100.0	3	3	11	21.10	AINAALAQR	95.0	44.6	25.0	927.54	0	9	0	0	2	43	51
									GSLNTYR	95.0	29.5	25.0	810.41	0	1	0	0	2	60	66
									EVTELIK	95.0	30.5	25.0	831.48	0	1	0	0	2	83	89
Transcriptional activator protein Pur-beta	PURB_HUMAN	PURB	33.22	100.0	4	4	8	10.60	GGGEQETQELASK	95.0	51.4	25.0	1333.62	0	2	0	0	2	25	37
									SEFLVR	95.0	29.7	25.0	750.41	0	2	0	0	2	121	126
									YGVFLR	95.0	34.0	25.0	754.42	0	3	0	0	2	241	246

									NAITVPFK	95.0	46.5	25.0	889.51	0	1	0	0	2	256	263
Transferrin receptor protein 1	TFR1_HUMAN	TFRC	84.86	100.0	9	10	45	13.00	LLNENSYVPR	95.0	71.1	25.0	1204.63	0	6	0	0	2	146	155
									SSGLPNIPVQTISR	95.0	65.2	25.0	1468.81	0	11	0	0	2	326	339
									LTVSNVLK	95.0	34.5	25.0	873.54	0	3	0	0	2	375	382
									ILNIFGVIK	95.0	37.0	25.0	1016.65	0	2	0	0	2	386	394
									GFVEPDHYVVVGAQR	95.0	76.3	25.0	1672.84	0	1	1	0	2	395	409
									LAQMFSDMVLK	95.0	63.4	25.0	1314.64	0	5	0	0	2	429	439
									AFTYINLDK	95.0	55.9	25.0	1084.57	0	6	0	0	2	478	486
									VSASPLLYTLIEK	95.0	76.1	25.0	1433.83	0	5	0	0	2	496	508
									YNSQLLSFVR	95.0	59.2	25.0	1226.65	0	5	0	0	2	614	623
Transforming growth factor beta-2	TGFB2_HUMAN	TGFB2	47.73	100.0	5	5	9	13.00	ERSDEEYYAK	95.0	31.0	25.0	1289.56	0	1	0	0	2	92	101
									IELYQILK	95.0	46.5	25.0	1019.61	0	3	0	0	2	166	173
									SKDLTSPTQR	95.0	27.1	25.0	1132.60	0	1	0	0	2	174	183
									FAGIDGTSTYTSGDQK	95.0	95.0	25.0	1647.75	0	2	0	0	2	250	265
									IEQLSNMIVK	95.0	41.9	25.0	1190.65	0	2	0	0	2	400	409
Transforming growth factor-beta-induced protein ig-h3	BGH3_HUMAN	TGFBI	74.66	100.0	14	21	251	20.90	RVLTDELK	95.0	33.2	25.0	973.57	0	4	0	0	2	179	186
									VLTDELK	95.0	49.7	25.0	817.47	0	5	0	0	2	180	186
									ADHHATNGVVHLIDK	95.0	62.9	25.0	1626.83	0	3	8	6	2	220	234
									IPSETLNR	95.0	53.2	25.0	929.51	0	20	0	0	2	288	295
									ILGDPEALR	95.0	46.9	25.0	983.55	0	34	0	0	2	296	304
									DLLNNHILK	95.0	43.0	25.0	1079.62	0	14	4	0	2	305	313
									QAGLGNHLSGSER	95.0	60.2	25.0	1325.66	0	12	6	0	2	397	409
									DGTPPIDAHTR	95.0	62.6	25.0	1179.58	0	21	5	0	2	422	432
									YLYHGQTLETLGGK	95.0	86.4	25.0	1579.81	0	12	12	0	2	448	461
									YGTLFTMDR	95.0	66.3	25.0	1119.51	0	23	0	0	2	488	496
									VLTPPMGTVMDVLK	95.0	68.2	25.0	1532.81	0	37	0	0	2	497	510
									SLQGDKLEVSLK	95.0	75.0	25.0	1316.74	0	7	7	0	2	591	602
									NNVVSVNK	95.0	29.3	25.0	873.48	0	1	0	0	2	603	610
									GDELADSALEIFK	95.0	66.0	25.0	1407.70	0	10	0	0	2	643	655
Transgelin	TAGL_HUMAN	TAGLN	22.59	100.0	6	7	25	33.30	LVNSLYPDGSKPVK	95.0	39.8	25.0	1516.84	0	1	6	0	2	65	78
									VPENPPSMVFK	95.0	29.1	25.0	1260.63	0	1	0	0	2	79	89
									QMEQVAQFLK	95.0	57.4	25.0	1237.62	0	6	0	0	2	90	99
									AAEDYGVIK	95.0	55.1	25.0	965.49	0	5	0	0	2	100	108
									TLMALGSLAVTK	95.0	37.3	25.0	1220.69	0	1	0	0	2	129	140
									EFTESQLQEGK	95.0	74.6	25.0	1295.61	0	5	0	0	2	162	172
Transgelin-2	TAGL2_HUMAN	TAGLN2	22.37	100.0	7	8	85	40.20	DVGRPQPGR	95.0	35.8	25.0	981.52	0	6	0	0	2	41	49
									IQASTMAFK	95.0	28.0	25.0	1012.51	0	1	0	0	2	80	88
									QMEQISQFLQAAER	95.0	86.1	25.0	1694.82	0	4	2	0	2	89	102
									TLMNLGGLAVAR	95.0	86.1	25.0	1231.68	0	34	0	0	2	128	139
									NFSDNQLQEGK	95.0	72.5	25.0	1279.59	0	28	0	0	2	161	171
									NVIGLQMGTNR	95.0	43.3	25.0	1218.63	0	6	0	0	2	172	182
									GASQAGMTGYGMPR	95.0	42.5	25.0	1415.60	0	4	0	0	2	183	196
Transitional endoplasmic reticulum ATPase	TERA_HUMAN	VCP	89.31	100.0	23	24	194	26.20	GDDLSTAILK	95.0	55.8	25.0	1032.56	0	2	0	0	2	9	18
									MDELQLFR	95.0	63.7	25.0	1067.52	0	46	0	0	2	46	53
									KGDIFLVR	95.0	50.4	25.0	947.57	0	7	0	0	2	148	155
									GDIFLVR	95.0	46.7	25.0	819.47	0	10	0	0	2	149	155
									AIGVKPPR	95.0	44.2	25.0	837.53	0	3	0	0	2	232	239
									GILLYGPPGTGK	95.0	35.7	25.0	1172.67	0	13	0	0	2	240	251
									LAGESESNLR	95.0	70.6	25.0	1075.54	0	10	0	0	2	278	287
									RIVSQLLTLMDGLK	95.0	54.3	25.0	1602.93	0	2	0	0	2	323	336
									IVSQLLTLMDGLK	95.0	####	25.0	1446.82	0	9	0	0	2	324	336

									AHVIVMAATNRPNSIDPALR	95.0	25.9	25.0	2162.15	0	0	2	0	2	339	358
									EVDIGIPDATGR	95.0	63.5	25.0	1242.63	0	35	0	0	2	366	377
									LEILQIHTK	95.0	35.5	25.0	1094.66	0	0	6	0	2	378	386
									WALSQSNPSALR	95.0	86.2	25.0	1329.69	0	4	0	0	2	454	465
									ELQELVQYPVEHPDK	95.0	82.7	25.0	1823.92	0	6	4	0	2	488	502
									GVLFYGPPGCGK	95.0	53.2	25.0	1251.62	0	2	0	0	2	513	524
									AIANECQANFISIK	95.0	79.3	25.0	1578.79	0	2	0	0	2	530	543
									VINQILTEMDGMSTK	95.0	86.5	25.0	1711.82	0	10	0	0	2	600	614
									VINQILTEMDGMSTKK	95.0	33.1	25.0	1839.92	0	1	0	0	2	600	615
									DVDLEFLAK	95.0	51.8	25.0	1049.55	0	11	0	0	2	669	677
									ESIESEIR	95.0	37.9	25.0	962.48	0	2	0	0	2	701	708
									ESIESEIRR	95.0	30.3	25.0	1118.58	0	4	0	0	2	701	709
									KYEMFAQTLQQSR	95.0	87.5	25.0	1645.80	0	2	0	0	2	754	766
									YEMFAQTLQQSR	95.0	71.0	25.0	1517.71	0	1	0	0	2	755	766
Transketolase	TKT_HUMAN	TKT	67.86	100.0	18	23	146	24.40	KISSDLDGHPVPK	95.0	51.5	25.0	1392.75	0	2	4	0	2	102	114
									ISSDLDGHPVPK	95.0	67.6	25.0	1264.65	0	13	8	0	2	103	114
									LGQSDPAPLQHQMDIYQK	95.0	52.2	25.0	2085.01	0	5	14	0	2	187	204
									HQPTAIIAK	95.0	43.1	25.0	978.57	0	6	0	0	2	233	241
									MPSLPSYK	95.0	42.0	25.0	938.47	0	2	0	0	2	303	310
									KAYGQALAK	95.0	33.4	25.0	949.55	0	2	0	0	2	319	327
