Supplementary Information Table 1 Proteins and peptides identified from In-gel, In-solution, and On-filter digestion techniques.

Digestion method : In-gel
File conversion : PepArML batch uploader
Search engine : PepArML
Database : IPI Human
Specific cleavage : trypsin
Fixed modification : Carbamidomethyl (C)
Variable modification : Oxidation (M), Deamidation (NQ)
Data Processing : In-house tool - Coverage Table 1.7 with Parsimony
FDR < 10%

Uniprot Accession number	Description	Number of peptides	Sequence Coverage	Start	End	Length	Left AA	peptide	Right AA	FDR	start_scan	end_scan	precursor_mz	assumed_charge	precursor_neutral_mass	calc_neutral_pep_mass	massdiff	leftaa	rightaa	modifications	number of agreed search engine	peptide_length	c13peak	misscleavages
A4UGR9	Xin actin-binding repeat-containing protein 2	1	0.36%	2604	2616	12	R	VTVQLPTESIQK	N	5.88%	3816	3816	448.5704956	3	1342.688012	1342.734377	-0.046365624	R	N	Q11:+0.984	2	12	0	0
A6ND48	Olfactory receptor 14I1	1	2.25%	218	225	7	Q	IFSTVLR	I	8.93%	1494	1494	418.07	2	834.1243499	834.4963344	-0.37198448	R	I	-	2	7	0	0
A6NMY6	Putative annexin A2-like protein	2	7.37%	88	104	16	K	SALSGHLETVILGLLK	T	0.81%	7739	7739	551.3342285	3	1650.97921	1649.971604	1.007606675	K	T	-	5	16	1	0
				169	178	9	K	LMVALAKGR	R	5.66%	3092	3092	488.2734985	2	974.531347	973.5733537	0.957993246	K	R	M2:+15.994	1	9	1	1
A7KAX9	Rho GTPase-activating protein 32	1	1.15%	1313	1337	24	R	SAEQPPVVGQVQAATNIGLNNSHK	V	6.49%	6035	6035	821.0797119	3	2460.215661	2460.224446	-0.008785802	R	V	Q4:+0.984,Q12:+0.984	2	24	0	0
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal	11	26.44%	62	85	23	R	AASAATAAPTATPAAQESGTIPK	K	5.24%	7636	7636	695.7423096	3	2084.203454	2083.043309	1.160144111	R	K	Q16:+0.984	1	23	1	0
				129	143	14	K	EWIQNTLGVNVEHK	T	2.32%	3459	3459	834.4295044	2	1666.843359	1665.847466	0.995892941	K	T	-	3	14	1	0
				147	169	22	K	ASLNPSDTPPSVVNEDFLHDLK	E	6.40%	5341	5341	799.0639648	3	2394.168419	2394.170317	-0.001897285	K	E	-	1	22	0	0
				253	265	12	R	TIISLDTSQMNR	I	0.81%	3012	3012	689.8519897	2	1377.688329	1377.692212	-0.003882204	R	I	-	3	12	0	0
				265	289	24	R	ILWVDENNLTAHVEAGITGQELER	Q	1.93%	6118	6118	903.4589233	3	2707.353295	2706.361306	0.991989276	R	Q	-	2	24	1	0
				323	337	14	K	NIYGNIEDLVVHIK	M	0.81%	6485	6485	814.4484863	2	1626.881323	1625.877703	1.003619304	K	M	-	4	14	1	0
				389	406	17	K	YGSVAFPNFEQGVACLR	E	0.81%	5709	5709	958.4606323	2	1914.905615	1913.908952	0.996662992	K	E	C15:+57.021	3	17	1	0
				456	476	20	K	GFDPNQLSVATLLFEGDREK	V	2.64%	6645	6645	746.3807373	3	2236.118737	2235.117159	1.001578026	K	V	-	3	20	1	1
				624	640	16	K	QWLKESISDVGFGMLK	S	5.40%	3741	3741	618.6533813	3	1852.936669	1853.923404	-0.986734957	K	S	Q1:+0.984,M14:+15.995	1	16	-1	1
				628	640	12	K	ESISDVGFGMLK	S	1.93%	5190	5190	642.326355	2	1282.63706	1281.627486	1.009573897	K	S	-	5	12	1	0
				643	655	12	K	EYVDPNNIFGNR	N	0.81%	3975	3975	719.3383789	2	1436.661108	1436.668439	-0.007330811	K	N	-	5	12	0	0
O00159	Myosin-Ic	3	4.70%	105	125	20	R	GVSFYEVPPHLFAVADTVYR	A	0.81%	6860	6860	756.7225952	3	2267.144311	2266.142251	1.002059285	R	A	-	5	20	1	0
				361	378	17	K	GEELLSPLNLEQAAYAR	D	0.81%	5905	5905	937.480896	2	1872.946142	1872.958139	-0.011996744	K	D	-	5	17	0	0
				605	618	13	K	MSLLQLVEILQSK	E	0.81%	8742	8742	751.4379883	2	1500.860326	1500.858549	0.001777675	K	E	-	5	13	0	0
O00264	Membrane-associated progesterone receptor component 1	1	7.18%	105	119	14	K	FYGPEGPYGVFAGR	D	2.26%	4541	4541	759.3696289	2	1516.723608	1515.71466	1.008947277	K	D	-	5	14	1	0
O00299	Chloride intracellular channel protein 1	7	42.74%	29	37	8	R	LFMVLWLK	G	0.81%	7381	7381	525.3137817	2	1048.611913	1048.614342	-0.002428883	R	G	-	5	8	0	0
				37	49	12	K	GVTFNVTTVDTK	R	2.64%	2695	2695	641.3337402	2	1280.65183	1280.661228	-0.009397483	K	R	-	4	12	0	0
				95	113	18	K	LAALNPESNTAGLDIFAK	F	0.81%	5093	5093	922.99	2	1843.96435	1843.967975	-0.003625128	K	F	-	4	18	0	0
				119	131	12	K	NSNPALNDNLEK	G	3.61%	757	757	664.8240356	2	1327.632421	1327.636804	-0.004382847	K	G	-	2	12	0	0
				138	165	27	K	VLDNYLTSPLPEEVDETSAEDEGVSQR	K	1.97%	5042	5042	998.7970581	3	2993.367699	2991.383283	1.98441646	K	K	-	4	27	2	0
				166	183	17	K	FLDGNELTLADCNLLPK	L	6.88%	5982	5982	968.2596436	2	1934.503637	1931.965798	2.537839149	K	L	C12:+57.021	1	17	3	0
				195	204	9	R	GFTIPEAFR	G	5.28%	4725	4725	519.2702637	2	1036.524877	1036.534177	-0.009299312	R	G	-	1	9	0	0
O00400	Acetyl-coenzyme A transporter 1	6	19.49%	49	63	14	R	EALLGDTGTGDFLK	A	0.81%	4477	4477	719.3649292	2	1436.714208	1435.719471	0.994737158	R	A	-	5	14	1	0
				122	135	13	K	LLWAPLVDAVYVK	N	0.81%	7261	7261	744.4359741	2	1486.856298	1485.859534	0.996764282	K	N	-	5	13	1	0
				141	172	31	K	SWLVPTQYILGLFMIYLSTQVDRLLGNTDDR	T	5.24%	8691	8691	1208.890625	3	3623.6484	3626.880689	-3.232289608	K	T	-	1	31	-1	1
				321	334	13	K	IGFSAADAVTGLK	L	0.81%	4057	4057	625.8452759	2	1249.674902	1248.671399	1.003503086	K	L	-	5	13	1	0
				342	365	23	K	EHLALLAVPMVPLQIILPLIISK	Y	0.81%	10716	10716	841.5203857	3	2521.537682	2520.548109	0.989573531	K	Y	-	4	23	1	0
				365	378	13	K	YTAGPQPLNTFYK	A	0.81%	3500	3500	750.378418	2	1498.741186	1498.745626	-0.00444043	K	A	-	3	13	0	0
O00422	Histone deacetylase complex subunit SAP18	3	27.45%	24	31	7	K	TCPLLLR	V	5.79%	2363	2363	435.7720642	2	869.5284783	871.4944916	-1.966013222	K	V	C2:+57.021	2	7	-1	0
				48	67	19	R	GNVPSSELQIYTWMDATLK	E	0.81%	7095	7095	718.6887207	3	2153.042687	2152.051054	0.991632925	R	E	-	1	19	1	0
				126	142	16	K	FQIGDYLDIAITPPNR	A	2.83%	6657	6657	917.4771729	2	1832.938696	1831.946846	0.991850015	K	A	-	5	16	1	0
O00592	Podocalyxin	1	2.33%	398	411	13	R	LASVPGSQTVVVK	E	2.26%	1612	1612	642.8778687	2	1283.740087	1283.744898	-0.004810735	R	E	-	2	13	0	0
O14495	Lipid phosphate phosphohydrolase 3	1	3.54%	281	292	11	K	TTLSLPAPAIR	K	6.06%	3118	3118	570.3375854	2	1138.659521	1138.671005	-0.011483774	K	K	-	1	11	0	0
O14672	Disintegrin and metalloproteinase domain-containing protein 10	6	9.22%	30	45	15	R	HYEGLSYNVDSLHQK	H	3.04%	1830	1830	597.6206055	3	1789.838341	1788.843109	0.99523255	R	H	-	2	15	1	0
				123	131	8	R	FEGFIQTR	G	0.81%	2748	2748	499.2578735	2	996.500097	996.5028764	-0.002779426	R	G	-	5	8	0	0
				131	142	11	R	GGTFYVEPAER	Y	1.93%	1748	1748	613.7960205	2	1225.576391	1224.577498	0.998892824	R	Y	-	5	11	1	0
				239	251	12	R	EAVIAQISSHVK	A	0.81%	2699	2699	641.354126	2	1280.692602	1280.708847	-0.016244895	R	A	-	5	12	0	0
				251	266	15	K	AIDTIYQTTDFSGIR	N	0.81%	4391	4391	851.4315796	2	1700.847509	1699.841712	1.005797348	K	N	-	5	15	1	0
				291	299	8	R	FPNIGVEK	F	0.81%	2239	2239	452.2459412	2	902.4762322	902.4861637	-0.009931436	R	F	-	1	8	0	0
O14735	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	5	30.52%	1	18	17	M	PDENIFLFVPNLIGYAR	I	0.81%	8565	8565	989.52771	2	1977.03977	1977.035995	0.003774786	M	I	-	3	17	0	0
				62	73	11	R	FGAMLDMLTDR	C	2.88%	5730	5730	635.7956543	2	1269.575659	1268.589327	0.986331122	R	C	-	3	11	1	0
				121	132	11	K	MIDLSGNPVLR	I	0.81%	3920	3920	607.8311157	2	1213.646581	1213.64889	-0.002308715	K	I	-	5	11	0	0
				173	186	13	R	MGLWVTAPIALLK	S	0.81%	7517	7517	706.9193726	2	1411.823095	1411.826126	-0.003031283	R	S	-	5	13	0	0
				186	199	13	K	SLISVIHLITAAR	N	0.81%	6984	6984	697.4290161	2	1392.842382	1392.845281	-0.002898637	K	N	-	5	13	0	0
O14966	Ras-related protein Rab-7L1	1	5.42%	58	69	11	R	LQLWDIAGQER	F	0.81%	4844	4844	664.8539429	2	1327.692236	1327.688446	0.003790006	R	F	-	5	11	0	0
O14980	Exportin-1	34	45.00%	22	44	22	K	LDINLLDNVVNCLYHGEGAQQR	M	5.15%	7712	7712	848.0870972	3	2541.237816	2541.227705	0.010111848	K	M	N8:+0.984,C12:+57.021	1	22	0	0
				62	76	14	R	VDTILEFSQNMNTK	Y	0.81%	4704	4704	820.4023438	2	1638.789037	1638.79232	-0.003282364	R	Y	-	5	14	0	0
				76	88	12	K	YYGLQILENVIK	T	0.81%	7434	7434	726.9093628	2	1451.803076	1451.802413	0.000662586	K	T	-	5	12	0	0
				104	112	8	K	YVVGLIIK	T	2.26%	4141	4141	452.7953186	2	903.5749871	903.5793358	-0.004348705	K	T	-	5	8	0	0
				129	139	10	K	LNMILVQILK	Q	0.81%	6681	6681	592.8741455	2	1183.732641	1183.736249	-0.003607608	K	Q	-	5	10	0	0
				144	158	14	K	HWPTFISDIVGASR	T	2.26%	6465	6465	793.9146729	2	1585.813696	1584.804873	1.008823063	K	T	-	4	14	1	0
				158	179	21	R	TSESLCQNNMVILKLLSEEVF	D	5.75%	7078	7078	819.394104	3	2455.158837	2454.201733	0.957103492	R	D	C6:+57.021,N9:+0.984	1	21	1	1
				172	190	18	K	LLSEEVFDFSSGQITQVK	S	0.81%	6034	6034	1014.526184	2	2027.036718	2026.025884	1.010834076	K	S	-	5	18	1	0
				231	245	14	R	FLNWIPLGYIFETK	L	0.81%	9115	9115	580.9831543	3	1739.925988	1739.928676	-0.002688445	R	L	-	4	14	0	0
				245	253	8	K	LISTLIYK	F	0.81%	3341	3341	475.7991333	2	949.5826165	949.5848152	-0.00219867	K	F	-	1	8	0	0
				253	261	8	K	FLNVPMFR	N	0.81%	5075	5075	512.2740479	2	1022.532446	1022.537155	-0.004708913	K	N	-	5	8	0	0
				295	305	10	K	QMLPLNTNIR	L	0.81%	3449	3449	601.33	2	1200.64435	1198.649224	1.995125512	K	L	-	4	10	2	0
				406	415	9	R	QLYLPMLFK	V	2.59%	6093	6093	584.8232422	2	1167.630834	1167.636285	-0.005451113	R	V	M6:+15.995	2	9	0	0
				423	442	19	R	MAKPEEVLVVENDQGEVVR	E	0.81%	3374	3374	714.3674927	3	2140.079003	2140.083417	-0.004413973	R	E	-	2	19	0	0
				446	455	9	K	DTDSINLYK	N	4.60%	1550	1550	534.7589111	2	1067.502172	1067.513501	-0.011328622	K	N	-	2	9	0	0
				458	474	16	R	ETLVYLTHLDYVDTER	I	0.81%	5087	5087	984.4932861	2	1966.970922	1965.968369	1.002553138	R	I	-	5	16	1	0
				479	492	13	K	LHNQVNGTEWSWK	N	5.33%	8095	8095	800.8374634	2	1599.659277	1597.763736	1.89554067	K	N	-	1	13	2	0
				492	515	23	K	NLNTLCWAIGSISGAMHEEDEKR	F	4.76%	7089	7089	658.81	4	2631.2087	2631.205256	0.003444144	K	F	N3:+0.984,C6:+57.021	2	23	0	1
				515	522	7	R	FLVTVIK	D	4.89%	3627	3627	410.269989	2	818.5243279	818.5265719	-0.002243957	R	D	-	1	7	0	0
				537	553	16	K	AIIASNIMYIVGQYPR	F	0.81%	6580	6580	905.4888916	2	1808.962133	1807.965474	0.996659475	K	F	-	5	16	1	0
				656	674	18	K	YMLLPNQVWDSIIQQATK	N	0.81%	8657	8657	716.711731	3	2147.111718	2147.108509	0.003208399	K	N	-	5	18	0	0
				674	686	12	K	NVDILKDPETVK	Q	0.81%	1580	1580	686.38	2	1370.74435	1369.745292	0.99905796	K	Q	-	3	12	1	1
				700	712	12	K	AVGHPFVIQLGR	I	0.81%	3682	3682	431.917572	3	1292.729241	1292.735336	-0.00609528	K	I	-	5	12	0	0
				712	722	10	R	IYLDMLNVYK	C	0.81%	5674	5674	636.3347778	2	1270.653906	1270.663143	-0.009237592	R	C	-	2	10	0	0
				712	741	29	R	IYLDMLNVYKCLSENISAAIQANGEMVTK	Q	6.03%	6395	6395	831.6915894	4	3322.735057	3322.563544	0.171513262	R	Q	M5:+15.994,C11:+57.021,	1	29	0	1
				757	765	8	K	LISGWVSR	S	0.81%	2632	2632	459.2628784	2	916.5101068	916.5130471	-0.00294038	K	S	-	4	8	0	0
				765	790	25	R	SNDPQMVAENFVPPLLDAVLIDYQR	N	2.26%	9567	9567	1423.713989	2	2845.412328	2843.416379	1.99594958	R	N	-	4	25	2	0
				796	810	14	R	EPEVLSTMAIIVNK	L	0.81%	5890	5890	772.9234619	2	1543.831274	1542.832728	0.99854574	R	L	-	5	14	1	0
				872	883	11	K	LVLDSIIWAFK	H	0.81%	7711	7711	653.3862305	2	1304.756811	1303.754006	1.002804834	K	H	-	4	11	1	0
				957	983	26	K	ISTSLNPGNPVNNQIFLQEYVANLLK	S	0.81%	8356	8356	1444.268433	2	2886.521215	2885.528705	0.992509682	K	S	-	5	26	1	0
				983	995	12	K	SAFPHLQDAQVK	L	0.81%	1989	1989	670.8497314	2	1339.683813	1339.688446	-0.004632845	K	L	-	5	12	0	0
				995	1012	17	K	LFVTGLFSLNQDIPAFK	E	0.81%	8017	8017	956.0103149	2	1910.00498	1909.034932	0.970047403	K	E	-	5	17	1	0
				1023	1038	15	K	EFAGEDTSDLFLEER	E	0.81%	4878	4878	879.3966064	2	1756.777563	1756.779171	-0.001608293	K	E	-	5	15	0	0
				1052	1071	19	R	QMSVPGIFNPHEIPEEMCD	-	4.96%	4315	4315	561.8040161	4	2243.184764	2244.947597	-1.762833051	R	-	M2:+15.994,C18:+57.021	1	19	-1	0
O15034	RIMS-binding protein 2	1	1.24%	289	302	13	I	DDIGEDIVPYPRK	I	8.66%	2951	2951	506.2616577	3	1515.761498	1515.756919	0.004578689	I	I	-	1	13	0	1
O15068	Guanine nucleotide exchange factor DBS	1	1.06%	361	373	12	R	EVKAILDAASQK	I	9.37%	1364	1364	638.3151245	2	1274.614599	1272.692512	1.922086503	R	I	Q11:+0.984	3	12	2	1
O15111	Inhibitor of nuclear factor kappa-B kinase subunit alpha	1	1.61%	287	299	12	R	GGPVDLTLKQPR	C	5.83%	2304	2304	428.2450562	3	1281.711693	1280.708831	1.002862161	R	C	Q10:+0.984	2	12	1	1
O15144	Actin-related protein 2/3 complex subunit 2	5	31.67%	18	52	34	K	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK	T	3.70%	7340	7340	910.44	4	3637.7287	3635.716854	2.011846144	K	T	-	1	34	2	0
				65	77	12	K	ELQAHGADELLK	R	0.81%	1287	1287	662.3436279	2	1322.671606	1322.683026	-0.011420189	K	R	-	5	12	0	0
				106	117	11	K	DSIVHQAGMLK	R	0.81%	1244	1244	599.8162842	2	1197.616918	1197.61759	-0.000671641	K	R	-	5	11	0	0
				203	230	27	R	EPPLELKDTDAAVGDNIGYITFVLFPR	H	3.66%	8317	8317	998.1859741	3	2991.534447	2989.543687	1.990760347	R	H	-	2	27	2	1
				237	248	11	R	DNTINLIHTFR	D	0.81%	3801	3801	672.3568115	2	1342.697973	1342.699345	-0.001371737	R	D	-	5	11	0	0
O15169	Axin-1	1	0.93%	803	811	8	R	AVTLGQFK	E	9.94%	1193	1193	432.7476196	2	863.4795892	863.475249	0.004340138	R	E	Q6:+0.984	1	8	0	0
O15427	Monocarboxylate transporter 4	3	7.31%	216	224	8	R	LLDLSVFR	D	1.97%	5336	5336	481.7897034	2	961.5637567	961.559663	0.00409361	R	D	-	5	8	0	0
				415	428	13	K	EPQPEVAAAEEEK	L	3.06%	710	710	714.3417969	2	1426.667944	1425.66235	1.00559347	K	L	-	5	13	1	0
				428	441	13	K	LHKPPADSGVDLR	E	0.81%	689	689	468.9237671	3	1403.747826	1403.752109	-0.004282482	K	E	-	3	13	0	0
O15439	Multidrug resistance-associated protein 4	14	15.77%	21	32	11	R	VFFWWLNPLFK	I	0.81%	9010	9010	749.411377	2	1496.807104	1495.801625	1.005478906	R	I	-	5	11	1	0
				52	70	18	R	SQHLGEELQGFWDKEVLR	A	0.81%	5696	5696	724.366394	3	2170.075707	2170.080714	-0.005006567	R	A	-	3	18	0	1
				188	204	16	K	TTTGQIVNLLSNDVNK	F	8.19%	4833	4833	857.4802246	2	1712.944799	1715.905375	-2.960575589	K	F	-	1	16	-1	0
				274	284	10	R	TMNEVITGIR	I	5.14%	2730	2730	567.3007202	2	1132.58579	1132.591041	-0.005250442	R	I	-	1	10	0	0
				293	303	10	K	SFSNLITNLR	K	2.61%	4716	4716	583.8245239	2	1165.633398	1163.629868	2.003529732	K	K	-	2	10	2	0
				408	421	13	K	MVHVQDFTAFWDK	A	5.29%	5641	5641	541.9247437	3	1622.750756	1622.755146	-0.004390427	K	A	-	1	13	0	0
				421	451	30	K	ASETPTLQGLSFTVRPGELLAVVGPVGAGK	S	0.81%	7045	7045	984.8820801	3	2951.622765	2951.59677	0.025995554	K	S	Q8:+0.984	3	30	0	0
				451	474	23	K	SSLLSAVLGELAPSHGLVSVHGR	I	0.81%	7414	7414	763.4277954	3	2287.259911	2285.249176	2.01073503	K	I	-	2	23	2	0
				474	490	16	R	IAYVSQQPWVFSGTLR	S	0.81%	5581	5581	926.4869995	2	1850.958349	1850.967915	-0.009566433	R	S	-	5	16	0	0
				622	632	10	K	SGIDFGSLLK	K	5.76%	5233	5233	518.7861328	2	1035.556616	1035.560057	-0.003441503	K	K	-	1	10	0	0
				633	650	17	K	DNEESEQPPVPGTPTLR	N	5.03%	2479	2479	622.7060547	3	1865.094689	1865.864282	-0.769593314	K	N	N2:+0.984	1	17	-1	0
				652	670	18	R	TFSESSVWSQQSSRPSLK	D	9.23%	3024	3024	681.331543	3	2040.971154	2040.97523	-0.004076014	R	D	Q10:+0.984	1	18	0	0
				807	815	8	K	APVLFFDR	N	1.93%	4423	4423	482.7650146	2	963.5143792	963.5177982	-0.003418951	K	N	-	5	8	0	0
				1081	1090	9	K	SSLISALFR	L	0.81%	6037	6037	497.2877808	2	992.5599114	992.5654767	-0.005565293	K	L	-	5	9	0	0
O15498	Synaptobrevin homolog YKT6	3	19.19%	71	88	17	R	NDSLAGVVIADNEYPSR	V	0.81%	3805	3805	910.9414673	2	1819.867284	1818.874803	0.992481594	R	V	-	5	17	1	0
				88	96	8	R	VAFTLLEK	V	4.40%	3842	3842	460.7748108	2	919.5339715	919.537865	-0.00389345	R	V	-	2	8	0	0
				150	163	13	K	IILHNTMESLLER	G	0.81%	4457	4457	523.6177979	3	1567.829918	1567.83921	-0.009291917	K	G	-	2	13	0	0
O15551	Claudin-3	3	19.09%	64	80	16	K	VYDSLLALPQDLQAAR	A	0.81%	5931	5931	886.9779053	2	1771.94016	1771.946846	-0.006685141	K	A	-	5	16	0	0
O43150	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	1	0.80%	421	429	8	K	EIISEVQR	M	6.58%	1025	1025	487.7587585	2	973.501867	973.5080059	-0.006138846	K	M	Q7:+0.984	1	8	0	0
O43155	Leucine-rich repeat transmembrane protein FLRT2	1	1.67%	475	486	11	K	QHLSLVNLEPR	S	8.56%	954	954	436.5795898	3	1306.715294	1306.68808	0.027214267	K	S	Q1:+0.984,N7:+0.984	1	11	0	0
O43280	Trehalase	1	2.40%	486	500	14	R	AQEVAFQLAQNWIR	T	4.03%	1199	1199	558.6279297	3	1672.860314	1672.868536	-0.008221593	R	T	-	1	14	0	0
O43521	Bcl-2-like protein 11	2	14.65%	135	153	18	R	QAEPADMRPEIWIAQELR	R	3.00%	5809	5809	718.3634644	3	2152.066918	2152.073521	-0.00660287	R	R	-	3	18	0	0
				154	165	11	R	IGDEFNAYYAR	R	2.46%	3011	3011	660.3046875	2	1318.593725	1317.598962	0.99476304	R	R	-	4	11	1	0
O43566	Regulator of G-protein signaling 14	1	1.41%	335	343	8	R	GLSLPDIK	V	1.93%	461	461	421.7590332	2	841.5024163	841.4909147	0.011501614	R	V	-	1	8	0	0
O43760	Synaptogyrin-2	2	8.93%	19	29	10	R	FLTQPQVVAR	A	0.81%	1947	1947	579.8314819	2	1157.647314	1157.655689	-0.008375053	R	A	-	4	10	0	0
				136	146	10	K	DVLVGADSVR	A	0.81%	1195	1195	515.7781372	2	1029.540624	1029.54547	-0.00484529	K	A	-	5	10	0	0
O43808	Peroxisomal membrane protein PMP34	5	28.66%	46	66	20	K	TTHMVLLEIIKEEGLLAPYR	G	2.83%	7103	7103	582.57	4	2326.2487	2325.276638	0.972062312	K	G	-	3	20	1	1
				103	130	27	K	DLVVGFVAGVVNVLLTTPLWVVNTRLK	L	5.41%	3991	3991	974.4523315	3	2920.33352	2921.710633	-1.377113563	K	L	-	2	27	-1	1

				199	213	14	K	LSSLDVFIIGAVAK	A	0.81%	6772	6772	717.3859253	2	1432.756201	1431.833713	0.922487426	K	A	-	5	14	1	0
				213	231	18	K	AIATTVTYPLQTVQSILR	F	2.80%	7061	7061	988.5623779	2	1975.109106	1974.114974	0.994131995	K	F	-	5	18	1	0
				248	257	9	R	NILYLLHQR	V	3.76%	3954	3954	585.328186	2	1168.640722	1168.671673	-0.030951258	R	V	-	5	9	0	0
O60469	Down syndrome cell adhesion molecule	1	0.40%	1010	1018	8	K	HLQNGIIR	G	5.23%	2411	2411	475.7789612	2	949.5422723	949.5457443	-0.003471997	K	G	-	1	8	0	0
O75106	Retina-specific copper amine oxidase	1	4.10%	118	149	31	R	EALAIVLFGGQPQPNVSELVVGPLPHPSYMR	D	5.75%	6141	6141	831.9362793	4	3323.713817	3316.716553	6.997264196	R	D	Q11:+0.984,N15:+0.984	1	31	7	0
O75116	Rho-associated protein kinase 2	1	0.72%	749	759	10	K	VENLLLEAEK	R	6.41%	5575	5575	579.3220215	2	1156.628393	1156.63395	-0.005557527	K	R	-	1	10	0	0
O75323	Protein NipSnap homolog 2	6	32.87%	75	91	16	K	LQFHNVKPECLEAYNK	I	0.81%	2515	2515	664.3331909	3	1989.976098	1988.977366	0.99873205	K	I	C10:+57.021	4	16	1	0
				129	143	14	R	YEGGYPALTEVMNK	L	0.81%	4125	4125	786.8779297	2	1571.740209	1570.733742	1.006467127	R	L	-	5	14	1	0
				164	181	17	R	KNQLLLEFSFWNEPVPR	S	1.93%	6921	6921	1059.558105	2	2117.100561	2116.110557	0.990003778	R	S	-	3	17	1	1
				181	190	9	R	SGPNIYELR	S	3.64%	2244	2244	524.772583	2	1047.529516	1047.534905	-0.005388968	R	S	-	1	9	0	0
				190	208	18	R	SYQLRPGTMIEWGNYWAR	A	2.26%	5916	5916	743.3529053	3	2227.035241	2227.06329	-0.028049724	R	A	-	3	18	0	0
				255	275	20	K	HGWEELVYYTVPLIQEMESR	I	2.26%	8284	8284	1240.106079	2	2478.196508	2478.188945	0.007563387	K	I	-	5	20	0	0
O75335	Liprin-alpha-4	1	2.28%	649	665	16	R	GGMLSASAETLPAGFR	V	8.19%	1994	1994	527.5953979	3	1579.762719	1579.766525	-0.003805944	R	V	M3:+15.995	1	16	0	0
O75365	Protein tyrosine phosphatase type IVA 3	1	8.67%	110	125	15	R	APVLVALALIESGMK	Y	0.81%	8486	8486	756.4404907	2	1510.865331	1510.879284	-0.013952883	R	Y	-	5	15	0	0
O75369	Filamin-B	6	3.69%	49	60	11	R	LIALLEVLSQK	R	0.81%	7373	7373	613.3911743	2	1224.766699	1225.764571	-0.997872191	R	R	-	4	11	-1	0
				931	946	15	K	SPFTVGVAAPLDLSK	I	4.11%	5050	5050	752.3924561	2	1502.769262	1500.818791	1.950470701	K	I	-	2	15	2	0
				1207	1219	12	K	YGGELVPHFPAR	V	2.80%	3466	3466	448.5662842	3	1342.675377	1341.682966	0.992411123	K	V	-	4	12	1	0
				1423	1436	13	K	VKIAGPGLGSGVR	A	5.40%	5421	5421	605.8708496	2	1209.726049	1209.719352	0.006697323	K	A	-	2	13	0	1
				1872	1893	21	K	DGTCTVTYLPTLPGDYSILVK	Y	0.81%	5180	5180	771.734314	3	2312.179467	2312.160535	0.018931919	K	Y	C4:+57.021	1	21	0	0
				1919	1943	24	K	LGSAADFLLDISETDLSSLTASIK	A	0.81%	9777	9777	823.1009521	3	2466.279381	2466.274113	0.005268085	K	A	-	5	24	0	0
O75443	Alpha-tectorin	1	0.37%	1454	1462	8	R	NVIQCDPR	Q	6.94%	3445	3445	501.7489624	2	1001.482275	1000.475547	1.006727621	R	Q	C5:+57.021	1	8	1	0
O75445	Usherin	1	0.31%	4121	4137	16	R	LDPFTLYTLTLEACTR	A	5.02%	3145	3145	639.0048218	3	1913.99099	1912.959984	1.03100602	R	A	C14:+57.021	2	16	1	0
O75578	Integrin alpha-10	2	3.17%	194	223	29	K	LFIDPEQIQVGLVQYGESPVHEWSLGDFR	T	4.73%	8438	8438	1120.560669	3	3358.658532	3360.61899	-1.960458428	K	T	Q7:+0.984,Q9:+0.984,Q14	2	29	-1	0
				445	453	8	R	LFLSGAPR	F	4.85%	1743	1743	430.75	2	859.4843499	859.4915834	-0.007233448	R	F	-	1	8	0	0
O75787	Renin receptor	2	5.43%	238	246	8	K	ILVDALQK	F	4.69%	1962	1962	450.2810974	2	898.5465447	898.548764	-0.002219256	K	F	-	1	8	0	0
				287	298	11	K	NPASPYNLAYK	Y	2.61%	2100	2100	619.31073	2	1236.60581	1236.613884	-0.008073751	K	Y	-	5	11	0	0
O76094	Signal recognition particle 72 kDa protein	5	11.18%	73	84	11	K	VLANNSLSFEK	A	3.51%	1813	1813	611.3214111	2	1220.627172	1220.640098	-0.012926246	K	A	-	2	11	0	0
				241	254	13	R	TEEALQLYNQIIK	L	0.81%	5326	5326	781.9208374	2	1561.826025	1561.83517	-0.009145011	R	L	-	5	13	0	0
				254	275	21	K	LKPTDVGLLAVIANNIITINK	D	1.93%	8784	8784	741.1149902	3	2220.321496	2219.325301	0.996194415	K	D	-	4	21	1	0
				300	310	10	K	KQLQAIEFNK	A	5.54%	1740	1740	407.2322998	3	1218.673424	1218.660818	0.012606014	K	A	N9:+0.984	2	10	0	1
				356	376	20	K	AIELLQEFSDQHPENAAEIK	L	4.06%	5060	5060	761.3807983	3	2281.11892	2282.106638	-0.987718228	K	L	Q11:+0.984	2	20	-1	0
O94779	Contactin-5	1	0.82%	638	647	9	R	NILLMHAGR	Y	9.51%	1530	1530	521.2910156	2	1040.566381	1039.558766	1.00761485	R	Y	M5:+15.994	2	9	1	0
O94911	ATP-binding cassette sub-family A member 8	1	1.64%	938	964	26	R	LNCFPVLMDIVSNGLLGMVKPSVHIR	T	8.28%	6093	6093	976.8543091	3	2927.539452	2925.527469	2.011983494	R	T	C3:+57.021,N13:+0.984,M	1	26	2	0
O94973	AP-2 complex subunit alpha-2	3	4.69%	497	515	18	K	VGGYILGEFGNLIAGDPR	S	0.81%	7290	7290	924.4830933	2	1846.950536	1846.957745	-0.007208213	K	S	-	5	18	0	0
				537	546	9	R	ALLLSTYIK	F	0.81%	4596	4596	511.8180237	2	1021.620397	1020.621929	0.998468243	R	F	-	5	9	1	0
				546	563	17	K	FVNLFPEVKPTIQDVLR	S	2.31%	6906	6906	672.3820801	3	2014.122765	2014.125145	-0.00237939	K	S	-	3	17	0	0
O95210	Starch-binding domain-containing protein 1	1	2.23%	172	180	8	K	LPSSNLLK	N	3.21%	2919	2919	436.7573547	2	871.4990594	871.5014638	-0.002404447	K	N	N5:+0.984	2	8	0	0
O95232	Luc7-like protein 3	3	6.02%	87	98	11	R	YLQSLLAEVER	R	0.81%	5168	5168	661.364563	2	1320.713476	1319.708512	1.004963457	R	R	-	5	11	1	0
				87	99	12	R	YLQSLLAEVERR	I	3.49%	4658	4658	493.2780457	3	1476.810662	1475.809624	1.001038251	R	I	-	3	12	1	1
				173	187	14	R	STTSTIESFAAQEK	Q	0.81%	2872	2872	750.3632813	2	1498.710912	1498.715114	-0.004201708	R	Q	-	5	14	0	0
O95295	SNARE-associated protein Snapin	2	29.41%	22	48	26	R	DLFAEGLLEFLRPAVQQLDSHVHAVR	E	8.70%	9172	9172	741.1488037	4	2960.563915	2961.534822	-0.97090762	R	E	Q16:+0.984,Q17:+0.984	2	26	-1	0
				91	105	14	R	VVLVNNILQNAQER	L	0.81%	4269	4269	805.4524536	2	1608.889257	1608.89475	-0.005493189	R	L	-	5	14	0	0
O95297	Myelin protein zero-like protein 1	1	4.83%	138	151	13	K	NPPDIVVQPGHIR	L	0.81%	1741	1741	481.2670593	3	1440.777703	1440.783743	-0.006040261	K	L	-	3	13	0	0
O95445	Apolipoprotein M	1	3.72%	171	178	7	K	AFLLTPR	N	5.86%	2949	2949	409.2496338	2	816.4836175	816.4857697	-0.002152182	K	N	-	1	7	0	0
O95716	Ras-related protein Rab-3D	4	24.20%	41	60	19	R	YADDSFTPAFVSTVGIDFK	V	0.81%	6558	6558	1040.998291	2	2079.980932	2078.983685	0.997247151	R	V	-	5	19	1	0
				72	83	11	K	LQIWDTAGQER	Y	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				85	93	8	R	TITTAYYR	G	0.81%	822	822	494.7568359	2	987.4980218	987.5025421	-0.004520293	R	G	-	3	8	0	0
				121	136	15	K	TYSWDNAQVILVGNK	C	1.93%	4737	4737	854.9362793	2	1707.856909	1706.862782	0.994126994	K	C	-	2	15	1	0
O95782	AP-2 complex subunit alpha-1	6	8.29%	464	481	17	R	VLQIVTNRDDVQGYAAK	T	4.73%	2544	2544	631.0101929	3	1890.007103	1889.984672	0.022431301	R	T	Q12:+0.984	2	17	0	1
				498	516	18	K	VGGYILGEFGNLIAGDPR	S	0.81%	7290	7290	924.4830933	2	1846.950536	1846.957745	-0.007208213	K	S	-	5	18	0	0
				538	547	9	R	ALLLSTYIK	F	0.81%	4596	4596	511.8180237	2	1021.620397	1020.621929	0.998468243	R	F	-	5	9	1	0
				832	843	11	R	DFLTPPLLSVR	F	4.82%	6309	6309	629.3605347	2	1256.705419	1256.712869	-0.007450216	R	F	-	2	11	0	0
				845	856	11	R	YGGAPQALTLK	L	2.64%	2142	2142	559.8148804	2	1117.614111	1117.613155	0.000955358	R	L	-	3	11	0	0
				863	878	15	K	FFQPTEMAAQDFFQR	W	0.81%	6199	6199	932.435791	2	1862.855932	1861.845752	1.010179583	K	W	-	5	15	1	0
O95858	Tetraspanin-15	1	4.08%	117	129	12	R	NQTIDFLNDNIR	R	4.82%	1726	1726	487.9017029	3	1460.681634	1461.721202	-1.039568949	R	R	-	2	12	-1	0