									IIALDGDTK	95.0	30.8	25.0	945.53	0	2	0	0	2	335	343
									NSTFSEIFK	95.0	27.1	25.0	1072.53	0	1	0	0	2	344	352
									NSTFSEIFKK	95.0	39.8	25.0	1200.63	0	3	2	0	2	344	353
									AFDQIR	95.0	37.3	25.0	749.39	0	10	0	0	2	396	401
									SVPTSTVFYPSDGVATEK	95.0	91.6	25.0	1884.92	0	6	0	0	2	439	456
									AVELAANTK	95.0	43.7	25.0	916.51	0	8	0	0	2	457	465
									VLDPFTIKPLDR	95.0	48.9	25.0	1413.81	0	7	2	0	2	531	542
									KLILDSAR	95.0	57.3	25.0	915.56	0	13	0	0	2	543	550
									LILDSAR	95.0	34.8	25.0	787.47	0	1	0	0	2	544	550
									SGKPAELLK	95.0	49.3	25.0	942.56	0	6	0	0	2	595	603
									MFGIDR	95.0	29.6	25.0	754.36	0	4	0	0	2	604	609
									DAIAQAVR	95.0	52.5	25.0	843.47	0	25	0	0	2	610	617
Translation initiation factor eIF-2B subunit alpha	EI2BA_HUMAN	EIF2B1	33.70	100.0	3	3	4	10.20	DKGETIQGLR	95.0	37.1	25.0	1116.60	0	2	0	0	2	37	46
									DGATILTHAYSR	95.0	57.6	25.0	1304.66	0	1	0	0	2	121	132
									VLEAAVAAK	95.0	29.7	25.0	871.52	0	1	0	0	2	137	145
Translation initiation factor eIF-2B subunit beta	EI2BB_HUMAN	EIF2B2	38.97	100.0	5	5	9	17.40	SDESDQQESLHK	95.0	41.1	25.0	1402.61	0	2	0	0	2	100	111
									TILANGALR	95.0	28.4	25.0	928.56	0	1	0	0	2	238	246
									AVTGTHTLALAAK	95.0	75.9	25.0	1253.72	0	2	0	0	2	247	259
									LSPQFPNEEDSFHK	95.0	49.3	25.0	1674.78	0	2	0	0	2	274	287
									LMSELYHPDDHVL	95.0	67.0	25.0	1584.74	0	2	0	0	2	339	351
Translationally-controlled tumor protein	TCTP_HUMAN	TPT1	19.58	100.0	3	4	5	17.40	GKLEEQRPER	95.0	32.2	25.0	1241.66	0	2	0	0	2	101	110
									VKPFMTGAAEQIK	95.0	46.1	25.0	1435.76	0	1	1	0	2	111	123
									HILANFK	95.0	27.6	25.0	842.49	0	1	0	0	2	124	130
Translin	TSN_HUMAN	TSN	26.17	100.0	6	9	27	21.10	KVVQSLEQTAR	95.0	38.1	25.0	1258.71	0	1	0	0	2	26	36
									TKFPAEQYYR	95.0	59.6	25.0	1302.65	0	2	4	0	2	77	86
									EAVTEILGIEPDR	95.0	79.4	25.0	1441.75	0	4	0	0	2	117	129
									EAVTEILGIEPDREK	95.0	65.9	25.0	1698.89	0	4	4	0	2	117	131
									KVEEVVYDLSIR	95.0	97.6	25.0	1449.79	0	4	2	0	2	204	215
									VEEVVYDLSIR	95.0	81.4	25.0	1321.70	0	2	0	0	2	205	215
Translin-associated protein X	TSNAX_HUMAN	TSNAX	33.10	100.0	4	4	10	16.20	DVNSSSPVMLAFK	95.0	70.0	25.0	1410.69	0	2	0	0	2	28	40
									TIFLLHR	95.0	41.6	25.0	899.55	0	4	0	0	2	70	76

									ITSAPDMEDILTESEIK	95.0	87.0	25.0	1907.92	0	1	0	0	2	77	93
									SLISMDEINK	95.0	37.3	25.0	1165.58	0	3	0	0	2	141	150
Transmembrane emp24 domain-containing protein 10	TMEDA_HUMAN	TMED10	24.96	100.0	3	3	11	14.60	ITDSAGHILYSK	95.0	74.4	25.0	1304.68	0	4	0	0	2	76	87
									IPDQLVILDMK	95.0	59.0	25.0	1300.72	0	5	0	0	2	117	127
									LKPLEVELR	95.0	56.5	25.0	1096.67	0	0	2	0	2	144	152
Transmembrane protein 132A	T132A_HUMAN	TMEM132A	110.09	100.0	4	4	8	5.38	MAGRTTAAPR	95.0	31.6	25.0	1047.54	0	1	0	0	2	5	14
									AVSVEAAVTPAEPYAR	95.0	42.0	25.0	1630.84	0	1	0	0	2	125	140
									VPGPAEGPAEPAAEASDEAERR	95.0	41.8	25.0	2206.04	0	0	1	0	2	514	535
									VSVLELR	95.0	42.7	25.0	815.50	0	5	0	0	2	634	640
Transportin-1	TNPO1_HUMAN	TNPO1	102.34	100.0	13	15	48	16.80	ESQSPDTTIQR	95.0	31.0	25.0	1261.60	0	2	0	0	2	29	39
									SLSGLILK	95.0	35.1	25.0	830.53	0	1	0	0	2	74	81
									ATVGILITTIASK	95.0	68.3	25.0	1287.79	0	3	0	0	2	116	128
									ALVMLLEVR	95.0	76.4	25.0	1059.62	0	19	0	0	2	246	254
									LLPHMHNIVEYMLQR	95.0	27.3	25.0	1925.97	0	0	2	1	2	258	272
									LIPVLVNGMK	95.0	59.9	25.0	1099.65	0	2	0	0	2	308	317
									YSDIDIILLK	95.0	37.0	25.0	1192.68	0	3	0	0	2	318	327
									GDVEEDETIPDSEQDIRPR	95.0	51.1	25.0	2200.00	0	1	2	0	2	328	346
									DELLPHILPLLK	95.0	29.6	25.0	1400.85	0	1	0	0	2	400	411
									QSSFALLGDLTK	95.0	77.2	25.0	1279.69	0	6	0	0	2	693	704
									TLLENTAITIGR	95.0	64.5	25.0	1301.74	0	1	0	0	2	774	785
									DNEEKDSAFR	95.0	39.8	25.0	1210.53	0	2	0	0	2	814	823
									FSDQFPLPLK	95.0	51.8	25.0	1191.64	0	2	0	0	2	880	889
TRIO and F-actin-binding protein	TARA_HUMAN	TRIOBP	261.36	100.0	3	3	3	0.93	NYGFQIHTK	95.0	28.1	25.0	1107.56	0	1	0	0	2	1853	1861
									LSEEIEK	95.0	28.4	25.0	847.44	0	1	0	0	2	2022	2028
									EIEQLK	95.0	35.5	25.0	759.42	0	1	0	0	2	2338	2343
Triosephosphate isomerase	TPIS_HUMAN	TPI1	26.65	100.0	10	16	232	40.20	KQSLGELIGTLNAAK	95.0	75.0	25.0	1542.89	0	6	3	0	2	19	33
									QSLGELIGTLNAAK	95.0	68.2	25.0	1414.79	0	25	1	0	2	20	33
									IAVAAQNCYK	95.0	42.3	25.0	1137.57	0	4	0	0	2	60	69
									VTNGAFTGEISPGMIK	95.0	96.0	25.0	1637.82	0	10	2	0	2	70	85
									RHVFGESDELIGQK	95.0	76.3	25.0	1614.82	0	2	3	0	2	100	113
									HVFGESDELIGQK	95.0	79.2	25.0	1458.72	0	30	4	0	2	101	113
									VVFEQTK	95.0	41.5	25.0	850.47	0	10	0	0	2	143	149
									TATPQQAQEVHEK	95.0	78.6	25.0	1466.72	0	39	15	0	2	176	188
									SNVSDAVAQSTR	95.0	####	25.0	1234.60	0	76	0	0	2	195	206
									IIYGGSVTGATCK	95.0	99.2	25.0	1326.67	0	2	0	0	2	207	219
Tripeptidyl-peptidase 1	TPP1_HUMAN	TPP1	61.23	100.0	3	4	12	8.17	LSELVQAVSDPSSPQYGK	95.0	98.9	25.0	1904.96	0	2	0	0	2	61	78
									LFGGNFAHQASVAR	95.0	####	25.0	1474.75	0	6	2	0	2	246	259
									LYQQHGAGLFDVTR	95.0	65.8	25.0	1604.82	0	2	0	0	2	507	520
Tripeptidyl-peptidase 2	TPP2_HUMAN	TPP2	138.33	100.0	11	11	47	8.97	DGEIVGLSGR	95.0	46.8	25.0	1002.52	0	2	0	0	2	86	95
									NGVAPGAQILSIK	95.0	54.0	25.0	1267.74	0	6	0	0	2	283	295
									LSTMETGTGLIR	95.0	56.4	25.0	1294.67	0	6	0	0	2	301	312
									ANNIDYTVHSVR	95.0	58.9	25.0	1388.69	0	2	0	0	2	468	479
									VPITAVIAAK	95.0	40.7	25.0	982.63	0	17	0	0	2	629	638
									FVLHAVQLVK	95.0	30.7	25.0	1153.71	0	0	3	0	2	688	697
									GTLTEAFPVLGGK	95.0	40.1	25.0	1289.71	0	3	0	0	2	716	728
									LKDLPFIVSHR	95.0	55.4	25.0	1324.77	0	0	2	0	2	903	913
									DLPFIVSHR	95.0	43.0	25.0	1083.59	0	2	0	0	2	905	913
									LDSSDIYNELK	95.0	88.3	25.0	1296.63	0	2	0	0	2	1036	1046
									LHQLDAEKER	95.0	28.1	25.0	1238.65	0	0	2	0	2	1060	1069
tRNA pseudouridine synthase A	TRUA_HUMAN	PUS1	47.45	100.0	3	3	7	7.26	TIEDDLVSALVR	95.0	64.7	25.0	1330.72	0	3	0	0	2	111	122
									EGLEFAVIR	95.0	53.3	25.0	1033.57	0	2	0	0	2	275	283

									APGLGLVLER	95.0	59.1	25.0	1024.62	0	2	0	0	2	328	337
Tropomyosin alpha-1 chain	TPM1_HUMAN	TPM1	32.69	99.5	2	2	4	25.00	LDKENALDR	95.0	24.6	25.0	1073.56	0	0	2	0	2	13	21
									QLEDELVSLQK	95.0	55.2	25.0	1301.69	0	2	0	0	2	38	48
									ATDAEADVASLNR	95.0	89.9	25.0	1332.64	0	6	0	0	2	78	90
									RIQLVEEELDR	95.0	40.7	25.0	1399.75	0	2	2	0	2	91	101
									IQLVEEELDR	95.0	72.7	25.0	1243.65	0	14	0	0	2	92	101
									LATALQK	95.0	32.6	25.0	744.46	0	2	0	0	2	106	112
									MEIQEIQLK	95.0	45.4	25.0	1147.60	0	6	0	0	2	141	149
									KLVIIESDLER	95.0	46.3	25.0	1314.76	0	2	0	0	2	168	178
Tropomyosin alpha-3 chain	TPM3_HUMAN	TPM3	32.80	100.0	5	6	25	21.10	LDKENALDR	95.0	24.6	25.0	1073.56	0	0	2	0	2	13	21
									AADAEAEVASLNR	95.0	65.2	25.0	1316.64	0	7	0	0	2	78	90
									RIQLVEEELDR	95.0	40.7	25.0	1399.75	0	2	2	0	2	91	101
									IQLVEEELDR	95.0	72.7	25.0	1243.65	0	14	0	0	2	92	101
									LATALQK	95.0	32.6	25.0	744.46	0	2	0	0	2	106	112
									MELQEIQLK	95.0	45.4	25.0	1147.60	0	6	0	0	2	141	149
									KLVIIEGDLER	95.0	63.0	25.0	1284.75	0	3	3	0	2	168	178
									LVIIEGDLER	95.0	71.5	25.0	1156.66	0	4	0	0	2	169	178
Tropomyosin alpha-4 chain	TPM4_HUMAN	TPM4	28.50	100.0	12	16	75	32.30	KIQALQQQADEAEDR	95.0	####	25.0	1742.87	0	2	4	0	2	13	27
									IQALQQQADEAEDR	95.0	96.2	25.0	1614.77	0	5	0	0	2	14	27
									EKAEGDVAALNR	95.0	66.1	25.0	1272.65	0	10	2	0	2	43	54
									AEGDVAALNR	95.0	49.9	25.0	1015.52	0	8	0	0	2	45	54
									RIQLVEEELDR	95.0	40.7	25.0	1399.75	0	2	2	0	2	55	65
									IQLVEEELDR	95.0	72.7	25.0	1243.65	0	14	0	0	2	56	65
									LATALQK	95.0	32.6	25.0	744.46	0	2	0	0	2	70	76
									MEIQEMQLK	95.0	38.7	25.0	1181.55	0	6	0	0	2	105	113
									KLVILEGELER	95.0	60.0	25.0	1298.77	0	7	4	0	2	132	142
									LVILEGELER	95.0	63.0	25.0	1170.67	0	5	0	0	2	133	142
									AEVSELK	95.0	33.8	25.1	775.42	0	1	0	0	2	147	153
									TIDDLEEK	95.0	27.9	25.0	962.47	0	1	0	0	2	216	223
Tryptophanyl-tRNA synthetase, cytoplasmic	SYWC_HUMAN	WARS	53.15	100.0	13	17	69	26.50	AGNASKDEIDSAVK	95.0	45.3	25.0	1404.70	0	5	6	0	2	28	41
									GIDYDKLIVR	95.0	70.2	25.0	1191.67	0	2	2	0	2	97	106
									IDKELINR	95.0	45.9	25.0	1000.58	0	4	0	0	2	112	119
									GIFFSHR	95.0	35.3	25.0	863.45	0	3	0	0	2	135	141
									DMNQVLDAYENK	95.0	67.0	25.0	1455.64	0	2	0	0	2	142	153
									KPFYLYTGR	95.0	37.9	25.0	1144.62	0	5	1	0	2	154	162
									DIIACGFDINK	95.0	57.1	25.0	1265.62	0	2	0	0	2	221	231
									MSASDPNSSIFLTDTAK	95.0	####	25.0	1800.83	0	8	0	0	2	350	366
									DYTSGAMLTGELK	95.0	96.1	25.0	1401.66	0	7	0	0	2	419	431
									DYTSGAMLTGELKK	95.0	63.1	25.0	1529.75	0	4	0	0	2	419	432
									ALIEVLQPLIAEHQAR	95.0	55.8	25.0	1801.03	0	3	2	0	2	433	448
									KLSFDFQ	95.0	58.9	25.0	884.45	0	12	0	0	2	465	471
									LSFDFQ	95.0	25.2	25.0	756.36	1	0	0	0	2	466	471
Tubulin-folding cofactor B	TBCB_HUMAN	TBCB	27.31	100.0	3	3	12	11.50	SLTIAEFK	95.0	29.2	25.0	908.51	0	2	0	0	2	31	38
									LGEYEDVSR	95.0	52.1	25.0	1067.50	0	4	0	0	2	95	103
									YTISQEAYDQR	95.0	79.9	25.0	1373.63	0	6	0	0	2	107	117
Tubulin-specific chaperone A	TBCA_HUMAN	TBCA	12.84	100.0	3	3	8	34.30	AEDGENYDIKK	95.0	38.0	25.0	1281.60	0	4	0	0	2	42	52
									RLEAAYLDLQR	95.0	44.3	25.0	1347.74	0	0	2	0	2	70	80
									ILENEKDLEEAEEYK	95.0	91.3	25.0	1851.89	0	2	0	0	2	81	95
Tubulin--tyrosine ligase-like protein 12	TTL12_HUMAN	TTLL12	74.39	100.0	5	6	13	9.47	QQLQQVPGLLHR	95.0	26.1	25.0	1416.81	0	0	2	0	2	133	144
									FNQTYQLAHGTAEEK	95.0	78.3	25.0	1736.82	0	2	3	0	2	173	187
									DLDTGEEVTR	95.0	60.0	25.0	1134.53	0	2	0	0	2	231	240

									DFAYGETDPLIR	95.0	74.6	25.0	1396.67	0	2	0	0	2	241	252
									AFALNDLDDYEK	95.0	80.2	25.0	1413.65	0	2	0	0	2	499	510
Tubulointerstitial nephritis antigen-like	TINAL_HUMAN	TINAGL1	52.37	100.0	3	5	11	7.49	ELAPGLHLR	95.0	52.8	25.0	1005.58	0	5	0	0	2	30	38
									LGSNDKEIMK	95.0	35.7	25.0	1150.58	0	1	1	0	2	346	355
									GGIYSHTPVSLGRPER	95.0	27.3	25.0	1725.90	0	2	2	0	2	378	393
Tumor necrosis factor alpha-induced protein 2	TNAP2_HUMAN	TNFAIP2	72.65	100.0	4	4	9	6.57	ELAAAAAAGGVSEEELVR	95.0	85.3	25.0	1742.89	0	1	0	0	2	103	120
									VEALYELLR	95.0	63.4	25.0	1105.63	0	2	0	0	2	125	133
									DQVLGVLR	95.0	31.9	25.0	899.53	0	2	0	0	2	134	141
									AFNEFLER	95.0	48.9	25.0	1025.51	0	4	0	0	2	404	411
Tumor protein D54	TPD54_HUMAN	TPD52L2	22.22	100.0	3	3	18	14.60	VEEEIVTLR	95.0	65.5	25.0	1087.60	0	5	0	0	2	56	64
									LGLSTLGELK	95.0	64.3	25.0	1030.61	0	10	0	0	2	81	90
									TQETLSQAGQK	95.0	61.7	25.0	1190.60	0	3	0	0	2	129	139
Twinfilin-1	TWF1_HUMAN	TWF1	40.27	100.0	4	5	13	10.30	HQTLQGVAFPISR	95.0	68.4	25.0	1453.79	0	5	2	0	2	172	184
									EAFQALEK	95.0	54.9	25.0	935.48	0	4	0	0	2	185	192
									YHFFLYK	95.0	28.8	25.0	1017.52	0	1	0	0	2	236	242