O95864	Fatty acid desaturase 2	3	10.59%	58	73	15	R	VIGHYAGEDATDAFR	A	0.81%	2234	2234	811.880127	2	1621.744604	1620.753231	0.991372866	R	A	-	5	15	1	0
				73	84	11	R	AFHPDLEFVGK	F	0.81%	3661	3661	630.3249512	2	1258.634252	1258.634619	-0.000366808	R	F	-	5	11	0	0
				84	105	21	K	FLKPLLIGELAPEEPSQDHGK	N	4.90%	5027	5027	580.3131104	4	2317.221141	2317.231795	-0.010653442	K	N	-	1	21	0	0
O95970	Leucine-rich glioma-inactivated protein 1	2	3.23%	320	328	8	K	IQDIEILK	I	6.36%	1176	1176	487.271637	2	972.5276238	971.5538934	0.973730406	K	I	Q2:+0.984	3	8	1	0
				513	523	10	K	FQELNVQAPR	S	7.56%	2075	2075	601.8007202	2	1201.58579	1201.609117	-0.023326658	K	S	Q7:+0.984	2	10	0	0
O95996	Adenomatous polyposis coli protein 2	1	0.91%	1687	1708	21	R	AIQEGANSIVTWLHQAAAATR	E	5.29%	5586	5586	1104.554932	2	2207.094213	2208.128711	-1.034497679	R	E	Q15:+0.984	1	21	-1	0
O96005	Cleft lip and palate transmembrane protein 1	9	19.58%	209	224	15	K	NLLTGETEADPEMIK	R	0.81%	3754	3754	831.4099731	2	1660.804296	1659.80255	1.001746033	K	R	-	5	15	1	0
				209	225	16	K	NLLTGETEADPEMIKR	A	0.81%	3164	3164	606.3083496	3	1815.901574	1815.903661	-0.00208762	K	A	-	5	16	0	1
				304	314	10	R	VSFCPLSLWR	W	0.81%	6464	6464	633.3297119	2	1264.643774	1263.642947	1.000826796	R	W	C4:+57.021	5	10	1	0
				314	324	10	R	WQLYAAQSTK	S	0.81%	2717	2717	598.3085938	2	1194.601537	1194.603319	-0.001781492	R	S	-	5	10	0	0
				324	346	22	K	SPWNFLGDELYEQSDEEQDSVK	V	0.81%	6327	6327	1308.572632	2	2615.129614	2614.134719	0.994894416	K	V	-	4	22	1	0
				376	394	18	K	NDIQFWNSRQSLEGLSVR	S	5.40%	7104	7104	717.9777222	3	2150.909691	2152.007212	-1.097520128	K	S	N1:+0.984,Q4:+0.984,N7:	1	18	-1	1
				534	542	8	K	SVAHLPWR	M	0.81%	2175	2175	483.2678833	2	964.5201165	964.5242805	-0.00416399	K	M	-	5	8	0	0
				547	562	15	K	ALNTFIDDLFAFVIK	M	0.81%	10236	10236	864.4760742	2	1726.936498	1725.934156	1.002342782	K	M	-	5	15	1	0
				634	666	32	R	EEASTSLPTKPTQGASSASEPQEAPPKPAEDK	K	3.45%	686	686	1089.529297	3	3265.564416	3264.563373	1.001042889	R	K	-	3	32	1	0
P00505	Aspartate aminotransferase, mitochondrial	9	24.42%	107	122	15	K	ASAELALGENSEVLK	S	0.81%	3349	3349	765.8980103	2	1529.78037	1529.793699	-0.013328428	K	S	-	5	15	0	0
				125	139	14	R	FVTVQTISGTGALR	I	0.81%	3728	3728	725.4039917	2	1448.792333	1448.798725	-0.006391226	R	I	-	5	14	0	0
				139	147	8	R	IGASFLQR	F	0.81%	2239	2239	446.25	2	890.4843499	890.4973971	-0.013047136	R	F	-	5	8	0	0
				287	296	9	R	VGAFTMVCK	D	0.81%	2031	2031	507.2515564	2	1012.487463	1011.487693	0.999769913	R	D	C8:+57.021	5	9	1	0
				309	325	16	K	ILIRPMYSNPPLNGAR	I	5.33%	5266	5266	610.3384399	3	1827.991845	1827.965606	0.026238632	K	I	M6:+15.994,N13:+0.984	1	16	0	0
				325	337	12	R	IAAAILNTPDLR	K	0.81%	3663	3663	634.3685303	2	1266.72141	1266.729582	-0.008171741	R	K	-	5	12	0	0
				325	338	13	R	IAAAILNTPDLRK	Q	0.81%	2923	2923	466.2797241	3	1395.815697	1394.824545	0.991151899	R	Q	-	3	13	1	1
				338	345	7	K	QWLQEVK	V	4.21%	1915	1915	465.7525024	2	929.4893548	929.4970627	-0.007707925	K	V	-	2	7	0	0
				407	430	23	R	ISVAGVTSSNVGYLAHAIHQVTK	-	3.06%	5692	5692	588.8234863	4	2351.262645	2352.243741	-0.981095648	R	-	N10:+0.984	3	23	-1	0
P00568	Adenylate kinase isoenzyme 1	1	7.22%	63	77	14	K	GQLVPLETVLDMLR	D	0.81%	8823	8823	793.4552612	2	1584.894872	1583.859262	1.035610837	K	D	Q2:+0.984	3	14	1	0
P00734	Prothrombin	2	3.86%	384	399	15	K	SPQELLCGASLISDR	W	0.81%	4750	4750	823.4089966	2	1644.802343	1644.813654	-0.011311028	K	W	C7:+57.021	2	15	0	0
				599	608	9	K	YGFYTHVFR	L	4.09%	3443	3443	596.3406372	2	1190.665624	1188.571625	2.093999582	K	L	-	2	9	2	0
P01111	GTPase NRas	5	25.93%	5	16	11	K	LVVVGAGGVGK	S	0.81%	1008	1008	478.2988586	2	954.5820672	954.5862122	-0.004144971	K	S	-	5	11	0	0
				16	41	25	K	SALTIQLIQNHFVDEYDPTIEDSYR	K	0.81%	6394	6394	990.147522	3	2967.419091	2966.429779	0.989311494	K	K	-	3	25	1	0
				31	41	10	E	YDPTIEDSYR	K	0.81%	1352	1352	629.7790527	2	1257.542455	1257.551343	-0.008887595	E	K	-	5	10	0	0
				31	42	11	E	YDPTIEDSYRK	Q	4.45%	733	733	462.8866272	3	1385.636406	1385.646306	-0.009899648	E	Q	-	1	11	0	1
				135	147	12	K	SYGIPFIETSAK	T	0.81%	4872	4872	656.8412476	2	1311.666845	1311.671064	-0.004219227	R	T	-	5	12	0	0
P01833	Polymeric immunoglobulin receptor	1	1.96%	360	375	15	K	GVAGGSVAVLCPYNR	K	9.49%	561	561	507.5881042	3	1519.740838	1519.744831	-0.003992888	K	K	C11:+57.021,N14:+0.984	1	15	0	0
P01893	Putative HLA class I histocompatibility antigen, alpha chain H	7	31.22%	45	59	14	R	FISVGYVDDTQFVR	F	0.81%	4793	4793	823.4122925	2	1644.808935	1644.814769	-0.005833743	R	F	-	5	14	0	0
				135	155	20	R	GYEQHAYDGKDYIALNEDLR	S	0.81%	3266	3266	790.7041016	3	2369.08883	2369.092401	-0.003571057	R	S	-	3	20	0	1
				155	169	14	R	SWTAADMAAQITKR	K	3.62%	4569	4569	517.2526855	3	1548.734582	1548.771859	-0.037277479	R	K	-	3	14	0	1
				194	205	11	R	YLENGKETLQR	A	0.81%	674	674	676.3446655	2	1350.673681	1350.677925	-0.004244041	R	A	N4:+0.984	5	11	0	1
				226	243	17	R	CWALGFYPAEITLTWQR	D	0.81%	7963	7963	1057.524414	2	2113.033178	2112.013401	1.019776861	R	D	C1:+57.021,Q16:+0.984	3	17	1	0
				243	267	24	R	DGEDQTQDTELVETRPAGDGTFQK	W	0.81%	2338	2338	880.0667725	3	2637.176842	2636.183795	0.993047535	R	W	-	2	24	1	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.81%	2533	2533	714.3683472	2	1426.721044	1426.720474	0.000570112	K	Y	-	4	13	0	0
P02647	Apolipoprotein A-I	1	5.99%	85	101	16	R	EQLGPVTQEFWDNLEK	E	0.81%	6239	6239	966.9629517	2	1931.910253	1931.926504	-0.016250928	R	E	-	5	16	0	0
P02649	Apolipoprotein E	1	3.79%	280	292	12	K	SWFEPLVEDMQR	Q	0.81%	5905	5905	768.8529053	2	1535.69016	1535.707862	-0.017701229	K	Q	-	5	12	0	0
P02786	Transferrin receptor protein 1	30	47.63%	6	22	16	R	SAFSNLFGGEPLSYTR	F	0.81%	6030	6030	873.4227905	2	1744.829931	1744.842046	-0.012115105	R	F	-	5	16	0	0
				39	53	14	K	LAVDEEENADNNTK	A	0.81%	633	633	781.3518066	2	1560.687963	1560.690356	-0.002392783	K	A	-	5	14	0	0
				120	129	9	R	RLYWDDLKR	K	6.08%	2406	2406	633.3444824	2	1264.673315	1263.672402	1.000913188	R	K	-	1	9	1	2
				121	128	7	R	LYWDDLK	R	4.11%	4015	4015	477.2422791	2	952.468908	951.4701793	0.998728753	R	R	-	2	7	1	0
				121	129	8	R	LYWDDLKR	K	2.83%	3115	3115	554.7888794	2	1107.562109	1107.57129	-0.009181715	R	K	-	4	8	0	1
				134	145	11	K	LDSTDFTGTIK	L	0.81%	2656	2656	599.2987061	2	1196.581762	1196.59248	-0.010717507	K	L	-	4	11	0	0
				145	155	10	K	LLNENSYVPR	E	0.81%	1534	1534	604.303894	2	1206.592138	1203.624783	2.967355326	K	E	-	2	10	3	0
				155	174	19	R	EAGSQKDENLALYVENQFR	E	0.81%	5466	5466	1106.542847	2	2211.070043	2210.060372	1.009671143	R	E	-	3	19	1	1
				161	174	13	K	DENLALYVENQFR	E	0.81%	6350	6350	805.8954468	2	1609.775243	1609.773632	0.001611403	K	E	-	5	13	0	0
				193	205	12	K	DSAQNSVIIVDK	N	0.81%	1191	1191	644.8388062	2	1287.661962	1287.667042	-0.005079335	K	N	-	5	12	0	0
				208	224	16	R	LVYLVENPGGYVAYSK	A	0.81%	4369	4369	886.9655151	2	1771.91538	1770.919234	0.996146369	R	A	-	5	16	1	0
				267	287	20	K	VANAESLNAIGVLIYMDQTK	F	0.81%	7299	7299	717.3772583	3	2149.1083	2149.108903	-0.00060357	K	F	-	5	20	0	0
				325	339	14	R	SSGLPNIPVQTISR	A	0.81%	3502	3502	734.9082031	2	1467.800756	1467.804538	-0.003782062	R	A	-	3	14	0	0
				385	394	9	K	ILNIFGVIK	G	0.81%	6175	6175	508.8267212	2	1015.637792	1015.642999	-0.005206505	K	G	-	5	9	0	0
				394	409	15	K	GFVEPDHYVVVGAQR	D	0.81%	2795	2795	558.281189	3	1671.820092	1671.836901	-0.016809273	K	D	-	4	15	0	0
				418	428	10	K	SGVGTALLLK	L	0.81%	3215	3215	479.8	2	957.5843499	957.5858778	-0.001527928	K	L	-	3	10	0	0
				428	439	11	K	LAQMFSDMVLK	D	0.81%	5355	5355	641.8294067	2	1281.643163	1281.646114	-0.002950627	K	D	-	4	11	0	0
				428	446	18	K	LAQMFSDMVLKDGFQPSR	S	0.81%	5437	5437	691.3408203	3	2070.998986	2069.991416	1.007569706	K	S	Q15:+0.984	3	18	1	1
				446	477	31	R	SIIFASWSAGDFGSVGATEWLEGYLSSLHLK	A	1.97%	9600	9600	1110.891235	3	3329.650231	3327.645192	2.005038887	R	A	-	2	31	2	0
				477	486	9	K	AFTYINLDK	A	0.81%	3636	3636	542.7863159	2	1083.556982	1083.560057	-0.003075292	K	A	-	5	9	0	0
				486	495	9	K	AVLGTSNFK	V	0.81%	933	933	468.7600098	2	935.5043695	935.5076274	-0.003257997	K	V	-	5	9	0	0
				495	508	13	K	VSASPLLYTLIEK	T	0.81%	5939	5939	717.4138184	2	1432.811987	1432.817729	-0.005742033	K	T	-	5	13	0	0
				514	531	17	K	HPVTGQFLYQDSNWASK	V	0.81%	3389	3389	989.4716187	2	1976.927587	1976.938072	-0.010484647	K	V	-	2	17	0	0
				588	600	12	R	AAAEVAGQFVIK	L	0.81%	3161	3161	602.3381348	2	1202.660619	1202.665919	-0.005299781	R	L	-	2	12	0	0
				600	613	13	K	LTHDVELNLDYER	Y	0.81%	3109	3109	539.600769	3	1615.778832	1615.784197	-0.005364783	K	Y	-	1	13	0	0
				613	623	10	R	YNSQLLSFVR	D	0.81%	4790	4790	613.8284912	2	1225.641332	1225.645518	-0.004185778	R	D	-	5	10	0	0
				633	646	13	K	EMGLSLQWLYSAR	G	0.81%	6925	6925	777.3933716	2	1552.771093	1552.770796	0.00029674	K	G	-	4	13	0	0
				655	665	10	R	LTTDFGNAEK	T	0.81%	758	758	549.3002319	2	1096.584814	1094.5244	2.060413931	R	T	-	1	10	2	0
				680	693	13	R	VEYHFLSPYVSPK	E	0.81%	3698	3698	783.4082642	2	1564.800878	1564.792577	0.008301712	R	E	-	5	13	0	0
				698	717	19	R	HVFWGSGSHTLPALLENLK	L	0.81%	5868	5868	702.7062378	3	2105.095238	2105.105806	-0.010567789	R	L	-	2	19	0	0
P04049	RAF proto-oncogene serine/threonine-protein kinase	1	4.94%	111	143	32	R	LDWNTDAASLIGEELQVDFLDHVPLTTHNFAR	K	9.64%	6394	6394	910.2441406	4	3636.945262	3637.768874	-0.823611364	R	K	N4:+0.984	1	32	-1	0
P04114	Apolipoprotein B-100	1	0.31%	804	818	14	R	TLQGIPQMIGEVIR	K	9.06%	3314	3314	524.6173096	3	1570.828454	1570.838946	-0.010492201	R	K	Q7:+0.984,M8:+15.995	1	14	0	0
P04233	HLA class II histocompatibility antigen gamma chain	8	37.50%	21	35	14	R	DLISNNEQLPMLGR	R	0.81%	3743	3743	808.9071045	2	1615.798559	1614.803639	0.994920384	R	R	M11:+15.995	3	14	1	0
				46	77	31	R	GALYTGFSILVTLLLAGQATTAYFLYQQQGR	L	3.27%	12321	12321	842.7001953	4	3366.769481	3363.786711	2.982769666	R	L	-	1	31	3	0
				77	94	17	R	LDKLTVTSQNLQLENLR	M	0.81%	3642	3642	662.3684082	3	1984.081749	1984.095301	-0.013551511	R	M	-	1	17	0	1
				80	94	14	K	LTVTSQNLQLENLR	M	0.81%	3817	3817	814.9492188	2	1627.882787	1627.889331	-0.006543228	K	M	-	5	14	0	0
				159	167	8	K	GSFPENLR	H	0.81%	1571	1571	460.7261963	2	919.4367425	919.4399262	-0.003183678	K	H	N6:+0.984	2	8	0	0
				170	179	9	K	NTMETIDWK	V	2.88%	2704	2704	569.2635498	2	1136.51145	1136.517207	-0.005757567	K	V	-	3	9	0	0
				179	195	16	K	VFESWMHHWLLFEMSR	H	0.81%	7138	7138	712.6654053	3	2134.972741	2133.991706	0.98103434	K	H	-	5	16	1	0
				272	288	16	S	ESLELEDPSSGLGVTK	Q	0.81%	3528	3528	831.416687	2	1660.817724	1659.820308	0.997416287	S	Q	-	5	16	1	0
P04264	Keratin, type II cytoskeletal 1	31	56.52%	12	29	17	R	SGGGFSSGSAGIINYQR	R	0.81%	2854	2854	829.4005127	2	1656.785375	1656.785594	-0.000218465	R	R	-	4	17	0	0
				54	117	63	G	SFGAGGGFGSRSLVNLGGSKSISISVARGGGRGSGFGGGYGGGGFGGGGFGGGGFGGGGIGGG	G	5.08%	7586	7586	1773.24292	3	5316.705285	5314.542969	2.162315654	G	G	-	1	63	2	4
				65	74	9	R	SLVNLGGSK	S	3.89%	1247	1247	438.25	2	874.4843499	873.4919774	0.992372552	R	S	-	4	9	1	0
				74	82	8	K	SISISVAR	G	4.85%	2876	2876	416.53	2	831.0443499	831.4814126	-0.437062728	K	G	-	1	8	0	0
				185	197	12	K	SLNNQFASFIDK	V	0.81%	4619	4619	692.3415527	2	1382.667455	1382.683026	-0.015570579	K	V	-	4	12	0	0

				185	199	14	K	SLNNQFASFIDKVR	F	0.81%	5311	5311	820.4326782	2	1638.849706	1637.852551	0.997155237	K	F	-	4	14	1	1
				190	197	7	Q	FASFIDK	V	0.81%	2431	2431	414.2163696	2	826.4170892	826.4225007	-0.005411526	K	V	-	2	7	0	0
				199	211	12	R	FLEQQNQVLQTK	W	0.81%	1313	1313	738.3967285	2	1474.777807	1474.777989	-0.000182153	R	W	-	5	12	0	0
				199	223	24	R	FLEQQNQVLQTKWELLQQVDTSTR	T	0.81%	5580	5580	978.5136719	3	2932.517541	2932.493033	0.024507817	R	T	Q10:+0.984	2	24	0	1
				223	239	16	R	THNLEPYFESFINNLR	R	0.81%	7207	7207	997.4928589	2	1992.970068	1992.969372	0.000695661	R	R	-	4	16	0	0
				223	240	17	R	THNLEPYFESFINNLRR	R	3.27%	6542	6542	717.3656616	3	2149.07351	2149.070483	0.003026559	R	R	-	1	17	0	1
				267	277	10	R	NKYEDEINKR	T	6.55%	635	635	436.8881226	3	1307.640893	1307.646975	-0.00608222	K	T	-	1	10	0	2
				277	288	11	R	TNAENEFVTIK	K	0.81%	2069	2069	633.347168	2	1264.678686	1264.629928	0.048758146	R	K	-	4	11	0	0
				277	289	12	R	TNAENEFVTIKK	D	0.81%	987	987	465.2479858	3	1392.720482	1392.724891	-0.004408448	R	D	-	3	12	0	1
				343	355	12	R	SLDLDSIIAEVK	A	0.81%	6381	6381	651.8609009	2	1301.706152	1301.707844	-0.001692106	R	A	-	5	12	0	0
				343	364	21	R	SLDLDSIIAEVKAQYEDIAQK	S	0.81%	8563	8563	783.7446289	3	2348.210412	2349.195119	-0.984707321	R	S	Q20:+0.984	2	21	-1	1
				355	364	9	K	AQYEDIAQK	S	5.44%	685	685	534.2723999	2	1066.52915	1064.513835	2.015314589	K	S	-	1	9	2	0
				364	386	22	K	SKAEAESLYQSKYEELQITAGR	H	5.17%	3214	3214	835.0856934	3	2502.233605	2500.244544	1.989060566	K	H	-	1	22	2	2
				376	386	10	K	YEELQITAGR	H	0.81%	1661	1661	590.3015747	2	1178.587499	1178.593148	-0.005648858	K	H	-	4	10	0	0
				395	403	8	K	IEISELNR	V	0.81%	1786	1786	487.2677307	2	972.5198113	972.5240059	-0.00419451	K	V	-	5	8	0	0
				417	432	15	K	QISNLQQSISDAEQR	G	0.81%	2890	2890	859.4231567	2	1716.830663	1715.843837	0.986826333	K	G	-	5	15	1	0
				417	438	21	K	QISNLQQSISDAEQRGENALK	D	7.85%	4857	4857	777.3997803	3	2329.175866	2328.166963	1.008903052	K	D	-	1	21	1	1
				441	455	14	K	NKLNDLEDALQQAK	E	0.81%	4003	4003	800.4205322	2	1598.825414	1598.826396	-0.000981627	K	E	-	5	14	0	1
				441	460	19	K	NKLNDLEDALQQAKEDLAR	L	5.66%	5999	5999	728.7124023	3	2183.113732	2183.118221	-0.004489513	K	L	-	1	19	0	2
				443	455	12	K	LNDLEDALQQAK	E	0.81%	3464	3464	678.3550415	2	1354.694433	1356.688505	-1.9940724	K	E	-	4	12	-1	0
				443	460	17	K	LNDLEDALQQAKEDLAR	L	0.81%	6061	6061	648.0007324	3	1940.978722	1941.964331	-0.985608606	K	L	Q10:+0.984	2	17	-1	1
				463	472	9	R	DYQELMNTK	L	0.81%	1985	1985	571.262146	2	1140.508642	1140.512122	-0.003479824	R	L	-	5	9	0	0
				483	492	9	R	TLLEGEESR	M	1.93%	825	825	517.2576904	2	1032.499731	1032.50875	-0.009018997	R	M	-	4	9	0	0
				518	549	31	R	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR	G	2.51%	670	670	1192.984253	2	2383.952856	2382.944567	1.008288627	R	G	-	5	31	1	0
				549	588	39	R	GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR	G	3.91%	667	667	1105.438599	3	3313.292321	3311.300844	1.991477226	R	G	-	4	39	2	0
				588	616	28	R	GGSGGGGGGSSGGRGSGGGSSGGSIGGR	G	9.21%	8202	8202	1041.147949	2	2080.280248	2078.907394	1.372854726	R	G	-	1	28	1	1
P04626	Receptor tyrosine-protein kinase erbB-2	1	1.91%	1072	1096	24	R	SPLAPSEGAGSDVFDGDLGMGAAK	G	9.53%	4208	4208	567.0096436	4	2264.007274	2264.025775	-0.018501221	R	G	M20:+15.994	2	24	0	0
P04792	Heat shock protein beta-1	12	70.73%	4	12	8	R	RVPFSLLR	G	0.81%	3680	3680	494.3055115	2	986.5953729	986.6025309	-0.007158043	R	G	-	4	8	0	1
				5	12	7	R	VPFSLLR	G	2.83%	4086	4086	416.19	2	830.3643499	830.5014198	-0.13706984	R	G	-	3	7	0	0
				12	20	8	R	GPSWDPFR	D	2.26%	4195	4195	481.2261658	2	960.4366815	960.4453615	-0.008679993	R	D	-	5	8	0	0
				12	27	15	R	GPSWDPFRDWYPHSR	L	4.24%	5342	5342	635.2924805	3	1902.853966	1901.859762	0.994204486	R	L	-	5	15	1	1
				27	37	10	R	LFDQAFGLPR	L	0.81%	4947	4947	582.8125	2	1163.60935	1162.61349	0.995860288	R	L	-	3	10	1	0
				37	56	19	R	LPEEWSQWLGGSSWPGYVR	P	4.46%	7111	7111	1118.537476	2	2235.059301	2233.05925	2.000051284	R	P	-	1	19	2	0
				37	75	38	R	LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR	A	0.81%	7378	7378	1366.027222	3	4095.05819	4092.053385	3.004805215	R	A	-	2	38	3	0
				56	75	19	R	PLPPAAIESPAVAAPAYSR	A	4.06%	3509	3509	940.0089111	2	1878.002172	1877.004695	0.99747729	R	A	-	1	19	1	0
				79	89	10	R	QLSSGVSEIR	H	2.26%	759	759	538.2908325	2	1074.566015	1074.566933	-0.000918433	R	H	-	2	10	0	0
				96	112	16	R	VSLDVNHFAPDELTVK	T	0.81%	4020	4020	595.307373	3	1782.898644	1783.899211	-1.000567099	R	T	N6:+0.984	3	16	-1	0
				140	171	31	R	KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	L	0.81%	5238	5238	1076.552124	3	3226.632897	3226.631895	0.001001598	R	L	Q12:+0.984	3	31	0	1
				171	188	17	K	LATQSNEITIPVTFESR	A	0.81%	4332	4332	953.4962158	2	1904.976782	1904.984353	-0.007571895	K	A	-	2	17	0	0
P04839	Cytochrome b-245 heavy chain	10	19.47%	43	54	11	R	KLLGSALALAR	A	1.93%	3313	3313	556.8584595	2	1111.701269	1111.707724	-0.006455575	R	A	-	3	11	0	1
				44	54	10	K	LLGSALALAR	A	0.81%	3763	3763	492.8122864	2	983.6089227	983.6127613	-0.00383863	K	A	-	5	10	0	0
				271	284	13	K	WIVGPMFLYLCER	L	0.81%	7826	7826	842.4321899	2	1682.84873	1682.830826	0.017904307	K	L	C11:+57.021	5	13	0	0
				306	313	7	K	TIELQMK	K	3.82%	1569	1569	431.7389526	2	861.4622552	861.4629865	-0.000731319	K	K	-	2	7	0	0
				318	328	10	K	MEVGQYIFVK	C	0.81%	4505	4505	607.8190308	2	1213.622411	1212.621278	1.001133147	K	C	-	5	10	1	0
				334	356	22	K	LEWHPFTLTSAPEEDFFSIHIR	I	0.81%	7265	7265	892.1106567	3	2673.308495	2671.307085	2.001410055	L	A	-	2	22	2	0
				458	468	10	L	QLLESQMQER	N	6.00%	6329	6329	633.3201294	2	1264.624609	1261.597233	3.027375821	L	N	Q1:+0.984	1	10	3	0
				508	521	13	K	TLYGRPNWDNEFK	T	2.34%	3329	3329	820.8974609	2	1639.779272	1638.779052	1.000220035	K	T	-	3	13	1	0
				531	548	17	R	IGVFLCGPEALAETLSK	Q	0.81%	6955	6955	902.977356	2	1803.939062	1803.943606	-0.00454395	R	Q	C6:+57.021	5	17	0	0
				559	567	8	R	GVHFIFNK	E	0.81%	2781	2781	481.2655945	2	960.5155389	960.5181325	-0.002593611	R	E	-	5	8	0	0
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	3	11.27%	130	143	13	R	LWADHGVQACFGR	S	3.80%	2858	2858	506.2410278	3	1515.699608	1515.70365	-0.004041504	R	S	C10:+57.021	1	13	0	0
				162	177	15	R	IAQSDYIPTQQDVLR	T	0.81%	3377	3377	873.9559326	2	1745.896215	1745.89481	0.001405146	R	T	-	5	15	0	0
				181	193	12	K	TTGIVETHFTFK	D	0.81%	3124	3124	690.8656006	2	1379.715551	1379.708512	0.007038652	K	D	-	5	12	0	0
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	33	37.73%	45	53	8	K	LSLDELHR	K	1.97%	2024	2024	490.7912292	2	979.5668084	981.5243402	-1.957531768	K	K	-	5	8	-1	0
				74	91	17	R	DGPNALTPPPTTPEWIK	F	0.81%	4405	4405	918.48	2	1834.94435	1832.930861	2.01348872	R	F	-	2	17	2	0
				153	162	9	K	SSKIMESFK	N	9.79%	5552	5552	537.2686768	2	1072.521703	1071.527129	0.994574588	K	N	M5:+15.995	2	9	1	1
				162	173	11	K	NMVPQQALVIR	N	0.81%	3450	3450	634.8587036	2	1267.701757	1267.707074	-0.005316549	K	E	-	2	11	0	0
				177	194	17	K	MSINAEEVVVGDLVEVK	G	0.81%	6198	6198	915.9781494	2	1829.940649	1829.944464	-0.003814804	K	G	-	5	17	0	0
				212	227	15	K	VDNSSLTGESEPQTR	S	0.81%	703	703	810.3778687	2	1618.740087	1618.743454	-0.003367015	K	S	-	5	15	0	0
				212	240	28	K	VDNSSLTGESEPQTRSPDFTNENPLETR	N	6.04%	6749	6749	780.9	4	3119.5687	3121.395942	-1.827241744	K	N	Q13:+0.984,N23:+0.984	1	28	-1	1
				227	240	13	R	SPDFTNENPLETR	N	0.81%	3188	3188	760.8604126	2	1519.705175	1518.695047	1.010127771	R	N	-	3	13	1	0
				240	255	15	R	NIAFFSTNCVEGTAR	G	0.81%	4169	4169	844.4005737	2	1686.785497	1685.782688	1.002809101	R	G	C9:+57.021	4	15	1	0
				255	264	9	R	GIVVYTGDR	T	0.81%	959	959	490.2635803	2	978.5115106	978.5134411	-0.001930571	R	T	-	5	9	0	0
				385	413	28	R	MTVAHMWFDNQIHEADTTENQSGVSFDK	T	0.81%	4781	4781	1080.81189	3	3239.412194	3238.397162	1.015031761	R	T	Q11:+0.984	4	28	1	0
				413	423	10	K	TSATWLALSR	I	0.81%	3891	3891	553.2998657	2	1104.584081	1104.592754	-0.008672827	K	I	-	1	10	0	0
				430	444	14	R	AVFQANQENLPILK	R	0.81%	4395	4395	793.4414063	2	1584.867162	1583.867139	1.000023868	R	R	-	5	14	1	0
				445	458	13	R	AVAGDASESALLK	C	0.81%	1545	1545	616.3283691	2	1230.641088	1230.645578	-0.004489591	R	C	-	5	13	0	0
				476	487	11	K	IVEIPFNSTNK	Y	0.81%	3495	3495	632.3321533	2	1262.648657	1261.655399	0.993257969	K	Y	N7:+0.984	4	11	1	0
				494	508	14	K	NPNTSEPQHLLVMK	G	0.81%	2353	2353	804.4098511	2	1606.804052	1606.813724	-0.009671812	K	G	-	4	14	0	0
				526	551	25	K	EQPLDEELKDAFQNAYLELGGLGER	V	2.34%	8171	8171	945.4642334	3	2833.369225	2833.377015	-0.007790301	K	V	-	4	25	0	1
				535	551	16	K	DAFQNAYLELGGLGER	V	0.81%	5882	5882	876.9752808	2	1751.934911	1751.84786	0.087051675	K	V	-	5	16	0	0
				612	625	13	K	VIMVTGDHPITAK	A	0.81%	1053	1053	461.2533569	3	1380.736596	1380.743519	-0.006923207	K	A	-	4	13	0	0
				614	625	11	I	MVTGDHPITAK	A	3.30%	1028	1028	585.3	2	1168.58435	1168.591041	-0.006690872	I	A	-	1	11	0	0
				629	647	18	K	GVGIISEGNETVEDIAAR	L	0.81%	4571	4571	915.4666748	2	1828.9177	1828.916668	0.001031753	K	L	-	4	18	0	0
				647	658	11	R	LNIPVSQVNPR	D	0.81%	2535	2535	618.8556519	2	1235.695654	1235.698616	-0.002962745	R	D	-	5	11	0	0
				671	683	12	K	DMTSEQLDDILK	Y	0.81%	4636	4636	704.3363037	2	1406.656957	1406.659908	-0.00295113	K	Y	-	5	12	0	0
				683	692	9	K	YHTEIVFAR	T	0.81%	2046	2046	568.7987061	2	1135.581762	1134.582189	0.999572557	K	T	-	2	9	1	0
				698	707	9	K	LIIVEGCQR	Q	0.81%	1443	1443	544.298645	2	1086.58164	1086.585098	-0.003457705	K	Q	C7:+57.021	5	9	0	0
				707	726	19	R	QGAIVAVTGDGVNDSPALK	K	0.81%	3081	3081	906.4755859	2	1810.935522	1810.942489	-0.006966781	R	K	-	5	19	0	0
				707	727	20	R	QGAIVAVTGDGVNDSPALKK	A	3.00%	2284	2284	647.3521729	3	1939.033043	1939.037452	-0.004408277	R	A	-	2	20	0	1
				726	743	17	K	KADIGVAMGIAGSDVSK	Q	0.81%	2888	2888	809.9247437	2	1617.833837	1617.839604	-0.005767127	K	Q	-	5	17	0	1
				727	743	16	K	ADIGVAMGIAGSDVSK	Q	0.81%	3097	3097	497.5944824	3	1489.759972	1489.744641	0.01533093	K	Q	-	1	16	0	0
				743	766	23	K	QAADMILLDDNFASIVTGVEEGR	L	0.81%	8318	8318	822.413147	3	2464.215966	2464.179152	0.036813374	K	L	Q1:+0.984	3	23	0	0
				766	773	7	R	LIFDNLK	K	4.12%	3708	3708	431.7551575	2	861.4946649	861.4960001	-0.001335211	R	K	-	2	7	0	0
				766	774	8	R	LIFDNLKK	S	2.26%	2581	2581	495.8017273	2	989.5878045	989.5909632	-0.003158698	R	S	-	5	8	0	1
				893	911	18	R	WINDVEDSYGQQWTYEQR	K	3.23%	4492	4492	1159.008667	2	2316.001684	2316.008337	-0.006652632	R	K	-	5	18	0	0
P05109	Protein S100-A8	3	31.18%	7	18	11	K	ALNSIIDVYHK	Y	0.81%	3383	3383	424.9031677	3	1271.686028	1271.687383	-0.001354946	K	Y	-	4	11	0	0
				36	47	11	K	LLETECPQYIR	K	0.81%	2531	2531	711.3546753	2	1420.693701	1420.701584	-0.007883734	K	K	C6:+57.021	5	11	0	0
				49	56	7	K	GADVWFK	E	4.33%	3072	3072	411.7106018	2	821.4055535	821.407185	-0.001631419	K	E	-	1	7	0	0
P05141	ADP/ATP translocase 2	24	66.11%	10	23	13	K	DFLAGGVAAAISK	T	0.81%	4705	4705	611.3071899	2	1220.59873	1218.660834	1.937895931	K	T	-	5	13	2	0
				33	43	10	K	LLLQVQHASK	Q	0.81%	967	967	568.8419189	2	1135.668188	1135.671339	-0.003151109	K	Q	-	5	10	0	0
				35	43	8	L	LQVQHASK	Q	5.83%	914	914	455.7539673	2	909.4922845	909.5032107	-0.010926254	L	Q	-	1	8	0	0
				63	72	9	K	EQGVLSFWR	G	0.81%	5380	5380	561.2883911	2	1120.561132	1120.566539	-0.005407245	K	G	-	3	9	0	0
				72	80	8	R	GNLANVIR	Y	3.57%	1131	1131	428.7650452	2	855.5144403	855.492646	0.021794228	R	Y	-	2	8	0	0
				80	92	12	R	YFPTQALNFAFK	D	0.81%	6120	6120	724.3757324	2	1446.735815	1445.734333	1.001481524	R	D	-	5	12	1	0
				80	94	14	R	YFPTQALNFAFKDK	Y	0.81%	5266	5266	845.4324951	2	1688.84934	1688.85624	-0.00689935	R	Y	-	5	14	0	1
				82	92	10	F	PTQALNFAFK	D	6.03%	6151	6151	569.3172607	2	1136.618871	1135.602591	1.01628082	F	D	-	1	10	1	0
				96	106	10	K	QIFLGGVDKR	T	0.81%	1661	1661	566.8251343	2	1131.634618	1131.640039	-0.005420285	K	T	-	3	10	0	1
				111	138	27	R	YFAGNLASGGAAGATSLCFVYPLDFAR	T	0.81%	7170	7170	1399.680054	2	2797.344457	2796.321271	1.023186654	R	T	N5:+0.984,C18:+57.021	3	27	1	0
				126	138	12	T	SLCFVYPLDFAR	T	3.96%	6585	6585	744.3701782	2	1486.724706	1486.727405	-0.002698675	T	T	C3:+57.021	1	12	0	0
				155	163	8	R	GLGDCLVK	I	0.81%	1414	1414	431.2280273	2	860.4404046	860.4421216	-0.001717025	R	I	C5:+57.021	2	8	0	0
				171	188	17	K	GLYQGFNVSVQGIIIYR	A	0.81%	9145	9145	965.4608154	2	1928.905981	1927.020329	1.885651395	R	A	Q4:+0.984	2	17	2	0
				188	199	11	R	AAYFGIYDTAK	G	0.81%	3621	3621	610.3012085	2	1218.586767	1218.592086	-0.005318624	R	G	-	5	11	0	0
				206	235	29	K	NTHIVISWMIAQTVTAVAGLTSYPFDTVR	R	0.81%	9945	9945	798.92	4	3191.6487	3191.632504	0.016195504	K	R	Q12:+0.984	3	29	0	0
				215	235	20	M	IAQTVTAVAGLTSYPFDTVR	R	4.77%	5759	5759	1056.059204	2	2110.102758	2109.110617	0.992141371	M	R	-	1	20	1	0
				244	259	15	R	KGTDIMYTGTLDCWR	K	0.81%	4078	4078	908.9190063	2	1815.822363	1815.827925	-0.005562505	R	K	C13:+57.021	5	15	0	1
				245	259	14	K	GTDIMYTGTLDCWR	K	0.81%	4706	4706	845.3707886	2	1688.725927	1687.732962	0.992965084	K	K	C12:+57.021	1	14	1	0
				272	280	8	K	GAWSNVLR	G	0.81%	2962	2962	451.7452393	2	901.4748284	901.4769959	-0.002167508	K	G	-	5	8	0	0
				280	295	15	R	GMGGAFVLVLYDEIK	K	0.81%	7497	7497	806.43	2	1610.84435	1610.837813	0.006536552	R	K	-	4	15	0	0