									QLQMDVIR	95.0	30.0	25.0	1018.54	0	1	0	0	2	286	293
Tyrosine-protein kinase-like 7	PTK7_HUMAN	PTK7	118.37	100.0	6	6	21	6.73	FAQGSSLSFAAVDR	95.0	####	25.0	1455.72	0	2	0	0	2	79	92
									HPASEAEIQPQTQVTLR	95.0	32.5	25.0	1904.98	0	0	2	0	2	133	149
									VVLAPQDVVVAR	95.0	57.2	25.0	1265.76	0	7	0	0	2	227	238
									VFTAGSEER	95.0	40.8	25.0	995.48	0	2	0	0	2	332	340
									NQMLISEDSR	95.0	41.1	25.0	1208.56	0	4	0	0	2	448	457
									SEFGEVFLAK	95.0	47.7	25.0	1126.58	0	4	0	0	2	805	814
Tyrosine-protein phosphatase non-receptor type 1	PTN1_HUMAN	PTPN1	49.95	100.0	4	4	18	10.10	LTLISEDIK	95.0	45.0	25.0	1031.60	0	2	0	0	2	142	150
									QLELENLTTQETR	95.0	96.8	25.0	1574.80	0	4	0	0	2	157	169
									MGLIQTADQLR	95.0	32.6	25.0	1261.66	0	2	0	0	2	258	268
									FSYLAVIEGAK	95.0	63.2	25.0	1197.65	0	10	0	0	2	269	279
Tyrosyl-tRNA synthetase, cytoplasmic	SYYC_HUMAN	YARS	59.13	100.0	11	11	49	21.60	NLQEVLGEEK	95.0	41.8	25.0	1158.60	0	2	0	0	2	17	26
									VSYYENVIK	95.0	38.6	25.0	1114.58	0	1	0	0	2	94	102
									AMLESIGVPLEK	95.0	73.7	25.0	1302.70	0	10	0	0	2	103	114
									EYTLDVYR	95.0	36.5	25.0	1058.52	0	2	0	0	2	128	135
									VDAQFGGIDQR	95.0	69.6	25.0	1205.59	0	4	0	0	2	179	189
									SEFVILR	95.0	34.8	25.0	863.50	0	4	0	0	2	273	279
									DFAAEVVHPGDLK	95.0	25.7	25.0	1397.71	0	0	2	0	2	298	310
									LLDPIR	94.7	26.5	25.0	726.45	0	1	0	0	2	320	325
									HPDADSLYVEK	95.0	27.1	25.0	1273.61	0	1	0	0	2	381	391
									IDVGEAEPR	95.0	57.5	25.0	985.50	0	9	0	0	2	392	400
									TVVSGLVQFVPK	95.0	71.4	25.0	1273.75	0	13	0	0	2	401	412
									LQADFK	95.0	27.9	25.0	721.39	0	1	0	0	2	491	496
U1 small nuclear ribonucleoprotein A	SNRPA_HUMAN	SNRPA	31.26	100.0	3	3	9	8.87	GQAFVIFK	95.0	37.0	25.0	909.52	0	3	0	0	2	53	60
									EVSSATNALR	95.0	70.2	25.0	1047.54	0	5	0	0	2	61	70
									DALQGFK	95.0	27.6	25.0	778.41	0	1	0	0	2	262	268
U2 small nuclear ribonucleoprotein A'	RU2A_HUMAN	SNRPA1	28.40	100.0	5	5	11	13.70	KLDGFPLLR	95.0	34.7	25.0	1058.64	0	3	0	0	2	56	64
									LDGFPLLR	95.0	29.0	25.0	930.54	0	1	0	0	2	57	64
									SLTYLSILR	95.0	58.1	25.0	1065.63	0	4	0	0	2	114	122
									LYVIYK	95.0	26.9	25.0	798.48	0	1	0	0	2	133	138
									GLLQSGQIPGR	95.0	40.9	25.0	1125.64	0	2	0	0	2	222	232
U4/U6.U5 tri-snRNP-associated protein 2	SNUT2_HUMAN	USP39	65.36	100.0	2	2	8	5.31	TFQITK	95.0	40.0	25.0	737.42	0	2	0	0	2	310	315
									TIVTDVFQGSMR	95.0	65.8	25.0	1369.68	0	6	0	0	2	343	354
									EYLSEEVQAVHK	95.0	82.8	25.0	1431.71	0	2	0	0	2	482	493
U5 small nuclear ribonucleoprotein 200 kDa	U520_HUMAN	SNRNP200	244.50	100.0	12	12	36	5.66	DEPTGEVLSLVGK	95.0	30.2	25.0	1343.71	0	1	0	0	2	34	46
									EIDLLLGQTDDTR	95.0	84.5	25.0	1488.75	0	6	0	0	2	156	168

helicase								YAQAGFEGFK	95.0	53.1	25.0	1117.53	0	4	0	0	2	470	479
								IIYIAPMR	95.0	35.9	25.0	992.56	0	2	0	0	2	538	545
								SLVQEMVGSFGK	95.0	71.8	25.0	1297.65	0	3	0	0	2	546	557
								GPVLEALVAR	95.0	41.9	25.0	1024.62	0	3	0	0	2	625	634
								DTLGLFLR	95.0	40.5	25.0	934.54	0	7	0	0	2	746	753
								GDPLLDQR	95.0	31.0	25.0	913.47	0	2	0	0	2	945	952
								TGNFQVTELGR	95.0	55.9	25.0	1221.62	0	4	0	0	2	976	986
								VFSLSSEFK	95.0	27.4	25.0	1043.54	0	1	0	0	2	1017	1025
								MLLQSSEGR	95.0	26.8	25.0	1036.51	0	1	0	0	2	1367	1375
								KPVIVFVPSR	95.0	64.1	25.0	1141.71	0	2	0	0	2	1557	1566
Ubiquitin carboxyl-terminal hydrolase 14	UBP14_HUMAN	USP14	56.05	100.0	5	6	37	15.20	AQLFALTGVQPAR	95.0	####	25.0	1371.77	0	8	0	0	2	31	43
								ASGEMASAQYITAALR	95.0	####	25.0	1655.81	0	6	0	0	2	142	157
								LEAIEDDSVKETDSSSASAATPSK	95.0	77.2	25.0	2438.14	0	1	4	0	2	215	238
								LPAYLTIQMVR	95.0	66.3	25.0	1320.73	0	8	0	0	2	320	330
								RVEIMEEESEQ	95.0	66.9	25.0	1394.61	0	10	0	0	2	484	494
Ubiquitin carboxyl-terminal hydrolase 5	UBP5_HUMAN	USP5	95.77	100.0	5	5	13	7.11	DGLGGLPDIVR	95.0	30.6	25.0	1111.61	0	1	0	0	2	134	144
								VTSAVEALLSADSASR	95.0	50.4	25.0	1576.82	0	2	0	0	2	147	162
								EVQDGIAPR	95.0	30.2	25.0	984.51	0	1	0	0	2	407	415
								SSENPNEVFR	95.0	41.8	25.0	1178.54	0	3	0	0	2	453	462
								SAADSISESVPVGPK	95.0	####	25.0	1443.73	0	6	0	0	2	779	793
Ubiquitin carboxyl-terminal hydrolase 7	UBP7_HUMAN	USP7	128.29	100.0	10	10	20	9.98	AVYMMPTEGDDSSK	95.0	31.2	25.0	1562.64	0	2	0	0	2	241	254
								VFYELQHSDKPVGTK	95.0	23.8	25.0	1747.90	0	0	1	0	2	263	277
								FMYDPQTDQNIK	95.0	55.5	25.0	1515.68	0	3	0	0	2	409	420
								FDDDVVSR	95.0	36.6	25.0	952.44	0	2	0	0	2	480	487
								RPAMLDNEADGNK	95.0	30.8	25.0	1446.66	0	1	0	0	2	634	646
								FDKDHDVMLFLK	95.0	23.2	25.0	1523.76	0	0	1	0	2	679	690
								EEEITLYPDK	95.0	32.3	25.0	1236.60	0	2	0	0	2	905	914
								LLEIVSYK	95.0	39.3	25.0	964.57	0	4	0	0	2	941	948
								IQSLLDIQEK	95.0	47.9	25.0	1186.67	0	2	0	0	2	1024	1033
								FAIVMMGR	95.0	35.8	25.0	956.47	0	2	0	0	2	1040	1047
Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3_HUMAN	UCHL3	26.16	100.0	5	5	14	28.70	SQGQDVTSSVYFMK	95.0	74.7	25.0	1592.73	0	2	0	0	2	75	88
								FLEESVSMSPEER	95.0	82.5	25.0	1555.69	0	4	0	0	2	122	134
								YLENYDAIR	95.0	60.2	25.0	1156.56	0	2	0	0	2	137	145
								VTHETSAHEGQTEAPSIDEK	95.0	37.4	25.0	2165.99	0	0	5	0	2	146	165
								FMERDPDELR	95.0	20.2	25.0	1323.60	0	0	1	0	2	212	221
Ubiquitin carboxyl-terminal hydrolase isozyme L5	UCHL5_HUMAN	UCHL5	37.59	100.0	4	4	22	12.50	LDTIFFAK	95.0	41.6	25.0	954.53	0	5	0	0	2	74	81