				280	296	16	R	GMGGAFVLVLYDEIKK	Y	0.81%	6943	6943	585.984436	3	1754.929833	1754.927777	0.002056481	R	Y	M2:+15.995	1	16	0	1
				280	298	18	R	GMGGAFVLVLYDEIKKYT	-	5.82%	8731	8731	668.6871338	3	2003.037926	2003.043784	-0.005857473	R	-	-	1	18	0	2
				282	296	14	M	GGAFVLVLYDEIKK	Y	4.79%	7128	7128	776.4417725	2	1550.867895	1550.870827	-0.002932086	M	Y	-	1	14	0	1
				286	296	10	F	VLVLYDEIKK	Y	4.15%	2998	2998	610.366394	2	1218.717138	1218.722372	-0.00523353	F	Y	-	1	10	0	1
P05362	Intercellular adhesion molecule 1	11	22.56%	56	66	10	K	LLGIETPLPK	K	1.93%	4342	4342	540.8354492	2	1079.655248	1079.659043	-0.00379453	K	K	-	5	10	0	0
				104	115	11	K	TFLTVYWTPER	V	0.81%	5768	5768	706.8626709	2	1411.709692	1411.713598	-0.003906083	K	V	-	5	11	0	0
				115	129	14	R	VELAPLPSWQPVGK	N	0.81%	5122	5122	760.9254761	2	1519.835302	1519.839861	-0.004559028	R	N	-	5	14	0	0
				158	176	18	K	REPAVGEPAEVTTTVLVR	R	0.81%	3392	3392	963.0256958	2	1924.035742	1923.042537	0.99320445	K	R	-	4	18	1	1
				159	176	17	R	EPAVGEPAEVTTTVLVR	R	0.81%	3918	3918	884.4740601	2	1766.93247	1766.941426	-0.008955883	R	R	-	5	17	0	0
				273	287	14	K	ASVSVTAEDEGTQR	L	0.81%	646	646	725.3451538	2	1448.674658	1448.674312	0.000345633	K	L	-	3	14	0	0
				339	353	14	K	VTLNGVPAQPLGPR	A	1.93%	2916	2916	710.4028931	2	1418.790136	1418.788144	0.001991821	K	A	N4:+0.984	3	14	0	0
				433	449	16	K	DGTFPLPIGESVTVTR	D	0.81%	5348	5348	844.9525146	2	1687.889379	1687.878097	0.011281945	K	D	-	5	16	0	0
				468	478	10	R	KVTVNVLSPR	Y	0.81%	1055	1055	556.8384399	2	1111.66123	1111.671339	-0.010109117	R	Y	-	5	10	0	1
				469	478	9	K	VTVNVLSPR	Y	0.81%	1919	1919	492.7927856	2	983.5699212	983.5763758	-0.006454575	K	Y	-	4	9	0	0
				519	532	13	K	GTPMKPNTQATPP	-	8.37%	670	670	670.3397217	2	1338.663793	1338.660183	0.003610151	K	-	-	2	13	0	0
P06239	Tyrosine-protein kinase Lck	2	5.11%	340	358	18	K	LLDMAAQIAEGMAFIEER	N	5.30%	6125	6125	670.05	3	2007.126525	2006.980533	0.145992224	K	N	-	1	18	0	0
				379	387	8	K	IADFGLAR	L	2.46%	2579	2579	431.742218	2	861.468786	861.4708479	-0.002061973	K	D	-	4	8	0	0
P06576	ATP synthase subunit beta, mitochondrial	26	68.24%	94	109	15	R	LVLEVAQHLGESTVR	T	0.81%	3781	3781	825.9645386	2	1649.913427	1649.910066	0.00336098	R	T	-	4	15	0	0
				109	121	12	R	TIAMDGTEGLVR	G	0.81%	2481	2481	632.3219604	2	1262.628271	1261.633634	0.994636818	R	G	-	5	12	1	0
				124	143	19	K	VLDSGAPIKIPVGPETLGR	I	0.81%	4432	4432	640.3666992	3	1918.076623	1918.088759	-0.012136448	K	I	-	4	19	0	1
				133	143	10	K	IPVGPETLGR	I	0.81%	1768	1768	520.776062	2	1039.536474	1037.586941	1.949533439	K	I	-	4	10	2	0
				143	155	12	R	IMNVIGEPIDER	G	0.81%	3319	3319	693.3572998	2	1384.69895	1384.702048	-0.003098479	R	G	-	5	12	0	0
				143	159	16	R	IMNVIGEPIDERGPIK	T	0.81%	3626	3626	891.4873047	2	1780.958959	1779.955303	1.003656367	R	T	-	4	16	1	1
				161	188	27	K	QFAPIHAEAPEFMEMSVEQEILVTGIK	V	0.81%	7317	7317	1015.840393	3	3044.497704	3043.503481	0.994223503	K	V	-	2	27	1	0
				188	198	10	K	VVDLLAPYAK	G	0.81%	4040	4040	544.8189087	2	1087.622167	1087.627743	-0.005575425	K	G	-	3	10	0	0
				201	212	11	K	IGLFGGAGVGK	T	0.81%	3177	3177	488.2828674	2	974.5500848	974.554912	-0.004827233	K	T	-	5	11	0	0
				212	225	13	K	TVLIMELINNVAK	A	0.81%	7907	7907	729.9257202	2	1457.83579	1456.832334	1.003456342	K	A	-	5	13	1	0
				216	239	23	I	MELINNVAKAHGGYSVFAGVGER	T	5.96%	4697	4697	812.3886719	3	2434.142541	2434.205411	-0.062870983	I	T	M1:+15.994	1	23	0	1
				225	239	14	K	AHGGYSVFAGVGER	T	0.81%	1999	1999	704.3429565	2	1406.670263	1405.673858	0.996404774	K	T	-	4	14	1	0
				239	259	20	R	TREGNDLYHEMIESGVINLK	D	3.04%	5156	5156	773.7145996	3	2318.120324	2317.137243	0.983080244	R	D	-	2	20	1	1
				241	259	18	R	EGNDLYHEMIESGVINLK	D	0.81%	5672	5672	688.3372803	3	2061.988366	2059.988454	1.999911956	R	D	-	2	18	2	0
				264	279	15	K	VALVYGQMNEPPGAR	A	0.81%	2565	2565	801.4032593	2	1600.790868	1600.803159	-0.012290685	K	A	-	5	15	0	0
				281	294	13	R	VALTGLTVAEYFR	D	0.81%	6272	6272	720.3991699	2	1438.78269	1438.782012	0.000677956	R	D	-	5	13	0	0
				281	310	29	R	VALTGLTVAEYFRDQEGQDVLLFIDNIFR	F	0.81%	10430	10430	1115.250244	3	3342.727257	3342.71359	0.013666838	R	F	Q15:+0.984	2	29	0	1

				294	310	16	R	DQEGQDVLLFIDNIFR	F	0.81%	9336	9336	961.4853516	2	1920.955053	1920.958139	-0.003085611	R	F	-	5	16	0	0
				310	324	14	R	FTQAGSEVSALLGR	I	0.81%	4354	4354	718.3797607	2	1434.743871	1434.746689	-0.00281754	R	I	-	5	14	0	0
				324	345	21	R	IPSAVGYQPTLATDMGTMQER	I	0.81%	4352	4352	1134.050049	2	2266.084448	2265.076952	1.007495128	R	I	-	4	21	1	0
				369	387	18	D	PAPATTFAHLDATTVLSR	A	5.52%	4203	4203	934.9911499	2	1867.96665	1867.979208	-0.012558699	D	A	-	1	18	0	0
				387	406	19	R	AIAELGIYPAVDPLDSTSR	I	0.81%	5595	5595	664.52	3	1990.536525	1987.026218	3.510306544	R	I	-	2	19	4	0
				406	422	16	R	IMDPNIVGSEHYDVAR	G	0.81%	2753	2753	605.9586182	3	1814.852379	1815.846131	-0.993751404	R	G	N5:+0.984	5	16	-1	0
				432	456	24	K	SLQDIIAILGMDELSEEDKLTVSR	A	0.81%	7998	7998	892.7973022	3	2675.368432	2674.373511	0.994920626	K	A	-	3	24	1	1
				462	480	18	R	FLSQPFQVAEVFTGHMGK	L	0.81%	6498	6498	675.0083618	3	2022.00161	2022.987316	-0.985705495	R	L	Q7:+0.984	4	18	-1	0
				489	519	30	K	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	A	0.81%	7925	7925	1117.546875	3	3349.61715	3350.616914	-0.999764048	K	A	Q16:+0.984	5	30	-1	0
P06702	Protein S100-A9	4	49.12%	10	25	15	R	NIETIINTFHQYSVK	L	0.81%	6026	6026	903.9731445	2	1805.930639	1805.931196	-0.000556545	R	L	-	3	15	0	0
				25	38	13	K	LGHPDTLNQGEFK	E	1.93%	906	906	485.9115295	3	1454.711114	1454.715389	-0.004275281	K	E	-	3	13	0	0
				57	72	15	K	VIEHIMEDLDTNADK	Q	0.81%	3386	3386	871.9172363	2	1741.818823	1741.819263	-0.000440336	K	Q	-	5	15	0	0
				72	85	13	K	QLSFEEFIMLMAR	L	0.81%	8589	8589	808.40448	2	1614.79331	1613.794569	0.998740465	K	L	-	4	13	1	0
P06733	Alpha-enolase	26	68.43%	15	28	13	R	GNPTVEVDLFTSK	G	2.26%	4036	4036	703.8647461	2	1405.713842	1405.708906	0.004935668	R	G	-	5	13	0	0
				32	50	18	R	AAVPSGASTGIYEALELR	D	0.81%	4939	4939	902.9730835	2	1803.930517	1803.936675	-0.006157976	R	D	-	5	18	0	0
				71	80	9	K	TIAPALVSK	K	3.03%	910	910	450.2796936	2	898.5437371	898.548764	-0.005026873	K	K	-	3	9	0	0
				92	103	11	K	LMIEMDGTENK	S	0.81%	2376	2376	641.2987671	2	1280.581884	1279.578822	1.003061756	K	S	-	5	11	1	0
				109	120	11	N	AILGVSLAVCK	A	7.30%	4167	4167	566.8056641	2	1131.595678	1129.652449	1.943229029	N	A	C10:+57.021	1	11	2	0
				132	162	30	R	HIADLAGNSEVILPVPAFNVINGGSHAGNK	L	0.81%	5848	5848	1005.525208	3	3013.552147	3011.546465	2.005682167	R	L	N19:+0.984	2	30	2	0
				162	179	17	K	LAMQEFMILPVGAANFR	E	0.81%	7565	7565	954.4934082	2	1906.971166	1906.979745	-0.00857833	K	E	-	5	17	0	0
				183	193	10	R	IGAEVYHNLK	N	0.81%	814	814	572.8063965	2	1143.597143	1142.608404	0.988738617	R	N	-	4	10	1	0
				202	221	19	K	DATNVGDEGGFAPNILENK	E	0.81%	4303	4303	981.4700928	2	1960.924535	1959.917396	1.007139363	K	E	-	4	19	1	0
				202	228	26	K	DATNVGDEGGFAPNILENKEGLELLK	T	0.81%	5903	5903	915.1310425	3	2742.369652	2742.371202	-0.001549367	K	T	-	1	26	0	1
				221	228	7	K	EGLELLK	T	6.14%	2791	2791	401.2380676	2	800.4604852	800.4643656	-0.00388041	K	T	-	1	7	0	0
				233	253	20	K	AGYTDKVVIGMDVAASEFFR	S	0.81%	7199	7199	1089.045166	2	2176.074682	2175.067038	1.007643479	K	S	-	5	20	1	1
				239	253	14	K	VVIGMDVAASEFFR	S	0.81%	6424	6424	771.9013672	2	1541.787084	1539.775547	2.011536919	K	S	-	1	14	2	0
				245	253	8	D	VAASEFFR	S	4.59%	2924	2924	463.7383728	2	925.4610955	925.4657626	-0.004667043	D	S	-	1	8	0	0
				253	262	9	R	SGKYDLDFK	S	0.81%	1466	1466	536.7672729	2	1071.518896	1071.523672	-0.00477571	R	S	-	5	9	0	1
				256	269	13	K	YDLDFKSPDDPSR	Y	0.81%	2646	2646	518.9034424	3	1553.686852	1553.699798	-0.012946348	K	Y	-	4	13	0	1
				269	281	12	R	YISPDQLADLYK	S	0.81%	4715	4715	713.364563	2	1424.713476	1424.718743	-0.005266935	R	S	-	5	12	0	0
				281	306	25	K	SFIKDYPVVSIEDPFDQDDWGAWQK	F	0.81%	7140	7140	996.1348877	3	2985.381188	2984.386852	0.994336198	K	F	-	3	25	1	1
				285	306	21	K	DYPVVSIEDPFDQDDWGAWQK	F	0.81%	7085	7085	1255.55	2	2509.08435	2509.107382	-0.023032128	K	F	-	3	21	0	0
				286	306	20	D	YPVVSIEDPFDQDDWGAWQK	F	7.03%	6839	6839	1198.541748	2	2395.067846	2394.080439	0.987407094	D	F	-	1	20	1	0
				294	306	12	D	PFDQDDWGAWQK	F	4.51%	3828	3828	746.8225708	2	1491.629492	1491.641889	-0.012397894	D	F	-	1	12	0	0
				306	326	20	K	FTASAGIQVVGDDLTVTNPK	R	0.81%	4763	4763	1017.532959	2	2033.050268	2032.047682	1.002585785	K	R	-	4	20	1	0
				335	343	8	K	SCNCLLLK	V	0.81%	1246	1246	504.2519836	2	1006.488317	1006.493043	-0.004725515	K	V	C2:+57.021,C4:+57.021	5	8	0	0
				343	358	15	K	VNQIGSVTESLQACK	L	0.81%	2723	2723	817.4135742	2	1632.811498	1632.813654	-0.002155754	K	L	C14:+57.021	3	15	0	0
				358	372	14	K	LAQANGWGVMVSHR	S	0.81%	2639	2639	764.3735352	2	1526.73142	1525.745963	0.985457297	K	S	N5:+0.984	5	14	1	0
				372	394	22	R	SGETEDTFIADLVVGLCTGQIK	T	0.81%	7848	7848	785.7214355	3	2354.140832	2352.151427	1.989404729	R	T	C17:+57.021	5	22	2	0
P06744	Glucose-6-phosphate isomerase	6	16.31%	57	73	16	K	NLVTEDVMRMLVDLAK	S	5.56%	2781	2781	924.468689	2	1846.921728	1846.95324	-0.031511758	K	S	N1:+0.984	1	16	0	1
				83	96	13	R	MFNGEKINYTEGR	A	5.34%	5243	5243	518.9543457	3	1553.839562	1558.708574	-4.869012443	R	A	N8:+0.984	1	13	-1	1
				194	211	17	K	TLAQLNPESSLFIIASK	T	0.81%	6333	6333	916.5124512	2	1831.009252	1831.009112	0.000140664	K	T	-	4	17	0	0
				211	226	15	K	TFTTQETITNAETAK	E	0.81%	1211	1211	828.9137573	2	1655.811865	1654.804992	1.006872664	K	E	-	5	15	1	0
				423	438	15	K	ILLANFLAQTEALMR	G	0.81%	8950	8950	852.4794922	2	1702.943334	1702.94401	-0.000675585	K	G	-	5	15	0	0
				466	481	15	K	VFEGNRPTNSIVFTK	L	0.81%	1961	1961	855.4507446	2	1708.885839	1707.894416	0.99142317	K	L	-	4	15	1	0
P06756	Integrin alpha-V	5	6.87%	63	72	9	R	MFLLVGAPK	A	0.81%	4668	4668	488.2877808	2	974.5599114	974.5623067	-0.002395237	R	A	-	4	9	0	0
				198	224	26	R	VLLGGPGSFYWQGQLISDQVAEIVSK	Y	3.69%	8604	8604	931.4908447	3	2791.449059	2791.443229	0.005830252	R	Y	Q19:+0.984	1	26	0	0
				646	660	14	K	IYIGDDNPLTLIVK	A	0.81%	6801	6801	787.4380493	2	1572.860449	1572.876306	-0.015857735	K	A	-	5	14	0	0
				718	728	10	K	AGTQLLAGLR	F	2.26%	3409	3409	500.2954407	2	998.5752313	998.5872748	-0.012043564	K	F	-	4	10	0	0
				742	755	13	K	FDLQIQSSNLFDK	V	2.32%	5383	5383	777.8303223	2	1553.644994	1553.772569	-0.127574965	K	V	-	5	13	0	0
P07237	Protein disulfide-isomerase	6	16.93%	31	42	11	K	SNFAEALAAHK	Y	2.59%	1459	1459	580.2987061	2	1158.581762	1157.582918	0.998844229	K	Y	-	5	11	1	0
				81	97	16	K	VDATEESDLAQQYGVR	G	0.81%	3045	3045	891.4208374	2	1780.826025	1779.827518	0.998506397	K	G	-	5	16	1	0
				132	162	30	R	TGPAATTLPDGAAAESLVESSEVAVIGFFK	D	0.81%	8990	8990	979.8305054	3	2936.468041	2934.486232	1.981809385	R	D	-	5	30	2	0
				132	170	38	R	TGPAATTLPDGAAAESLVESSEVAVIGFFKDVESDSAK	Q	1.93%	10290	10290	942.7191772	4	3766.845409	3765.847259	0.998149784	R	Q	-	4	38	1	1
				195	207	12	K	YQLDKDGVVLFK	K	5.88%	3733	3733	475.9304199	3	1424.767785	1423.771113	0.996671886	K	K	-	2	12	1	1
				254	263	9	K	THILLFLPK	S	0.81%	4197	4197	541.3405151	2	1080.66538	1080.669548	-0.004167743	K	S	-	5	9	0	0
P07384	Calpain-1 catalytic subunit	1	2.66%	174	193	19	K	LVFVHSAEGNEFWSALLEK	A	2.59%	7015	7015	726.3756714	3	2176.103539	2175.100052	1.003487008	K	A	-	2	19	1	0
P07858	Cathepsin B	2	10.62%	245	263	18	K	NGPVEGAFSVYSDFLLYK	S	2.26%	7438	7438	1003.502686	2	2004.989721	2004.983291	0.006430214	K	S	-	5	18	0	0
				263	281	18	K	SGVYQHVTGEMMGGHAIR	I	4.05%	2521	2521	644.3014526	3	1929.880883	1929.882534	-0.001651418	K	I	Q5:+0.984	3	18	0	0
P07900	Heat shock protein HSP 90-alpha	18	28.14%	60	74	14	R	YESLTDPSKLDSGK	E	0.81%	1146	1146	770.8803711	2	1539.745092	1538.746414	0.99867782	R	E	-	5	14	1	1
				87	100	13	R	TLTIVDTGIGMTK	A	0.81%	3975	3975	675.373291	2	1348.730932	1348.7272	0.003731799	R	A	-	2	13	0	0
				100	112	12	K	ADLINNLGTIAK	S	0.81%	3991	3991	621.8555908	2	1241.695532	1241.697948	-0.002416159	K	S	-	5	12	0	0
				153	173	20	K	HNDDEQYAWESSAGGSFTVR	T	1.96%	3699	3699	752.9908447	3	2255.949059	2254.95155	0.997509156	K	T	-	2	20	1	0
				185	201	16	K	VILHLKEDQTEYLEER	R	0.81%	3053	3053	672.3508911	3	2014.029198	2014.037117	-0.007919164	K	R	-	3	16	0	1
				191	201	10	K	EDQTEYLEER	R	0.81%	859	859	656.2865601	2	1310.55747	1310.562636	-0.005165995	K	R	-	5	10	0	0
				209	224	15	K	HSQFIGYPITLFVEK	E	6.32%	6319	6319	890.86	2	1779.70435	1777.940304	1.764046328	K	E	-	2	15	2	0
				283	292	9	K	YIDQEELNK	T	1.96%	738	738	576.2792358	2	1150.542822	1150.550615	-0.007793056	K	T	-	3	9	0	0
				299	314	15	R	NPDDITNEEYGEFYK	S	3.06%	3499	3499	917.3980103	2	1832.78037	1832.774086	0.006284684	R	S	-	3	15	0	0
				314	327	13	K	SLTNDWEDHLAVK	H	0.81%	3679	3679	509.9179688	3	1526.730431	1526.736518	-0.006087094	K	H	-	2	13	0	0
				327	338	11	K	HFSVEGQLEFR	A	0.81%	3482	3482	674.8355103	2	1347.65537	1347.657146	-0.001775068	K	A	-	5	11	0	0
				345	355	10	R	RAPFDLFENR	K	0.81%	4027	4027	632.8256226	2	1263.635595	1263.636016	-0.000421019	R	K	-	4	10	0	1
				386	400	14	R	GVVDSEDLPLNISR	E	0.81%	3971	3971	757.3966675	2	1512.777685	1512.778383	-0.000698223	R	E	-	3	14	0	0
				436	443	7	K	FYEQFSK	N	6.08%	1068	1068	474.7229309	2	947.4302117	947.4388791	-0.008667376	K	N	-	1	7	0	0
				489	499	10	K	HIYYITGETK	D	8.03%	903	903	612.8172607	2	1223.618871	1223.618635	0.00023674	K	D	-	1	10	0	0
				489	510	21	K	HIYYITGETKDQVANSAFVER	L	0.81%	2911	2911	814.7399292	3	2441.196312	2440.202286	0.994026966	K	L	-	4	21	1	1
				631	647	16	K	KHLEINPDHSIIETLR	Q	3.41%	2732	2732	639.3468018	3	1915.01693	1915.016307	0.000623473	K	Q	N6:+0.984	1	16	0	1
				632	647	15	K	HLEINPDHSIIETLR	Q	0.81%	3858	3858	596.3199463	3	1785.936364	1785.937344	-0.000979797	K	Q	-	5	15	0	0
P07954	Fumarate hydratase, mitochondrial	16	53.92%	51	61	10	R	IEYDTFGELK	V	0.81%	3583	3583	607.7996216	2	1213.583593	1213.586666	-0.003072764	R	V	-	2	10	0	0
				61	74	13	K	VPNDKYYGAQTVR	S	0.81%	687	687	504.2574768	3	1509.748955	1509.757588	-0.008632692	K	S	-	4	13	0	1
				101	115	14	R	AAAEVNQDYGLDPK	I	0.81%	1043	1043	746.3538818	2	1490.692114	1489.704884	0.987229856	R	I	-	5	14	1	0
				131	160	29	K	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	A	0.81%	5924	5924	1091.533447	3	3271.576867	3270.572758	1.004109021	K	A	Q17:+0.984	2	29	1	0
				160	172	12	R	AIEMLGGELGSK	I	0.81%	1658	1658	612.3492432	2	1222.682836	1219.611921	3.070914984	R	I	M4:+15.995	2	12	3	0
				183	213	30	K	SQSSNDTFPTAMHIAAAIEVHEVLLPGLQK	L	0.81%	6991	6991	802.1650391	4	3204.628856	3203.628497	1.000358866	K	L	-	1	30	1	0
				221	230	9	K	SKEFAQIIK	I	0.81%	1032	1032	532.8083496	2	1063.601049	1062.607342	0.993707523	K	I	-	5	9	1	1
				233	256	23	R	THTQDAVPLTLGQEFSGYVQQVK	Y	0.81%	5732	5732	1274.654907	2	2547.294164	2545.281264	2.012900133	R	Y	-	2	23	2	0
				268	284	16	R	IYELAAGGTAVGTGLN	T	9.15%	3834	3834	753.8874512	2	1505.759252	1505.772569	-0.013317152	R	T	-	1	16	0	0
				268	286	18	R	IYELAAGGTAVGTGLNTR	I	0.81%	3359	3359	882.9625854	2	1763.909521	1762.921359	0.988161682	R	I	-	5	18	1	0
				296	311	15	K	VAALTGLPFVTAPNK	F	0.81%	5078	5078	749.9350586	2	1497.854467	1497.855511	-0.001044068	K	F	-	5	15	0	0
				296	337	41	K	VAALTGLPFVTAPNKFEALAAHDALVELSGAMNTTACSLMK	I	2.26%	9259	9259	1058.795898	4	4231.152294	4231.136246	0.016047654	K	I	N14:+0.984,C37:+57.021	3	41	0	1
				350	371	21	R	SGLGELILPENEPGSSIMPGK	V	0.81%	5347	5347	1063.044556	2	2124.073461	2124.077269	-0.003807616	R	V	-	4	21	0	0
				400	414	14	N	GHFELNVFKPMMIK	N	1.97%	5182	5182	564.2969971	3	1689.867516	1689.873488	-0.005972381	N	N	-	1	14	0	0
				447	467	20	K	LMNESLMLVTALNPHIGYDK	A	0.81%	6277	6277	754.0477905	3	2259.119896	2259.12791	-0.008013338	K	A	N13:+0.984	3	20	0	0
				483	504	21	K	ETAIELGYLTAEQFDEWVKPK	D	0.81%	8146	8146	823.4202271	3	2467.237206	2467.215854	0.021351672	K	D	Q13:+0.984	4	21	0	0
P08195	4F2 cell-surface antigen heavy chain	26	43.65%	9	17	8	S	IAVVSIPR	Q	4.76%	1267	1267	428.7652893	2	855.5149285	853.5385336	1.976394925	S	Q	-	1	8	2	0
				111	122	11	K	EVELNELEPEK	Q	2.80%	2921	2921	664.8310547	2	1327.646459	1327.650723	-0.004263529	K	Q	-	4	11	0	0
				111	140	29	K	EVELNELEPEKQPMNAASGAAMSLAGAEK	N	4.65%	5035	5035	1006.152954	3	3015.435387	3014.421252	1.014135633	K	N	Q12:+0.984	1	29	1	1
				122	140	18	K	QPMNAASGAAMSLAGAEK	N	4.47%	3177	3177	853.4052734	2	1704.794897	1704.781089	0.013808067	K	N	N4:+0.984	2	18	0	0
				147	160	13	K	VAEDEAEAAAAAK	F	0.81%	603	603	623.3012085	2	1244.586767	1244.588457	-0.00168992	K	F	-	5	13	0	0
				160	171	11	K	FTGLSKEELLK	V	0.81%	2750	2750	632.8571777	2	1263.698705	1263.70745	-0.008744395	K	V	-	4	11	0	1
				171	180	9	K	VAGSPGWVR	T	0.81%	872	872	464.7533875	2	927.4911248	927.492646	-0.001521202	K	T	-	4	9	0	0
				226	245	19	R	IGDLQAFQGHGAGNLAGLK	G	0.81%	3747	3747	622.998291	3	1865.971398	1866.958792	-0.987393793	R	G	Q8:+0.984	2	19	-1	0
				245	255	10	K	GRLDYLSSLK	V	0.81%	2985	2985	576.3248901	2	1150.63413	1150.634619	-0.000488879	K	V	-	5	10	0	1
				247	255	8	R	LDYLSSLK	V	0.81%	3473	3473	469.7625427	2	937.5094354	937.5120442	-0.002608783	R	V	-	5	8	0	0
				257	266	9	K	GLVLGPIHK	N	0.81%	2012	2012	468.7728271	2	935.5300042	932.5807328	2.949271401	K	N	-	1	9	3	0
				266	287	21	K	NQKDDVAQTDLLQIDPNFGSK	E	0.81%	4824	4824	783.0574951	3	2346.14901	2346.133916	0.015094648	K	E	Q8:+0.984	1	21	0	1
				269	287	18	K	DDVAQTDLLQIDPNFGSK	E	0.81%	5446	5446	988.984375	2	1975.9531	1974.953447	0.999652624	K	E	-	3	18	1	0
				269	298	29	K	DDVAQTDLLQIDPNFGSKEDFDSLLQSAK	K	0.81%	6940	6940	1071.192627	3	3210.554406	3208.541181	2.013225219	K	K	-	1	29	2	1
				287	298	11	K	EDFDSLLQSAK	K	3.89%	4344	4344	627.8049316	2	1253.594213	1251.598293	1.995919977	K	K	-	4	11	2	0
				303	313	10	R	VILDLTPNYR	G	0.81%	3744	3744	602.3391724	2	1202.662695	1202.665919	-0.003224585	R	G	-	5	10	0	0
				313	329	16	R	GENSWFSTQVDTVATK	V	0.81%	4129	4129	885.4186401	2	1768.82163	1768.82679	-0.005159807	R	V	-	5	16	0	0
				329	348	19	K	VKDALEFWLQAGVDGFQVR	D	0.81%	7314	7314	727.0525513	3	2178.134179	2177.126935	1.007243201	K	D	-	4	19	1	1
				429	439	10	R	WCSWSLSQAR	L	0.81%	3729	3729	640.7935181	2	1279.571386	1279.576324	-0.004937875	R	L	C2:+57.021	5	10	0	0
				439	451	12	R	LLTSFLPAQLLR	L	0.81%	7240	7240	686.4212036	2	1370.826757	1370.828568	-0.001810901	R	L	-	5	12	0	0
				510	524	14	K	GQSEDPGSLLSLFR	R	0.81%	6749	6749	754.6520996	2	1507.288549	1504.752168	2.536380835	K	R	-	2	14	3	0
				515	524	9	D	PGSLLSLFR	R	4.33%	6088	6088	495.2904663	2	988.5652825	988.5705621	-0.005279559	D	R	-	1	9	0	0
				534	555	21	R	SLLHGDFHAFSAGPGLFSYIR	H	0.81%	6476	6476	764.7213745	3	2291.140648	2291.148734	-0.008085169	R	H	-	1	21	0	0
				592	603	11	K	ADLLLSTQPGR	E	2.26%	2507	2507	585.8271484	2	1169.638647	1169.640433	-0.001785965	K	E	-	3	11	0	0
				592	613	21	K	ADLLLSTQPGREEGSPLELER	L	0.81%	4204	4204	771.0692749	3	2310.18435	2309.186301	0.998048483	K	L	-	4	21	1	1
				613	625	12	R	LKLEPHEGLLLR	F	0.81%	3145	3145	709.4271851	2	1416.83872	1416.845281	-0.006560747	R	F	-	4	12	0	1
P08237	6-phosphofructokinase, muscle type	15	26.15%	16	35	19	K	AIAVLTSGGDAQGMNAAVR	A	0.81%	3234	3234	901.9653931	2	1801.915136	1800.915229	0.999907021	K	A	-	5	19	1	0
				39	47	8	R	VGIFTGAR	V	0.81%	1562	1562	410.7366333	2	819.4576165	819.4602832	-0.002666686	R	V	-	5	8	0	0
				47	66	19	R	VFFVHEGYQGLVDGGDHIK	E	0.81%	4169	4169	706.6868896	3	2117.037194	2116.037786	0.999407785	R	E	-	2	19	1	0
				184	201	17	R	IMEIVDAITTTAQSHQR	T	0.81%	4674	4674	638.9959717	3	1913.96444	1913.951659	0.012781287	R	T	Q16:+0.984	1	17	0	0
				201	210	9	R	TFVLEVMGR	H	0.81%	4820	4820	526.2828979	2	1050.550146	1050.553199	-0.003052798	R	H	-	5	9	0	0
				397	420	23	K	SGSHTVAVMNVGAPAAGMNAAVR	S	2.83%	3173	3173	723.69104	3	2168.049645	2168.04664	0.003005317	K	S	N10:+0.984	3	23	0	0
				432	445	13	R	VLVVHDGFEGLAK	G	0.81%	3565	3565	462.6105347	3	1384.808129	1382.755797	2.052331876	R	G	-	1	13	2	0
				445	466	21	K	GQIEEAGWSYVGGWTGQGGSK	L	0.81%	5120	5120	1077.490112	2	2152.964575	2152.981393	-0.016818879	K	L	-	5	21	0	0
				475	487	12	K	KSFEQISANITK	F	0.81%	1788	1788	683.3729858	2	1364.730322	1364.729976	0.000345392	K	F	-	5	12	0	1
				476	487	11	K	SFEQISANITK	F	0.81%	2871	2871	619.8291016	2	1237.642553	1236.635013	1.007539973	K	F	-	5	11	1	0
				603	615	12	R	DLQANVEHLVQK	M	0.81%	3463	3463	697.8754883	2	1393.735326	1392.736124	0.999202259	R	M	-	5	12	1	0
				656	673	17	K	NVLGHMQQGGSPTPFDR	N	3.05%	2791	2791	614.2993774	3	1839.874657	1839.868613	0.006044084	K	N	-	2	17	0	0
				699	714	15	R	IFANTPDSGCVLGMR	K	0.81%	3857	3857	819.3933716	2	1636.771093	1636.769682	0.001411252	R	K	C10:+57.021	5	15	0	0
				716	727	11	R	ALVFQPVAELK	D	3.78%	4743	4743	607.8583374	2	1213.701025	1213.707056	-0.006031059	R	D	-	2	11	0	0
				716	735	19	R	ALVFQPVAELKDQTDFEHR	I	3.65%	4968	4968	748.7173462	3	2243.128563	2243.122229	0.006334918	R	I	Q13:+0.984	2	19	0	1
P08473	Neprilysin	4	7.20%	159	177	18	K	LLPDIYGWPVATENWEQK	Y	2.26%	6913	6913	1081.042114	2	2160.068578	2158.073503	1.995075532	K	Y	-	4	18	2	0
				261	275	14	R	LPIDENQLALEMNK	V	0.81%	4283	4283	814.425415	2	1626.83518	1626.828705	0.006474694	R	V	-	4	14	0	0
				374	385	11	R	FIMDLVSSLSR	T	0.81%	6357	6357	634.3403931	2	1266.665136	1266.664206	0.000930221	R	T	-	4	11	0	0
				437	448	11	K	HVVEDLIAQIR	E	0.81%	4296	4296	646.8692017	2	1291.722753	1291.724831	-0.002077936	K	E	-	5	11	0	0
P08574	Cytochrome c1, heme protein, mitochondrial	12	44.00%	84	99	15	A	SDLELHPPSYPWSHR	G	4.33%	3711	3711	911.4434814	2	1820.871313	1819.864179	1.007134307	A	G	-	1	15	1	0
				98	111	13	H	RGLLSSLDHTSIR	R	7.53%	2516	2516	485.6044922	3	1453.790001	1453.800122	-0.010120085	H	R	-	1	13	0	1
				99	107	8	R	GLLSSLDH	T	4.32%	10203	10203	421.7583313	2	841.5010125	840.4341281	1.066884438	R	T	-	1	8	1	0
				99	111	12	R	GLLSSLDHTSIR	R	2.34%	3478	3478	433.5720825	3	1297.692772	1297.69901	-0.006237937	R	R	-	1	12	0	0

				133	146	13	R	HLVGVCYTEDEAK	E	E	0.81%	805	805	760.8536987	2	1519.691747	1519.697227	-0.005479827	R	E	C6:+57.021	5	13	0	0
				146	170	24	K	ELAAEVEVQDGPNEDGEMFMRPGK	L	L	1.97%	4160	4160	884.0732422	3	2649.196251	2648.173416	1.022835123	K	L	N13:+0.984	3	24	1	0
				170	186	16	K	LFDYFPKPYPNSEAAR	A	A	0.81%	4114	4114	639.3178711	3	1914.930138	1914.915196	0.014942633	K	A	N11:+0.984	2	16	0	0
				186	202	16	R	AANNGALPPDLSYIVR	A	A	0.81%	4945	4945	836.9403076	2	1671.864965	1670.862766	1.002199226	R	A	N4:+0.984	3	16	1	0
				204	228	24	R	HGGEDYVFSLLTGYCEPPTGVSLR	E	E	0.81%	6899	6899	886.0894775	3	2655.244958	2653.247787	1.997170585	R	E	C15:+57.021	5	24	2	0
				268	275	7	K	DVCTFLR	W	W	0.81%	2770	2770	455.7244263	2	909.4332025	909.4373706	-0.004168141	K	W	C3:+57.021	3	7	0	0
				291	307	16	K	MLMMMALLVPLVYTIK	R	R	0.81%	10536	10536	935.0217285	2	1868.027807	1866.0255	2.002307135	K	R	-	2	16	2	0
				296	307	11	M	ALLVPLVYTIK	R	R	9.69%	6094	6094	615.399231	2	1228.782812	1228.779493	0.003319338	M	R	-	1	11	0	0
P08575	Receptor-type tyrosine-protein phosphatase C	2	1.76%	291	303	12	K	TLILDVPPGVEK	F	F	1.93%	4026	4026	640.8757935	2	1279.735937	1279.73875	-0.00281311	K	F	-	5	12	0	0
				649	660	11	R	LFLAEFQSIPR	V	V	0.81%	5742	5742	660.8688354	2	1319.722021	1319.723769	-0.001747702	R	V	-	5	11	0	0
P08754	Guanine nucleotide-binding protein G(k) subunit alpha	3	12.15%	70	86	16	K	VVVYSNTIQSIIAIIR	A	A	5.56%	3991	3991	597.2961426	3	1788.864953	1790.018917	-1.153964194	K	A	N6:+0.984,Q9:+0.984	1	16	-1	0
				161	176	15	R	ISQSNYIPTQQDVLR	T	T	5.35%	5698	5698	588.6292725	3	1762.864342	1763.857709	-0.993366793	R	T	Q3:+0.984,Q10:+0.984,Q1	1	15	-1	0
				180	192	12	K	TTGIVETHFTFK	D	D	0.81%	3124	3124	690.8656006	2	1379.715551	1379.708512	0.007038652	K	D	-	5	12	0	0
P08842	Steryl-sulfatase	3	8.40%	98	120	22	R	TGVFLFTASSGGLPTDEITFAK	L	L	0.81%	6780	6780	1131.080444	2	2260.145239	2258.147062	1.998176648	R	L	-	5	22	2	0
				263	274	11	R	LTVEAAQFIQR	N	N	0.81%	3485	3485	638.3557129	2	1274.695776	1274.698282	-0.002506347	R	N	-	5	11	0	0
				393	409	16	K	IDEPTSNMDIFPTVAK	L	L	0.81%	4595	4595	889.44	2	1776.86435	1776.860399	0.003950456	K	L	-	5	16	0	0
P08865	40S ribosomal protein SA	8	34.58%	17	40	23	K	FLAAGTHLGGTNLDFQMEQYIYK	R	R	0.81%	5499	5499	873.4290771	3	2617.263756	2617.252258	0.011498533	K	R	N12:+0.984	2	23	0	0
				17	41	24	K	FLAAGTHLGGTNLDFQMEQYIYKR	K	K	5.66%	6041	6041	698.3585815	4	2789.403026	2789.348369	0.054657068	K	K	M17:+15.995,Q19:+0.984	1	24	0	1
				41	52	11	R	KSDGIYIINLK	R	R	0.81%	3600	3600	632.3721924	2	1262.728735	1262.723434	0.005300494	R	R	-	4	11	0	1
				63	80	17	R	AIVAIENPADVSVISSR	N	N	0.81%	4266	4266	871.4814453	2	1740.947241	1739.94176	1.005480297	R	N	-	5	17	1	0