								LYELDGLR	95.0	44.2	25.0	978.53	0	7	0	0	2	175	182
								NQMLIEEEVQK	95.0	62.8	25.0	1376.67	0	4	0	0	2	267	277
								TLAEHQQLIPLVEK	95.0	43.2	25.0	1618.92	0	0	6	0	2	302	315
Ubiquitin conjugation factor E4 A	UBE4A_HUMAN	UBE4A	122.55	100.0	3	3	7	3.28	VFVEYIQPK	95.0	59.6	25.0	1122.62	0	4	0	0	2	309	317
								DAQQSSSPAADNLR	95.0	45.9	25.0	1459.68	0	2	0	0	2	545	558
								ESIKDLADYASK	95.0	32.1	25.0	1339.67	0	1	0	0	2	763	774
Ubiquitin thioesterase OTUB1	OTUB1_HUMAN	OTUB1	31.27	100.0	5	8	44	23.60	IQQEIAVQNPLVSER	95.0	####	25.0	1723.93	0	12	1	0	2	37	51
								EYAEDDNIYQQK	95.0	65.3	25.0	1515.66	0	7	0	0	2	60	71
								LLTSGYLQR	95.0	63.5	25.0	1050.59	0	10	0	0	2	177	185
								FFEHFIEGGR	95.0	64.5	25.0	1238.60	0	5	4	0	2	189	198
								GEGGTTNPHIFPEGSEPK	95.0	69.1	25.0	1853.87	0	2	3	0	2	239	256
Ubiquitin-conjugating enzyme E2 K	UBE2K_HUMAN	UBE2K	22.39	100.0	4	4	18	21.00	GEIAGPPDTPYEGGR	95.0	69.9	25.0	1515.71	0	4	0	0	2	41	55
								YQLEIK	95.0	34.6	25.0	793.45	0	3	0	0	2	56	61
								IPETYPFNPPK	95.0	51.3	25.0	1302.67	0	7	0	0	2	62	72
								NAVIVALSSK	95.0	62.3	25.0	1001.60	0	4	0	0	2	177	186

Ubiquitin-conjugating enzyme E2 L3	UB2L3_HUMAN	UBE2L3	17.84	100.0	2	3	18	15.60	ELEEIR	95.0	30.7	25.0	788.41	0	2	0	0	2	10	15
									IYHPNIDEK	95.0	35.2	25.0	1128.57	0	4	5	0	2	74	82
									ADLAEEYSK	95.0	47.0	25.0	1025.48	0	9	0	0	2	123	131
Ubiquitin-conjugating enzyme E2 N	UBE2N_HUMAN	UBE2N	17.12	100.0	3	3	24	19.10	LLAEPVPGIK	95.0	45.7	25.0	1036.64	0	7	0	0	2	15	24
									IYHPNVDK	95.0	29.4	25.0	985.51	0	1	0	0	2	75	82
									TNEAQAIETAR	95.0	76.3	25.0	1203.60	0	16	0	0	2	131	141
Ubiquitin-conjugating enzyme E2 variant 1	UB2V1_HUMAN	UBE2V1	16.48	100.0	5	5	15	26.50	LLEELEEGQK	95.0	54.9	25.0	1187.62	0	4	0	0	2	17	26
									TIYENR	95.0	32.4	25.0	795.40	0	1	0	0	2	58	63
									YPEAPPFVR	95.0	30.4	25.0	1075.56	0	2	0	0	2	75	83
									AISVLAK	95.0	61.1	25.0	701.46	0	6	0	0	2	104	110
									VVLQELR	95.0	30.8	25.0	856.53	0	2	0	0	2	119	125
Ubiquitin-conjugating enzyme E2 variant 2	UB2V2_HUMAN	UBE2V2	16.34	99.5	2	2	8	26.20	LLEELEEGQK	95.0	54.9	25.0	1187.62	0	4	0	0	2	15	24
									YPEAPPSVR	95.0	31.5	25.0	1015.52	0	3	0	0	2	73	81
									VVLQELR	95.0	30.8	25.0	856.53	0	2	0	0	2	117	123
									LPQPPEGQTYNN	95.0	37.3	25.0	1357.64	0	5	0	0	2	134	145
Ubiquitin-like modifier-activating enzyme 1	UBA1_HUMAN	UBA1	117.83	100.0	16	19	106	17.30	NGSEADIDEGLYSR	95.0	####	25.0	1525.68	0	6	0	0	2	44	57
									LQTSSVLVSGLR	95.0	77.7	25.0	1259.73	0	14	0	0	2	70	81
									GLGVEIAK	95.0	34.0	25.0	786.47	0	6	0	0	2	82	89
									NIILGGVK	95.0	40.3	25.0	813.52	0	7	0	0	2	90	97
									LVVADTR	95.0	38.6	25.0	773.45	0	8	0	0	2	186	192
									GGIVSQVK	95.0	42.8	25.0	787.47	0	4	0	0	2	289	296
									ALPAVQQNNLDEDLIR	95.0	65.4	25.0	1808.95	0	2	0	0	2	369	384
									YDGQVAVFGSDLQEK	95.0	84.3	25.0	1655.79	0	6	0	0	2	451	465
									LKSDTAAAAVR	95.0	37.3	25.0	1102.62	0	2	2	0	2	527	537
									KPLLESGTLGTK	95.0	64.2	25.0	1243.73	0	3	0	0	2	593	604
									DEFEGLFK	95.0	35.5	25.0	984.47	0	6	0	0	2	650	657
									QPAENVNQYLTDPK	95.0	78.2	25.0	1616.79	0	11	0	0	2	658	671
									LAGTQPLEVLEAVQR	95.0	82.4	25.0	1623.91	0	6	2	0	2	679	693
									ATLPSPDKLPGFK	95.0	30.8	25.0	1370.77	0	1	3	0	2	831	843
									AENYDIPSADR	95.0	48.8	25.0	1250.56	0	6	0	0	2	870	880
									LDQPMTEIVSR	95.0	60.7	25.0	1304.65	0	11	0	0	2	1011	1021
Ubiquitin-like protein 4A	UBL4A_HUMAN	UBL4A	17.76	100.0	3	4	10	18.50	LNLVVKPLEK	95.0	40.5	25.0	1152.74	0	3	4	0	2	67	76
									VLEQLQR	95.0	37.1	25.0	885.52	0	2	0	0	2	115	121
									FLHPEVTETMEK	95.0	34.9	25.0	1476.70	0	0	1	0	2	142	153
UDP-glucose 4-epimerase	GALE_HUMAN	GALE	38.26	100.0	4	5	10	12.10	GGGSLPESLR	95.0	32.3	25.0	972.51	0	1	0	0	2	41	50
									AVGESVQKPLDYYR	95.0	53.6	25.0	1624.83	0	2	0	0	2	93	106
									FFIEEMIR	95.0	34.9	25.0	1100.54	0	2	0	0	2	162	169
									DYIHVVDLAK	95.0	55.4	25.0	1172.63	0	3	2	0	2	240	249
UDP-glucose 6-dehydrogenase	UGDH_HUMAN	UGDH	55.01	100.0	5	6	10	10.10	EADLVFISVNTPTK	95.0	53.8	25.0	1533.82	0	4	0	0	2	81	94
									IIDSLFNTVTDK	95.0	47.1	25.0	1365.73	0	1	0	0	2	318	329
									IIDSLFNTVTDKK	95.0	47.8	25.0	1493.82	0	1	1	0	2	318	330
									MLKPAFIFDGR	95.0	43.3	25.0	1310.69	0	2	0	0	2	432	442
									RIPYAPSGEIPK	95.0	36.2	25.0	1327.74	0	1	0	0	2	470	481
UDP-glucose:glycoprotein glucosyltransferase 1	UGGG1_HUMAN	UGGT1	177.18	100.0	8	8	15	4.95	INYVFR	95.0	33.4	25.0	811.45	0	1	0	0	2	223	228
									DLSQNFPTK	95.0	35.3	25.0	1049.53	0	2	0	0	2	348	356
									ILETTTFFQR	95.0	43.2	25.0	1255.67	0	4	0	0	2	659	668
									TAAVANSMNYLTK	95.0	89.0	25.0	1399.69	0	2	0	0	2	732	744
									ISMINNPAK	95.0	36.2	25.0	1003.52	0	2	0	0	2	793	801
									VEEDVASDLVMK	95.0	30.6	25.0	1350.65	0	1	0	0	2	938	949
									VDALLSAQPK	95.0	60.1	25.0	1041.59	0	2	0	0	2	950	959
									IMMLSVLK	95.0	38.2	25.0	966.54	0	1	0	0	2	1273	1280

UMP-CMP kinase	KCY_HUMAN	CMPK1	22.21	100.0	3	3	10	10.70	KNPDSQYGELIEK	95.0	84.6	25.0	1520.76	0	2	0	0	2	43	55
									NPDSQYGELIEK	95.0	59.2	25.0	1392.66	0	4	0	0	2	44	55
									FLIDGFPR	95.0	38.0	25.0	964.53	0	4	0	0	2	89	96
UPF0027 protein C22orf28	CV028_HUMAN	C22orf28	55.19	100.0	9	10	21	19.00	SYNDELQFLEK	95.0	63.2	25.0	1385.66	0	2	0	0	2	4	14
									GGGVGGFLPAMK	95.0	34.2	25.0	1106.57	0	2	0	0	2	56	67
									QIGNVAALPGIVHR	95.0	61.0	25.0	1444.84	0	2	3	0	2	68	81