				89	102	13	K	FAAATGATPIAGR	F	F	0.81%	857	857	602.3269043	2	1202.638159	1202.640767	-0.002608574	K	F	-	5	13	0	0
				102	117	15	R	FTPGTFTNQIQAAFR	E	E	4.85%	5805	5805	567.9719849	3	1700.892479	1697.852551	3.039928342	R	E	-	1	15	3	0
				120	128	8	R	LLVVTDPR	A	A	0.81%	1396	1396	457.7843628	2	913.5530755	911.544013	2.009062538	R	A	-	2	8	2	0
				166	180	14	K	GAHSVGLMWWMLAR	E	E	0.81%	6811	6811	538.9365845	3	1613.786278	1613.795907	-0.00962843	K	E	-	5	14	0	0
P08962	CD63 antigen	2	5.04%	108	120	12	R	DKVMSEFNNNFR	Q	Q	0.81%	2843	2843	750.8399048	2	1499.664159	1499.68271	-0.018550062	R	Q	-	5	12	0	1
				110	120	10	K	VMSEFNNNFR	Q	Q	0.81%	2479	2479	629.2888184	2	1256.561987	1256.560803	0.001183351	K	Q	-	4	10	0	0
P09104	Gamma-enolase	4	14.75%	32	50	18	R	AAVPSGASTGIYEALELR	D	D	0.81%	4939	4939	902.9730835	2	1803.930517	1803.936675	-0.006157976	R	D	-	5	18	0	0
				109	120	11	N	AILGVSLAVCK	A	A	7.30%	4167	4167	566.8056641	2	1131.595678	1129.652449	1.943229029	N	A	C10:+57.021	1	11	2	0
				330	343	13	R	AVEEKACNCLLLK	V	V	8.06%	4257	4257	774.9144897	2	1547.813329	1547.767805	0.045523924	R	V	C7:+57.021,N8:+0.984,C9	3	13	0	1
				372	394	22	R	SGETEDTFIADLVVGLCTGQIK	T	T	0.81%	7848	7848	785.7214355	3	2354.140832	2352.151427	1.989404729	R	T	C17:+57.021	5	22	2	0
P09382	Galectin-1	3	23.70%	29	37	8	K	SFVLNLGK	D	D	0.81%	3136	3136	439.257843	2	876.500036	876.5068991	-0.006863165	K	D	-	5	8	0	0
				100	108	8	K	LPDGYEFK	F	F	0.81%	1798	1798	484.7376099	2	967.4595696	967.4650939	-0.005524265	K	F	-	5	8	0	0
				112	128	16	R	LNLEAINYMAADGDFK	I	I	0.81%	5400	5400	892.9262085	2	1783.836767	1783.845084	-0.0083168	R	I	-	5	16	0	0
P09429	High mobility group protein B1	3	23.26%	96	112	16	K	RPPSAFFLFCSEYRPK	I	I	0.81%	4695	4695	668.0014038	3	2000.980736	2000.992622	-0.011885358	K	I	C10:+57.021	5	16	0	0
				112	127	15	K	IKGEHPGLSIGDVAK	K	K	0.81%	888	888	507.6173401	3	1519.828545	1519.835838	-0.007293248	K	K	-	5	15	0	1
				127	146	19	K	KLGEMWNNTAADDKQPYEK	K	K	8.14%	1529	1529	747.347229	3	2239.018212	2237.04228	1.975931564	K	K	-	1	19	2	2
P09601	Heme oxygenase 1	6	32.99%	100	113	13	R	WQEVIPYTPAMQR	Y	Y	2.26%	4180	4180	810.9018555	2	1619.788061	1617.797345	1.990715386	R	Y	-	4	13	2	0
				123	136	13	R	TEPELLVAHAYTR	Y	Y	0.81%	2815	2815	750.3952026	2	1498.774755	1498.777989	-0.003233911	R	Y	-	5	13	0	0
				136	148	12	R	YLGDLSGGQVLK	K	K	0.81%	3176	3176	626.3482666	2	1250.680883	1248.671399	2.009484531	R	K	-	2	12	2	0
				153	177	24	K	ALDLPSSGEGLAFFTFPNIASATK	F	F	0.81%	7784	7784	1228.134766	2	2454.253881	2453.247839	1.006042402	K	F	-	4	24	1	0
				185	196	11	R	MNSLEMTPAVR	Q	Q	0.81%	2010	2010	625.3041992	2	1248.592748	1247.600226	0.992521918	R	Q	-	3	11	1	0
				204	226	22	K	TAFLLNIQLFEELQELLTHDTK	D	D	0.81%	9712	9712	873.1326294	3	2616.374413	2615.384667	0.98974628	K	D	-	2	22	1	0
P09848	Lactase-phlorizin hydrolase	1	0.47%	886	895	9	K	FSSQPKFER	D	D	3.94%	4879	4879	563.7774048	2	1125.539159	1125.545454	-0.006294542	K	D	Q4:+0.984	2	9	0	1
P0CG47	Polyubiquitin-B	6	20.52%	11	27	16	K	TITLEVEPSDTIENVK	A	A	0.81%	3946	3946	894.4653931	2	1786.915136	1786.920022	-0.004885771	K	A	-	2	16	0	0
				29	42	13	K	IQDKEGIPPDQQR	L	L	0.81%	609	609	508.5975037	3	1522.769036	1522.773966	-0.004930534	K	L	-	3	13	0	1
				54	63	9	R	TLSDYNIQK	E	E	0.81%	722	722	541.277771	2	1080.539892	1080.545135	-0.005243384	R	E	-	3	9	0	0
				54	72	18	R	TLSDYNIQKESTLHLVLR	L	L	2.36%	3951	3951	711.0545044	3	2130.140038	2129.148065	0.991973136	R	L	-	2	18	1	1
				63	72	9	K	ESTLHLVLR	L	L	0.81%	2470	2470	535.7610474	2	1069.506445	1066.61349	2.892955015	K	L	-	1	9	3	0
				64	72	8	E	STLHLVLR	L	L	5.24%	2354	2354	469.7915344	2	937.5674188	937.5708964	-0.003477656	E	L	-	1	8	0	0
P10966	T-cell surface glycoprotein CD8 beta chain	4	23.81%	18	30	12	G	NSVLQQTPAYIK	V	V	3.69%	2429	2429	681.3712158	2	1360.726782	1360.735062	-0.008280007	G	V	-	1	12	0	0
				58	77	19	R	QAPSSDSHHEFLALWDSAK	G	G	1.93%	4304	4304	1063.996704	2	2125.977758	2124.986479	0.991279355	R	G	-	4	19	1	0
				128	146	18	K	GTQLSVVDFLPTTAQPTK	K	K	0.81%	5815	5815	952.0108032	2	1902.005956	1902.00984	-0.003883563	K	K	-	5	18	0	0
				128	147	19	K	GTQLSVVDFLPTTAQPTKK	S	S	2.26%	5134	5134	1016.557617	2	2031.099584	2030.104803	0.994781231	K	S	-	5	19	1	1
P11142	Heat shock cognate 71 kDa protein	30	53.41%	3	25	22	K	GPAVGIDLGTTYSCVGVFQHGK	V	V	0.81%	4680	4680	755.0428467	3	2262.105065	2262.109837	-0.004771649	K	V	C14:+57.021	3	22	0	0
				25	36	11	K	VEIIANDQGNR	T	T	0.81%	665	665	614.8173828	2	1227.619116	1227.62076	-0.001644431	K	T	-	4	11	0	0
				36	49	13	R	TTPSYVAFTDTER	L	L	0.81%	2691	2691	744.3525391	2	1486.689428	1486.693985	-0.004556643	R	L	-	5	13	0	0
				56	71	15	K	NQVAMNPTNTVFDAK	R	R	0.81%	2829	2829	825.3998413	2	1648.784033	1648.787903	-0.003870543	K	R	-	5	15	0	0
				56	72	16	K	NQVAMNPTNTVFDAKR	L	L	3.96%	2018	2018	602.9715576	3	1805.891198	1804.889014	1.0021835	K	L	-	1	16	1	1
				76	88	12	R	RFDDAVVQSDMK	H	H	0.81%	787	787	705.8366089	2	1409.657568	1409.660911	-0.003343763	R	H	-	5	12	0	1
				77	88	11	R	FDDAVVQSDMK	H	H	0.81%	1262	1262	627.7894897	2	1253.563329	1253.5598	0.003529108	R	H	-	2	11	0	0
				88	102	14	K	HWPFMVVNDAGRPK	V	V	0.81%	3542	3542	551.9472656	3	1652.818322	1652.824563	-0.006241501	K	V	-	3	14	0	0
				112	126	14	K	SFYPEEVSSMVLTK	M	M	0.81%	5172	5172	808.8944092	2	1615.773168	1615.780358	-0.007189801	K	M	-	5	14	0	0
				126	137	11	K	MKEIAEAYLGK	T	T	0.81%	1615	1615	417.84	3	1250.496525	1251.653307	-1.156781904	K	T	-	4	11	-1	1
				128	137	9	K	EIAEAYLGK	T	T	0.81%	1305	1305	497.263855	2	992.5120599	992.5178578	-0.005797959	K	T	-	5	9	0	0
				137	155	18	K	TVTNAVVTVPAYFNDSQR	Q	Q	0.81%	4379	4379	992.49646	2	1982.97727	1981.974501	1.00276837	K	Q	N14:+0.984	4	18	1	0
				159	171	12	K	DAGTIAGLNVLR	I	I	0.81%	4092	4092	600.3395996	2	1198.663549	1198.666982	-0.003432749	K	I	-	5	12	0	0
				171	187	16	R	IINEPTAAAIAYGLDK	K	K	0.81%	4486	4486	830.4503174	2	1658.884985	1658.887934	-0.002948978	R	K	-	5	16	0	0
				171	188	17	R	IINEPTAAAIAYGLDKK	V	V	0.81%	3878	3878	596.6674805	3	1786.978966	1786.982897	-0.003930514	R	V	-	1	17	0	1
				193	220	27	R	NVLIFDLGGGTFDVSILTIEDGIFEVK	S	S	0.81%	10258	10258	971.8449097	3	2912.511254	2910.52664	1.984614052	R	S	-	5	27	2	0
				220	236	16	K	STAGDTHLGGEDFDNR	M	M	0.81%	693	693	846.3651733	2	1690.714697	1690.718302	-0.003605496	K	M	-	5	16	0	0
				236	246	10	R	MVNHFIAEFK	R	R	0.81%	3026	3026	412.5450745	3	1234.611748	1234.616862	-0.005113323	R	R	-	5	10	0	0
				236	247	11	R	MVNHFIAEFKR	K	K	0.81%	2162	2162	464.5777588	3	1390.709801	1390.717973	-0.008171497	R	K	-	3	11	0	1
				237	246	9	M	VNHFIAEFK	R	R	8.53%	3101	3101	554.2919922	2	1106.568334	1103.576376	2.991958511	M	R	-	1	9	3	0
				299	311	12	R	ARFEELNADLFR	G	G	0.81%	4216	4216	740.8770752	2	1479.7385	1479.747023	-0.008522961	R	G	-	5	12	0	1
				301	311	10	R	FEELNADLFR	G	G	0.81%	4757	4757	627.3096924	2	1252.603735	1252.608798	-0.005063586	R	G	-	5	10	0	0
				325	342	17	K	LDKSQIHDIVLVGGSTR	I	I	0.81%	2634	2634	613.3433838	3	1837.006676	1837.005758	0.000918695	K	I	-	3	17	0	1
				328	342	14	K	SQIHDIVLVGGSTR	I	I	0.81%	2206	2206	741.9139404	2	1481.812231	1480.799787	1.012443579	K	I	-	5	14	1	0
				348	357	9	K	LLQDFFNGK	E	E	0.81%	4230	4230	541.286499	2	1080.557348	1080.560391	-0.003043409	K	E	-	3	9	0	0
				348	361	13	K	LLQDFFNGKELNK	S	S	0.81%	4570	4570	522.940979	3	1565.799462	1565.808939	-0.009477452	K	S	N12:+0.984	1	13	0	1
				361	384	23	K	SINPDEAVAYGAAVQAAILSGDK	S	S	0.81%	6889	6889	754.0526123	3	2259.134362	2259.138288	-0.003926414	K	S	-	2	23	0	0
				384	415	31	K	SENVQDLLLLDVTPLSLGIETAGGVMTVLIK	R	R	0.81%	11452	11452	1080.596313	3	3238.765465	3237.778181	0.987283958	K	R	-	5	31	1	0
				423	447	24	K	QTQTFTTYSDNQPGVLIQVYEGER	A	A	0.81%	5299	5299	926.1138306	3	2775.318017	2773.3195	1.998516163	K	A	-	2	24	2	0
				539	550	11	K	NSLESYAFNMK	A	A	0.81%	2516	2516	660.2999268	2	1318.584203	1318.586435	-0.002231356	K	A	M10:+15.995	3	11	0	0
P11166	Solute carrier family 2, facilitated glucose transporter member 1	5	10.16%	232	249	17	R	GTADVTHDLQEMKEESR	Q	Q	1.93%	2629	2629	649.6303711	3	1945.867638	1944.884717	0.982921289	R	Q	-	2	17	1	1
				255	264	9	K	KVTILELFR	S	S	2.88%	5361	5361	559.8504028	2	1117.685156	1117.685926	-0.00077076	K	S	-	4	9	0	1
				256	264	8	K	VTILELFR	S	S	2.46%	6790	6790	495.800293	2	989.5849359	989.5909632	-0.006027351	K	S	-	2	8	0	0
				468	492	24	R	QGGASQSDKTPEELFHPLGADSQV	-	-	3.02%	4213	4213	833.3960571	3	2497.164696	2498.156108	-0.991411413	R	-	Q6:+0.984	3	24	-1	1
				477	492	15	K	TPEELFHPLGADSQV	-	-	1.93%	4691	4691	820.4052124	2	1638.794775	1638.788948	0.005826901	K	-	-	3	15	0	0
P11215	Integrin alpha-M	1	1.82%	549	570	21	R	GAVYLFHGTSGSGISPSHSQR	I	I	5.98%	4689	4689	716.0153198	3	2145.022484	2145.023911	-0.001426999	R	I	Q20:+0.984	2	21	0	0
P11277	Spectrin beta chain, erythrocyte	1	1.17%	1870	1895	25	K	AEAIQNKEQEVSAAWQALLDACAGR	R	R	8.26%	7807	7807	911.4439087	3	2731.308251	2729.307412	2.000839362	K	R	Q16:+0.984,C22:+57.021	1	25	2	1
P11279	Lysosome-associated membrane glycoprotein 1	4	8.39%	137	146	9	K	TVESITDIR	A	A	0.81%	1992	1992	517.27771	2	1032.53977	1032.545135	-0.005365454	K	A	-	5	9	0	0
				326	337	11	R	ALQATVGNSYK	C	C	0.81%	696	696	576.305542	2	1150.595434	1150.598234	-0.002799648	R	C	-	5	11	0	0
				348	356	8	K	AFSVNIFK	V	V	0.81%	4699	4699	463.2601013	2	924.5045526	924.5068991	-0.002346563	K	V	-	5	8	0	0
				356	363	7	K	VWVQAFK	V	V	0.81%	3079	3079	439.249176	2	876.482702	876.4857697	-0.003067709	K	V	-	5	7	0	0
P11413	Glucose-6-phosphate 1-dehydrogenase	4	8.54%	136	152	16	R	LFYLALPPTVYEAVTK	N	N	5.15%	7347	7347	914.0081787	2	1826.000707	1824.007321	1.993386726	R	N	-	2	16	2	0
				166	175	9	R	IIVEKPFGR	D	D	0.81%	1011	1011	529.8189087	2	1057.622167	1057.628411	-0.006244081	R	D	-	4	9	0	0
				219	227	8	R	IFGPIWNR	D	D	0.81%	4169	4169	501.776947	2	1001.538244	1001.544682	-0.006437661	R	D	-	5	8	0	0
				246	257	11	R	GGYFDEFGIIR	D	D	5.24%	9133	9133	637.8533325	2	1273.691015	1272.613884	1.077131327	R	D	-	1	11	1	0
P11532	Dystrophin	1	0.41%	2160	2175	15	R	TLNATGEEIIQQSSK	T	T	7.76%	3691	3691	540.6010742	3	1618.779748	1617.820976	0.958771224	R	T	-	3	15	1	0
P11717	Cation-independent mannose-6-phosphate receptor	4	1.81%	1030	1039	9	K	GTADAFIVR	F	F	0.81%	2285	2285	475.2590027	2	948.5023553	948.5028764	-0.000521125	K	F	-	5	9	0	0
				1052	1065	13	K	FLHQDIDSGQGIR	N	N	0.81%	1059	1059	495.918335	3	1484.73153	1484.737187	-0.005657117	K	N	-	4	13	0	0
				1582	1593	11	R	YVDQVLQLVYK	D	D	0.81%	5362	5362	684.3807983	2	1366.745947	1366.749649	-0.003702392	R	D	-	5	11	0	0
				1714	1726	12	K	VPIDGPPIDIGR	V	V	0.81%	3668	3668	624.8502197	2	1247.684789	1247.687383	-0.002593627	K	V	-	5	12	0	0
P12235	ADP/ATP translocase 1	22	66.11%	10	23	13	K	DFLAGGVAAAVSK	T	T	1.97%	3909	3909	603.8291626	2	1205.642675	1204.645184	0.997491323	K	T	-	3	13	1	0
				33	43	10	K	LLLQVQHASK	Q	Q	0.81%	967	967	568.8419189	2	1135.668188	1135.671339	-0.003151109	K	Q	-	5	10	0	0
				35	43	8	L	LQVQHASK	Q	Q	5.83%	914	914	455.7539673	2	909.4922845	909.5032107	-0.010926254	L	Q	-	1	8	0	0
				63	72	9	K	EQGFLSFWR	G	G	2.90%	6173	6173	585.2902832	2	1168.564916	1168.566539	-0.001623066	K	G	-	3	9	0	0
				72	80	8	R	GNLANVIR	Y	Y	3.57%	1131	1131	428.7650452	2	855.5144403	855.492646	0.021794228	R	Y	-	2	8	0	0
				80	92	12	R	YFPTQALNFAFK	D	D	0.81%	6120	6120	724.3757324	2	1446.735815	1445.734333	1.001481524	R	D	-	5	12	1	0
				80	94	14	R	YFPTQALNFAFKDK	Y	Y	0.81%	5266	5266	845.4324951	2	1688.84934	1688.85624	-0.00689935	R	Y	-	5	14	0	1
				82	92	10	F	PTQALNFAFK	D	D	6.03%	6151	6151	569.3172607	2	1136.618871	1135.602591	1.01628082	F	D	-	1	10	1	0
				96	105	9	K	QLFLGGVDR	H	H	3.42%	2917	2917	502.7749329	2	1003.534216	1003.545076	-0.010859981	K	H	-	1	9	0	0
				111	138	27	R	YFAGNLASGGAAGATSLCFVYPLDFAR	T	T	0.81%	7170	7170	1399.680054	2	2797.344457	2796.321271	1.023186654	R	T	N5:+0.984,C18:+57.021	3	27	1	0
				126	138	12	T	SLCFVYPLDFAR	T	T	3.96%	6585	6585	744.3701782	2	1486.724706	1486.727405	-0.002698675	T	T	C3:+57.021	1	12	0	0
				152	163	11	R	EFHGLGDCIIK	I	I	1.93%	2995	2995	644.8226318	2	1287.629614	1287.627691	0.00192272	R	I	C8:+57.021	4	11	0	0
				171	188	17	R	GLYQGFNVSVQGIIIYR	A	A	0.81%	9145	9145	965.4608154	2	1928.905981	1927.020329	1.885651395	R	A	Q4:+0.984	2	17	2	0
				188	199	11	R	AAYFGVYDTAK	G	G	0.81%	2828	2828	603.2936401	2	1204.57163	1204.576435	-0.004805263	R	G	-	5	11	0	0
				206	235	29	K	NVHIFVSWMIAQSVTAVAGLVSYPFDTVR	R	R	4.89%	10147	10147	1075.553345	3	3223.636559	3223.636675	-0.000115996	K	R	N1:+0.984,M9:+15.994	1	29	0	0
				244	259	15	R	KGADIMYTGTVDCWR	K	K	0.81%	3459	3459	886.9069214	2	1771.798193	1771.80171	-0.003517627	R	K	C13:+57.021	5	15	0	1
				245	259	14	K	GADIMYTGTVDCWR	K	K	0.81%	4085	4085	823.3636475	2	1644.711645	1643.706747	1.004897658	K	K	C12:+57.021	5	14	1	0
				272	280	8	K	GAWSNVLR	G	G	0.81%	2962	2962	451.7452393	2	901.4748284	901.4769959	-0.002167508	K	G	-	5	8	0	0
				280	295	15	R	GMGGAFVLVLYDEIK	K	K	0.81%	7497	7497	806.43	2	1610.84435	1610.837813	0.006536552	R	K	-	4	15	0	0
				280	296	16	R	GMGGAFVLVLYDEIKK	Y	Y	0.81%	6943	6943	585.984436	3	1754.929833	1754.927777	0.002056481	R	Y	M2:+15.995	1	16	0	1
				282	296	14	M	GGAFVLVLYDEIKK	Y	Y	4.79%	7128	7128	776.4417725	2	1550.867895	1550.870827	-0.002932086	M	Y	-	1	14	0	1
				286	296	10	F	VLVLYDEIKK	Y	Y	4.15%	2998	2998	610.366394	2	1218.717138	1218.722372	-0.00523353	F	Y	-	1	10	0	1
P12259	Coagulation factor V	3	1.66%	513	527	14	R	DIASGLIGLLLICK	S	S	0.81%	9033	9033	743.9396973	2	1485.863744	1484.86317	1.000574051	R	S	C13:+57.021	5	14	1	0
				1969	1982	13	K	EVIITGIQTQGAK	H	H	0.81%	2584	2584	679.3858643	2	1356.756078	1356.761276	-0.005197932	K	H	-	5	13	0	0
				2189	2199	10	K	NFFNPPIISR	F	F	1.93%	4744	4744	603.3249512	2	1204.634252	1203.640039	0.994213504	K	F	-	3	10	1	0
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	8	40.24%	29	41	12	K	SEDFSLPAYMDR	R	R	0.81%	4517	4517	716.3156738	2	1430.615698	1429.618378	0.997319656	K	R	-	5	12	1	0
				29	42	13	K	SEDFSLPAYMDRR	D	D	1.93%	3809	3809	793.8668213	2	1585.717993	1585.719489	-0.001496574	K	D	-	4	13	0	1
				42	53	11	R	DHPLPEVAHVK	H	H	0.81%	698	698	414.8956909	3	1241.663598	1240.656417	1.007180466	R	H	-	5	11	1	0
				67	78	11	K	ASWSSLSMDEK	V	V	0.81%	2794	2794	622.3325195	2	1242.649389	1239.54415	3.105238759	K	V	-	2	11	3	0
				67	83	16	K	ASWSSLSMDEKVELYR	I	I	0.81%	4478	4478	634.3061523	3	1899.894982	1899.903661	-0.008679417	K	I	-	2	16	0	1
				85	95	10	K	FKESFAEMNR	G	G	0.81%	943	943	629.7941284	2	1257.572607	1257.581204	-0.008597644	K	G	-	5	10	0	1
				122	135	13	K	HYVYGPLPQSFDK	E	E	0.81%	2803	2803	776.3859863	2	1550.756323	1549.756525	0.99979724	K	E	-	3	13	1	0
				122	140	18	K	HYVYGPLPQSFDKEWVAK	Q	Q	1.93%	4212	4212	1083.546509	2	2165.077368	2163.078923	1.998444906	K	Q	-	3	18	2	1
P13473	Lysosome-associated membrane glycoprotein 2	3	7.07%	132	144	12	K	GILTVDELLAIR	I	I	0.81%	7056	7056	656.8918457	2	1311.768041	1311.776198	-0.008156794	K	I	-	5	12	0	0
				144	152	8	R	IPLNDLFR	C	C	0.81%	5014	5014	494.7878113	2	987.5599725	986.554912	1.005060463	R	C	-	5	8	1	0
				280	289	9	K	YLDFVFAVK	N	N	0.81%	6096	6096	551.3027344	2	1100.589819	1100.590629	-0.00081021	K	N	-	5	9	0	0
P13498	Cytochrome b-245 light chain	4	29.74%	127	139	12	R	GEQWTPIEPKPR	E	E	0.81%	1746	1746	719.8829956	2	1437.750341	1436.74121	1.009131547	R	E	-	3	12	1	0
				149	164	15	K	QPPSNPPPRPPAEAR	K	K	4.72%	673	673	797.4089355	2	1592.802221	1592.805484	-0.00326333	K	K	Q1:-17.027	1	15	0	0
				164	193	29	R	KKPSEEEAAVAAGGPPGGPQVNPIPVTDE	V	V	7.51%	3112	3112	948.1472168	3	2841.418175	2841.403215	0.014960687	R	V	N22:+0.984	1	29	0	1

				164	195	31	R	KKPSEEEAAVAAGGPPGGPQVNPIPVTDEVV	-	0.81%	4210	4210	1014.534485	3	3040.579979	3039.540043	1.03993687	R	-	Q20:+0.984	4	31	1	1
P13591	Neural cell adhesion molecule 1	3	4.90%	19	37	18	S	LQVDIVPSQGEISVGESK	F	5.96%	4223	4223	942.9977417	2	1883.979833	1883.984019	-0.00418581	S	F	-	1	18	0	0
				165	177	12	R	FIVLSNNYLQIR	G	0.81%	5640	5640	740.42	2	1478.82435	1478.824545	-0.000195424	R	G	-	5	12	0	0
				592	604	12	K	GLGEISAASEFK	T	0.81%	3397	3397	605.3154297	2	1208.615209	1207.608464	1.006745351	K	T	-	4	12	1	0
P13598	Intercellular adhesion molecule 2	1	5.82%	135	151	16	R	VPTVEPLDSLTLFLFR	G	2.46%	9496	9496	924.5283813	2	1847.041113	1846.024033	1.017079263	R	G	-	5	16	1	0
P13796	Plastin-2	6	12.28%	68	76	8	R	ISFDEFIK	I	3.00%	4933	4933	499.7607117	2	997.5057733	997.5120442	-0.006270892	R	I	-	1	8	0	0
				263	272	9	K	LSPEELLLR	W	0.81%	4825	4825	535.3169556	2	1068.618261	1068.617906	0.000354717	K	W	-	4	9	0	0
				297	309	12	K	AYYHLLEQVAPK	G	2.26%	3235	3235	478.2632446	3	1431.766259	1430.755797	1.010461759	K	G	-	2	12	1	0
				542	564	22	K	DPKISTSLPVLDLIDAIQPGSI	N	5.83%	4879	4879	766.364563	3	2296.070214	2291.262426	4.807787653	K	N	-	1	22	5	1
				596	610	14	R	VYALPEDLVEVNPK	M	0.81%	4718	4718	793.9212646	2	1585.826879	1584.839921	0.986958449	R	M	-	5	14	1	0
				610	622	12	K	MVMTVFACLMGK	G	4.98%	5453	5453	710.86	2	1419.70435	1418.642729	1.061621416	K	G	M3:+15.995,C8:+57.021,M	1	12	1	0
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	1	3.96%	23	39	16	R	QQPPDLVEFAVEYFTR	L	6.47%	9190	9190	647.3294678	3	1938.964928	1937.952325	1.012603232	R	L	-	1	16	1	0
P13987	CD59 glycoprotein	3	29.69%	25	39	14	S	LQCYNCPNPTADCK	T	4.79%	662	662	871.3623047	2	1740.708959	1739.705169	1.003790391	S	T	C3:+57.021,C6:+57.021,C	1	14	1	0
				66	78	12	K	FEHCNFNDVTTR	L	0.81%	858	858	770.331665	2	1538.64768	1538.656759	-0.009079314	K	L	C4:+57.021	5	12	0	0
				78	90	12	R	LRENELTYYCCK	K	0.81%	1453	1453	824.8734131	2	1647.731176	1647.737584	-0.006407484	R	K	C10:+57.021,C11:+57.021	4	12	0	1
P14174	Macrophage migration inhibitory factor	2	17.39%	1	12	11	M	PMFIVNTNVPR	A	0.81%	3841	3841	644.3447876	2	1286.673925	1286.680525	-0.006599453	M	A	-	3	11	0	0
				78	87	9	K	LLCGLLAER	L	0.81%	3990	3990	522.7949829	2	1043.574316	1043.579284	-0.004968236	K	L	C3:+57.021	4	9	0	0
P14618	Pyruvate kinase isozymes M1/M2	37	67.80%	32	43	11	R	LDIDSPPITAR	N	0.81%	2657	2657	599.3256226	2	1196.635595	1196.640098	-0.004503395	R	N	-	4	11	0	0
				43	56	13	R	NTGIICTIGPASR	S	0.81%	2092	2092	680.3549194	2	1358.694189	1358.697168	-0.002978749	R	S	C6:+57.021	5	13	0	0
				56	66	10	R	SVETLKEMIK	S	3.00%	696	696	597.3241577	2	1192.632665	1192.636408	-0.003742386	R	S	M8:+15.994	1	10	0	1
				73	89	16	R	LNFSHGTHEYHAETIK	N	0.81%	649	649	942.4545898	2	1882.89353	1882.896207	-0.002677384	R	N	-	3	16	0	0
				92	106	14	R	TATESFASDPILYR	P	1.97%	3806	3806	787.94	2	1573.86435	1569.767484	4.096865864	R	P	-	1	14	4	0
				92	115	23	R	TATESFASDPILYRPVAVALDTK	G	0.81%	5665	5665	1233.145996	2	2464.276342	2464.284953	-0.008610508	R	G	-	5	23	0	0
				92	120	28	R	TATESFASDPILYRPVAVALDTKGPEIR	T	0.81%	5666	5666	1006.870911	3	3017.589257	3016.586949	1.002308054	R	T	-	5	28	1	1
				101	115	14	D	PILYRPVAVALDTK	G	8.16%	3963	3963	778.9592285	2	1555.902807	1554.91336	0.989446487	D	G	-	1	14	1	0
				106	115	9	R	PVAVALDTK	G	4.94%	960	960	457.2697449	2	912.5238397	912.5280286	-0.004188894	R	G	-	1	9	0	0
				141	151	10	K	ITLDNAYMEK	C	1.93%	2230	2230	599.2935791	2	1196.571508	1196.574722	-0.003213933	K	C	-	4	10	0	0
				151	162	11	K	CDENILWLDYK	N	0.81%	5214	5214	734.8414917	2	1467.667333	1467.66995	-0.002616434	K	N	C1:+57.021	4	11	0	0
				173	186	13	K	IYVDDGLISLQVK	Q	0.81%	5226	5226	731.9140015	2	1461.812353	1461.807892	0.00446057	K	Q	-	5	13	0	0
				188	206	18	K	GADFLVTEVENGGSLGSK	K	0.81%	5096	5096	890.9338989	2	1779.852148	1779.852655	-0.000507108	K	K	N11:+0.984	5	18	0	0
				206	224	18	K	KGVNLPGAAVDLPAVSEK	D	0.81%	3598	3598	882.9944458	2	1763.973242	1763.978146	-0.004904246	K	D	-	4	18	0	1
				206	230	24	K	KGVNLPGAAVDLPAVSEKDIQDLK	F	3.76%	4896	4896	826.7943726	3	2477.359643	2476.353701	1.005941604	K	F	-	1	24	1	2
				207	224	17	K	GVNLPGAAVDLPAVSEK	D	0.81%	4171	4171	818.9472656	2	1635.878881	1635.883183	-0.004301462	K	D	-	5	17	0	0
				207	230	23	K	GVNLPGAAVDLPAVSEKDIQDLK	F	0.81%	5452	5452	1175.642456	2	2349.269262	2348.258738	1.010524213	K	F	-	4	23	1	1
				230	246	16	K	FGVEQDVDMVFASFIR	K	0.81%	9017	9017	930.4487305	2	1858.881811	1858.892368	-0.010557422	K	K	-	4	16	0	0
				230	247	17	K	FGVEQDVDMVFASFIRK	A	0.81%	8264	8264	663.3382568	3	1986.991295	1986.987331	0.003963972	K	A	-	3	17	0	1
				278	294	16	R	RFDEILEASDGIMVAR	G	0.81%	5078	5078	911.4603271	2	1820.905004	1820.909081	-0.004076799	R	G	-	2	16	0	1
				294	305	11	R	GDLGIEIPAEK	V	0.81%	3147	3147	571.3074341	2	1140.599218	1140.60265	-0.003432172	R	V	-	4	11	0	0
				319	336	17	R	AGKPVICATQMLESMIK	K	0.81%	6236	6236	938.9910889	2	1875.966528	1875.961583	0.004944574	R	K	C7:+57.021	4	17	0	0
				322	336	14	K	PVICATQMLESMIK	K	3.91%	6759	6759	810.9067993	2	1619.797949	1619.808042	-0.010093775	K	K	C4:+57.021	1	14	0	0
				342	367	25	R	AEGSDVANAVLDGADCIMLSGETAK	G	0.81%	6669	6669	836.7267456	3	2507.156762	2509.130854	-1.9740926	R	G	C16:+57.021,M18:+15.99	2	25	-1	0
				367	376	9	K	GDYPLEAVR	M	0.81%	1734	1734	510.2598572	2	1018.504064	1018.508356	-0.004291501	K	M	-	5	9	0	0
				383	399	16	R	EAEAAIYHLQLFEELR	R	0.81%	6084	6084	966.4942017	2	1930.972753	1930.978874	-0.006120856	R	R	-	4	16	0	0
				383	400	17	R	EAEAAIYHLQLFEELRR	L	0.81%	5337	5337	1044.543945	2	2087.072241	2087.079985	-0.007744703	R	L	-	3	17	0	1
				400	422	22	R	LAPITSDPTEATAVGAVEASFK	C	0.81%	5980	5980	725.7146606	3	2174.120507	2174.110676	0.00983039	R	C	-	5	22	0	0
				422	433	11	K	CCSGAIIVLTK	S	0.81%	2508	2508	611.3184204	2	1220.621191	1220.624785	-0.003594636	K	S	C1:+57.021,C2:+57.021	1	11	0	0
				447	455	8	R	APIIAVTR	N	4.38%	2380	2380	421.757019	2	841.498388	839.5228835	1.975504478	R	N	-	1	8	2	0
				467	475	8	R	GIFPVLCK	D	0.81%	4134	4134	467.2641907	2	932.5127313	932.5148927	-0.002161404	R	D	C7:+57.021	4	8	0	0
				467	489	22	R	GIFPVLCKDPVQEAWAEDVDLR	V	0.81%	6599	6599	853.0964966	3	2556.266015	2556.267794	-0.001779398	R	V	C7:+57.021	2	22	0	1
				475	489	14	K	DPVQEAWAEDVDLR	V	0.81%	4758	4758	548.2577515	3	1641.749779	1641.763461	-0.013682077	K	V	-	5	14	0	0
				489	498	9	R	VNFAMNVGK	A	0.81%	2047	2047	490.7904358	2	979.5652215	978.4956837	1.069537846	R	A	-	5	9	1	0
				504	523	19	K	KGDVVIVLTGWRPGSGFTN	T	4.79%	5503	5503	1002.540955	2	2003.066259	2002.063607	1.00265226	K	T	-	1	19	1	1
				504	526	22	K	KGDVVIVLTGWRPGSGFTNTMR	V	1.93%	5231	5231	1196.135254	2	2390.254858	2390.252882	0.001975364	K	V	-	2	22	0	1
				505	526	21	K	GDVVIVLTGWRPGSGFTNTMR	V	0.81%	5928	5928	755.0591431	3	2262.153954	2262.157919	-0.003965153	K	V	-	3	21	0	0
P14625	Endoplasmin	14	21.42%	43	67	24	R	TDDEVVQREEEAIQLDGLNASQIR	E	2.32%	5127	5127	911.1091309	3	2730.303917	2728.315128	1.988789666	R	E	Q14:+0.984	2	24	2	1
				75	84	9	K	FAFQAEVNR	M	0.81%	2669	2669	541.2698364	2	1080.524023	1080.535239	-0.01121646	K	M	-	5	9	0	0
				87	95	8	K	LIINSLYK	N	1.93%	3623	3623	482.2950439	2	962.5744378	962.5800642	-0.005626349	K	N	-	2	8	0	0
				102	114	12	R	ELISNASDALDK	I	0.81%	2148	2148	638.3244019	2	1274.633154	1274.635407	-0.002253441	R	I	-	5	12	0	0
				102	116	14	R	ELISNASDALDKIR	L	0.81%	3775	3775	515.612793	3	1543.814904	1543.820582	-0.005678526	R	Y	-	1	14	0	1
				142	156	14	K	NLLHVTDTGVGMTR	E	0.81%	2970	2970	757.8964233	2	1513.777197	1512.771859	1.0053376	K	E	-	5	14	1	0
				142	161	19	K	NLLHVTDTGVGMTREELVK	N	4.12%	3474	3474	705.3789063	3	2113.113244	2111.104487	2.008756982	K	N	-	1	19	2	1
				270	285	15	K	YSQFINFPIYVWSSK	T	0.81%	7510	7510	940.4749756	2	1878.934301	1877.935218	0.99908286	K	T	-	4	15	1	0
				384	395	11	K	SILFVPTSAPR	G	0.81%	3744	3744	594.3421021	2	1186.668554	1186.671005	-0.00245057	K	G	-	5	11	0	0
				415	428	13	R	VFITDDFHDMMPK	Y	0.81%	5081	5081	798.3553467	2	1594.695043	1594.715985	-0.020941409	R	Y	-	5	13	0	0
				434	448	14	K	GVVDSDDLPLNVSR	E	0.81%	3642	3642	743.3813477	2	1484.747045	1484.747083	-3.77115E-05	K	E	-	5	14	0	0
				474	493	19	K	IADDKYNDTFWKEFGTNIK	L	5.76%	4780	4780	769.3806763	3	2305.118554	2304.10626	1.012293969	K	L	-	1	19	1	2
				511	530	19	R	FQSSHHPTDITSLDQYVER	M	0.81%	3515	3515	754.0241699	3	2259.049035	2260.039621	-0.990586458	R	M	Q2:+0.984	2	19	-1	0
				683	690	7	K	TFEINPR	H	4.33%	1112	1112	438.7320557	2	875.4484612	875.4501125	-0.00165124	K	H	-	5	7	0	0
P14868	Aspartyl-tRNA synthetase, cytoplasmic	6	14.77%	110	121	11	K	ESIVDVEGVVR	K	0.81%	3366	3366	602.3253784	2	1202.635107	1200.635013	2.000093684	K	K	-	2	11	2	0
				151	171	20	R	LPLQLDDAVRPEAEGEEEGR	A	0.81%	3426	3426	742.03	3	2223.066525	2223.065502	0.001023304	R	A	Q4:+0.984	3	20	0	0
				264	273	9	K	VFSIGPVFR	A	2.32%	4854	4854	511.290741	2	1020.565832	1020.575647	-0.009815602	K	A	-	3	9	0	0
				453	460	7	K	AYIDSFR	F	6.49%	2235	2235	435.772644	2	869.529638	870.4235634	-0.893925354	K	F	-	2	7	-1	0
				460	475	15	R	FGAPPHAGGGIGLER	V	0.81%	1081	1081	479.2489929	3	1434.723504	1434.736793	-0.01328924	R	V	-	1	15	0	0
				475	487	12	R	VTMLFLGLHNVR	Q	0.81%	5096	5096	700.3985596	2	1398.781469	1398.780573	0.000895997	R	Q	-	5	12	0	0
P14923	Junction plakoglobin	3	6.44%	426	444	18	K	TLVTQNSGVEALIHAILR	A	1.97%	8248	8248	646.0401001	3	1935.096825	1935.078907	0.017918173	K	A	Q5:+0.984	2	18	0	0
				477	487	10	R	LNYGIPAIVK	L	6.51%	4167	4167	544.8609009	2	1087.706152	1086.643727	1.062424542	R	L	-	2	10	1	0
				582	602	20	R	LNTIPLFVQLLYSSVENIQR	V	0.81%	10176	10176	783.4331055	3	2347.275841	2346.294729	0.98111195	R	V	-	4	20	1	0
P15153	Ras-related C3 botulinum toxin substrate 2	9	57.29%	43	66	23	N	VMVDSKPVNLGLWDTAGQEDYDR	L	9.37%	4892	4892	870.0802612	3	2607.217309	2607.227515	-0.010206669	N	L	-	1	23	0	0
				49	66	17	K	PVNLGLWDTAGQEDYDR	L	4.29%	4948	4948	974.9525146	2	1947.889379	1947.896267	-0.006887447	K	L	-	1	17	0	0
				66	94	28	R	LRPLSYPQTDVFLICFSLVSPASYENVR	A	0.81%	7949	7949	1091.889771	3	3272.645836	3271.658255	0.987581035	R	A	Q8:+0.984,C15:+57.021	4	28	1	0
				102	116	14	R	HHCPSTPIILVGTK	L	0.81%	1527	1527	520.614624	3	1558.820397	1558.828516	-0.008119242	R	L	C3:+57.021	5	14	0	0
				116	128	12	K	LDLRDDKDTIEK	L	4.17%	747	747	730.8804321	2	1459.745214	1459.751834	-0.006619798	K	L	-	1	12	0	2
				132	147	15	K	KLAPITYPQGLALAK	E	0.81%	3979	3979	792.4752197	2	1582.934789	1582.944661	-0.009871251	K	E	-	4	15	0	1
				133	147	14	K	LAPITYPQGLALAK	E	0.81%	4467	4467	728.9327393	2	1455.849828	1454.849697	1.000130948	K	E	-	4	14	1	0
				153	163	10	K	YLECSALTQR	G	0.81%	1586	1586	620.8023682	2	1239.589086	1239.591305	-0.002219104	K	G	C4:+57.021	5	10	0	0
				166	174	8	K	TVFDEAIR	A	0.81%	2550	2550	475.7470398	2	949.4784295	949.486892	-0.008462498	K	A	-	3	8	0	0
P15311	Ezrin	3	5.80%	237	246	9	K	IGFPWSEIR	N	0.81%	5500	5500	552.793396	2	1103.571142	1103.576376	-0.005233872	K	N	-	5	9	0	0
				263	273	10	K	APDFVFYAPR	L	2.83%	4293	4293	593.3498535	2	1184.684057	1181.586941	3.097116447	K	L	-	2	10	3	0
				412	427	15	K	SQEQLAAELAEYTAK	I	0.81%	4453	4453	826.9143066	2	1651.812963	1650.810077	1.002885937	K	I	-	3	15	1	0
P15509	Granulocyte-macrophage colony-stimulating factor receptor subunit alpha	1	2.75%	28	39	11	R	TVAPASSLNVR	F	4.01%	826	826	558.3037109	2	1114.591772	1114.598218	-0.006446165	R	F	N9:+0.984	2	11	0	0
P15924	Desmoplakin	40	19.19%	84	94	10	R	AELIVQPELK	Y	2.26%	3164	3164	570.3330078	2	1138.650366	1138.659771	-0.009405671	R	Y	-	5	10	0	0
				94	103	9	K	YGDGIQLTR	S	0.81%	1408	1408	511.7642822	2	1021.512914	1021.519255	-0.006340451	K	S	-	5	9	0	0
				141	150	9	R	LLQLQEQMR	A	0.81%	2717	2717	579.8174438	2	1157.619238	1157.622675	-0.003437665	R	A	-	4	9	0	0
				199	222	23	R	AEMDMVAWGVDLASVEQHINSHR	G	2.34%	7093	7093	650.0549927	4	2596.188671	2594.20059	1.988080519	R	G	-	1	23	2	0
				245	260	15	K	SAIYQLEEEYENLLK	A	0.81%	7429	7429	922.4606934	2	1842.905737	1840.909457	1.996279535	K	A	-	5	15	2	0
				270	281	11	R	QLQNIIQATSR	E	0.81%	2032	2032	636.3539429	2	1270.692236	1270.699345	-0.007109042	R	E	-	4	11	0	0
				407	423	16	K	NMPLQHLLEQIKELEK	E	3.49%	7405	7405	655.03	3	1962.066525	1962.060831	0.005694096	K	E	-	3	16	0	1
				578	592	14	K	TIADLELHYQEFIR	N	0.81%	5664	5664	874.9624023	2	1747.909155	1746.894082	1.015072928	K	N	-	5	14	1	0
				689	705	16	K	NLPLADQGSSHHITVK	I	1.98%	989	989	858.9522705	2	1715.888891	1715.895479	-0.006587728	K	I	-	4	16	0	0
				710	727	17	K	SVQNDSQAIAEVLNQLK	D	0.81%	6686	6686	619.6588745	3	1855.953148	1855.963952	-0.010803929	K	D	-	3	17	0	0
				771	785	14	R	ALLQAILQTEDMLK	V	0.81%	7785	7785	795.27	2	1588.52435	1585.874927	2.649422704	R	V	-	1	14	3	0
				812	821	9	K	KIKNDLNLK	K	4.89%	776	776	544.7756958	2	1087.535742	1085.64444	1.89130165	K	K	N4:+0.984	1	9	2	2
				834	855	21	K	AQQIHSQTSQQYPLYDLDLGK	F	0.81%	4341	4341	812.0722046	3	2433.193139	2433.1812	0.011938498	K	F	Q10:+0.984	2	21	0	0
				959	982	23	K	DYELQLASYTSGLETLLNIPIKR	T	5.54%	8374	8374	880.7592163	3	2639.254174	2638.374131	0.880043254	K	T	Q5:+0.984,N18:+0.984	1	23	1	1
				982	1002	20	R	TMIQSPSGVILQEAADVHAR	Y	0.81%	4860	4860	708.3609619	3	2122.059411	2124.052086	-1.992674914	R	Y	Q4:+0.984,Q12:+0.984	1	20	-1	0
				1002	1009	7	R	YIELLTR	S	0.81%	3329	3329	454.264679	2	906.5137078	906.5174638	-0.00375601	R	S	-	3	7	0	0
				1033	1042	9	K	IEVLEEELR	L	1.93%	3661	3661	565.3091431	2	1128.602636	1128.60265	-1.42032E-05	K	L	-	3	9	0	0
				1056	1064	8	K	FLDQNLQK	Y	3.15%	978	978	503.2701721	2	1004.524694	1004.529091	-0.004397058	K	Y	-	2	8	0	0
				1247	1255	8	R	DLKDEIVR	L	1.93%	1396	1396	494.2737732	2	986.5318963	986.5396559	-0.007759629	R	L	-	4	8	0	1
				1255	1267	12	R	LNDSILQATEQR	R	0.81%	2905	2905	694.3672485	2	1386.718847	1386.710303	0.008543566	R	R	-	4	12	0	0
				1352	1363	11	R	NNYDEEIISLK	N	0.81%	3677	3677	669.8322754	2	1337.648901	1336.651057	0.997843549	R	N	-	4	11	1	0
				1363	1374	11	K	NQFETEINITK	T	0.81%	3106	3106	668.8432007	2	1335.670751	1335.667042	0.003709727	K	T	-	5	11	0	0
				1443	1452	9	R	KQQLEVELR	Q	3.03%	993	993	571.8288574	2	1141.642065	1141.645518	-0.003453356	R	Q	-	3	9	0	1
				1558	1572	14	R	FQNSLKELQLQKQK	V	5.30%	8418	8418	868.2927246	2	1734.569799	1732.935915	1.633883763	R	V	N3:+0.984,Q9:+0.984	1	14	2	2
				1611	1626	15	K	ITNLTQQLEQASIVK	K	0.81%	4830	4830	843.4740601	2	1684.93247	1684.935947	-0.003476523	K	K	-	5	15	0	0
				1705	1715	10	R	LQSLTENLTK	E	0.81%	1940	1940	573.8206787	2	1145.625707	1145.629199	-0.003492042	R	E	-	4	10	0	0
				1759	1780	21	S	NNRTLELQGLINDLQRERENL	R	5.29%	5528	5528	846.7836914	3	2537.327599	2537.331008	-0.003409349	S	R	-	1	21	0	3
				1762	1775	13	R	TLELQGLINDLQR	E	0.81%	6576	6576	756.9202271	2	1511.824804	1511.830753	-0.00594901	R	E	-	5	13	0	0
				1857	1868	11	K	QQIQNDLNQWK	T	3.17%	2406	2406	708.862915	2	1415.71018	1413.700073	2.010106966	K	T	-	1	11	2	0
				1965	1972	7	K	LVFDGLR	K	1.97%	3519	3519	410.2392883	2	818.4629266	818.4650342	-0.00210766	K	K	-	3	7	0	0
				1999	2013	14	K	SVEEVASEIQPFLR	G	0.81%	5944	5944	802.4202881	2	1602.824926	1602.825333	-0.000407252	K	G	-	5	14	0	0
				2038	2063	25	K	LISPESTVMLLEAQAATGGIIDPHR	N	8.84%	7583	7583	874.1326294	3	2619.374413	2618.373786	1.000627416	K	N	-	1	25	1	0
				2091	2103	12	K	AITGFDDPFSGK	T	2.36%	4359	4359	629.3427734	2	1256.669897	1253.592814	3.077082931	K	T	-	2	12	3	0
				2123	2145	22	R	LLEAQIASGGVVDPVNSVFLPK	D	0.81%	6338	6338	1128.052734	2	2254.089819	2252.241631	1.84818759	R	D	-	3	22	2	0
				2191	2205	14	R	IEPHTGLLLLSVQK	R	0.81%	4370	4370	516.9735107	3	1547.897057	1546.908275	0.988782003	R	R	-	1	14	1	0
				2206	2214	8	R	SMSFQGIR	Q	0.81%	2081	2081	463.2331848	2	924.4507195	924.4487334	0.001986133	R	Q	-	4	8	0	0
				2279	2309	30	K	IGLVRPGTALELLEAQAATGFIVDPVSNLR	L	0.81%	8656	8656	780.9413452	4	3119.734081	3120.718282	-0.984201125	K	L	Q16:+0.984	3	30	-1	0
				2413	2430	17	K	GFFDPNTEENLTYLQLK	E	0.81%	6210	6210	1015.508362	2	2029.001074	2027.984019	1.017054425	K	E	-	5	17	1	0
				2639	2649	10	R	GIVDSITGQR	L	5.92%	2181	2181	524.2754517	2	1046.535253	1044.556369	1.978884568	R	L	-	4	10	2	0
				2725	2744	19	R	FLEFQYLTGGLVDPEVHGR	I	0.81%	6489	6489	726.3729858	3	2176.095482	2176.095301	0.0001814	R	I	-	5	19	0	0
P15941	Mucin-1	1	1.35%	1108	1125	17	R	EGTINVHDVETQFNQYK	T	9.06%	3961	3961	675.324585	3	2022.95028	2020.949031	2.001249171	R	T	-	1	17	2	0
P16188	HLA class I histocompatibility antigen, A-30 alpha chain	9	39.73%	45	59	14	R	FIAVGYVDDTQFVR	F	0.81%	4994	4994	815.911377	2	1629.807104	1628.819854	0.987249842	R	F	-	5	14	1	0
				72	89	17	R	APWIEQERPEYWDQETR	N	1.93%	4000	4000	745.3441772	3	2233.009057	2233.007593	0.001464002	R	N	Q6:+0.984	3	17	0	0
				135	155	20	R	GYEQHAYDGKDYIALNEDLR	S	0.81%	3266	3266	790.7041016	3	2369.08883	2369.092401	-0.003571057	R	S	-	3	20	0	1
				181	193	12	R	AYLEGTCVEWLR	R	0.81%	4971	4971	749.3571167	2	1496.698583	1495.712483	0.98610003	R	R	C7:+57.021	5	12	1	0
				194	205	11	R	YLENGKETLQR	T	0.81%	674	674	676.3446655	2	1350.673681	1350.677925	-0.004244041	R	A	N4:+0.984	5	11	0	1
				226	243	17	R	CWALGFYPAEITLTWQR	D	0.81%	7963	7963	1057.524414	2	2113.033178	2112.013401	1.019776861	R	D	C1:+57.021,Q16:+0.984	3	17	1	0
				243	267	24	R	DGEDQTQDTELVETRPAGDGTFQK	W	0.81%	2338	2338	880.0667725	3	2637.176842	2636.183795	0.993047535	R	W	-	2	24	1	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.81%	2533	2533	714.3683472	2	1426.721044	1426.720474	0.000570112	K	Y	-	4	13	0	0
				280	297	17	R	YTCHVQHEGLPKPLTLR	W	0.81%	2076	2076	1025.535522	2	2049.055395	2048.062098	0.993296514	R	W	C3:+57.021	4	17	1	0
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	26	31.09%	7	30	23	K	TVEEVLGHFGVNESTGLSLEQVK	K	0.81%	5718	5718	1237.630249	2	2473.244848	2471.254381	1.990467183	K	K	-	4	23	2	0
				7	31	24	K	TVEEVLGHFGVNESTGLSLEQVKK	L	0.81%	5158	5158	868.4573975	3	2602.348717	2599.349344	2.999373343	K	L	-	2	24	3	1

				35	47	12	R	WGSNELPAEEGK	T	0.81%	1333	1333	659.3081665	2	1316.600683	1315.604441	0.996241688	R	T	-	5	12	1	0
				110	128	18	R	NAENAIEALKEYEPEMGK	V	4.85%	4847	4847	679.3275146	3	2034.959069	2035.940819	-0.981750431	R	V	N4:+0.984	2	18	-1	1
				143	158	15	K	DIVPGDIVEIAVGDK	V	0.81%	6103	6103	770.421814	2	1538.827978	1538.819185	0.008792522	K	V	-	5	15	0	0
				143	164	21	K	DIVPGDIVEIAVGDKVPADIR	L	0.81%	6463	6463	1096.605347	2	2191.195043	2190.189595	1.005447799	K	L	-	5	21	1	1
				174	189	15	R	VDQSILTGESVSVIK	H	0.81%	3847	3847	787.9446411	2	1573.873632	1573.856299	0.017332971	R	H	-	3	15	0	0
				205	218	13	K	NMLFSGTNIAAGK	A	0.81%	3672	3672	663.35	2	1324.68435	1322.665268	2.019081432	K	A	-	2	13	2	0
				218	234	16	K	AMGVVVATGVNTEIGK	I	0.81%	3323	3323	773.4185181	2	1544.821386	1544.823226	-0.001839891	K	I	-	5	16	0	0
				234	246	12	K	IRDEMVATEQER	T	0.81%	691	691	738.8594971	2	1475.703344	1475.703839	-0.000494931	K	T	-	5	12	0	1
				252	262	10	K	LDEFGEQLSK	V	2.26%	1935	1935	583.2862549	2	1164.55686	1164.566265	-0.00940505	K	V	-	2	10	0	0
				352	365	13	K	TGTLTTNQMSVCR	M	0.81%	810	810	734.8470459	2	1467.678442	1467.680532	-0.002090667	K	M	C12:+57.021	5	13	0	0
				436	451	15	K	VGEATETALTCLVEK	M	0.81%	4068	4068	810.9082031	2	1619.800756	1619.807172	-0.006415598	K	M	C11:+57.021	4	15	0	0
				451	460	9	K	MNVFDTELK	G	0.81%	2847	2847	556.7640991	2	1111.512548	1111.522043	-0.009495326	K	G	M1:+15.995	3	9	0	0
				549	559	10	R	EWGSGSDTLR	C	3.02%	1009	1009	554.7659912	2	1107.516332	1106.499248	1.01708463	R	C	-	4	10	1	0
				572	585	13	R	EEMHLEDSANFIK	Y	0.81%	3316	3316	782.3602905	2	1562.704931	1561.708256	0.996675279	R	Y	-	4	13	1	0
				619	628	9	R	VIMITGDNK	G	0.81%	949	949	495.766449	2	989.5172479	989.5215641	-0.004316259	R	G	-	4	9	0	0
				636	650	14	R	RIGIFGQDEDVTSK	A	0.81%	2802	2802	783.4039917	2	1564.792333	1563.789282	1.003051166	R	A	-	4	14	1	1
				637	650	13	R	IGIFGQDEDVTSK	A	0.81%	3515	3515	704.8501587	2	1407.684667	1407.688171	-0.003503697	R	A	-	4	13	0	0
				655	666	11	R	EFDELNPSAQR	D	0.81%	1751	1751	653.3060913	2	1304.596533	1304.59969	-0.003157671	R	D	-	5	11	0	0
				685	712	27	K	IVEFLQSFDEITAMTGDGVNDAPALKK	A	4.24%	7313	7313	970.8184204	3	2909.431786	2909.436824	-0.005037938	K	A	Q6:+0.984	1	27	0	1
				711	727	16	K	KAEIGIAMGSGTAVAK	T	0.81%	1648	1648	752.4187622	2	1502.821874	1502.812661	0.00921311	K	T	-	5	16	0	1
				712	727	15	K	AEIGIAMGSGTAVAK	T	0.81%	2714	2714	688.8696899	2	1375.72373	1374.717698	1.006031715	K	T	-	5	15	1	0
				727	750	23	K	TASEMVLADDNFSTIVAAVEEGR	A	0.81%	7836	7836	809.7197876	3	2426.135888	2424.147868	1.988019817	K	A	-	3	23	2	0
				824	835	11	K	EPLISGWLFFR	Y	0.81%	7748	7748	683.3752441	2	1364.734838	1363.728854	1.005984321	K	Y	-	5	11	1	0
				971	984	13	K	ISLPVILMDETLK	F	0.81%	7469	7469	736.4274902	2	1470.83933	1470.836751	0.002579677	K	F	-	5	13	0	0
P17081	Rho-related GTP-binding protein RhoQ	1	4.88%	159	169	10	C	YVECSALTQK	G	0.81%	717	717	599.7892456	2	1197.562841	1197.569507	-0.006666125	K	G	C4:+57.021	5	10	0	0
P17152	Transmembrane protein 11	5	30.21%	58	66	8	K	YIVIEPTR	I	0.81%	1760	1760	495.7831726	2	989.5506951	989.5545777	-0.003882553	K	I	-	3	8	0	0
				73	83	10	R	WITVGNCLHK	T	0.81%	2435	2435	614.3151855	2	1226.614721	1226.622546	-0.007824826	R	T	C7:+57.021	5	10	0	0
				133	142	9	K	YQVEYDAYK	L	3.89%	1306	1306	589.7692871	2	1177.522924	1177.529151	-0.006226749	K	L	-	2	9	0	0
				145	161	16	R	LPLHTLTSSTPVVLVR	K	0.81%	4262	4262	867.0142822	2	1732.012914	1732.024702	-0.011787635	R	K	-	5	16	0	0
				169	184	15	R	LHNTIALAALVYCVK	K	0.81%	5440	5440	562.9797363	3	1685.915734	1684.932981	0.982752472	R	K	C13:+57.021	5	15	1	0
P17181	Interferon alpha/beta receptor 1	1	1.26%	179	186	7	R	IENIYSR	H	9.12%	1050	1050	448.7151794	2	895.4147088	893.4606772	1.954031599	R	H	-	2	7	2	0
P17987	T-complex protein 1 subunit alpha	21	51.26%	11	33	22	R	STGETIRSQNVMAAASIANIVK	S	5.67%	8218	8218	1141.098389	2	2280.181127	2279.131528	1.049599232	R	S	Q9:+0.984,N10:+0.984,M1	1	22	1	1
				18	33	15	R	SQNVMAAASIANIVK	S	0.81%	4454	4454	758.9105835	2	1515.805517	1515.80791	-0.00239328	R	S	-	3	15	0	0
				43	63	20	K	MLVDDIGDVTITNDGATILK	L	0.81%	5859	5859	1052.545898	2	2103.076147	2103.076935	-0.000787741	K	L	-	4	20	0	0
				49	63	14	I	GDVTITNDGATILK	L	4.05%	2808	2808	709.3874512	2	1416.759252	1416.74602	0.013231976	K	Q	-	3	14	0	0
				73	102	29	K	VLCELADLQDKEVGDGTTSVVIIAAELLK	N	2.32%	8366	8366	1034.555298	3	3100.642418	3098.641618	2.000800539	K	N	C3:+57.021	2	29	2	1
				111	122	11	K	IHPTSVISGYR	L	5.02%	972	972	615.3348389	2	1228.654028	1228.656417	-0.002389514	K	L	-	1	11	0	0
				130	145	15	R	YINENLIVNTDELGR	D	0.81%	4299	4299	881.9530029	2	1761.890356	1761.889725	0.000631131	R	D	-	5	15	0	0
				159	180	21	K	IIGINGDFFANMVVDAVLAIK	Y	4.21%	10744	10744	741.0726318	3	2220.19442	2219.20241	0.992010556	K	Y	-	1	21	1	0
				189	199	10	R	YPVNSVNILK	A	0.81%	2913	2913	573.8278198	2	1145.63999	1145.644455	-0.004465896	R	A	-	5	10	0	0
				233	243	10	K	IACLDFSLQK	T	0.81%	3896	3896	597.3386841	2	1192.661718	1193.610978	-0.949260052	K	T	C3:+57.021	4	10	-1	0
				247	264	17	K	LGVQVVITDPEKLDQIR	Q	0.81%	4577	4577	962.0479736	2	1922.080297	1922.083674	-0.003376438	K	Q	-	5	17	0	1
				298	309	11	K	YFVEAGAMAVR	R	0.81%	3024	3024	607.3037109	2	1212.591772	1212.596126	-0.004354357	K	R	-	5	11	0	0
				321	355	34	K	ASGATILSTLANLEGEETFEAAMLGQAEEVVQER	I	0.81%	9202	9202	1189.244507	3	3564.710045	3563.730122	0.979923668	K	I	-	4	34	1	0
				370	378	8	R	TSASIILR	G	0.81%	1048	1048	431.26	2	860.5043499	859.5127128	0.991637112	R	G	-	5	8	1	0
				390	400	10	R	SLHDALCVVK	R	0.81%	1227	1227	571.3058472	2	1140.596044	1140.595662	0.000381872	R	R	C7:+57.021	5	10	0	0
				433	443	10	R	EQLAIAEFAR	S	0.81%	3801	3801	574.3071289	2	1146.598608	1146.603319	-0.004711179	R	S	-	5	10	0	0
				443	466	23	R	SLLVIPNTLAVNAAQDSTDLVAK	L	0.81%	6437	6437	1177.152588	2	2352.289526	2352.290038	-0.000512275	R	L	-	4	23	0	0
				450	466	16	N	TLAVNAAQDSTDLVAK	L	4.27%	2462	2462	809.4285278	2	1616.841406	1615.841712	0.999693832	N	L	-	1	16	1	0
				484	496	12	K	WIGLDLSNGKPR	D	0.81%	3709	3709	452.9125671	3	1355.714226	1355.71973	-0.005503928	K	D	N8:+0.984	3	12	0	0
				499	510	11	K	QAGVFEPTIVK	V	0.81%	2625	2625	594.8329468	2	1187.650243	1187.65502	-0.004776709	K	V	-	5	11	0	0
				515	526	11	K	FATEAAITILR	I	0.81%	4200	4200	603.34552	2	1204.67539	1204.681569	-0.006179353	K	I	-	5	11	0	0
P18084	Integrin beta-5	3	4.26%	176	185	9	R	LGFGSFVDK	D	2.64%	3746	3746	485.2536926	2	968.4917352	968.4967284	-0.004993226	R	D	-	3	9	0	0
				176	196	20	R	LGFGSFVDKDISPFSYTAPR	Y	3.00%	6248	6248	735.7088013	3	2204.102929	2203.094967	1.007962017	R	Y	-	5	20	1	1
				365	379	14	K	NIIQLIINAYNSIR	S	1.93%	10231	10231	823.4800415	2	1644.944433	1643.935887	1.00854604	K	S	-	3	14	1	0
P18827	Syndecan-1	3	11.94%	100	117	17	K	EGEAVVLPEVEPGLTAR	E	0.81%	4348	4348	883.8952637	2	1765.774877	1764.925776	0.849101424	K	E	-	4	17	1	0
				230	249	19	R	NQSPVDQGATGASQGLLDR	K	0.81%	2370	2370	957.9708252	2	1913.926	1912.923878	1.002121863	R	K	-	4	19	1	0
				230	250	20	R	NQSPVDQGATGASQGLLDRK	E	3.40%	1749	1749	681.3477783	3	2041.01986	2042.002842	-0.982981743	R	E	Q14:+0.984	3	20	-1	1
P19086	Guanine nucleotide-binding protein G(z) subunit alpha	1	3.66%	130	143	13	R	LWADPGAQACFSR	S	7.41%	1028	1028	494.2336426	3	1479.677453	1478.660766	1.01668619	R	S	Q8:+0.984,C10:+57.021	1	13	1	0
P20336	Ras-related protein Rab-3A	11	22.27%	24	35	11	K	ILIIGNSSVGK	T	3.80%	3185	3185	550.8336792	2	1099.651708	1099.660106	-0.008397226	K	T	-	2	11	0	0
				41	60	19	R	YADDSFTPAFVSTVGIDFK	V	0.81%	6558	6558	1040.998291	2	2079.980932	2078.983685	0.997247151	R	V	-	5	19	1	0
				72	83	11	K	LQIWDTAGQER	Y	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				85	93	8	R	TITTAYYR	G	0.81%	822	822	494.7568359	2	987.4980218	987.5025421	-0.004520293	R	G	-	3	8	0	0
				22	33	11	K	LVLLGESAVGK	S	0.81%	3455	3455	543.3295898	2	1084.64353	1084.649207	-0.005676888	K	S	-	3	11	0	0
				70	81	11	K	FEIWDTAGQER	Y	0.81%	3794	3794	676.3134766	2	1350.611303	1350.620426	-0.009122603	K	Y	-	5	11	0	0
				81	91	10	R	YHSLAPMYYR	G	0.81%	1956	1956	650.8092651	2	1299.60288	1299.607025	-0.004145007	R	G	-	5	10	0	0
				91	110	19	R	GAQAAIVVYDITNEESFAR	A	0.81%	5626	5626	1028.013306	2	2054.010961	2053.011631	0.999330336	R	A	-	5	19	1	0
				120	134	14	R	QASPNIVIALSGNK	A	1.93%	3718	3718	706.397644	2	1410.779638	1410.783074	-0.003436458	R	A	-	3	14	0	0
				165	179	14	K	TSMNVNEIFMAIAK	K	1.93%	6758	6758	785.397644	2	1568.779638	1567.773834	1.00580403	K	K	-	3	14	1	0
				197	209	12	R	GVDLTEPTQPTR	N	0.81%	791	791	657.3352051	2	1312.65476	1312.662291	-0.007530452	R	N	-	4	12	0	0
P20618	Proteasome subunit beta type-1	1	7.47%	109	127	18	K	AMTTGAIAAMLSTILYSR	R	1.93%	3956	3956	624.6723633	3	1870.993615	1869.96924	1.024375116	K	R	-	1	18	1	0
P20645	Cation-dependent mannose-6-phosphate receptor	1	8.66%	99	123	24	K	ETVVGRLNETHIFNGSNWIMLIYK	G	5.31%	7236	7236	940.4511719	3	2818.330041	2818.399518	-0.069477887	K	G	E1:-18.011,N8:+0.984,N14	1	24	0	1
P21333	Filamin-A	24	15.22%	76	87	11	R	LIALLEVLSQK	K	0.81%	7373	7373	613.3911743	2	1224.766699	1225.764571	-0.997872191	R	R	-	4	11	-1	0
				367	376	9	K	SPFEVYVDK	S	3.19%	3112	3112	543.3173828	2	1084.619116	1082.528423	2.090692985	K	S	-	2	9	2	0
				383	400	17	K	VTAQGPGLEPSGNIANK	T	0.81%	930	930	827.4350586	2	1652.854467	1651.852945	1.00152198	K	T	-	5	17	1	0
				684	700	16	K	TGVAVNKPAEFTVDAK	H	0.81%	2004	2004	824.4454956	2	1646.875341	1645.867533	1.007808579	K	H	-	4	16	1	0
				921	936	15	R	DVDIIDHHDNTYTVK	Y	4.21%	1992	1992	595.9498291	3	1784.826012	1783.837689	0.988323137	R	Y	-	2	15	1	0
				936	958	22	K	YTPVQQGPVGVNVTYGGDPIPK	S	0.81%	3988	3988	1143.596924	2	2285.178198	2285.169194	0.009003208	K	S	-	5	22	0	0
				982	994	12	K	VDVGKDQEFTVK	S	6.31%	919	919	455.5727234	3	1363.694695	1363.698342	-0.003646674	K	S	-	1	12	0	1
				1071	1087	16	K	AFGPGLQGGSAGSPAR	F	0.81%	1065	1065	715.8626099	2	1429.70957	1428.710972	0.998597567	K	F	-	4	16	1	0
				1234	1246	12	K	YGGQPVPNFPSK	L	1.93%	1857	1857	645.8267212	2	1289.637792	1289.640433	-0.002640457	K	L	-	4	12	0	0
				1296	1312	16	R	VANPSGNLTETYVQDR	G	0.81%	2248	2248	882.4360352	2	1762.85642	1762.848588	0.007832137	R	G	-	5	16	0	0
				1381	1399	18	R	GAGTGGLGLAVEGPSEAK	M	3.40%	2694	2694	785.9112549	2	1569.80686	1569.799847	0.007012814	R	M	-	4	18	0	0
				1464	1477	13	R	ANLPQSFQVDTSK	A	4.59%	2556	2556	718.3606567	2	1434.705663	1433.715054	0.990608941	R	A	-	2	13	1	0
				1477	1486	9	K	AGVAPLQVK	V	3.82%	920	920	441.7735901	2	881.5315301	881.5334482	-0.001918152	K	V	-	3	9	0	0
				1515	1532	17	R	EGPYSISVLYGDEEVPR	S	0.81%	4920	4920	955.4579468	2	1908.900243	1908.91052	-0.010276285	R	S	-	5	17	0	0
				1549	1573	24	K	ASGPGLNTTGVPASLPVEFTIDAK	D	0.81%	5859	5859	1172.119019	2	2342.222387	2341.216539	1.005848421	K	D	-	5	24	1	0
				1573	1592	19	K	DAGEGLLAVQITDPEGKPK	K	3.69%	4072	4072	647.3434448	3	1939.006859	1937.010568	1.996291097	K	K	-	1	19	2	0
				1621	1633	12	K	YGGDEIPFSPYR	V	0.81%	4062	4062	700.8284302	2	1399.64121	1399.640827	0.000383512	K	V	-	5	12	0	0
				1725	1753	28	R	FGGEHVPNSPFQVTALAGDQPSVQPPLR	S	1.96%	5300	5300	982.8337402	3	2945.477746	2944.483152	0.994593367	R	S	-	2	28	1	0
				1937	1951	14	K	YNEQHVPGSPFTAR	V	7.43%	1617	1617	535.2598267	3	1602.756005	1601.758651	0.997354212	K	V	-	1	14	1	0
				1964	1993	29	K	VGSAADIPINISETDLSLLTATVVPPSGR	E	0.81%	8251	8251	965.5209351	3	2893.53933	2892.544415	0.994914832	K	E	-	3	29	1	0
				2119	2133	14	K	FADQHVPGSPFSVK	V	0.81%	2833	2833	506.256897	3	1515.747216	1514.751774	0.995441494	K	V	-	3	14	1	0
				2310	2333	23	K	FNEEHIPDSPFVVPVASPSGDAR	R	0.81%	5081	5081	823.4032593	3	2467.186303	2467.16555	0.02075264	K	R	N2:+0.984	2	23	0	0
				2346	2367	21	K	VNQPASFAVSLNGAKGAIDAK	V	5.66%	4592	4592	1030.949341	2	2059.883032	2060.04255	-0.159518407	K	V	N2:+0.984,Q3:+0.984,N12	1	21	0	1
				2484	2500	16	R	VTYTPMAPGSYLISIK	Y	0.81%	5677	5677	871.4666138	2	1740.917577	1739.916792	1.000785363	R	Y	-	5	16	1	0
P21796	Voltage-dependent anion-selective channel protein 1	19	77.03%	20	28	8	K	GYGFGLIK	L	0.81%	3338	3338	427.7394104	2	853.4631707	853.4697853	-0.006614551	K	L	-	1	8	0	0
				32	53	21	K	TKSENGLEFTSSGSANTETTK	V	2.26%	805	805	730.6714478	3	2188.990868	2188.997147	-0.006279098	K	V	N5:+0.984	5	21	0	1
				34	53	19	K	SENGLEFTSSGSANTETTK	V	0.81%	1129	1129	980.4407959	2	1958.865942	1958.870506	-0.004563819	K	V	-	4	19	0	0
				63	74	11	R	WTEYGLTFTEK	W	0.81%	4050	4050	688.3335571	2	1374.651464	1373.650329	1.001135354	R	W	-	5	11	1	0
				74	93	19	K	WNTDNTLGTEITVEDQLAR	G	0.81%	4956	4956	726.3461914	3	2176.015099	2175.044388	0.970711371	K	G	-	2	19	1	0
				96	109	13	K	LTFDSSFSPNTGK	K	0.81%	2854	2854	701.3380737	2	1400.660497	1399.661956	0.998541181	K	K	-	5	13	1	0
				96	110	14	K	LTFDSSFSPNTGKK	N	0.81%	2319	2319	510.2576904	3	1527.749596	1527.756919	-0.007323167	K	N	-	1	14	0	1
				120	139	19	R	EHINLGCDMDFDIAGPSIR	G	0.81%	5222	5222	721.6786499	3	2162.012475	2158.977109	3.035365747	R	G	C7:+57.021	2	19	3	0
				139	161	22	R	GALVLGYEGWLAGYQMNFETAK	S	0.81%	7012	7012	812.0656128	3	2433.173363	2433.167566	0.005796931	R	S	M16:+15.995	3	22	0	0
				139	163	24	R	GALVLGYEGWLAGYQMNFETAKSR	V	5.52%	3908	3908	893.0809326	3	2676.219323	2677.283706	-1.064383236	R	V	Q15:+0.984,M16:+15.994	1	24	-1	1
				163	174	11	R	VTQSNFAVGYK	T	0.81%	1067	1067	607.3121948	2	1212.60874	1212.613884	-0.005144064	R	T	-	3	11	0	0
				174	197	23	K	TDEFQLHTNVNDGTEFGGSIYQK	V	0.81%	4001	4001	867.7340088	3	2600.178551	2599.182672	0.995878847	K	V	-	3	23	1	0
				200	218	18	K	KLETAVNLAWTAGNSNTR	F	0.81%	3415	3415	974.0082397	2	1946.000829	1945.001735	0.999094564	K	F	-	5	18	1	1
				201	218	17	K	LETAVNLAWTAGNSNTR	F	0.81%	4026	4026	910.4660645	2	1818.916479	1817.890772	1.025707114	K	F	N6:+0.984	3	17	1	0
				224	236	12	K	YQIDPDACFSAK	V	0.81%	3036	3036	708.3202515	2	1414.624853	1413.623	1.001853338	K	V	C8:+57.021	5	12	1	0
				236	252	16	K	VNNSSLIGLGYTQTLK	P	4.41%	4189	4189	854.9778442	2	1707.940038	1706.920296	1.019741917	K	P	-	1	16	1	0
				236	256	20	K	VNNSSLIGLGYTQTLKPGIK	L	0.81%	4101	4101	1052.092773	2	2102.169897	2102.173551	-0.003654605	K	L	-	3	20	0	0
				256	266	10	K	LTLSALLDGK	N	0.81%	4897	4897	515.8060303	2	1029.59641	1029.607007	-0.010596821	K	N	-	2	10	0	0
				256	274	18	K	LTLSALLDGKNVNAGGHK	L	0.81%	3576	3576	452.7547302	4	1806.987621	1806.995193	-0.007572094	K	L	-	1	18	0	1
P21926	CD9 antigen	4	9.65%	119	126	7	K	EVQEFYK	D	4.59%	849	849	471.7312927	2	941.4469354	941.4494438	-0.002508463	K	D	-	1	7	0	0
				119	131	12	K	EVQEFYKDTYNK	L	0.81%	1009	1009	782.373291	2	1562.730932	1562.725285	0.005647103	K	L	-	4	12	0	1
				169	179	10	K	KDVLETFTVK	S	0.81%	3335	3335	590.3340454	2	1178.652441	1178.654686	-0.002245116	K	S	-	5	10	0	1
				170	179	9	K	DVLETFTVK	S	0.81%	3900	3900	526.2861938	2	1050.556738	1050.559723	-0.002985105	K	S	-	5	9	0	0
P21964	Catechol O-methyltransferase	6	42.80%	58	86	28	R	ILNHVLQHAEPGNAQSVLEAIDTYCEQK	E	9.30%	5346	5346	795.3887939	4	3177.523876	3177.539597	-0.015721123	R	E	N13:+0.984,C25:+57.021	1	28	0	0
				98	125	27	K	IVDAVIQEHQPSVLLELGAYCGYSAVR	M	3.70%	6170	6170	997.1775513	3	2988.509179	2986.521777	1.987401417	K	M	C21:+57.021	3	27	2	0
				135	151	16	R	LITIEINPDCAAITQR	M	0.81%	4750	4750	914.4819946	2	1826.948339	1826.955567	-0.00722831	R	M	C10:+57.021	5	16	0	0
				151	159	8	R	MVDFAGVK	D	0.81%	2016	2016	433.7244873	2	865.4333245	865.4367717	-0.003447183	R	D	-	4	8	0	0
				196	211	15	R	YLPDTLLLEECGLLR	K	0.81%	6717	6717	902.9775391	2	1803.939428	1803.943606	-0.004177739	R	K	C11:+57.021	5	15	0	0