									TNLDESDVQPVK	95.0	76.9	25.0	1344.66	0	3	0	0	2	129	140
									IASPEGQDYLK	95.0	39.5	25.0	1220.62	0	2	0	0	2	298	308
									SSMTFLTR	95.0	43.5	25.0	958.47	0	1	0	0	2	322	329
									VEQHVVDGK	95.0	29.1	25.0	1010.53	0	1	0	0	2	358	366
									NLDFQDVLDK	95.0	35.9	25.0	1206.60	0	3	0	0	2	442	451
									LADMGIAIR	95.0	75.8	25.0	975.53	0	2	0	0	2	452	460
UPF0364 protein C6orf211	CF211_HUMAN	C6orf211	51.16	100.0	4	5	10	7.03	IPQILTK	95.0	36.6	25.0	812.52	0	3	0	0	2	25	31
									LRNELQTDKPFIPLVEK	95.0	38.6	25.0	2040.15	0	0	2	0	2	65	81
									NELQTDKPFIPLVEK	95.0	52.5	25.0	1770.96	0	2	2	0	2	67	81
									AHLILFK	95.0	35.3	25.0	841.53	0	1	0	0	2	359	365
UPF0368 protein Cxorf26	CX026_HUMAN	CXorf26	26.04	100.0	3	3	5	15.50	LISSVDPQFLK	95.0	43.8	25.0	1246.70	0	2	0	0	2	53	63
									VDDQIYSEFR	95.0	41.1	25.0	1271.59	0	1	0	0	2	67	76
									IDVLDPEELKSESAK	95.0	19.9	25.0	1672.86	0	0	2	0	2	84	98
UPF0424 protein C1orf128	CA128_HUMAN	C1orf128	24.16	100.0	3	3	18	12.80	GLAYGLYLR	95.0	54.0	25.0	1025.58	0	1	0	0	2	26	34
									DLTGELEYATK	95.0	61.4	25.0	1239.61	0	12	0	0	2	132	142
									VFYIGLR	95.0	45.6	25.0	867.51	0	5	0	0	2	167	173
UPF0568 protein C14orf166	CN166_HUMAN	C14orf166	28.05	100.0	4	4	9	14.80	YKDLVPDNSK	95.0	26.7	25.0	1178.61	0	1	0	0	2	99	108
									HDDYLVMLK	95.0	45.3	25.0	1149.56	0	2	0	0	2	146	154
									EGLPVALDK	95.0	46.2	25.0	941.53	0	2	0	0	2	177	185
									LLHIEELR	95.0	48.8	25.0	1022.60	0	4	0	0	2	206	213
Uridine 5'-monophosphate synthase	PYR5_HUMAN	UMPS	52.20	100.0	3	3	5	6.04	FGDFVLK	95.0	27.4	25.0	825.45	0	2	0	0	2	23	29
									SGLSSPIYIDLR	95.0	39.2	25.0	1320.72	0	1	0	0	2	30	41
									VTDAIVLLDR	95.0	84.0	25.0	1114.65	0	2	0	0	2	146	155
Uridine phosphorylase 1	UPP1_HUMAN	UPP1	33.92	100.0	4	4	31	14.20	HNFPALFGDVK	95.0	57.4	25.0	1244.64	0	2	0	0	2	44	54
									AEFEQIVLGK	95.0	67.6	25.0	1133.62	0	18	0	0	2	165	174
									QAYLEAAYAAGVR	95.0	97.1	25.0	1382.71	0	2	0	0	2	233	245
									LEGDQISSPR	95.0	63.4	25.0	1101.55	0	9	0	0	2	276	285
Urokinase-type plasminogen activator	UROK_HUMAN	PLAU	48.49	100.0	5	5	51	13.20	SDALQLGLGK	95.0	91.9	25.0	1001.56	0	16	0	0	2	109	118
									KPSSPPEELK	95.0	38.2	25.0	1111.60	0	4	0	0	2	156	165
									KEDYIVYLGR	95.0	54.9	25.0	1255.67	0	6	0	0	2	232	241
									FEVENLILHK	95.0	39.6	25.0	1241.69	0	17	0	0	2	254	263
									DYSADTLAHHNDIALLK	95.0	37.7	25.0	1896.95	0	0	8	0	2	264	280
UTP--glucose-1-phosphate uridylyltransferase	UGPA_HUMAN	UGP2	56.92	100.0	8	8	17	17.30	AMSQDGASQFQEVIR	95.0	85.3	25.0	1682.78	0	4	0	0	2	11	25
									GLPDNISSVLNK	95.0	27.3	25.0	1256.68	0	1	0	0	2	96	107
									IYTFNQSR	95.0	29.6	25.0	1028.52	0	1	0	0	2	185	192
									LQEQNAIDMEIIVNAK	95.0	75.7	25.0	1844.94	0	2	0	0	2	342	357
									SFENSLGINVPR	95.0	82.5	25.0	1332.69	0	2	0	0	2	378	389
									VQDYLR	95.0	35.9	25.0	793.42	0	2	0	0	2	439	444
									IDIPPGAVLENK	95.0	38.9	25.0	1265.71	0	4	0	0	2	486	497
									IVSGNLR	95.0	28.0	25.0	758.45	0	1	0	0	2	498	504
UV excision repair protein RAD23 homolog A	RD23A_HUMAN	RAD23A	39.59	99.5	2	2	4	10.50	TLQQQTFK	95.0	31.8	25.0	993.54	0	1	0	0	2	9	16
									EDKSPSEESAPTTSPESVSGSVPSSGSSGR	95.0	77.2	25.0	2922.31	0	0	2	0	2	120	149
									SPSEESAPTTSPESVSGSVPSSGSSGR	95.0	23.7	25.0	2550.14	0	0	2	0	2	123	149
UV excision repair protein RAD23 homolog B	RD23B_HUMAN	RAD23B	43.15	100.0	5	5	10	11.70	TLQQQTFK	95.0	31.8	25.0	993.54	0	1	0	0	2	7	14
									NFVVVMVTKPK	95.0	60.2	25.0	1277.73	0	2	0	0	2	68	78

									EQVIAALR	95.0	36.3	25.0	899.53	0	3	0	0	2	205	212
									ASFNNPDR	95.0	48.7	25.0	920.42	0	2	0	0	2	213	220
									AVEYLLMGIPGDR	95.0	50.6	25.0	1449.74	0	2	0	0	2	221	233
Vacuolar protein sorting-associated protein 13C	VP13C_HUMAN	VPS13C	422.38	100.0	3	3	5	0.83	ENALSELDVPFK	95.0	34.5	25.0	1361.69	0	2	0	0	2	45	56
									NVQLLFAR	95.0	29.8	25.0	960.56	0	1	0	0	2	755	762
									AVSILGDEVFR	95.0	49.5	25.0	1205.65	0	2	0	0	2	1661	1671
Vacuolar protein sorting-associated protein 26A	VP26A_HUMAN	VPS26A	38.15	100.0	9	10	35	33.30	HYLFYDGESVSGK	95.0	63.5	25.0	1501.70	0	5	2	0	2	39	51
									SNTHEFVNLVK	95.0	41.5	25.0	1287.67	0	0	3	0	2	83	93
									ELALPGELTQSR	95.0	80.1	25.0	1313.71	0	6	0	0	2	94	105
									IYFLLVR	95.0	48.8	25.0	923.57	0	2	0	0	2	195	201
									IQHMELQLIK	95.0	43.7	25.0	1268.70	0	0	3	0	2	204	213
									EITGIGPSTTTETETIAK	95.0	####	25.0	1848.94	0	6	0	0	2	215	232
									YEIMDGAPVK	95.0	29.3	25.0	1138.55	0	1	0	0	2	233	242
									LFLAGYDPTPTMR	95.0	68.4	25.0	1497.74	0	5	0	0	2	250	262
									FESPESQASAEQPEM	95.0	47.3	25.0	1682.69	0	2	0	0	2	313	327
Vacuolar protein sorting-associated protein 29	VPS29_HUMAN	VPS29	20.49	100.0	4	5	18	22.00	TLAGDVHIVR	95.0	52.8	25.0	1080.62	0	1	4	0	2	51	60
									GDFDENLNYPEQK	95.0	52.1	25.0	1568.69	0	4	0	0	2	61	73
									VVTVGQFK	95.0	52.2	25.0	877.51	0	3	0	0	2	74	81
									FEAFEHENK	95.0	33.4	25.0	1150.52	0	6	0	0	2	119	127
Vacuolar protein sorting-associated protein 35	VPS35_HUMAN	VPS35	91.69	100.0	9	9	34	11.90	LLDEAIQAVK	95.0	53.9	25.0	1099.64	0	6	0	0	2	15	24
									ILVGTNLVR	95.0	49.4	25.0	984.62	0	4	0	0	2	218	226
									LSQLEGVNVER	95.0	63.1	25.0	1243.66	0	4	0	0	2	227	237
									NIIIALIDR	95.0	38.2	25.0	1040.65	0	3	0	0	2	297	305
									VLETTVEIFNK	95.0	73.9	25.0	1292.71	0	1	0	0	2	372	382
									LNLEHIATSSAVSK	95.0	92.8	25.0	1469.80	0	4	0	0	2	383	396