				212	234	22	K	GTVLLADNVICPGAPDFLAHVR	G	0.81%	6068	6068	779.4091797	3	2335.204064	2334.21497	0.989093518	K	G	C11:+57.021	5	22	1	0
P22732	Solute carrier family 2, facilitated glucose transporter member 5	1	2.20%	466	477	11	K	TFIEINQIFTK	M	0.81%	5730	5730	677.3742065	2	1352.732763	1352.733999	-0.001235906	K	M	-	5	11	0	0
P22888	Lutropin-choriogonadotropic hormone receptor	1	2.29%	563	579	16	K	DTKIAKKMAILIFTDF	T	9.01%	8118	8118	930.2904663	2	1858.565283	1855.032491	3.532791865	K	T	K6:+1.000	1	16	4	3
P22897	Macrophage mannose receptor 1	11	10.99%	59	72	13	R	WVSESQIMSVAFK	L	0.81%	5912	5912	756.3833618	2	1510.751074	1510.748998	0.002075305	R	L	-	4	13	0	0
				299	314	15	R	YLNWLPGSPSAEPGK	S	0.81%	4714	4714	808.9152222	2	1615.814794	1614.804204	1.010590352	R	S	-	4	15	1	0
				491	502	11	R	SQGPEIVEVEK	G	3.04%	1110	1110	608.3185425	2	1214.621435	1213.619029	1.002406217	R	G	-	4	11	1	0
				561	573	12	K	YFWTGLSDIQTK	G	0.81%	5526	5526	730.3668213	2	1458.717993	1457.719077	0.998915338	K	G	-	5	12	1	0
				604	616	12	R	TGIAGGLWDVLK	C	0.81%	6399	6399	615.3478394	2	1228.680029	1228.681569	-0.001540681	R	C	-	3	12	0	0
				681	701	20	R	ALGGDLASINNKEEQQTIWR	L	0.81%	4184	4184	748.385498	3	2242.133019	2243.118206	-0.985186811	R	L	N11:+0.984	3	20	-1	1
				808	816	8	K	DYQYYFSK	E	8.14%	2900	2900	558.2996826	2	1114.583715	1112.481472	2.102242834	K	E	-	2	8	2	0
				830	845	15	R	NFGDLVSIQSESEKK	F	0.81%	3354	3354	840.9226074	2	1679.829565	1679.836626	-0.007061628	R	F	-	4	15	0	1
				1001	1026	25	K	DSTFSAWTGLNDVNSEHTFLWTDGR	G	0.81%	6769	6769	953.4336548	3	2857.277489	2856.262698	1.014791043	K	G	N14:+0.984	4	25	1	0
				1265	1285	20	R	MGSSLVSIESAAESSFLSYR	V	0.81%	7200	7200	1061.514038	2	2121.012426	2120.009583	1.002842908	R	V	-	5	20	1	0
				1292	1301	9	K	TNFWIGLFR	N	0.81%	7342	7342	577.3113403	2	1152.607031	1152.60801	-0.000979688	K	N	-	5	9	0	0
P23276	Kell blood group glycoprotein	2	4.51%	267	281	14	K	VQEHSSLSISITSR	L	3.66%	3509	3509	772.9049683	2	1543.794286	1543.784181	0.010105243	K	L	Q2:+0.984	2	14	0	0
				358	377	19	R	DFLQSHMILGLVVTLSPAL	D	9.04%	8623	8623	685.7181396	3	2054.130944	2053.128182	1.002761689	R	D	-	1	19	1	0
P23634	Plasma membrane calcium-transporting ATPase 4	2	2.66%	59	75	16	K	TSPVEGLSGNPADLEK	R	0.81%	2921	2921	807.40271	2	1612.78977	1612.794427	-0.004657342	K	R	-	5	16	0	0
				811	828	17	K	EASDIILTDDNFTSIVK	A	0.81%	5462	5462	940.9865112	2	1879.957372	1879.941486	0.015886789	K	A	-	4	17	0	0

P24666	Low molecular weight phosphotyrosine protein phosphatase	3	20.25%	19	28	9	R	SPIAEAVFR	K	0.81%	3117	3117	495.2702026	2	988.5247552	988.5341766	-0.009421383	R	K	-	5	9	0	0
				29	41	12	K	LVTDQNISENWR	V	0.81%	2915	2915	738.3652344	2	1474.714819	1473.721202	0.993616198	K	V	-	4	12	1	0
				113	124	11	K	IELLGSYDPQK	Q	1.93%	3516	3516	632.8272705	2	1263.638891	1261.655414	1.983476752	K	Q	-	5	11	2	0
P25054	Adenomatous polyposis coli protein	1	0.32%	2228	2237	9	R	TMIHIPGVR	N	8.84%	4651	4651	513.2677002	2	1024.51975	1022.569517	1.950232959	R	N	-	2	9	2	0
P25705	ATP synthase subunit alpha, mitochondrial	28	55.15%	45	58	13	K	TGTAEMSSILEER	I	0.81%	3345	3345	712.3375244	2	1422.659399	1422.666056	-0.00665774	K	I	-	5	13	0	0
				58	73	15	R	ILGADTSVDLEETGR	V	0.81%	3086	3086	788.3945923	2	1574.773534	1574.778777	-0.005242614	R	V	-	5	15	0	0
				73	83	10	R	VLSIGDGIAR	V	0.81%	2285	2285	500.791626	2	999.5676019	999.5712904	-0.003688551	R	V	-	5	10	0	0
				88	103	15	R	NVQAEEMVEFSSGLK	G	0.81%	4355	4355	834.3960571	2	1666.776464	1666.787234	-0.010770246	R	G	-	5	15	0	0
				103	123	20	K	GMSLNLEPDNVGVVVFGNDK	L	0.81%	6093	6093	1055.04	2	2108.06435	2103.030653	5.033696968	K	L	-	1	20	5	0
				103	126	23	K	GMSLNLEPDNVGVVVFGNDKLIK	E	6.15%	6408	6408	820.4381104	3	2458.290856	2457.293744	0.997111671	K	E	-	1	23	1	1
				133	149	16	R	TGAIVDVPVGEELLGR	V	0.81%	5479	5479	812.9498291	2	1623.884008	1623.883183	0.000825491	R	V	-	5	16	0	0
				149	161	12	R	VVDALGNAIDGK	G	0.81%	1978	1978	586.317749	2	1170.619848	1170.624448	-0.004600385	R	G	-	5	12	0	0
				149	167	18	R	VVDALGNAIDGKGPIGSK	T	0.81%	2838	2838	570.9841309	3	1709.928917	1709.931196	-0.00227807	R	T	-	2	18	0	1
				194	204	10	K	AVDSLVPIGR	G	0.81%	2756	2756	513.7994385	2	1025.583227	1025.586941	-0.003713631	K	G	-	5	10	0	0
				207	214	7	R	ELIIGDR	Q	0.81%	1229	1229	408.2341003	2	814.4525506	814.4548635	-0.002312916	R	Q	-	2	7	0	0
				218	230	12	K	TSIAIDTIINQK	R	0.81%	3777	3777	658.8759766	2	1315.736303	1315.734727	0.001575805	K	R	-	5	12	0	0
				253	261	8	R	STVAQLVK	R	1.93%	917	917	423.2578125	2	844.4999749	844.5018138	-0.00183884	R	R	-	4	8	0	0
				305	316	11	K	HALIIYDDLSK	Q	0.81%	3042	3042	644.3495483	2	1286.683447	1286.687049	-0.003602072	K	Q	-	5	11	0	0
				316	329	13	K	QAVAYRQMSLLLR	R	4.94%	2530	2530	517.581665	3	1549.72152	1547.860614	1.860905549	K	R	-	1	13	2	1
				322	329	7	R	QMSLLLR	R	2.26%	3063	3063	430.7540894	2	859.4925286	859.4949553	-0.002426697	R	R	-	5	7	0	0
				334	347	13	R	EAYPGDVFYLHSR	L	0.81%	3494	3494	777.3710327	2	1552.726415	1552.731039	-0.004623514	R	L	-	5	13	0	0
				390	402	12	D	GQIFLETELFYK	G	3.49%	6099	6099	744.8963013	2	1487.776952	1486.770778	1.006174027	D	G	-	1	12	1	0
				402	416	14	K	GIRPAINVGLSVSR	V	0.81%	2918	2918	719.925293	2	1437.834936	1437.841592	-0.00665655	K	V	-	5	14	0	0
				405	416	11	R	PAINVGLSVSR	V	3.94%	2458	2458	558.2979126	2	1114.580175	1111.634953	2.945221715	R	V	-	1	11	3	0
				434	441	7	K	LELAQYR	E	0.81%	1078	1078	446.7465515	2	891.4774529	891.4814126	-0.003959701	K	E	-	5	7	0	0
				441	463	22	R	EVAAFAQFGSDLDAATQQLLSR	G	0.81%	8421	8421	1170.085205	2	2338.15476	2337.160086	0.994673772	R	G	-	4	22	1	0
				472	493	21	K	QGQYSPMAIEEQVAVIYAGVR	G	0.81%	6747	6747	1163.585571	2	2325.155493	2324.147165	1.008327282	K	G	M7:+15.995	1	21	1	0
				479	493	14	M	AIEEQVAVIYAGVR	G	6.13%	4518	4518	761.1685181	2	1520.321386	1516.824939	3.496446709	M	G	-	1	14	3	0
				493	503	10	R	GYLDKLEPSK	I	0.81%	1501	1501	575.3100586	2	1148.604467	1148.607736	-0.003268508	R	I	-	4	10	0	1
				506	527	21	K	FENAFLSHVVSQHQALLGTIR	A	0.81%	5602	5602	1184.634033	2	2367.252416	2367.23351	0.018905918	K	A	N3:+0.984	3	21	0	0
				539	553	14	K	LKEIVTNFLAGFEA	-	0.81%	7248	7248	776.9317017	2	1551.847753	1550.834441	1.013311832	K	-	-	5	14	1	1
				541	553	12	K	EIVTNFLAGFEA	-	0.81%	7438	7438	655.8356934	2	1309.655737	1309.655414	0.000322455	K	-	-	2	12	0	0
P26010	Integrin beta-7	13	26.57%	24	35	11	K	IPSTGDATEWR	N	0.81%	1138	1138	616.795166	2	1231.574682	1231.583312	-0.008629849	K	N	-	5	11	0	0
				100	116	16	R	GQQEVLQDQPLSQGAR	G	0.81%	1099	1099	877.4435425	2	1752.871435	1752.875472	-0.004036671	R	G	-	4	16	0	0
				129	143	14	R	VTLRPGEPQQLQVR	F	0.81%	1063	1063	540.9754639	3	1619.902916	1619.910735	-0.007818262	R	F	-	5	14	0	0
				190	199	9	R	IGFGSFVDK	T	0.81%	3643	3643	485.2541504	2	968.4926507	968.4967284	-0.004077699	R	T	-	3	9	0	0
				199	211	12	K	TVLPFVSTVPSK	L	0.81%	4029	4029	637.8684082	2	1273.721166	1273.728185	-0.007018898	K	L	-	5	12	0	0
				248	278	30	R	QSVSGNLDSPEGGFDAILQAALCQEQIGWR	N	3.65%	8752	8752	1083.528931	3	3247.563317	3246.524675	1.03864188	R	N	Q19:+0.984,C23:+57.021	4	30	1	0
				282	299	17	R	LLVFTSDDTFHTAGDGK	L	0.81%	4059	4059	608.6314087	3	1822.870751	1822.87374	-0.002989286	R	L	-	1	17	0	0
				321	361	40	R	STEFDYPSVGQVAQALSAANIQPIFAVTSAALPVYQELSK	L	2.88%	9908	9908	1054.042114	4	4212.137157	4211.131405	1.005752343	R	L	Q22:+0.984	2	40	1	0
				691	707	16	R	TLDNQLFFFLVEDDAR	G	0.81%	8024	8024	972.4777222	2	1942.939794	1941.94724	0.992554648	R	G	-	2	16	1	0
				719	747	28	K	GADHTQAIVLGCVGGIVAVGLGLVLAYR	L	8.93%	10469	10469	927.4786377	3	2779.412438	2778.520989	0.891448694	K	L	C12:+57.021	2	28	1	0
				747	755	8	R	LSVEIYDR	R	2.59%	2518	2518	497.7605896	2	993.5055291	993.5131068	-0.007577689	R	R	-	5	8	0	0
				747	756	9	R	LSVEIYDRR	E	3.91%	1647	1647	575.81	2	1149.60435	1149.614218	-0.00986804	R	E	-	3	9	0	1
				779	789	10	K	SAITTTINPR	F	1.97%	867	867	537.300354	2	1072.585058	1072.587669	-0.002610904	K	F	-	5	10	0	0
P26012	Integrin beta-8	1	1.95%	295	310	15	K	LAGIVVPNDGNCHLK	N	4.59%	3991	3991	536.2828369	3	1605.825036	1605.829245	-0.004208898	K	N	C12:+57.021	2	15	0	0
P27105	Erythrocyte band 7 integral membrane protein	9	48.61%	77	93	16	K	GPGLFFILPCTDSFIK	V	0.81%	7851	7851	907.4725342	2	1812.929418	1810.932313	1.997105543	K	V	C10:+57.021	5	16	2	0
				125	144	19	R	VQNATLAVANITNADSATR	L	0.81%	3335	3335	965.4974976	2	1928.979345	1928.991564	-0.012219091	R	L	-	5	19	0	0
				144	152	8	R	LLAQTTLR	N	0.81%	859	859	458.2843323	2	914.5530145	914.554912	-0.001897545	F	N	-	5	8	0	0
				158	188	30	K	NLSQILSDREEIAHNMQSTLDDATDAWGIK	V	5.58%	7421	7421	843.9030151	4	3371.58076	3371.593947	-0.013186381	K	V	Q17:+0.984	2	30	0	1
				198	205	7	K	LPVQLQR	A	3.83%	918	918	427.2651062	2	852.5145623	852.5181325	-0.003570174	K	A	-	3	7	0	0
				220	232	12	K	VIAAEGEMNASR	A	0.81%	751	751	625.3062744	2	1248.596899	1246.597583	1.99931594	K	A	-	2	12	2	0
				235	251	16	K	EASMVITESPAALQLR	Y	0.81%	4468	4468	858.4512329	2	1714.886816	1714.892368	-0.00555254	K	Y	-	5	16	0	0
				251	263	12	R	YLQTLTTIAAEK	N	0.81%	3319	3319	676.3751221	2	1350.734594	1350.739478	-0.004884211	R	N	-	5	12	0	0
				263	283	20	K	NSTIVFPLPIDMLQGIIGAK	H	0.81%	9292	9292	1064.601929	2	2127.188207	2126.180946	1.007261278	K	H	-	4	20	1	0
P27797	Calreticulin	5	16.07%	24	36	12	K	EQFLDGDGWTSR	W	0.81%	3638	3638	705.8136597	2	1409.611669	1409.621154	-0.00948472	K	W	-	5	12	0	0
				73	87	14	R	FYALSASFEPFSNK	G	0.81%	5649	5649	804.3892822	2	1606.762914	1606.766756	-0.003841355	R	G	-	4	14	0	0
				87	98	11	K	GQTLVVQFTVK	H	5.40%	3787	3787	611.8147583	2	1221.613867	1218.697219	2.91664713	K	H	-	1	11	3	0
				143	151	8	K	VHVIFNYK	G	5.70%	2018	2018	510.2592773	2	1018.502905	1018.559997	-0.057092769	K	G	-	1	8	0	0
				185	207	22	K	IDNSQVESGSLEDDWDFLPPKK	I	4.90%	4982	4982	840.7381592	3	2519.191002	2518.186361	1.004641643	K	I	-	1	22	1	1
P27815	cAMP-specific 3',5'-cyclic phosphodiesterase 4A	1	1.13%	10	20	10	R	SLSLSLPGPR	E	5.30%	2541	2541	513.7984619	2	1025.581274	1025.586941	-0.005666756	R	E	-	1	10	0	0
P28290	Sperm-specific antigen 2	1	1.51%	947	966	19	K	SSVLPLYENTFQELQVMRR	S	9.61%	4963	4963	771.7330322	3	2312.175622	2311.1518	1.023821856	K	S	N9:+0.984,Q15:+0.984	2	19	1	1
P28827	Receptor-type tyrosine-protein phosphatase mu	1	1.17%	1422	1439	17	K	TLRNNKPNMVDLLDQYK	F	4.39%	2203	2203	688.3601074	3	2062.056847	2062.051707	0.005140018	K	F	Q15:+0.984	2	17	0	1
P28907	ADP-ribosyl cyclase 1	3	12.33%	47	58	11	R	QQWSGPGTTKR	F	5.27%	4228	4228	416.17	3	1245.486525	1245.61018	-0.123654784	R	F	Q1:+0.984	1	11	0	1
				127	140	13	R	IKDLAHQFTQVQR	D	4.79%	1553	1553	529.6182251	3	1585.8312	1582.857971	2.973229357	R	D	-	1	13	3	1
				234	247	13	K	VQTLEAWVIHGGR	E	0.81%	4639	4639	489.6018982	3	1465.782219	1464.783743	0.99847634	K	E	-	5	13	1	0
P29475	Nitric oxide synthase, brain	1	1.53%	870	892	22	R	DNFESAGPLANVRFSVFGLGSR	A	6.07%	8116	8116	781.3918457	3	2341.152062	2340.14984	1.002221669	R	A	N11:+0.984	1	22	1	1
P30464	HLA class I histocompatibility antigen, B-15 alpha chain	14	53.31%	30	38	8	R	YFYTAMSR	P	3.79%	2135	2135	519.7374268	2	1037.459203	1037.464049	-0.004845732	R	P	-	1	8	0	0
				45	59	14	R	FIAVGYVDDTQFVR	F	0.81%	4994	4994	815.911377	2	1629.807104	1628.819854	0.987249842	R	F	-	5	14	1	0
				72	86	14	R	APWIEQEGPEYWDR	E	0.81%	4756	4756	888.4016113	2	1774.787573	1774.795096	-0.007523264	R	N	-	5	14	0	0
				72	92	20	R	APWIEQEGPEYWDRETQISK	T	1.93%	4715	4715	821.7252197	3	2462.152184	2461.155001	0.997183116	R	T	-	2	20	1	1
				121	132	11	R	MYGCDVGPDGR	L	0.81%	721	721	613.7477417	2	1225.479833	1225.485127	-0.005293434	R	L	C4:+57.021	5	11	0	0
				135	169	34	R	GHDQSAYDGKDYIALNEDLSSWTAADTAAQITQR	K	4.10%	5794	5794	929.18	4	3712.6887	3711.692474	0.99622588	R	K	N16:+0.984	1	34	1	1
				155	169	14	S	SWTAADTAAQITQR	K	0.81%	3048	3048	760.3759155	2	1518.736181	1518.742666	-0.006485265	R	K	-	4	14	0	0
				181	193	12	R	AYLEGLCVEWLR	R	0.81%	6409	6409	754.8795166	2	1507.743383	1507.748869	-0.005485685	R	R	C7:+57.021	5	12	0	0
				194	205	11	R	YLENGKETLQR	A	0.81%	674	674	676.3446655	2	1350.673681	1350.677925	-0.004244041	R	A	N4:+0.984	5	11	0	1
				210	226	16	K	THVTHHPISDHEATLR	C	3.44%	605	605	463.4850159	4	1849.908763	1849.918339	-0.009576099	K	C	-	3	16	0	0
				226	243	17	R	CWALGFYPAEITLTWQR	D	0.81%	7963	7963	1057.524414	2	2113.033178	2112.013401	1.019776861	R	D	C1:+57.021,Q16:+0.984	3	17	1	0
				243	263	20	R	DGEDQTQDTELVETRPAGDR	T	1.93%	758	758	744.6696167	3	2230.985375	2230.993809	-0.008433806	R	T	-	2	20	0	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.81%	2533	2533	714.3683472	2	1426.721044	1426.720474	0.000570112	K	Y	-	4	13	0	0
				280	297	17	R	YTCHVQHEGLPKPLTLR	W	0.81%	2076	2076	1025.535522	2	2049.055395	2048.062098	0.993296514	R	W	C3:+57.021	4	17	1	0
P30511	HLA class I histocompatibility antigen, alpha chain F	4	15.03%	89	100	11	K	ANAQTDRVALR	N	5.04%	1251	1251	405.8804321	3	1214.617821	1214.636729	-0.018907525	K	N	Q4:+0.984	3	11	0	1
				191	202	11	R	YLENGKETLQR	A	0.81%	674	674	676.3446655	2	1350.673681	1350.677925	-0.004244041	R	A	N4:+0.984	5	11	0	1
				223	240	17	R	CWALGFYPAEITLTWQR	D	0.81%	7963	7963	1057.524414	2	2113.033178	2112.013401	1.019776861	R	D	C1:+57.021,Q16:+0.984	3	17	1	0
				264	277	13	K	WAAVVVPSGEEQR	Y	0.81%	2533	2533	714.3683472	2	1426.721044	1426.720474	0.000570112	K	Y	-	4	13	0	0
P30825	High affinity cationic amino acid transporter 1	3	6.36%	130	149	19	R	AWSATFDELIGRPIGEFSR	T	0.81%	6847	6847	718.3640137	3	2152.068566	2151.0749	0.993666008	R	T	-	4	19	1	0
				360	373	13	R	VIYAMAEDGLLFK	F	0.81%	5756	5756	735.388916	2	1468.762182	1468.763586	-0.001403721	R	C	-	5	13	0	0
				373	381	8	K	FLANVNDR	T	3.08%	805	805	474.7481079	2	947.4805657	947.4824753	-0.001909564	K	T	-	2	8	0	0
P31146	Coronin-1A	10	28.42%	29	45	16	R	VSQTTWDSGFCAVNPK	F	0.81%	3671	3671	899.4190063	2	1796.822363	1795.819468	1.002894815	R	F	C11:+57.021	4	16	1	0
				233	241	8	K	ILTTGFSR	M	0.81%	1001	1001	447.7544556	2	893.4932611	893.4970627	-0.003801675	K	M	-	5	8	0	0
				276	287	11	D	PDTNIVYLCGK	G	3.76%	2482	2482	640.3164673	2	1278.617284	1278.627357	-0.010072054	D	G	C9:+57.021	1	11	0	0
				293	313	20	R	YFEITSEAPFLHYLSMFSSK	E	0.81%	7883	7883	800.0405884	3	2397.09829	2396.139869	0.958420833	R	E	-	5	20	1	0
				344	354	10	R	CEPIAMTVPR	K	4.05%	2303	2303	588.3115234	2	1174.607397	1172.567734	2.039662611	R	K	C1:+57.021	2	10	2	0
				354	383	29	R	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	D	0.81%	7147	7147	1059.18103	3	3174.519616	3173.519307	1.00030854	R	D	Q6:+0.984	3	29	1	1
				383	393	10	R	DAGPLLISLK	D	1.96%	4418	4418	513.8134155	2	1025.611181	1025.612093	-0.000911673	R	D	-	5	10	0	0
				416	432	16	R	AAPEASGTPSSDAVSR	L	0.81%	646	646	752.8831177	2	1503.750585	1501.700861	2.04972424	R	L	-	2	16	2	0
				438	449	11	R	KLQATVQELQK	R	0.81%	669	669	643.3748779	2	1284.734106	1284.740147	-0.006041149	R	R	-	5	11	0	1
				439	449	10	K	LQATVQELQK	R	0.81%	947	947	579.3251343	2	1156.634618	1156.645184	-0.010565317	K	R	-	5	10	0	0
P32241	Vasoactive intestinal polypeptide receptor 1	1	1.75%	91	99	8	K	LFSSIQGR	N	6.26%	4478	4478	454.2526245	2	906.4895989	906.4923117	-0.002712753	K	N	-	1	8	0	0
P32246	C-C chemokine receptor type 1	2	7.32%	326	335	9	K	WLPFLSVDR	L	0.81%	6251	6251	566.8099976	2	1131.604345	1131.607676	-0.003330907	K	L	-	4	9	0	0
				338	355	17	R	VSSTSPSTGEHELSAGF	-	2.46%	2736	2736	846.8913574	2	1691.767065	1691.763855	0.003209412	R	-	-	5	17	0	0
P32942	Intercellular adhesion molecule 3	6	11.15%	62	71	9	K	IALETSLSK	E	0.81%	1265	1265	481.2814331	2	960.5472161	960.549158	-0.001941869	K	E	-	2	9	0	0
				147	156	9	R	TSLTVVLLR	W	0.81%	4432	4432	501.3201294	2	1000.624609	1000.628077	-0.003468347	R	W	-	3	9	0	0
				156	163	7	R	WEEELSR	Q	3.02%	831	831	475.2266846	2	948.4377191	947.4348564	1.002862653	R	Q	-	3	7	1	0
				163	181	18	R	QPAVEEPAEVTATVLASR	D	0.81%	4582	4582	934.9868774	2	1867.958105	1866.968703	0.989401427	R	D	-	3	18	1	0
				214	224	10	R	TFVLPVTPPR	L	0.81%	4212	4212	563.83	2	1125.64435	1125.654626	-0.010276264	R	L	-	4	10	0	0
				426	434	8	R	GNPYPELR	C	6.11%	1045	1045	473.2410584	2	944.4664666	944.4715763	-0.005109637	R	C	-	1	8	0	0
P33241	Lymphocyte-specific protein 1	1	5.01%	226	243	17	K	IDQWLEQYTQAIETAGR	T	0.81%	6244	6244	1011.997498	2	2021.979345	2020.985416	0.993928925	K	T	-	5	17	1	0
P34910	Protein EVI2B	2	6.25%	266	279	13	R	TSIISLTPWKPSK	S	0.81%	4488	4488	729.4262695	2	1456.836889	1456.828962	0.007926935	R	S	-	5	13	0	0
				290	305	15	K	LFESSENIEDSNNPK	T	0.81%	1451	1451	861.8931274	2	1721.770605	1721.77442	-0.003815269	K	T	-	4	15	0	0
P35232	Prohibitin	19	67.65%	4	35	31	K	VFESIGKFGLALAVAGGVVNSALYNVDAGHR	A	0.81%	8457	8457	783.9209595	4	3131.652538	3131.640366	0.012171979	K	A	N20:+0.984	3	31	0	1
				11	35	24	K	FGLALAVAGGVVNSALYNVDAGHR	A	0.81%	7353	7353	791.4213867	3	2371.240685	2371.228425	0.012259988	K	A	N13:+0.984	3	24	0	0
				43	63	20	R	GVQDIVVGEGTHFLIPWVQK	P	4.41%	6765	6765	741.7375488	3	2222.189171	2221.189536	0.999635556	R	P	-	1	20	1	0
				43	70	27	R	GVQDIVVGEGTHFLIPWVQKPIIFDCR	S	2.26%	7608	7608	781.6655884	4	3122.631053	3123.621082	-0.990028492	R	S	Q19:+0.984,C26:+57.021	2	27	-1	0
				83	93	10	K	DLQNVNITLR	I	0.81%	2890	2890	593.3300171	2	1184.644384	1184.651332	-0.006947708	K	I	-	5	10	0	0
				93	105	12	R	ILFRPVASQLPR	I	0.81%	3110	3110	466.2850342	3	1395.831627	1395.83505	-0.003422973	R	I	-	1	12	0	0
				95	105	10	L	FRPVASQLPR	I	5.17%	3277	3277	585.8399658	2	1169.664282	1169.666922	-0.002640655	L	I	-	1	10	0	0
				105	117	12	R	IFTSIGEDYDER	V	0.81%	2703	2703	722.8311157	2	1443.646581	1443.651785	-0.005204115	R	V	-	5	12	0	0
				105	128	23	R	IFTSIGEDYDERVLPSITTEILK	S	0.81%	6692	6692	881.1318359	3	2640.372033	2638.374162	1.997870957	R	S	-	4	23	2	1
				117	128	11	R	VLPSITTEILK	S	0.81%	4867	4867	607.37146	2	1212.72727	1212.732936	-0.005666414	R	S	-	5	11	0	0
				119	128	9	L	PSITTEILK	S	4.06%	4783	4783	501.2966919	2	1000.577734	1000.580458	-0.002724451	L	S	-	1	9	0	0
				133	143	10	R	FDAGELITQR	E	0.81%	3485	3485	575.2958374	2	1148.576025	1148.582583	-0.006558747	R	E	-	5	10	0	0
				157	177	20	R	AATFGLILDDVSLTHLTFGK	E	0.81%	7142	7142	707.0482788	3	2118.121361	2118.136103	-0.014741918	R	E	-	4	20	0	0
				166	177	11	D	DVSLTHLTFGK	E	3.60%	3791	3791	609.3292847	2	1216.642919	1216.645184	-0.002264536	D	E	-	1	11	0	0
				167	177	10	D	VSLTHLTFGK	E	6.36%	3219	3219	552.3126831	2	1102.609716	1101.618241	0.991475467	D	E	-	1	10	1	0
				219	239	20	K	AAELIANSLATAGDGLIELR	K	0.81%	6454	6454	1000.548889	2	1999.082128	1997.079317	2.002811648	K	K	-	2	20	2	0
				226	239	13	N	SLATAGDGLIELR	K	3.87%	4225	4225	658.3603516	2	1314.705053	1314.714326	-0.009273083	N	K	-	1	13	0	0
				239	253	14	R	KLEAAEDIAYQLSR	S	0.81%	4058	4058	804.4257202	2	1606.83579	1605.836232	0.999557958	R	S	-	5	14	1	1
				255	272	17	R	NITYLPAGQSVLLQLPQ	-	0.81%	6510	6510	928.5184937	2	1855.021337	1854.025096	0.996241217	R	-	-	4	17	1	0
P35579	Myosin-9	88	45.97%	8	29	21	K	YLYVDKNFINNPLAQADWAAK	K	0.81%	6047	6047	819.4195557	3	2455.235192	2454.221943	1.013249168	K	K	Q15:+0.984	3	21	1	1
				14	29	15	K	NFINNPLAQADWAAK	K	0.81%	5138	5138	836.9241943	2	1671.832739	1671.836901	-0.004162456	K	K	-	5	15	0	0
				29	38	9	K	KLVWVPSDK	S	0.81%	1485	1485	536.3112183	2	1070.606786	1070.612427	-0.005640533	K	S	-	4	9	0	1
				30	38	8	K	LVWVPSDK	S	4.65%	2288	2288	473.283783	2	944.5519158	942.5174638	2.034451998	K	S	-	2	8	2	0
				38	63	25	K	SGFEPASLKEEVGEEAIVELVENGK	K	4.46%	6739	6739	888.1136475	3	2661.317467	2659.322854	1.994612799	K	K	-	3	25	2	1
				38	64	26	K	SGFEPASLKEEVGEEAIVELVENGKK	V	4.83%	6133	6133	930.4744263	3	2788.399804	2787.417818	0.981986089	K	V	-	1	26	1	2
				125	139	14	K	NLPIYSEEIVEMYK	G	0.81%	5683	5683	864.4312134	2	1726.846777	1726.848772	-0.00199541	K	G	-	5	14	0	0
				143	159	16	R	HEMPPHIYAITDTAYR	S	0.81%	2684	2684	638.9754639	3	1913.902916	1913.909415	-0.006498862	R	S	-	4	16	0	0
				185	199	14	K	KVIQYLAYVASSHK	S	0.81%	3518	3518	536.3001099	3	1605.876854	1605.887874	-0.011019522	K	S	-	5	14	0	1
				186	199	13	K	VIQYLAYVASSHK	S	0.81%	3506	3506	493.6034241	3	1477.786797	1477.792911	-0.006113759	K	S	-	3	13	0	0
				209	225	16	R	QLLQANPILEAFGNAK	T	0.81%	6514	6514	576.3218384	3	1725.94204	1726.925366	-0.983326231	R	T	Q1:+0.984	2	16	-1	0
				272	289	17	R	TFHIFYYLLSGAGEHLK	T	0.81%	6744	6744	499.7619324	4	1995.016429	1995.02543	-0.009001004	R	T	-	4	17	0	0
				289	299	10	K	TDLLLEPYNK	Y	0.81%	3288	3288	603.3221436	2	1204.628637	1204.63395	-0.005313387	K	Y	-	5	10	0	0

				301	327	26	R	FLSNGHVTIPGQQDKDMFQETMEAMR	I	1.93%	5555	5555	753.8477783	4	3011.359813	3011.346298	0.013515273	R	I	N4:+0.984,Q19:+0.984	1	26	0	1
				316	341	25	K	DMFQETMEAMRIMGIPEEEQMGLLR	V	5.25%	5832	5832	1007.131897	3	3018.372216	3017.32943	1.042785814	K	V	M2:+15.994,Q4:+0.984,M	1	25	1	1
				327	341	14	R	IMGIPEEEQMGLLR	V	0.81%	5080	5080	808.4168091	2	1614.817968	1614.810948	0.00702026	R	V	-	2	14	0	0
				341	355	14	R	VISGVLQLGNIVFK	K	0.81%	6792	6792	743.9518433	2	1485.888036	1485.891897	-0.003860253	R	K	-	5	14	0	0
				341	356	15	R	VISGVLQLGNIVFKK	E	0.81%	6218	6218	808.4967651	2	1614.97788	1613.98686	0.991020361	R	E	-	3	15	1	1
				373	387	14	K	VSHLLGINVTDFTR	G	0.81%	4779	4779	786.4279175	2	1570.840185	1570.846737	-0.006552559	K	G	-	5	14	0	0
				407	419	12	K	EQADFAIEALAK	A	3.15%	4364	4364	653.336792	2	1304.657934	1304.661228	-0.003293968	K	A	-	3	12	0	0
				475	494	19	K	LQQLFNHTMFILEQEEYQR	E	0.81%	5887	5887	1235.109375	2	2468.2031	2466.200178	2.002921808	K	E	-	2	19	2	0
				563	576	13	K	DKADFCIIHYAGK	V	3.21%	2494	2494	513.253479	3	1536.736962	1536.739032	-0.002070524	K	V	C6:+57.021	1	13	0	1
				565	576	11	K	ADFCIIHYAGK	V	3.21%	3021	3021	647.8163452	2	1293.61704	1293.617126	-8.58023E-05	K	V	C4:+57.021	3	11	0	0
				576	587	11	K	VDYKADEWLMK	N	2.26%	3352	3352	699.8419189	2	1397.668188	1396.669685	0.998502619	K	N	-	4	11	1	1
				580	587	7	K	ADEWLMK	N	3.19%	2619	2619	446.7153931	2	891.4151361	891.4160363	-0.000900219	K	N	-	3	7	0	0
				587	613	26	K	NMDPLNDNIATLLHQSSDKFVSELWK	D	4.17%	7931	7931	758.8792114	4	3031.485546	3030.47577	1.009775383	K	D	M2:+15.995	1	26	1	1
				606	613	7	K	FVSELWK	D	0.81%	3402	3402	455.2478333	2	908.4800164	907.48035	0.999666432	K	D	-	2	7	1	0
				617	637	20	R	IIGLDQVAGMSETALPGAFK	T	0.81%	6480	6480	1009.532043	2	2017.048437	2017.055411	-0.006974262	R	T	-	5	20	0	0
				644	656	12	R	TVGQLYKEQLAK	L	0.81%	883	883	689.3895874	2	1376.763525	1376.766362	-0.002837003	R	L	-	5	12	0	1
				682	693	11	K	LDPHLVLDQLR	C	0.81%	4447	4447	660.373291	2	1318.730932	1317.740481	0.990450695	K	C	-	3	11	1	0
				686	693	7	H	LVLDQLR	C	4.62%	2871	2871	428.7654419	2	855.5152337	855.5177982	-0.002564459	R	C	-	1	7	0	0
				711	718	7	R	VVFQEFR	Q	0.81%	2467	2467	463.2526855	2	924.489721	923.486498	1.003223006	R	Q	-	5	7	1	0
				718	731	13	R	QRYEILTPNSIPK	G	0.81%	3185	3185	780.4313354	2	1558.847021	1557.851488	0.995532346	R	G	-	3	13	1	1
				720	731	11	R	YEILTPNSIPK	G	0.81%	3714	3714	637.8529663	2	1273.690283	1273.6918	-0.001517167	R	G	-	5	11	0	0
				745	755	10	K	ALELDSNLYR	I	0.81%	3202	3202	597.3027954	2	1192.589941	1192.608798	-0.018857532	K	I	-	2	10	0	0
				764	775	11	R	AGVLAHLEEER	D	0.81%	1639	1639	612.3220825	2	1222.628515	1222.630596	-0.002081409	R	D	-	5	11	0	0
				766	775	9	G	VLAHLEEER	D	4.70%	2262	2262	549.3168945	2	1096.618139	1094.572019	2.046120231	G	D	-	1	9	2	0
				842	856	14	R	QEEEMMAKEEELVK	V	0.81%	2326	2326	861.8985596	2	1721.781469	1721.785187	-0.003717635	R	V	-	4	14	0	1
				867	882	15	R	LTEMETLQSQLMAEK	L	0.81%	5088	5088	876.4296265	2	1750.843603	1750.848121	-0.004518494	R	L	-	5	15	0	0
				939	959	20	K	KMQQNIQELEEQLEEEESAR	Q	3.59%	4984	4984	821.0571899	3	2460.148095	2461.127845	-0.979750448	K	Q	Q7:+0.984	4	20	-1	1
				940	959	19	K	MQQNIQELEEQLEEEESAR	Q	2.26%	5266	5266	1167.025879	2	2332.036108	2332.048882	-0.012774284	K	Q	-	5	19	0	0
				1000	1014	14	R	IAEFTTNLTEEEEK	S	0.81%	3200	3200	827.401062	2	1652.786474	1652.778108	0.008365495	R	S	-	5	14	0	0
				1000	1016	16	R	IAEFTTNLTEEEEKSK	S	0.81%	2743	2743	935.46698	2	1868.91831	1867.9051	1.013209809	R	S	-	4	16	1	1
				1022	1035	13	K	NKHEAMITDLEER	L	0.81%	1155	1155	529.26	3	1584.756525	1584.756603	-7.804E-05	K	L	-	2	13	0	1
				1024	1035	11	K	HEAMITDLEER	L	0.81%	2137	2137	672.3135376	2	1342.611425	1342.618712	-0.007287133	K	L	-	5	11	0	0
				1050	1075	25	R	RKLEGDSTDLSDQIAELQAQIAELK	M	4.51%	6881	6881	924.8233032	3	2771.446435	2771.418865	0.027569884	R	M	Q13:+0.984	1	25	0	2
				1051	1075	24	R	KLEGDSTDLSDQIAELQAQIAELK	M	0.81%	7363	7363	1308.665039	2	2615.314428	2614.333754	0.980674533	R	M	-	3	24	1	1