									SEDPDQQYLILNTAR	95.0	87.2	25.0	1762.86	0	2	0	0	2	500	514
									AELAELPLR	95.0	64.5	25.0	1011.58	0	8	0	0	2	574	582
									YIYFYEK	95.0	30.2	25.0	1025.50	0	2	0	0	2	727	733
Valyl-tRNA synthetase	SYVC_HUMAN	VARS	140.46	100.0	3	3	11	3.40	SSAQDPQAVLGALGR	95.0	88.8	25.0	1469.77	0	7	0	0	2	123	137
									VQGSDSDEEVVVATTR	95.0	####	25.0	1691.81	0	2	0	0	2	522	537
									VPLEVQEADEAK	95.0	64.1	25.0	1327.67	0	2	0	0	2	1231	1242
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADV_HUMAN	ACADVL	70.37	100.0	10	10	32	17.30	FFEEVNDPAK	95.0	46.5	25.0	1195.56	0	1	0	0	2	112	121
									GILLFGTK	95.0	35.3	25.0	848.52	0	6	0	0	2	188	195
									ITAFVVER	95.0	41.6	25.0	934.54	0	3	0	0	2	279	286
									ASNTAEVFFDGVR	95.0	79.5	25.0	1412.68	0	3	0	0	2	304	316
									VPSENVLGEVGSGFK	95.0	85.7	25.0	1518.78	0	10	0	0	2	317	331
									IFEGTNDILR	95.0	42.6	25.0	1177.62	0	2	0	0	2	460	469
									NPFGNAGLLLGEAGK	95.0	59.2	25.0	1457.77	0	2	0	0	2	493	507
									ALEQFATVVEAK	95.0	55.5	25.0	1305.70	0	2	0	0	2	539	550
									GIVNEQFLLQR	95.0	30.4	25.0	1316.73	0	1	0	0	2	557	567
									GGVVTSNPLGF	95.0	56.7	25.0	1047.55	0	2	0	0	2	645	655
Vesicle-associated membrane protein-associated protein B/C	VAPB_HUMAN	VAPB	27.21	100.0	3	4	18	13.60	VEQVLSLEPQHELK	95.0	62.6	25.0	1648.89	0	3	1	0	2	4	17
									GPFTDVVTTNLK	95.0	99.2	25.0	1291.69	0	13	0	0	2	20	31
									LGNPTDR	95.0	27.4	25.0	772.39	0	1	0	0	2	32	38
Vesicle-trafficking protein SEC22b	SC22B_HUMAN	SEC22B	24.72	100.0	7	7	38	35.80	VLLTMIAR	95.0	47.5	25.0	932.56	0	7	0	0	1	2	9
									VADGLPLAASMQEDEQSGR	95.0	95.5	25.0	1989.92	0	6	0	0	2	10	28
									DLQQYQSQAK	95.0	48.5	25.0	1208.59	0	8	0	0	2	29	38
									LNEQSPTR	95.0	50.1	25.0	944.48	0	3	0	0	2	44	51
									LYIDSR	95.0	33.5	25.0	766.41	0	1	0	0	2	125	130
									NLGSINTELQDVQR	95.0	####	25.0	1586.81	0	9	0	0	2	134	147
									IMVANIEEVLQR	95.0	70.1	25.0	1430.77	0	4	0	0	2	148	159

Vimentin	VIME_HUMAN	VIM	53.63	100.0	6	6	21	16.70	ILLAELEQLK	95.0	61.3	25.0	1169.71	0	8	0	0	2	130	139
									EEAENTLQSFR	95.0	41.6	25.0	1323.62	0	3	0	0	2	197	207
									QDVDNASLAR	95.0	35.5	25.0	1088.53	0	1	0	0	2	208	217
									KVESLQEEIAFLK	95.0	86.4	25.0	1533.85	0	6	0	0	2	223	235
									FADLSEAANR	95.0	65.5	25.0	1093.53	0	2	0	0	2	295	304
									KLLEGEESR	95.0	51.6	25.0	1060.56	0	2	0	0	2	402	410
									LLEGEESR	95.0	35.4	25.0	932.47	0	5	0	0	2	403	410
									ETNLDSLPLVDTHSK	95.0	24.3	25.0	1668.84	0	0	1	0	2	425	439
Vinculin	VINC_HUMAN	VCL	123.78	100.0	38	42	666	36.10	ETVQTTEDQILK	95.0	72.1	25.0	1404.72	0	27	0	0	2	60	71
									ETVQTTEDQILKR	95.0	83.2	25.0	1560.82	0	2	0	0	2	60	72
									LVQAAQMLQSDPYSVPAR	95.0	80.3	25.0	1990.01	0	2	2	0	2	88	105
									DYLIDGSR	95.0	46.0	25.0	938.46	0	6	0	0	2	106	113
									VMLVNSMNTVK	95.0	52.0	25.0	1267.64	0	21	0	0	2	189	199
									ELLPVLISAMK	95.0	64.9	25.0	1229.72	0	32	0	0	2	200	210
									NQGIEEALK	95.0	52.0	25.0	1001.53	0	3	0	0	2	220	228
									MSAEINEIIR	95.0	79.6	25.0	1191.60	0	37	0	0	2	237	246
									ALASIDSK	95.0	57.5	25.0	804.45	0	4	0	0	2	269	276
									DPSASPGDAGEQAIR	95.0	97.4	25.0	1470.68	0	21	0	0	2	286	300
									QILDEAGK	95.0	30.9	25.0	873.47	0	3	0	0	2	301	308
									MLGQMTDQVADLR	95.0	91.5	25.0	1509.70	0	49	0	0	2	327	339
									AQQVSQGLDVLTAK	95.0	####	25.0	1457.80	0	56	3	0	2	353	366
									ERDDILR	95.0	33.5	25.0	916.48	0	2	0	0	2	427	433
									SLGEISALTSK	95.0	86.7	25.0	1105.61	0	41	0	0	2	434	444
									QVATALQNLQTK	95.0	96.2	25.0	1314.74	0	15	0	0	2	465	476
									WIDNPTVDDR	95.0	46.1	25.0	1230.58	0	3	0	0	2	503	512
									GVGQAAIR	95.0	49.0	25.0	771.45	0	2	0	0	2	513	520
									LANVMMGPYR	95.0	65.2	25.0	1183.56	0	16	0	0	2	529	538
									VDQLTAQLADLAAR	95.0	93.0	25.0	1484.81	0	14	0	0	2	548	561
									ALASQLQDSLK	95.0	76.3	25.0	1173.65	0	35	0	0	2	571	581
									LLAVAATAPPDAPNR	95.0	42.3	25.0	1476.82	0	2	0	0	2	608	622
									STVEGIQASVK	95.0	76.1	25.0	1118.61	0	29	0	0	2	656	666
									ELTPQVVSAAR	95.0	63.9	25.0	1170.65	0	38	0	0	2	670	680
									NPGNQAAYEHFETMK	95.0	68.0	25.0	1752.76	0	2	1	0	2	685	699
									MTGLVDEAIDTK	95.0	90.5	25.0	1308.64	0	55	0	0	2	709	720
									SLLDASEEAIK	95.0	32.2	25.0	1175.62	0	2	0	0	2	721	731
									SLLDASEEAIKK	95.0	36.5	25.0	1303.71	0	1	2	0	2	721	732
									VAMANIQPQMLVAGATSIAR	95.0	####	25.0	2074.08	0	4	0	0	2	739	758
									EVENSEDPKFR	95.0	31.0	25.0	1349.63	0	1	0	0	2	770	780
									TISPMVMDAK	95.0	36.0	25.0	1124.53	0	7	0	0	2	793	802
									AVAGNISDPGLQK	95.0	55.8	25.0	1269.68	0	30	0	0	2	803	815
									SFLDSGYR	95.0	52.1	25.0	944.45	0	8	0	0	2	816	823
									AGEVINQPMMMAAR	95.0	61.4	25.0	1566.71	0	15	0	0	2	890	903
									GNDIIAAAK	95.0	51.9	25.0	872.48	0	5	0	0	2	984	992
									MALLMAEMSR	95.0	47.2	25.0	1200.54	0	30	0	0	2	994	1003
									IPTISTQLK	95.0	36.5	25.0	1000.60	0	15	0	0	2	1056	1064
									TDAGFTLR	95.0	57.8	25.0	880.45	0	23	0	0	2	1118	1125
Visinin-like protein 1	VISL1_HUMAN	VSNL1	22.13	100.0	3	3	10	12.00	LAPEVMEDLVK	95.0	38.1	25.0	1259.66	0	2	0	0	2	8	18
									NKDDQITLDEFK	95.0	72.3	25.0	1465.72	0	6	0	0	2	161	172
									DDQITLDEFK	95.0	39.6	25.0	1223.58	0	2	0	0	2	163	172
Voltage-dependent anion-selective channel protein 2	VDAC2_HUMAN	VDAC2	31.55	100.0	3	3	5	11.90	LTFDTTFSPNTGK	95.0	48.2	25.0	1428.70	0	1	0	0	2	108	120