				1080	1091	11	K	KEEELQAALAR	V	0.81%	852	852	629.3386841	2	1256.661718	1256.672461	-0.010743164	R	A	-	5	11	0	1
				1105	1124	19	K	IRELESQISELQEDLESER	A	0.81%	5777	5777	1152.568237	2	2303.120825	2302.128846	0.991978713	K	A	-	4	19	1	1
				1107	1124	17	R	ELESQISELQEDLESER	A	0.81%	5751	5751	1017.481018	2	2032.946386	2032.943671	0.002715477	R	A	-	5	17	0	0
				1135	1162	27	R	DLGEELEALKTELEDTLDSTAAQQELR	S	0.81%	9251	9251	1006.833801	3	3017.477929	3016.472432	1.005496505	R	S	-	4	27	1	1
				1165	1173	8	R	EQEVNILK	K	3.51%	1324	1324	486.7706604	2	971.5256707	971.5287569	-0.003086167	R	K	-	2	8	0	0
				1174	1191	17	K	TLEEEAKTHEAQIQEMR	Q	0.81%	2890	2890	681.9980469	3	2042.970666	2041.973866	0.996799185	K	Q	-	4	17	1	1
				1193	1209	16	K	HSQAVEELAEQLEQTK	R	0.81%	4235	4235	920.4628906	2	1838.910131	1838.901018	0.009113474	K	R	-	5	16	0	0
				1193	1210	17	K	HSQAVEELAEQLEQTKR	V	0.81%	3843	3843	666.0061646	3	1994.995019	1995.002129	-0.007110316	K	V	-	4	17	0	1
				1217	1234	17	K	AKQTLENERGELANEVK	V	2.34%	799	799	965.5076904	2	1928.999731	1927.996315	1.003415619	K	V	-	1	17	1	2
				1219	1234	15	K	QTLENERGELANEVK	V	0.81%	1177	1177	865.4372559	2	1728.858862	1728.864238	-0.005376537	K	V	-	2	15	0	1
				1247	1260	13	R	KKVEAQLQELQVK	F	4.33%	1031	1031	771.4657593	2	1540.915868	1540.898439	0.017429763	R	F	K2:+1.000	1	13	0	2
				1248	1260	12	K	KVEAQLQELQVK	F	0.81%	1977	1977	707.4094849	2	1412.80332	1411.803476	0.999844071	K	F	-	3	12	1	1
				1249	1260	11	K	VEAQLQELQVK	F	0.81%	2614	2614	642.8615112	2	1283.707372	1283.708512	-0.001140059	K	F	-	5	11	0	0
				1277	1295	18	K	LQVELDNVTGLLSQSDSK	S	0.81%	5724	5724	973.5100708	2	1945.004492	1945.000398	0.004093986	K	S	-	5	18	0	0
				1301	1322	21	K	DFSALESQLQDTQELLQEENR	Q	2.26%	6891	6891	1247.090088	2	2492.164526	2492.166688	-0.002162291	K	Q	-	4	21	0	0
				1301	1324	23	K	DFSALESQLQDTQELLQEENRQK	L	3.59%	6336	6336	917.1120605	3	2748.312707	2749.304229	-0.991522223	K	L	N20:+0.984	2	23	-1	1
				1357	1370	13	K	QIATLHAQVADMK	K	1.98%	1582	1582	476.2553101	3	1425.742455	1425.728582	0.013873512	K	K	Q1:+0.984	1	13	0	0
				1392	1400	8	K	DLEGLSQR	H	4.64%	889	889	459.2373047	2	916.4589593	916.4614055	-0.002446241	K	H	-	2	8	0	0
				1415	1433	18	K	TRLQQELDDLLVDLDHQR	Q	1.97%	7185	7185	736.3859863	3	2206.134484	2206.134206	0.000278032	K	Q	-	5	18	0	1
				1417	1433	16	R	LQQELDDLLVDLDHQR	Q	0.81%	6354	6354	650.6651611	3	1948.972008	1948.985416	-0.013407834	R	Q	-	3	16	0	0
				1444	1454	10	K	KFDQLLAEEK	T	2.46%	1828	1828	610.8250122	2	1219.634374	1219.644849	-0.01047513	R	N	-	2	10	0	1
				1445	1454	9	K	FDQLLAEEK	T	0.81%	1847	1847	547.2832031	2	1092.550756	1091.549886	1.000869842	K	N	-	4	9	1	0
				1483	1497	14	R	ALEEAMEQKAELER	L	0.81%	2135	2135	824.4078369	2	1646.800024	1645.798133	1.001890276	R	L	-	5	14	1	1
				1528	1538	10	R	ALEQQVEEMK	T	0.81%	1651	1651	602.7937622	2	1203.571874	1203.580536	-0.00866141	R	T	-	4	10	0	0
				1528	1555	27	R	ALEQQVEEMKTQLEELEDELQATEDAK	L	2.26%	8113	8113	1050.169678	3	3147.485558	3146.481284	1.004274579	R	L	-	3	27	1	1
				1538	1555	17	K	TQLEELEDELQATEDAK	L	0.81%	5643	5643	981.4623413	2	1960.909033	1960.911308	-0.002275223	K	L	-	5	17	0	0
				1676	1694	18	K	SMEAEMIQLQEELAAAER	A	0.81%	6830	6830	683.6576538	3	2047.949486	2047.95544	-0.005953878	K	A	-	5	18	0	0
				1697	1716	19	R	QAQQERDELADEIANSSGK	G	2.46%	2237	2237	697.3283691	3	2088.961632	2087.971951	0.989681286	R	G	-	2	19	1	1
				1730	1751	21	R	IAQLEEELEEEQGNTELINDR	L	2.26%	4824	4824	1237.579468	2	2473.143285	2471.166354	1.976931803	R	L	-	5	21	2	0
				1730	1753	23	R	IAQLEEELEEEQGNTELINDRLK	K	3.00%	4915	4915	905.4581909	3	2713.351098	2712.345381	1.005716746	R	K	-	3	23	1	1
				1753	1770	17	K	KANLQIDQINTDLNLER	S	0.81%	3949	3949	1000.039551	2	1998.063451	1997.054164	1.009287035	K	S	-	4	17	1	1
				1754	1770	16	K	ANLQIDQINTDLNLER	S	0.81%	4705	4705	935.4874878	2	1868.959326	1868.959201	0.000124194	K	S	-	2	16	0	0
				1791	1802	11	K	VKLQEMEGTVK	S	0.81%	828	828	631.343811	2	1260.671972	1260.674771	-0.002798562	K	S	-	4	11	0	1
				1806	1815	9	K	ASITALEAK	I	0.81%	934	934	452.2608337	2	902.5060174	902.5072931	-0.00127572	K	I	-	3	9	0	0
				1815	1828	13	K	IAQLEEQLDNETK	E	0.81%	2617	2617	765.8849487	2	1529.754247	1529.757313	-0.003065955	K	E	-	5	13	0	0
				1815	1830	15	K	IAQLEEQLDNETKER	Q	0.81%	2233	2233	908.9552612	2	1815.894872	1814.901018	0.993854685	K	Q	-	3	15	1	1
				1842	1856	14	K	KLKDVLLQVDDERR	N	0.81%	1827	1827	576.3292236	3	1725.964196	1725.973729	-0.009533286	K	N	-	1	14	0	3
				1877	1888	11	R	QLEEAEEEAQR	A	2.46%	698	698	666.3067627	2	1330.597875	1330.600084	-0.002208897	R	A	-	4	11	0	0
				1898	1912	14	R	ELEDATETADAMNR	E	0.81%	1328	1328	783.8421021	2	1565.668554	1564.667513	1.001040878	R	E	-	4	14	1	0
				1922	1932	10	R	RGDLPFVVPR	R	0.81%	3523	3523	578.3342285	2	1154.652807	1154.656023	-0.003216217	R	R	-	5	10	0	1
				1923	1932	9	R	GDLPFVVPR	R	2.83%	3999	3999	500.2824402	2	998.5492303	998.554912	-0.005681725	R	R	-	2	9	0	0
P35611	Alpha-adducin	1	2.04%	452	467	15	R	GDEASEEGQNGSSPK	S	7.64%	5634	5634	498.5813599	3	1492.720604	1492.580106	0.140498886	R	S	Q9:+0.984,N10:+0.984	3	15	0	0
P35613	Basigin	3	12.99%	243	257	14	K	SESVPPVTDWAWYK	I	3.05%	5405	5405	833.4101563	2	1664.804662	1663.78822	1.016442924	K	I	-	2	14	1	0
				282	300	18	R	SELHIENLNMEADPGQYR	C	0.81%	3625	3625	706.6543579	3	2116.939599	2115.953115	0.986483322	R	C	N9:+0.984	1	18	1	0
				348	366	18	R	RKPEDVLDDDDAGSAPLK	S	0.81%	1023	1023	648.3241577	3	1941.948998	1939.948696	2.000301761	R	S	-	2	18	2	1
P36404	ADP-ribosylation factor-like protein 2	4	25.00%	18	29	11	R	LLMLGLDNAGK	T	1.98%	4284	4284	571.7672119	2	1141.518774	1143.632177	-2.113403596	R	T	-	2	11	-1	0
				104	114	10	R	ELQSLLVEER	L	2.80%	3421	3421	608.3286743	2	1214.641699	1214.650663	-0.008964599	R	L	-	5	10	0	0
				114	126	12	R	LAGATLLIFANK	Q	3.79%	5479	5479	617.8613892	2	1233.707128	1230.733605	2.973523328	R	Q	-	2	12	3	0
				126	139	13	K	QDLPGALSSNAIR	E	0.81%	2899	2899	671.3603516	2	1340.705053	1340.704824	0.000228981	K	E	-	4	13	0	0
P37802	Transgelin-2	10	58.79%	20	39	19	K	QYDADLEQILIQWITTQCR	K	0.81%	8762	8762	799.3942871	3	2395.159386	2393.16808	1.991306352	K	K	C18:+57.021	3	19	2	0
				79	88	9	K	IQASTMAFK	Q	1.93%	1117	1117	498.757782	2	995.4999139	995.5109994	-0.011085523	K	Q	-	2	9	0	0
				88	102	14	K	QMEQISQFLQAAER	Y	0.81%	5314	5314	839.9112549	2	1677.80686	1677.814452	-0.007592522	K	Y	-	3	14	0	0
				102	120	18	R	YGINTTDIFQTVDLWEGK	N	0.81%	7067	7067	1051.013672	2	2100.011694	2099.021133	0.990560694	R	N	-	2	18	1	0
				127	139	12	R	TLMNLGGLAVAR	D	0.81%	4294	4294	610.3352661	2	1218.654882	1215.664525	2.990357579	R	D	N4:+0.984	2	12	3	0
				139	153	14	R	DDGLFSGDPNWFPK	K	0.81%	5748	5748	798.87	2	1595.72435	1593.709969	2.014380824	R	K	-	1	14	2	0
				156	171	15	K	ENPRNFSDNQLQEGK	N	8.60%	7770	7770	889.7953491	2	1777.575048	1776.791436	0.78361221	K	N	N5:+0.984,N9:+0.984	1	15	1	1
				160	171	11	R	NFSDNQLQEGK	N	4.83%	727	727	640.2935181	2	1278.571386	1278.58404	-0.012654075	R	N	-	3	11	0	0
				171	182	11	K	NVIGLQMGTNR	G	0.81%	2515	2515	601.8184814	2	1201.621313	1201.623738	-0.002425125	K	G	-	5	11	0	0
				171	187	16	K	NVIGLQMGTNRGASQA	G	8.30%	3138	3138	545.5981445	3	1633.770958	1633.773036	-0.00207703	K	G	N1:+0.984,Q6:+0.984,M7:	1	16	0	1
P38570	Integrin alpha-E	1	0.93%	1155	1166	11	K	YQQLNLESIRK	A	4.82%	2506	2506	464.9258728	3	1391.754143	1391.74086	0.013283624	K	A	N5:+0.984	1	11	0	1
P38606	V-type proton ATPase catalytic subunit A	2	5.83%	142	163	21	R	VGSHITGGDIYGIVSENSLIK	H	0.81%	5090	5090	720.713623	3	2159.117394	2158.126995	0.990398861	R	H	-	5	21	1	0
				308	323	15	R	TALVANTSNMPVAAR	E	0.81%	1469	1469	758.4016113	2	1514.787573	1514.787509	6.34963E-05	R	E	-	5	15	0	0
P38646	Stress-70 protein, mitochondrial	22	48.31%	85	99	14	R	TTPSVVAFTADGER	L	0.81%	2759	2759	725.8601685	2	1449.704687	1449.709969	-0.005282262	R	L	-	5	14	0	0
				107	121	14	R	QAVTNPNNTFYATK	R	0.81%	725	725	785.3890381	2	1568.762426	1567.763067	0.99935874	R	R	-	2	14	1	0
				146	173	27	R	ASNGDAWVEAHGKLYSPSQIGAFVLMK	M	5.92%	9350	9350	959.8395996	3	2876.495324	2875.432698	1.062626116	R	M	-	1	27	1	1
				159	173	14	K	LYSPSQIGAFVLMK	M	0.81%	6282	6282	777.428772	2	1552.841894	1552.832334	0.009559857	K	M	-	2	14	0	0
				187	202	15	K	NAVITVPAYFNDSQR	Q	0.81%	4163	4163	847.9251709	2	1693.834692	1693.84238	-0.007688691	T	Q	-	4	15	0	0
				206	218	12	K	DAGQISGLNVLR	V	0.81%	3569	3569	621.8417969	2	1241.667944	1241.672796	-0.004851906	K	V	-	5	12	0	0
				218	234	16	R	VINEPTAAALAYGLDK	S	0.81%	4377	4377	549.2976074	3	1644.869347	1644.872284	-0.002936438	R	S	-	4	16	0	0
				265	284	19	K	STNGDTFLGGEDFDQALLR	H	0.81%	6042	6042	1028.971191	2	2055.926733	2055.93851	-0.01177722	K	H	N3:+0.984	5	19	0	0
				348	360	12	R	AQFEGIVTDLIR	R	0.81%	5943	5943	681.8724976	2	1361.729345	1361.719062	0.010283469	R	R	Q2:+0.984	3	12	0	0
				377	391	14	K	SDIGEVILVGGMTR	M	0.81%	4891	4891	723.8817749	2	1445.7479	1445.754812	-0.006912211	K	M	-	5	14	0	0
				394	405	11	K	VQQTVQDLFGR	A	0.81%	3483	3483	645.8414307	2	1289.667211	1289.672796	-0.005584328	K	A	-	2	11	0	0
				409	456	47	K	AVNPDEAVAIGAAIQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTK	L	1.93%	12916	12916	1148.380981	4	4589.492626	4588.48914	1.003485381	K	L	-	4	47	1	0
				468	485	17	K	SQVFSTAADGQTQVEIK	V	0.81%	2622	2622	904.9558105	2	1807.895971	1807.895204	0.000767006	K	V	-	5	17	0	0
				498	513	15	K	LLGQFTLIGIPPAPR	G	0.81%	6500	6500	797.4768066	2	1592.937963	1591.944995	0.992968249	K	G	-	4	15	1	0
				541	555	14	R	EQQIVIQSSGGLSK	D	0.81%	926	926	737.9022217	2	1473.788793	1472.783468	1.005324815	R	D	-	4	14	1	0
				541	563	22	R	EQQIVIQSSGGLSKDDIENMVK	N	1.93%	4308	4308	806.7423096	3	2417.203454	2418.194803	-0.991348913	R	N	N19:+0.984	2	22	-1	1
				576	595	19	K	ERVEAVNMAEGIIHDTETK	M	0.81%	4510	4510	714.6850586	3	2141.031701	2141.04228	-0.010579667	K	M	-	3	19	0	1
				578	595	17	R	VEAVNMAEGIIHDTETK	M	0.81%	4773	4773	929.4538574	2	1856.892065	1855.898576	0.993488796	R	M	-	5	17	1	0
				610	619	9	K	LKEEISKMR	E	5.29%	13064	13064	568.3876953	2	1134.759741	1132.627426	2.132314233	K	E	-	1	9	2	2
				625	646	21	K	DSETGENIRQAASSLQQASLK	L	5.92%	8018	8018	1117.17981	2	2232.343969	2232.098214	0.245754749	K	L	-	1	21	0	1
				646	653	7	K	LFEMAYK	K	0.81%	2757	2757	451.2258911	2	900.4361321	900.4415227	-0.005390597	K	K	-	4	7	0	0
				654	671	17	K	MASEREGSGSSGTGEQK	E	5.75%	4319	4319	571.9823608	3	1712.923607	1712.726239	0.197368624	K	E	M1:+15.994	1	17	0	1
P40763	Signal transducer and activator of transcription 3	3	7.40%	114	140	26	R	LLQTAATAAQQGGQANHPTAAVVTEK	Q	0.81%	818	818	859.4522095	3	2575.333153	2575.335425	-0.002271854	R	Q	-	4	26	0	0
				215	233	18	R	SIVSELAGLLSAMEYVQK	T	0.81%	10190	10190	647.0135498	3	1938.017174	1937.017963	0.999211374	R	T	-	5	18	1	0
				518	531	13	R	GLSIEQLTTLAEK	L	0.81%	5470	5470	701.8876953	2	1401.759741	1401.771507	-0.011766215	R	L	-	5	13	0	0
P40926	Malate dehydrogenase, mitochondrial	9	37.87%	26	45	19	K	VAVLGASGGIGQPLSLLLK	N	0.81%	6912	6912	897.5510254	2	1793.086401	1792.082217	1.004183733	K	N	-	5	19	1	0
				52	74	22	R	LTLYDIAHTPGVAADLSHIETK	A	0.81%	5599	5599	789.418396	3	2365.231713	2364.232523	0.999189852	R	A	-	4	22	1	0
				78	91	13	K	GYLGPEQLPDCLK	G	0.81%	4028	4028	745.3720703	2	1488.728491	1488.727799	0.000691505	K	G	C11:+57.021	4	13	0	0
				165	176	11	K	IFGVTTLDIVR	A	0.81%	5557	5557	617.361084	2	1232.706518	1232.712869	-0.006351583	K	A	-	4	11	0	0
				176	185	9	R	ANTFVAELK	G	4.46%	2437	2437	496.7725525	2	991.5294549	991.5338422	-0.004387348	R	G	-	1	9	0	0
				203	215	12	K	TIIPLISQCTPK	V	2.36%	4059	4059	685.8787231	2	1369.741796	1369.763456	-0.021660023	K	V	C9:+57.021	3	12	0	0
				215	229	14	K	VDFPQDQLTALTGR	I	2.26%	4888	4888	781.4034424	2	1560.791235	1559.794368	0.996867174	K	I	-	5	14	1	0
				241	257	16	K	AGAGSATLSMAYAGAR	F	0.81%	2347	2347	727.8514404	2	1453.687231	1453.69836	-0.011128853	K	F	-	5	16	0	0
				257	269	12	R	FVFSLVDAMNGK	E	0.81%	6087	6087	664.8394165	2	1327.663183	1326.664206	0.998977096	R	E	-	5	12	1	0
P41240	Tyrosine-protein kinase CSK	2	6.22%	94	107	13	R	LLYPPETGLFLVR	E	0.81%	6473	6473	759.442688	2	1516.869726	1516.865348	0.004378329	R	E	-	3	13	0	0
				244	259	15	R	HSNLVQLLGVIVEEK	G	0.81%	6920	6920	560.3218994	3	1677.942223	1676.946117	0.996105842	R	G	-	5	15	1	0
P42261	Glutamate receptor 1	2	3.20%	499	519	20	R	EEVIDFSKPFMSLGISIMIK	K	3.62%	5944	5944	762.3970947	3	2284.167809	2283.189463	0.978346004	R	K	-	1	20	1	0
				757	766	9	R	NPVNLAVLK	L	4.76%	2199	2199	485.29	2	968.5643499	968.5702122	-0.005862256	R	L	N1:+0.984,K9:+1.000	1	9	0	0
P43005	Excitatory amino acid transporter 3	1	5.15%	315	342	27	R	FAMGMAQALLTALMISSSSATLPVTFR	C	5.69%	5902	5902	939.1157837	3	2814.323876	2814.448215	-0.124339294	R	C	-	3	27	0	0
P43007	Neutral amino acid transporter A	10	34.40%	0	31	31	-	MEKSNETNGYLDSAQAGPAAGPGAPGTAAGR	A	5.65%	8499	8499	983.4761353	3	2947.404931	2947.325361	0.079570138	-	A	N5:+0.984,N8:+0.984	1	31	0	1
				3	31	28	K	SNETNGYLDSAQAGPAAGPGAPGTAAGR	A	1.93%	2230	2230	854.0610352	3	2559.15963	2558.163318	0.996311997	K	A	N5:+0.984	2	28	1	0
				41	63	22	R	QALVLLTVSGVLAGAGLGAALR	G	0.81%	9087	9087	684.0840454	3	2049.228661	2049.231007	-0.002345578	R	G	-	5	22	0	0
				69	84	15	R	TQVTYLAFPGEMLLR	M	0.81%	7254	7254	870.4626465	2	1738.909643	1737.912375	0.997267497	R	M	-	5	15	1	0
				165	176	11	K	ETVDSFLDLAR	N	0.81%	5400	5400	633.3189087	2	1264.622167	1264.629928	-0.007760409	K	N	-	3	11	0	0
				176	189	13	R	NLFPSNLVVAAFR	T	0.81%	7242	7242	724.9088135	2	1447.801977	1446.798331	1.003646329	R	T	-	3	13	1	0
				239	249	10	K	LGSEGEDLIR	F	0.81%	1592	1592	544.7830811	2	1087.550512	1087.550949	-0.000436955	K	F	-	3	10	0	0

				323	354	31	K	NPFRFLLGLLAPFATAFATCSSSATLPSMMK	C	5.58%	7841	7841	1116.980957	3	3347.919396	3346.69117	1.228225966	K	C	C20:+57.021	1	31	1	1
				457	480	23	R	TTTVVNVEGDALGAGILHHLNQK	A	0.81%	4932	4932	1194.647949	2	2387.280248	2386.260469	1.01977923	R	A	-	5	23	1	0
				501	528	27	K	SEEETSPLVTHQNPAGPVASAPELESK	E	2.64%	3020	3020	935.7848511	3	2804.331078	2804.335195	-0.004116473	K	E	N13:+0.984	2	27	0	0
P43121	Cell surface glycoprotein MUC18	3	5.88%	97	112	15	R	GATLALTQVTPQDER	I	0.81%	2868	2868	800.9232788	2	1599.830908	1598.826396	1.004511537	R	I	-	5	15	1	0
				251	263	12	K	VWLEVEPVGMLK	E	0.81%	6008	6008	700.38	2	1398.74435	1398.758106	-0.013756392	K	E	-	5	12	0	0
				388	399	11	R	GPVLQLHDLKR	E	3.38%	1469	1469	426.2514648	3	1275.730919	1275.729901	0.001018467	R	E	Q5:+0.984	2	11	0	1
P43403	Tyrosine-protein kinase ZAP-70	1	1.13%	186	193	7	K	FLLRPRK	E	3.93%	4057	4057	465.292572	2	928.569494	928.5970516	-0.027557589	K	E	-	3	7	0	1
P46059	Solute carrier family 15 member 1	1	2.54%	437	455	18	R	INISSPGSPVTAVTDDFK	Q	7.91%	2658	2658	924.4682007	2	1846.920751	1846.931255	-0.010503913	R	Q	-	1	18	0	0
P46940	Ras GTPase-activating-like protein IQGAP1	47	43.69%	80	88	8	K	LGNFFSPK	V	0.81%	3191	3191	455.75	2	909.4843499	908.475599	1.00875096	K	V	-	5	8	1	0
				111	130	19	R	HTDNVIQWLNAMDEIGLPK	I	0.81%	7838	7838	732.373291	3	2194.096398	2193.088837	1.007561359	R	I	-	3	19	1	0
				130	142	12	K	IFYPETTDIYDR	K	0.81%	3902	3902	766.8641968	2	1531.712743	1531.719471	-0.006727685	K	K	-	4	12	0	0
				174	186	12	K	VDFTEEEINNMK	T	0.81%	3359	3359	735.3330688	2	1468.650488	1467.655157	0.995330175	K	T	-	5	12	1	0
				191	201	10	K	YGIQMPAFSK	I	4.57%	4239	4239	571.2855225	2	1140.555395	1140.563763	-0.008368494	K	I	-	1	10	0	0
				201	230	29	K	IGGILANELSVDEAALHAAVIAINEAIDR	R	0.81%	10632	10632	740.9075928	4	2959.599071	2958.566198	1.032873206	K	R	N7:+0.984	2	29	1	0
				230	241	11	R	RIPADTFAALK	N	0.81%	2969	2969	601.8464355	2	1201.677221	1201.681904	-0.004682626	R	N	-	2	11	0	1
				241	266	25	K	NPNAMLVNLEEPLASTYQDILYQAK	Q	0.81%	8217	8217	946.6516724	3	2836.931542	2834.416045	2.515497442	K	Q	-	1	25	3	0
				269	276	7	K	MTNAKNR	T	5.34%	2285	2285	426.2189636	2	850.4222772	850.3957676	0.026509582	K	T	M1:+15.994,N3:+0.984	1	7	0	1
				302	326	24	K	VNTFSALANIDLALEQGDALALFR	A	0.81%	9581	9581	855.4598999	3	2563.356225	2562.33295	1.023274667	K	A	Q16:+0.984	3	24	1	0
				326	336	10	R	ALQSPALGLR	G	0.81%	2138	2138	513.3062744	2	1024.596899	1024.602925	-0.006026164	R	G	-	5	10	0	0
				336	348	12	R	GLQQQNSDWYLK	Q	0.81%	3254	3254	740.8666382	2	1479.717626	1478.715389	1.002237503	R	Q	-	3	12	1	0
				358	387	29	R	QSGQTDPLQKEELQSGVDAANSAAQQYQR	R	3.27%	3701	3701	1050.161987	3	3147.462487	3147.47046	-0.007972734	R	R	Q14:+0.984	4	29	0	1
				388	401	13	R	LAAVALINAAIQK	G	0.81%	5359	5359	648.9038086	2	1295.791967	1294.797268	0.99469922	R	G	-	5	13	1	0
				401	431	30	K	GVAEKTVLELMNPEAQLPQVYPFAADLYQK	E	4.94%	6530	6530	841.1809082	4	3360.692333	3362.710814	-2.018481756	K	E	Q29:+0.984	1	30	-1	1
				406	431	25	K	TVLELMNPEAQLPQVYPFAADLYQK	E	0.81%	7747	7747	960.1665039	3	2877.476037	2877.462266	0.013770159	K	E	-	3	25	0	0
				438	465	27	R	QSPEHNLTHPELSVAVEMLSSVALINR	A	4.82%	7884	7884	743.8878174	4	2971.519969	2971.507304	0.012665675	R	A	N6:+0.984	2	27	0	0
				465	477	12	R	ALESGDVNTVWK	Q	0.81%	2855	2855	659.8300171	2	1317.644384	1317.656477	-0.01209274	R	Q	-	5	12	0	0
				538	556	18	R	ILAIGLINEALDEGDAQK	T	0.81%	6891	6891	941.4776001	2	1880.93955	1882.004755	-1.065204453	G	T	-	5	18	-1	0
				556	567	11	K	TLQALQIPAAK	L	0.81%	3123	3123	577.3499146	2	1152.684179	1152.686655	-0.00247565	K	L	-	5	11	0	0
				567	585	18	K	LEGVLAEVAQHYQDTLIR	A	0.81%	6389	6389	685.699646	3	2054.075463	2055.063651	-0.988188052	K	A	Q10:+0.984	4	18	-1	0
				622	641	19	K	FALGIFAINEAVESGDVGK	T	0.81%	7306	7306	969.0057373	2	1935.995825	1935.99419	0.001634681	K	T	-	5	19	0	0
				722	738	16	R	EEIQSSISGVTAAYNR	E	0.81%	3310	3310	863.4261475	2	1724.836645	1723.837689	0.998955794	R	E	-	5	16	1	0
				738	751	13	R	EQLWLANEGLITR	L	4.01%	5267	5267	773.9	2	1545.78435	1543.788188	1.996161608	R	L	Q2:+0.984,N7:+0.984	3	13	2	0
				833	841	8	R	DHINDIIK	I	3.50%	931	931	484.2623596	2	966.5090692	966.5134411	-0.004371978	R	I	-	3	8	0	0
				856	870	14	K	TLINAEDPPMVVVR	K	0.81%	4233	4233	777.4216919	2	1552.827734	1552.828311	-0.000577595	K	K	-	5	14	0	0
				871	891	20	K	FVHLLDQSDQDFQEELDLMK	M	1.93%	6509	6509	817.7268677	3	2450.157128	2450.13114	0.025988379	K	M	Q7:+0.984	2	20	0	0
				891	901	10	K	MREEVITLIR	S	0.81%	3511	3511	420.575531	3	1258.703118	1258.706739	-0.00362147	K	S	-	3	10	0	1
				901	916	15	R	SNQQLENDLNLMDIK	I	0.81%	5316	5316	887.932312	2	1773.848974	1773.856711	-0.007737145	R	I	-	5	15	0	0
				924	935	11	K	ITLQDVVSHSK	K	0.81%	3005	3005	613.8409424	2	1225.666235	1225.666648	-0.000412874	K	K	-	5	11	0	0
				942	955	13	K	EQLSDMMMINKQK	G	5.44%	4154	4154	543.6328735	3	1627.875145	1626.741719	1.133426021	K	G	M7:+15.995,M8:+15.995	1	13	1	1
				966	988	22	R	EKLEAYQHLFYLLQTNPTYLAK	L	0.81%	6856	6856	671.6085205	4	2682.402782	2682.405737	-0.002954681	R	L	-	4	22	0	1
				988	997	9	K	LIFQMPQNK	S	0.81%	3731	3731	559.8029175	2	1117.590185	1117.595398	-0.005212943	K	S	-	4	9	0	0
				1063	1077	14	R	GQNALRQILAPVVK	E	5.51%	8680	8680	755.3839111	2	1508.752172	1507.872193	0.879979458	R	E	Q2:+0.984,N3:+0.984	1	14	1	1
				1096	1111	15	K	SWVNQMESQTGEASK	L	0.81%	3118	3118	841.3779907	2	1680.740331	1680.741347	-0.001015475	K	L	-	5	15	0	0
				1111	1128	17	K	LPYDVTPEQALAHEEVK	T	0.81%	3645	3645	646.9937744	3	1937.957848	1937.973454	-0.015606286	K	T	-	3	17	0	0
				1139	1155	16	R	AVTDKFLSAIVSSVDK	I	4.56%	14155	14155	840.7911377	2	1679.566625	1678.914148	0.652476847	R	I	-	1	16	1	1
				1144	1155	11	K	FLSAIVSSVDK	I	0.81%	4029	4029	583.3264771	2	1164.637304	1164.639036	-0.001731754	K	I	-	4	11	0	0
				1239	1261	22	K	MFLGDNAHLSIINEYLSQSYQK	F	0.81%	6597	6597	858.090332	3	2571.247521	2570.247522	0.999998622	K	F	-	3	22	1	0
				1397	1422	25	R	FQPGETLTEILETPATSEQEAEHQR	A	4.29%	5962	5962	948.1213989	3	2841.340722	2840.346444	0.994278113	R	A	-	2	25	1	0
				1465	1477	12	K	LTELGTVDPKNK	Y	5.49%	2325	2325	439.8965454	3	1316.666161	1314.703077	1.96308395	K	Y	N11:+0.984	1	12	2	1
				1477	1487	10	K	YQELINDIAR	D	0.81%	3431	3431	618.3204346	2	1234.625219	1233.635347	0.989871661	K	D	-	4	10	1	0
				1505	1516	11	K	LQQTYAALNSK	A	0.81%	802	802	618.8327637	2	1235.649877	1235.650997	-0.001120216	K	A	-	5	11	0	0
				1516	1528	12	K	ATFYGEQVDYYK	S	0.81%	3323	3323	742.8399658	2	1483.664282	1482.666707	0.997574329	K	S	-	5	12	1	0
				1571	1586	15	K	GVLLEIEDLQVNQFK	N	0.81%	6611	6611	873.4771118	2	1744.938574	1743.940698	0.997875961	K	N	-	5	15	1	0
				1586	1604	18	K	NVIFEISPTEEVGDFEVK	A	0.81%	6269	6269	1026.514282	2	2051.012914	2051.0099	0.003014773	K	A	-	5	18	0	0
				1604	1634	30	K	AKFMGVQMETFMLHYQDLLQLQYEGVAVMK	L	5.56%	7078	7078	892.9833984	4	3567.902294	3566.684599	1.217694646	K	L	M8:+15.995,Q16:+0.984,C	1	30	1	1
P48047	ATP synthase subunit O, mitochondrial	10	61.50%	26	40	14	K	LVRPPVQVYGIEGR	Y	0.81%	3288	3288	791.9605103	2	1581.90537	1581.899107	0.00626306	K	Y	-	4	14	0	0
				40	51	11	R	YATALYSAASK	Q	0.81%	940	940	573.7894287	2	1145.563207	1144.576435	0.986771886	R	Q	-	5	11	1	0
				51	64	13	K	QNKLEQVEKELLR	V	5.61%	5070	5070	544.3070679	3	1629.897728	1627.878066	2.019662405	K	V	Q1:+0.984,N2:+0.984	1	13	2	2
				73	84	11	K	VAASVLNPYVK	R	0.81%	2797	2797	580.8336182	2	1159.651586	1159.660106	-0.008519296	K	R	-	5	11	0	0
				98	117	19	K	ERFSPLTTNLINLLAENGR	L	1.93%	7008	7008	720.3889771	3	2158.143456	2158.138213	0.005243088	K	L	N9:+0.984	4	19	0	1
				100	117	17	R	FSPLTTNLINLLAENGR	L	0.81%	7629	7629	937.5137939	2	1873.011938	1872.010509	1.001429227	R	L	-	4	17	1	0
				117	136	19	R	LSNTQGVVSAFSTMMSVHR	G	0.81%	5651	5651	684.6759033	3	2051.004235	2050.992829	0.011406153	R	G	-	4	19	0	0
				136	158	22	R	GEVPCTVTSASPLEEATLSELK	T	0.81%	5256	5256	1159.574951	2	2317.134252	2317.135442	-0.00119012	R	T	C5:+57.021	5	22	0	0
				162	172	10	K	SFLSQGQVLK	L	0.81%	2973	2973	553.8108521	2	1105.606054	1105.613155	-0.007101282	K	L	-	4	10	0	0
				176	188	12	K	TDPSILGGMIVR	I	0.81%	4660	4660	629.8430786	2	1257.670507	1257.675105	-0.004597733	K	I	-	5	12	0	0
P48549	G protein-activated inward rectifier potassium channel 1	1	2.59%	287	300	13	S	MQTEQFEIVVILE	G	6.15%	8979	8979	798.9	2	1595.78435	1594.780094	1.0042564	S	G	M1:+15.995,Q2:+0.984	1	13	1	0
P48960	CD97 antigen	3	6.11%	303	323	20	K	LVDELMEAPGDVEALAPPVR	H	0.81%	6053	6053	707.7015991	3	2120.081322	2120.082354	-0.001031981	K	H	-	3	20	0	0
				323	339	16	R	HLIATQLLSNLEDIMR	I	0.81%	8221	8221	934.5216675	2	1867.027685	1866.003316	1.024369057	R	I	-	4	16	1	0
				441	456	15	R	LSAVNSIFLSHNNTK	E	7.42%	6398	6398	550.6158447	3	1648.824059	1646.815116	2.008943212	R	E	N5:+0.984,N12:+0.984,N1	1	15	2	0
P49327	Fatty acid synthase	62	38.43%	12	39	27	K	LPESENLQEFWDNLIGGVDMVTDDDRR	W	0.81%	9554	9554	1055.487061	3	3163.437707	3163.440406	-0.002699495	K	W	N13:+0.984	4	27	0	1
				41	49	8	K	AGLYGLPR	R	1.93%	2522	2522	423.744812	2	845.4739739	845.4759333	-0.001959345	K	R	-	4	8	0	0
				59	70	11	R	FDASFFGVHPK	Q	0.81%	4271	4271	417.93	3	1250.766525	1250.608404	0.158120608	R	Q	-	5	11	0	0
				101	122	21	R	GTHTGVWVGVSGSETSEALSR	D	0.81%	3199	3199	706.6790771	3	2117.013756	2116.018507	0.995249069	R	D	-	4	21	1	0
				224	235	11	R	SEGVVAVLLTK	K	0.81%	4493	4493	558.3338013	2	1114.651952	1114.659771	-0.007818757	R	K	-	5	11	0	0
				257	274	17	K	EQGVTFPSGDIQEQLIR	S	0.81%	4731	4731	959.49	2	1916.96435	1916.947952	0.016397576	K	S	Q2:+0.984	3	17	0	0
				274	298	24	R	SLYQSAGVAPESFEYIEAHGTGTK	V	0.81%	4417	4417	848.0718994	3	2541.192223	2541.202345	-0.010122062	R	V	-	3	24	0	0
				298	310	12	K	VGDPQELNGITR	A	0.81%	1467	1467	649.8376465	2	1297.659643	1297.662625	-0.002981967	K	A	-	5	12	0	0
				316	326	10	R	QEPLLIGSTK	S	4.05%	2078	2078	543.3126831	2	1084.609716	1084.612821	-0.003104845	R	S	-	1	10	0	0
				316	343	27	R	QEPLLIGSTKSNMGHPEPASGLAALAK	V	5.62%	4072	4072	680.8233643	4	2719.262157	2717.405799	1.856358327	R	V	N12:+0.984	1	27	2	1
				326	343	17	K	SNMGHPEPASGLAALAK	V	0.81%	2660	2660	551.2827759	3	1650.824853	1650.803538	0.021314949	K	V	N2:+0.984	2	17	0	0
				343	373	30	K	VLLSLEHGLWAPNLHFHSPNPEIPALLDGR	L	2.59%	7017	7017	836.6964722	4	3342.754589	3342.751313	0.003275216	K	L	N13:+0.984	3	30	0	0
				373	384	11	R	LQVVDQPLPVR	G	0.81%	2836	2836	632.3713379	2	1262.727026	1262.734668	-0.007641867	R	G	-	5	11	0	0
				384	422	38	R	GGNVGINSFGFGGSNVHIILRPNTQPPPAPAPHATLPR	L	3.04%	4992	4992	966.27	4	3861.0487	3858.007756	3.040943656	R	L	Q25:+0.984	1	38	3	0
				443	468	25	R	HSQDLAFLSMLNDIAAVPATAMPFR	G	0.81%	9038	9038	906.1245117	3	2715.35006	2715.351277	-0.0012171	R	G	-	4	25	0	0
				468	477	9	R	GYAVLGGER	G	0.81%	852	852	461.743927	2	921.4722039	920.4715763	1.000627668	R	G	-	2	9	1	0