									YQLDPTASISAK	95.0	30.2	25.0	1293.67	0	2	0	0	2	236	247

									LTLSALVDGK	95.0	61.8	25.0	1016.60	0	2	2	0	2	268	277
V-type proton ATPase catalytic subunit A	VATA_HUMAN	ATP6V1A	68.29	100.0	6	6	17	10.40	VGHSELVGEIIR	95.0	41.8	25.0	1308.73	0	2	0	0	2	45	56
									GVNVSALSR	95.0	32.4	25.0	902.51	0	2	0	0	2	121	129
									GNEMSEVLR	95.0	50.5	25.0	1050.49	0	4	0	0	2	281	289
									DFPELTMEVDGK	95.0	56.0	25.0	1396.63	0	4	0	0	2	290	301
									TALVANTSNMPVAAR	95.0	69.0	25.0	1531.79	0	4	0	0	2	309	323
									LASFYER	95.0	36.0	25.0	885.45	0	1	0	0	2	382	388
V-type proton ATPase subunit C 1	VATC1_HUMAN	ATP6V1C1	43.92	100.0	4	4	6	9.42	FNIPDLK	95.0	54.0	25.0	846.47	0	2	0	0	2	38	44
									GVTQIDNDLK	95.0	29.6	25.0	1102.57	0	1	0	0	2	128	137
									SLAEIVK	95.0	26.8	25.0	759.46	0	1	0	0	2	165	171
									QYETLAEMVVPR	95.0	42.5	25.0	1451.72	0	2	0	0	2	200	211
V-type proton ATPase subunit d 1	VA0D1_HUMAN	ATP6V0D1	40.31	100.0	3	3	7	9.69	LYPEGLAQLAR	95.0	37.0	25.0	1230.68	0	1	0	0	2	247	257
									NVADYYPEYK	95.0	35.3	25.0	1261.57	0	2	0	0	2	266	275
									LLFEGAGSNPGDK	95.0	69.2	25.0	1304.65	0	4	0	0	2	276	288
V-type proton ATPase subunit E 1	VATE1_HUMAN	ATP6V1E1	26.13	100.0	3	3	4	14.60	AEEEFNIEK	95.0	33.9	25.0	1108.52	0	1	0	0	2	34	42
									IQMSNLMNQAR	95.0	31.9	25.0	1337.63	0	1	0	0	2	70	80
									LDLIAQQMMPEVR	95.0	47.5	25.0	1575.79	0	2	0	0	2	200	212
WD repeat and HMG-box DNA-binding protein 1	WDHD1_HUMAN	WDHD1	125.95	100.0	3	3	9	2.92	IVDVMDSSQQK	95.0	45.7	25.0	1265.60	0	4	0	0	2	120	130
									GHDAPVLSLSFDPK	95.0	69.8	25.0	1482.76	0	2	0	0	2	134	147
									LLAIPVEK	95.0	36.9	25.0	882.57	0	3	0	0	2	201	208
WD repeat-containing protein 1	WDR1_HUMAN	WDR1	66.18	100.0	10	12	56	13.50	KVFASLPQVER	95.0	43.0	25.0	1273.73	0	1	1	0	2	7	17
									VFASLPQVER	95.0	43.0	25.0	1145.63	0	13	0	0	2	8	17
									YAPSGFYIASGDVSGK	95.0	97.5	25.0	1618.77	0	2	0	0	2	66	81
									YEYQPFAGK	95.0	36.7	25.0	1102.52	0	2	0	0	2	96	104
									IAVVGEGR	95.0	45.9	25.0	800.46	0	20	0	0	2	117	124
									VINSVDIK	95.0	63.2	25.0	887.52	0	2	0	0	2	148	155
									YTSLMLR	95.0	32.5	25.0	899.47	0	2	0	0	2	390	396
									DYSGQGVVK	95.0	30.0	25.0	952.47	0	1	0	0	2	397	405
									LYSILGTTLK	95.0	79.0	25.0	1108.66	0	8	0	0	2	471	480
									LYSILGTTLKDEGK	95.0	47.5	25.0	1537.85	0	1	3	0	2	471	484
WD repeat-containing protein 5	WDR5_HUMAN	WDR5	36.57	100.0	3	3	10	12.60	TLPAHSDPVSAVHFNR	95.0	46.4	25.0	1747.89	0	0	2	0	2	166	181
									TLIDDDNPPVSFVK	95.0	64.1	25.0	1559.80	0	4	0	0	2	208	221
									YILAATLDNTLK	95.0	55.0	25.0	1335.75	0	4	0	0	2	228	239
WD repeat-containing protein 82	WDR82_HUMAN	WDR82	35.06	100.0	3	3	4	4.79	LTDSVLR	94.5	26.4	25.0	803.46	0	1	0	0	2	3	9
									KYGVDLIR	95.0	30.5	25.0	963.56	0	1	0	0	2	63	70
									YGVDLIR	95.0	50.6	25.0	835.47	0	2	0	0	2	64	70
Xaa-Pro aminopeptidase 1	XPP1_HUMAN	XPNPEP1	69.90	100.0	4	4	11	7.87	SAGHHLIPVK	95.0	27.5	25.0	1058.61	0	0	3	0	2	138	147
									GGVTEISAADKAEEFR	95.0	33.7	25.0	1679.82	0	0	1	0	2	355	370
									TMHFGTPTAYEK	95.0	40.3	25.0	1398.64	0	2	0	0	2	430	441
									IENVVLVVPVK	95.0	75.7	25.0	1208.76	0	5	0	0	2	536	546
Xaa-Pro dipeptidase	PEPD_HUMAN	PEPD	54.53	100.0	5	5	33	9.53	VPLALFALNR	95.0	67.8	25.0	1113.68	0	24	0	0	2	18	27
									KNPAVQAGSIVVLQGGEETQR	95.0	31.5	25.0	2181.16	0	0	2	0	2	36	56
									NPAVQAGSIVVLQGGEETQR	95.0	####	25.0	2053.07	0	2	0	0	2	37	56
									TDMELEVLR	95.0	66.2	25.0	1121.55	0	2	0	0	2	188	196
									IDEPGLR	95.0	31.0	25.0	799.43	0	3	0	0	2	389	395
X-ray repair cross-complementing protein 5	XRCC5_HUMAN	XRCC5	82.69	100.0	13	13	82	17.10	KVITMFVQR	95.0	27.0	25.0	1137.65	0	1	0	0	2	36	44
									VITMFVQR	95.0	44.7	25.0	1009.55	0	1	0	0	2	37	44
									SQLDIIIHSLK	95.0	44.7	25.0	1266.74	0	5	0	0	2	145	155
									LGGHGPSFPLK	95.0	45.4	25.0	1109.61	0	0	6	0	2	185	195
									YGSDIVPFSK	95.0	58.2	25.0	1112.56	0	5	0	0	2	316	325
									FFMGNQVLK	95.0	31.4	25.0	1099.56	0	4	0	0	2	355	363

									ANPQVGVAFPHIK	95.0	35.9	25.0	1377.76	0	0	4	0	2	401	413
									TDTLEDLFPTTK	95.0	80.2	25.0	1380.69	0	30	0	0	2	470	481
									TLFPLIEAK	95.0	55.9	25.0	1031.61	0	4	0	0	2	535	543
									DQVTAQEIFQDNHEDGPTAK	95.0	46.6	25.0	2243.02	0	0	2	0	2	546	565
									FNNFLK	95.0	26.8	25.0	782.42	0	1	0	0	2	655	660
									EEASGSSVTAEEAK	95.0	97.0	25.0	1394.63	0	17	0	0	2	689	702
									EEASGSSVTAEEAKK	95.0	47.0	25.0	1522.72	0	2	0	0	2	689	703
X-ray repair cross-complementing protein 6	XRCC6_HUMAN	XRCC6	69.83	100.0	14	15	73	25.10	DSLIFLVDASK	95.0	62.0	25.0	1207.66	0	4	0	0	2	36	46
									NIYVLQELDNPGAK	95.0	####	25.0	1573.82	0	13	0	0	2	101	114
									ILELDQFK	95.0	39.8	25.0	1005.56	0	5	0	0	2	116	123
									IMLFTNEDNPHGNDSAK	95.0	88.2	25.0	1918.86	0	2	4	0	2	166	182
									DTGIFLDLMHLK	95.0	40.0	25.0	1418.74	0	3	0	0	2	195	206
									DIISIAEDEDLR	95.0	93.5	25.0	1388.69	0	11	0	0	2	219	230
									LEDLLR	95.0	35.7	25.0	758.44	0	9	0	0	2	239	244
									TFNTSTGGLLLPSDTK	95.0	88.8	25.0	1651.85	0	4	0	0	2	302	317
									TFNTSTGGLLLPSDTKR	95.0	85.6	25.0	1807.96	0	2	0	0	2	302	318
									IMATPEQVGK	95.0	49.0	25.0	1089.56	0	6	0	0	2	452	461
									SDSFENPVLQQHFR	95.0	65.4	25.0	1703.81	0	2	0	0	2	475	488
									LGSLVDEFK	95.0	58.9	25.0	1007.54	0	3	0	0	2	518	526
									ELVYPPDYNPEGK	95.0	54.1	25.0	1520.73	0	3	0	0	2	527	539
									KQELLEALTK	95.0	42.1	25.0	1172.69	0	2	0	0	2	596	605