				477	504	27	R	GGPEVQQVPAGERPLWFICSGMGTQWR	G	2.36%	6847	6847	1015.49	3	3043.446525	3042.458801	0.987724016	R	G	C19:+57.021	2	27	1	0
				504	512	8	R	GMGLSLMR	L	0.81%	3443	3443	432.724823	2	863.4339959	863.435727	-0.001731052	R	L	-	5	8	0	0
				522	533	11	R	SDEAVKPFGLK	V	0.81%	1148	1148	595.8238525	2	1189.632055	1189.634285	-0.002229746	R	V	-	4	11	0	0
				646	666	20	K	DTVTISGPQAPVFEFVEQLR	K	0.81%	8134	8134	745.3928223	3	2233.154992	2232.142645	1.012346437	K	K	-	5	20	1	0
				646	667	21	K	DTVTISGPQAPVFEFVEQLRK	E	4.59%	7632	7632	788.0879517	3	2361.24038	2360.237608	1.002771484	K	E	-	1	21	1	1
				676	700	24	R	TGGMAFHSYFMEAIAPPLLQELKK	V	0.81%	7512	7512	670.5956421	4	2678.351268	2678.360051	-0.008782673	R	V	-	3	24	0	1
				711	728	17	R	WLSTSIPEAQWHSSLAR	T	0.81%	4362	4362	657	3	1967.976525	1967.985356	-0.00883156	R	T	-	2	17	0	0
				802	825	23	R	LHLSGIDANPNALFFPPVEFPAPR	G	0.81%	6325	6325	825.44	3	2473.296525	2471.296126	2.00039856	R	G	-	1	23	2	0
				883	897	14	R	VLFPATGYLSIVWK	T	5.64%	7875	7875	797.4140015	2	1592.812353	1592.896648	-0.084294878	R	T	-	1	14	0	0
				901	927	26	R	ALGLGVEQLPVVFEDVVLHQATILPK	T	0.81%	9450	9450	697.4020996	4	2785.577098	2784.57895	0.99814819	R	T	-	2	26	1	0
				927	936	9	K	TGTVSLEVR	L	1.93%	1030	1030	481.2675476	2	960.5194451	960.5240059	-0.004560721	K	L	-	5	9	0	0
				957	967	10	K	VYQWDDPDPR	L	0.81%	2495	2495	645.78479	2	1289.55393	1289.567662	-0.013731722	K	L	-	4	10	0	0
				967	992	25	R	LFDHPESPTPNPTEPLFLAQAEVYK	E	0.81%	5830	5830	948.1466675	3	2841.416527	2839.406859	2.009668441	R	E	-	2	25	2	0
				997	1019	22	R	GYDYGPHFQGILEASLEGDSGR	L	0.81%	5807	5807	790.3640137	3	2368.068566	2367.076751	0.991815352	R	L	-	3	22	1	0
				1043	1051	8	K	HGLYLPTR	V	1.93%	1030	1030	478.7676392	2	955.5196282	955.5239462	-0.004317944	K	V	-	5	8	0	0
				1104	1116	12	R	RQQEQQVPILEK	F	1.97%	1051	1051	748.4140625	2	1494.812475	1494.815437	-0.00296236	R	F	-	4	12	0	1
				1105	1116	11	R	QQEQQVPILEK	F	2.32%	1887	1887	670.8600464	2	1339.704443	1338.714326	0.990116565	R	F	-	3	11	1	0
				1142	1151	9	K	GLVQALQTK	V	0.81%	2018	2018	481.260437	2	960.5052239	957.5494767	2.955747207	K	V	Q7:+0.984	2	9	3	0
				1158	1171	13	K	MVVPGLDGAQIPR	D	0.81%	4245	4245	676.8707886	2	1351.725927	1351.728203	-0.002276068	K	D	-	4	13	0	0
				1171	1180	9	R	DPSQQELPR	L	6.94%	676	676	535.2628174	2	1068.509985	1068.519983	-0.009998466	R	L	-	1	9	0	0
				1187	1208	21	R	LQLNGNLQLELAQVLAQERPK	L	2.32%	6919	6919	792.7792969	3	2375.314416	2375.31724	-0.002824663	R	L	Q13:+0.984	2	21	0	0
				1208	1225	17	K	LPEDPLLSGLLDSPALK	A	0.81%	7473	7473	889.5020752	2	1776.9885	1776.987314	0.001186807	K	A	-	5	17	0	0
				1241	1255	14	K	VVEVLAGHGHLYSR	I	5.79%	1089	1089	513.2791138	3	1536.813866	1535.820857	0.993009221	K	I	-	2	14	1	0
				1255	1275	20	R	IPGLLSPHPLLQLSYTATDR	H	0.81%	6101	6101	731.4061279	3	2191.194909	2191.200101	-0.005191859	R	H	-	4	20	0	0
				1337	1349	12	R	EGGFLLLHTLLR	G	0.81%	6669	6669	456.9371033	3	1367.787835	1367.792517	-0.004682162	R	G	-	1	12	0	0
				1404	1423	19	R	RPTPQDSPIFLPVDDTSFR	W	0.81%	5255	5255	730.710022	3	2189.106591	2187.096029	2.01056147	R	W	-	1	19	2	0
				1495	1507	12	K	VLQGDLVMNVYR	D	0.81%	3358	3358	711.8713989	2	1421.727148	1421.733768	-0.006620084	K	D	M8:+15.995	3	12	0	0
				1515	1538	23	R	HFLLEEDKPEEPTAHAFVSTLTR	G	0.81%	4637	4637	667.5897827	4	2666.327831	2666.334028	-0.006197469	R	G	-	4	23	0	0
				1591	1606	15	K	WTSQDSLLGMEFSGR	D	0.81%	5504	5504	857.9047852	2	1713.79392	1712.782818	1.011102513	K	D	-	4	15	1	0
				1711	1724	13	R	FPQLDSTSFANSR	D	0.81%	3728	3728	735.8560181	2	1469.696386	1468.694653	1.001732709	R	D	-	5	13	1	0
				1739	1752	13	K	GVDLVLNSLAEEK	L	0.81%	4902	4902	693.8793335	2	1385.743017	1385.740207	0.002810312	K	L	-	4	13	0	0
				1771	1787	16	K	FDLSQNHPLGMAIFLK	N	0.81%	6326	6326	916.4855957	2	1830.955541	1829.949824	1.005717758	K	N	-	3	16	1	0
				1851	1866	15	K	VVVQVLAEEPEAVLK	G	0.81%	4888	4888	812.4743652	2	1622.93308	1621.92907	1.004010173	K	G	-	5	15	1	0
				1934	1953	19	R	QGVQVQVSTSNISSLEGAR	G	0.81%	3618	3618	980.510437	2	1959.005224	1959.002129	0.003095095	R	G	-	5	19	0	0
				2026	2043	17	R	GNAGQSNYGFANSAMER	I	0.81%	2099	2099	887.3908691	2	1772.766088	1772.753643	0.012445329	R	I	-	5	17	0	0
				2125	2138	13	R	DLVEAVAHILGIR	D	0.81%	9334	9334	469.2750854	3	1404.801781	1404.808895	-0.007114036	R	D	-	5	13	0	0
				2168	2177	9	R	ELNLVLSVR	E	0.81%	4362	4362	521.8155518	2	1041.615453	1041.618241	-0.002787228	R	E	-	5	9	0	0
				2206	2220	14	K	EDGLAQQQTQLNLR	S	0.81%	2191	2191	807.4138794	2	1612.812109	1612.816894	-0.004785227	K	S	-	4	14	0	0
				2220	2233	13	R	SLLVNPEGPTLMR	L	0.81%	4041	4041	714.387207	2	1426.758764	1425.764983	0.993781327	R	L	-	5	13	1	0
				2233	2263	30	R	LNSVQSSERPLFLVHPIEGSTTVFHSLASR	L	2.59%	5704	5704	828.4416504	4	3309.735301	3307.731322	2.003979627	R	L	-	1	30	2	0
				2275	2294	19	R	AAPLDSIHSLAAYYIDCIR	Q	2.46%	7616	7616	717.367981	3	2149.080468	2148.066909	1.013558719	R	Q	C17:+57.021	5	19	1	0
				2382	2391	9	R	VLEALLPLK	G	0.81%	4739	4739	498.3273926	2	994.6391351	994.6426645	-0.003529404	R	G	-	4	9	0	0
				2396	2406	10	R	VAAAVDLIIK	S	0.81%	4092	4092	506.8211365	2	1011.626623	1011.632828	-0.006205219	R	S	-	5	10	0	0
				2438	2447	9	K	YHGNVMLLR	A	4.23%	1853	1853	551.2627563	2	1100.509863	1101.575331	-1.065468425	K	A	-	4	9	-1	0
				2471	2482	11	K	VSVHVIEGDHR	T	8.26%	678	678	417.77	3	1250.286525	1246.64183	3.644695136	K	T	-	1	11	4	0
				2482	2505	23	R	TLLEGSGLESIISIIHSSLAEPR	V	0.81%	9220	9220	808.1134033	3	2421.316735	2421.311502	0.005233097	R	V	-	4	23	0	0
P49368	T-complex protein 1 subunit gamma	23	49.17%	5	15	10	R	PVLVLSQNTK	R	4.92%	1195	1195	549.8280029	2	1097.640356	1097.644455	-0.004099685	R	R	-	1	10	0	0
				31	38	7	K	TIADIIR	T	3.69%	2283	2283	401.2450562	2	800.4744622	800.475599	-0.001136735	K	T	-	2	7	0	0
				48	68	20	K	MLLDPMGGIVMTNDGNAILR	E	0.81%	6674	6674	1066.040405	2	2130.06516	2130.063552	0.001608467	K	E	-	4	20	0	0
				127	138	11	R	KALDDMISTLK	K	0.81%	3246	3246	617.8386841	2	1233.661718	1233.663872	-0.00215342	R	K	-	2	11	0	1
				128	139	11	K	ALDDMISTLKK	I	0.81%	3271	3271	617.8382568	2	1233.660864	1233.663872	-0.003007912	K	I	-	4	11	0	1
				139	163	24	K	ISIPVDISDSDMMLNIINSSITTK	A	2.80%	8225	8225	1304.670288	2	2607.324926	2606.318305	1.006620756	K	A	-	4	24	1	0
				167	181	14	R	WSSLACNIALDAVK	M	0.81%	4975	4975	774.3950806	2	1546.774511	1546.780897	-0.006386243	R	M	C6:+57.021	5	14	0	0
				203	216	13	K	IPGGIIEDSCVLR	G	0.81%	3760	3760	714.8765869	2	1427.737524	1427.743783	-0.0062597	K	G	C10:+57.021	5	13	0	0
				237	248	11	R	IVLLDSSLEYK	K	0.81%	4292	4292	640.359436	2	1278.703222	1278.707115	-0.003893466	R	K	-	5	11	0	0
				237	249	12	R	IVLLDSSLEYKK	G	3.03%	3286	3286	704.4063721	2	1406.797094	1406.802079	-0.004984531	R	G	-	3	12	0	1
				294	306	12	K	GISDLAQHYLMR	A	0.81%	4463	4463	468.5732727	3	1402.696343	1402.702717	-0.006373669	K	A	-	3	12	0	0

				330	353	23	R	IVSRPEELREDDVGTGAGLLEIK	K	0.81%	3848	3848	624.8359985	4	2495.312694	2495.323129	-0.010435139	R	K	-	3	23	0	1
				370	377	7	K	ACTILLR	G	4.18%	1213	1213	424.25	2	846.4843499	845.4788415	1.00550844	K	G	C2:+57.021	2	7	1	0
				381	389	8	K	EILSEVER	N	2.61%	1356	1356	487.7596436	2	973.503637	973.5080214	-0.004384419	K	N	-	1	8	0	0
				389	399	10	R	NLQDAMQVCR	N	0.81%	1239	1239	617.7819824	2	1233.548315	1233.55896	-0.010645684	R	N	C9:+57.021	5	10	0	0
				399	425	26	R	NVLLDPQLVPGGGASEMAVAHALTEK	S	0.81%	6073	6073	1309.682617	2	2617.349584	2616.358136	0.991448727	R	S	-	4	26	1	0
				404	425	21	D	PQLVPGGGASEMAVAHALTEK	S	3.30%	4551	4551	688.3560791	3	2062.044762	2062.051723	-0.006960535	D	S	-	1	21	0	0
				427	438	11	K	AMTGVEQWPYR	A	0.81%	3223	3223	669.3146362	2	1336.613622	1336.623404	-0.009781227	K	A	-	5	11	0	0
				438	449	11	R	AVAQALEVIPR	T	0.81%	3388	3388	583.8465576	2	1165.677465	1165.681904	-0.004438486	R	T	-	5	11	0	0
				449	461	12	R	TLIQNCGASTIR	L	0.81%	740	740	667.3474121	2	1332.679174	1332.681517	-0.002343317	R	L	C6:+57.021	5	12	0	0
				491	502	11	K	ELGIWEPLAVK	L	0.81%	5543	5543	627.8564453	2	1253.697241	1253.70197	-0.004729879	K	L	-	5	11	0	0
				504	529	25	Q	TYKTAVETAVLLLRIDDIVSGHKKK	G	4.92%	7653	7653	933.64	3	2797.896525	2797.606562	0.289963008	Q	G	-	1	25	0	4
				507	518	11	K	TAVETAVLLLR	I	0.81%	5005	5005	593.3623047	2	1184.708959	1184.712869	-0.003910177	K	I	-	5	11	0	0
P49768	Presenilin-1	1	3.21%	380	395	15	K	LGLGDFIFYSVLVGK	A	0.81%	8745	8745	814.4644165	2	1626.913183	1626.902127	0.01105584	K	A	-	5	15	0	0
P49895	Type I iodothyronine deiodinase	1	3.61%	27	36	9	K	VLLILFPDR	V	4.30%	3489	3489	544.3066406	2	1086.597631	1084.664463	1.933168594	K	V	-	4	9	2	0
P50395	Rab GDP dissociation inhibitor beta	2	8.54%	118	137	19	K	VPSTEAEALASSLMGLFEK	R	0.81%	8805	8805	661.0095825	3	1980.005272	1978.992142	1.013130319	K	R	-	5	19	1	0
				174	193	19	K	FDLGQDVIDFTGHALALYR	T	4.42%	8389	8389	718.3811646	3	2152.120019	2151.063651	1.056367612	K	T	Q5:+0.984	3	19	1	0
P50443	Sulfate transporter	1	2.84%	330	351	21	K	APIPIELVVVVAATLASHFGK	L	0.81%	11360	11360	711.7561035	3	2132.244835	2131.240509	1.004326675	K	L	-	4	21	1	0
P50570	Dynamin-2	4	6.32%	66	77	11	R	RPLILQLIFSK	T	3.41%	7373	7373	664.4261475	2	1326.836645	1326.838739	-0.002093926	R	T	-	4	11	0	0
				113	123	10	K	GISPVPINLR	V	0.81%	3480	3480	533.3226318	2	1064.629614	1064.634225	-0.00461148	K	V	-	5	10	0	0
				123	142	19	R	VYSPHVLNLTLIDLPGITK	V	0.81%	7050	7050	699.0749512	3	2094.201378	2092.193224	2.008154212	R	V	-	1	19	2	0
				142	157	15	K	VPVGDQPPDIEYQIK	D	0.81%	3413	3413	849.9401855	2	1697.864721	1696.867198	0.99752279	K	D	-	5	15	1	0
P51148	Ras-related protein Rab-5C	8	53.24%	23	34	11	K	LVLLGESAVGK	S	0.81%	3455	3455	543.3295898	2	1084.64353	1084.649207	-0.005676888	K	S	-	3	11	0	0
				71	82	11	K	FEIWDTAGQER	Y	0.81%	3794	3794	676.3134766	2	1350.611303	1350.620426	-0.009122603	K	Y	-	5	11	0	0
				82	92	10	R	YHSLAPMYYR	G	0.81%	1956	1956	650.8092651	2	1299.60288	1299.607025	-0.004145007	R	G	-	5	10	0	0
				92	111	19	R	GAQAAIVVYDITNTDTFAR	A	0.81%	5641	5641	1013.513245	2	2025.010839	2025.016716	-0.005877094	R	A	-	5	19	0	0
				121	135	14	R	QASPNIVIALAGNK	A	0.81%	4113	4113	698.4016724	2	1394.787695	1394.78816	-0.000465177	R	A	-	5	14	0	0
				142	166	24	R	AVEFQEAQAYADDNSLLFMETSAK	T	0.81%	6034	6034	1340.61438	2	2679.21311	2677.221761	1.991348462	R	T	-	4	24	2	0
				166	180	14	K	TAMNVNEIFMAIAK	K	0.81%	6975	6975	776.8927612	2	1551.769872	1551.778919	-0.009046955	K	K	-	4	14	0	0
				198	210	12	R	GVDLQENNPASR	S	0.81%	685	685	650.3150635	2	1298.614477	1298.621488	-0.007011431	R	S	-	5	12	0	0
P51151	Ras-related protein Rab-9A	5	31.34%	9	20	11	K	VILLGDGGVGK	S	3.00%	2847	2847	515.2973633	2	1028.579076	1026.607342	1.971734867	K	S	-	1	11	2	0
				31	47	16	K	FDTQLFHTIGVEFLNK	D	0.81%	6794	6794	954.9951172	2	1907.974584	1907.978146	-0.003561473	K	D	-	3	16	0	0
				103	125	22	K	EFIYYADVKEPESFPFVILGNK	I	0.81%	7026	7026	869.447876	3	2605.320153	2604.31519	1.00496269	K	I	-	4	22	1	1
				112	125	13	K	EPESFPFVILGNK	I	7.26%	6156	6156	738.8881836	2	1475.760717	1475.766027	-0.005310292	K	I	-	1	13	0	0
				178	192	14	R	SDHLIQTDTVNLHR	K	0.81%	929	929	550.2820435	3	1647.822655	1647.832878	-0.010223093	R	K	-	4	14	0	0
P51159	Ras-related protein Rab-27A	5	30.77%	11	22	11	K	FLALGDSGVGK	T	4.82%	2809	2809	532.2906494	2	1062.565649	1062.570956	-0.005307348	K	T	-	1	11	0	0
				37	49	12	K	FITTVGIDFREK	R	4.98%	9804	9804	713.3862305	2	1424.756811	1424.766362	-0.00955087	K	R	-	2	12	0	1
				69	80	11	H	LQLWDTAGQER	F	0.81%	2932	2932	659.33	2	1316.64435	1315.65206	0.992289784	S	F	-	3	11	1	0
				90	111	21	R	DAMGFLLLFDLTNEQSFLNVR	N	3.95%	9635	9635	815.4133911	3	2443.216698	2443.20933	0.007367964	R	N	Q15:+0.984	1	21	0	0
				141	154	13	R	VVKEEEAIALAEK	Y	1.93%	1467	1467	715.3947754	2	1428.773901	1427.787157	0.986743861	R	Y	-	5	13	1	1
P51572	B-cell receptor-associated protein 31	11	40.24%	79	95	16	K	VNLQNNPGAMEHFHMK	L	0.81%	2435	2435	933.9433594	2	1865.871069	1865.866506	0.00456295	K	L	-	4	16	0	0
				101	117	16	R	NLYIAGFSLLLSFLLR	R	0.81%	11825	11825	921.5454102	2	1841.07517	1840.049839	1.025331673	R	R	N1:+0.984	3	16	1	0
				101	118	17	R	NLYIAGFSLLLSFLLRR	L	1.93%	10926	10926	666.395752	3	1996.163781	1995.16695	0.996831027	R	L	-	4	17	1	1
				117	137	20	R	RLVTLISQQATLLASNEAFK	K	0.81%	5915	5915	735.4169312	3	2203.227318	2202.237214	0.990103961	R	K	-	4	20	1	1
				117	138	21	R	RLVTLISQQATLLASNEAFKK	Q	5.65%	5252	5252	778.1192017	3	2331.33413	2330.332178	1.001952348	R	Q	-	1	21	1	2
				118	137	19	R	LVTLISQQATLLASNEAFK	K	0.81%	6274	6274	683.3845215	3	2047.130089	2047.120103	0.009986109	R	K	Q7:+0.984	2	19	0	0
				118	138	20	R	LVTLISQQATLLASNEAFKK	Q	3.38%	5432	5432	726.4209595	3	2176.239403	2174.231066	2.008336938	R	Q	-	1	20	2	1
				159	182	23	K	GAAVDGGKLDVGNAEVKLEEENR	S	5.40%	2669	2669	791.0667114	3	2370.176659	2370.166278	0.010380757	K	S	N13:+0.984	1	23	0	2
				167	182	15	K	LDVGNAEVKLEEENR	S	0.81%	2543	2543	858.4364624	2	1714.857275	1713.853339	1.003935597	K	S	-	5	15	1	1
				204	213	9	K	AENQVLAMR	K	0.81%	973	973	516.2671509	2	1030.518652	1030.522961	-0.004309434	K	K	-	5	9	0	0
				232	246	14	K	LQAAVDGPMDKKEE	-	3.89%	715	715	765.88	2	1529.74435	1529.739556	0.004794064	K	-	-	1	14	0	2
P51617	Interleukin-1 receptor-associated kinase 1	2	2.11%	79	91	12	R	VADLVHILTHLQ	L	7.27%	5238	5238	453.9361877	3	1358.785088	1357.771781	1.013306696	R	L	-	1	12	1	0
				79	94	15	R	VADLVHILTHLQLLR	A	3.85%	7415	7415	581.9411011	3	1742.799828	1740.041021	2.758807359	R	A	-	2	15	3	0
P51809	Vesicle-associated membrane protein 7	4	23.18%	74	83	9	R	AFNFLNEIK	K	0.81%	5354	5354	548.2937622	2	1094.571874	1094.576041	-0.004167122	R	K	-	5	9	0	0
				93	115	22	R	AQTALPYAMNSEFSSVLAAQLK	H	2.51%	6852	6852	781.4000244	3	2341.176598	2340.167131	1.009467074	R	H	N10:+0.984	2	22	1	0
				125	137	12	K	VMETQAQVDELK	G	0.81%	983	983	695.8449097	2	1389.674169	1389.680978	-0.006808984	K	G	-	5	12	0	0
				142	150	8	R	NIDLVAQR	G	5.48%	1077	1077	464.7619324	2	927.5082147	927.5137755	-0.005560798	R	G	-	1	8	0	0
P51828	Adenylate cyclase type 7	1	1.57%	906	923	17	R	LLNEIIADFDELLLKPK	F	3.03%	9035	9035	662.0515137	3	1983.131066	1983.129227	0.001839016	R	F	-	2	17	0	0
P52272	Heterogeneous nuclear ribonucleoprotein M	25	48.77%	17	37	20	K	MEEESGAPGVPSGNGAPGPK	G	0.81%	666	666	934.9157715	2	1867.815893	1867.825789	-0.009896447	K	G	N14:+0.984	4	20	0	0
				72	83	11	R	AFITNIPFDVK	W	0.81%	5328	5328	632.8492432	2	1263.682836	1263.68632	-0.003484096	R	W	-	5	11	0	0
				94	110	16	K	VGEVTYVELLMDAEGK	S	0.81%	6582	6582	876.9385376	2	1751.861425	1751.865151	-0.003725381	K	S	-	5	16	0	0
				126	134	8	K	KAAEVLNK	H	6.00%	1323	1323	438.2290344	2	874.4424188	872.4967128	1.94570596	K	H	N7:+0.984	1	8	2	1
				201	214	13	R	LGSTVFVANLDYK	V	0.81%	4125	4125	713.880127	2	1425.744604	1425.750377	-0.005773494	R	V	-	5	13	0	0
				219	232	13	K	LKEVFSMAGVVVR	A	0.81%	4055	4055	717.9074707	2	1433.799291	1433.806454	-0.00716221	K	A	-	5	13	0	1
				221	232	11	K	EVFSMAGVVVR	A	2.26%	4386	4386	597.3195801	2	1192.62351	1192.627426	-0.003916236	K	A	-	5	11	0	0
				244	277	33	R	GIGTVTFEQSIEAVQAISMFNGQLLFDRPMHVK	M	0.81%	9261	9261	1222.630859	3	3664.869103	3663.842909	1.026193701	R	M	N21:+0.984	1	33	1	0
				285	322	37	K	GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLNK	G	3.08%	5037	5037	955.9835815	4	3819.903026	3818.895095	1.007930772	K	G	Q10:+0.984	1	37	1	0
				322	345	23	K	GIGMGNIGPAGMGMEGIGFGINK	M	0.81%	6139	6139	1089.521729	2	2177.027807	2177.043151	-0.015343937	K	M	-	3	23	0	0
				345	362	17	K	MGGMEGPFGGGMENMGR	F	0.81%	4338	4338	858.3400879	2	1714.664526	1713.673153	0.991373053	K	F	-	4	17	1	0
				362	371	9	R	FGSGMNMGR	I	2.46%	749	749	478.7059631	2	955.3962762	955.4004041	-0.004127914	R	I	-	5	9	0	0
				371	381	10	R	INEILSNALK	R	0.81%	3125	3125	559.3150635	2	1116.614477	1113.63937	2.975106769	R	R	-	2	10	3	0
				371	382	11	R	INEILSNALKR	G	0.81%	2904	2904	635.8773193	2	1269.738989	1269.740481	-0.001492664	R	G	-	5	11	0	1
				388	410	22	K	QGGGGGGGSVPGIERMGPGIDR	L	5.07%	6503	6503	671.1415405	3	2010.401146	2009.921118	0.48002819	K	L	Q1:-17.027,Q1:+0.984,M1	1	22	0	1
				436	443	7	R	MGLVMDR	M	2.26%	1124	1124	411.2034302	2	820.3912103	820.3935278	-0.002317488	R	M	-	5	7	0	0
				456	471	15	R	MGPLGLDHMASSIER	M	0.81%	3841	3841	807.8968506	2	1613.778051	1612.770146	1.007905492	R	M	-	5	15	1	0
				485	496	11	R	MGAGMGFGLER	M	0.81%	3338	3338	564.3339233	2	1126.652197	1124.510683	2.141513608	R	M	-	2	11	2	0
				524	531	7	R	MGLSMER	M	4.57%	877	877	412.7525024	2	823.4893548	822.3727923	1.116562483	R	M	-	4	7	1	0
				531	543	12	R	MVPAGMGAGLER	M	0.81%	1648	1648	594.7958374	2	1187.576025	1187.579097	-0.003072275	R	M	-	1	12	0	0
				591	606	15	R	MGPAMGPALGAGIER	M	0.81%	3191	3191	714.3583984	2	1426.701147	1426.706089	-0.004941829	R	M	-	5	15	0	0
				606	621	15	R	MGLAMGGGGGASFDR	A	0.81%	3222	3222	692.3102417	2	1382.604833	1382.607103	-0.002269466	R	A	-	5	15	0	0
				627	650	23	R	GNFGGSFAGSFGGAGGHAPGVAR	K	0.81%	3249	3249	1018.48175	2	2034.947851	2033.945617	1.002234025	R	K	-	4	23	1	0
				658	667	9	R	NLPFDFTWK	M	5.37%	5893	5893	584.2929077	2	1166.570165	1166.576041	-0.005876106	R	M	-	2	9	0	0
				698	707	9	K	FESPEVAER	A	0.81%	732	732	532.2546997	2	1062.493749	1062.498185	-0.004435722	K	A	-	5	9	0	0
P52630	Signal transducer and activator of transcription 2	2	5.05%	124	148	24	R	AQLEQGEPVLETPVESQQHEIESR	I	2.90%	3280	3280	912.1165771	3	2733.326256	2732.325314	1.000942221	R	I	-	2	24	1	0
				248	267	19	R	APIDHGLEQLETWFTAGAK	L	0.81%	7534	7534	695.6828003	3	2084.024926	2083.037452	0.987474047	R	L	-	3	19	1	0
P53618	Coatomer subunit beta	25	39.77%	54	64	10	K	LPGLLMTIIR	F	0.81%	6640	6640	563.8532715	2	1125.690893	1125.694384	-0.003490775	K	F	-	5	10	0	0
				64	75	11	R	FVLPLQDHTIK	K	8.70%	3916	3916	438.92	3	1313.736525	1310.723419	3.01310628	R	K	Q6:+0.984	1	11	3	0
				107	117	10	K	DLQHPNEFIR	G	0.81%	2106	2106	635.3236084	2	1268.631567	1267.630931	1.000636021	K	G	-	4	10	1	0
				128	141	13	K	EAELLEPLMPAIR	A	0.81%	6059	6059	741.92	2	1481.82435	1480.795948	1.028401432	K	A	-	2	13	1	0
				153	164	11	R	NAVLAIYTIYR	N	0.81%	5350	5350	649.3729858	2	1296.730322	1295.723769	1.00655308	R	N	-	5	11	1	0
				164	185	21	R	NFEHLIPDAPELIHDFLVNEK	D	0.81%	8118	8118	831.0946045	3	2490.260338	2489.259072	1.001266213	R	D	-	5	21	1	0
				191	204	13	R	NAFMMLIHADQDR	A	0.81%	5077	5077	781.8665161	2	1561.717382	1560.717716	0.999666147	R	A	-	5	13	1	0
				261	279	18	K	YEAAGTLVTLSSAPTAIK	A	0.81%	4347	4347	897.4858398	2	1792.95603	1791.961827	0.994202576	K	A	-	5	18	1	0
				279	291	12	K	AAAQCYIDLIIK	E	0.81%	5758	5758	689.8751221	2	1377.734594	1377.732156	0.002437989	K	E	C5:+57.021	5	12	0	0
				316	327	11	R	VLQDLVMDILR	V	0.81%	7578	7578	657.8754883	2	1313.735326	1313.737705	-0.002378717	R	V	-	5	11	0	0
				327	337	10	R	VLSTPDLEVR	K	0.81%	2809	2809	564.8157959	2	1127.615942	1127.618635	-0.002692947	R	K	-	1	10	0	0
				339	351	12	K	TLQLALDLVSSR	N	0.81%	5402	5402	658.8863525	2	1315.757055	1314.750712	1.00634335	K	N	-	4	12	1	0
				351	361	10	R	NVEELVIVLK	K	2.59%	5337	5337	578.3518677	2	1154.688085	1154.691071	-0.002986104	R	K	-	4	10	0	0
				481	495	14	R	SLGEIPIVESEIKK	E	0.81%	4161	4161	771.946228	2	1541.876806	1540.871221	1.005585047	R	E	-	5	14	1	1
				495	513	18	K	EAGELKPEEEITVGPVQK	L	0.81%	2313	2313	977.5127563	2	1953.009863	1952.010234	0.999628687	K	L	-	5	18	1	0
				513	531	18	K	LVTEMGTYATQSALSSSR	P	4.33%	3540	3540	951.9702759	2	1901.924902	1900.92004	1.004861942	K	P	-	1	18	1	0
				513	534	21	K	LVTEMGTYATQSALSSSRPTK	K	0.81%	2852	2852	743.7111816	3	2228.11007	2227.115445	0.994624434	K	K	-	2	21	1	0
				577	597	20	K	QNSFVAEAMLLMATILHLGK	S	4.22%	10666	10666	735.0556641	3	2202.143517	2203.138166	-0.994648813	K	S	N2:+0.984,M9:+15.995	2	20	-1	0
				661	679	18	R	NVTVQPDDPISFMQLTAK	N	0.81%	6121	6121	1003.006836	2	2003.998022	2003.003376	0.994646299	R	N	-	4	18	1	0
				679	702	23	K	NEMNCKEDQFQLSLLAAMGNTQR	K	5.29%	3853	3853	900.7390137	3	2699.193566	2699.198441	-0.004875448	K	K	C5:+57.021,Q9:+0.984,N2	1	23	0	1
				767	786	19	K	LVEKPSPLTLAPHDFANIK	A	0.81%	4259	4259	523.2958374	4	2089.152049	2089.157173	-0.005123543	K	A	-	4	19	0	0
				790	814	24	K	VASTENGIIFGNIVYDVSGAASDR	N	3.61%	7026	7026	819.7453613	3	2456.212609	2456.17068	0.041929352	K	N	N6:+0.984,N12:+0.984	2	24	0	0
				852	871	19	K	VTVNTNMVDLNDYLQHILK	S	3.70%	7403	7403	744.0545044	3	2229.140038	2230.130352	-0.990313464	K	S	Q15:+0.984	3	19	-1	0
				898	928	30	R	SIFGEDALANVSIEKPIHQGPDAAVTGHIR	I	0.81%	4850	4850	1048.878296	3	3143.611413	3142.604709	1.006704015	R	I	Q19:+0.984	3	30	1	0
				932	943	11	K	SQGMALSLGDK	I	5.21%	3650	3650	562.2651367	2	1122.514623	1121.538756	0.975867134	K	I	M4:+15.995	1	11	1	0
P53680	AP-2 complex subunit sigma	2	10.56%	3	10	7	R	FILIQNR	A	3.06%	2592	2592	452.2719116	2	902.5281732	902.5337826	-0.005609414	R	A	-	3	7	0	0
				45	53	8	K	HTNFVEFR	N	3.41%	1206	1206	525.2601929	2	1048.504736	1048.509024	-0.00428877	K	N	-	2	8	0	0
P53985	Monocarboxylate transporter 1	2	6.40%	224	236	12	K	DLHDANTDLIGR	H	3.82%	1441	1441	447.2227173	3	1338.644677	1338.652788	-0.008111729	K	H	-	1	12	0	0
				459	479	20	K	ESKEEETSIDVAGKPNEVTK	A	3.08%	690	690	731.0286865	3	2190.062584	2189.069934	0.992650578	K	A	-	5	20	1	1
P54105	Methylosome subunit pICln	2	16.03%	30	43	13	K	GLGTGTLYIAESR	L	0.81%	3088	3088	669.3512573	2	1336.686865	1336.698676	-0.01181148	K	L	-	5	13	0	0
				43	68	25	R	LSWLDGSGLGFSLEYPTISLHALSR	D	0.81%	8120	8120	907.4793701	3	2719.414635	2718.401714	1.012921384	R	D	-	5	25	1	0
P54578	Ubiquitin carboxyl-terminal hydrolase 14	1	2.63%	30	43	13	K	AQLFALTGVQPAR	Q	0.81%	4117	4117	686.3968506	2	1370.778051	1370.76703	0.011020708	K	Q	-	4	13	0	0
P54709	Sodium/potassium-transporting ATPase subunit beta-3	11	43.37%	7	17	10	K	SLNQSLAEWK	L	0.81%	3338	3338	588.3040161	2	1174.592382	1174.598234	-0.005851405	K	L	-	5	10	0	0
				17	31	14	K	LFIYNPTTGEFLGR	T	0.81%	5725	5725	814.9281006	2	1627.840551	1626.840589	0.999961668	K	T	-	5	14	1	0
				71	97	26	K	YRDQIPSPGLMVFPKPVTALEYTFSR	S	0.81%	7185	7185	754.1448975	4	3012.54829	3011.557898	0.990391452	K	S	-	3	26	1	1
				73	86	13	R	DQIPSPGLMVFPK	P	4.62%	5156	5156	714.8786011	2	1427.741552	1427.74827	-0.006717852	R	P	-	1	13	0	0
				86	97	11	K	PVTALEYTFSR	S	3.21%	3892	3892	642.3312988	2	1282.646948	1282.655749	-0.008800936	K	S	-	1	11	0	0
				97	112	15	R	SDPTSYAGYIEDLKK	F	0.81%	3909	3909	843.9142456	2	1685.812841	1685.814828	-0.001987165	R	F	-	5	15	0	1
				99	112	13	D	PTSYAGYIEDLKK	F	4.01%	3251	3251	495.5916138	3	1483.751366	1483.755857	-0.004490491	D	F	-	1	13	0	1
				174	188	14	K	MNRIIGLKPEGVPR	I	5.34%	8016	8016	798.41	2	1594.80435	1594.897814	-0.093463736	K	I	M1:+15.995	1	14	0	1
				177	188	11	R	IIGLKPEGVPR	I	0.81%	1512	1512	589.8658447	2	1177.716039	1177.718289	-0.002249787	R	I	-	5	11	0	0
				194	213	19	K	NEDIPNVAVYPHNGMIDLK	Y	0.81%	4578	4578	713.6873169	3	2138.038476	2138.046637	-0.008161796	K	Y	-	3	19	0	0
				221	244	23	K	LHVGYLQPLVAVQVSFAPNNTGK	E	0.81%	5803	5803	818.4446411	3	2452.310448	2452.311426	-0.00097826	K	E	Q7:+0.984	3	23	0	0
P55061	Bax inhibitor 1	3	8.44%	6	15	9	R	KINFDALLK	F	3.21%	4134	4134	531.3206787	2	1060.625707	1060.628077	-0.002369714	R	F	-	2	9	0	1
				7	15	8	K	INFDALLK	F	0.81%	5003	5003	467.2733459	2	932.5310418	932.5331139	-0.002072105	K	F	-	5	8	0	0
				219	230	11	R	KLMMILAMNEK	D	3.04%	6050	6050	661.3627319	2	1320.709814	1320.696771	0.013043235	R	D	-	2	11	0	1
P55160	Nck-associated protein 1-like	12	17.39%	175	189	14	R	LGQMVLEYDHPLKK	L	1.93%	2982	2982	557.6359253	3	1669.884301	1669.886161	-0.001859833	R	L	-	2	14	0	1
				349	365	16	K	ELETVLADEPGLLGPK	A	0.81%	5204	5204	840.9542847	2	1679.892919	1679.898164	-0.0052448	K	A	-	5	16	0	0
				423	435	12	K	VIQQYHLQYLAR	F	0.81%	3054	3054	766.9202271	2	1531.824804	1530.830693	0.994110662	K	F	-	4	12	1	0
				500	513	13	K	APLHLHENPDLAK	V	0.81%	654	654	486.282135	3	1455.82293	1453.767759	2.055171197	K	V	-	1	13	2	0
				513	523	10	K	VMNLIVFHSR	M	1.93%	4009	4009	406.2269897	3	1215.657494	1214.659395	0.99809899	K	M	-	5	10	1	0
				719	745	26	R	AIVWLAGYNATTQEIVRPSELLAGVK	A	2.59%	7299	7299	934.1830444	3	2799.525658	2798.533063	0.992595677	R	A	-	3	26	1	0
				745	764	19	K	AYIGFIQSLAQFLGADASR	V	0.81%	9528	9528	1015.026001	2	2028.036352	2027.047622	0.988729441	K	V	-	5	19	1	0
				799	820	21	R	QASSGTIILSPAMQAFVSLPR	E	0.81%	7246	7246	1088.08606	2	2174.156469	2173.156522	0.999946813	R	E	-	5	21	1	0
				838	850	12	R	ALAELLGPYGMK	F	0.81%	5285	5285	631.8447266	2	1261.673803	1261.674042	-0.000239179	R	F	-	5	12	0	0
				850	868	18	K	FLSENLMWHVTSQIVELK	K	1.93%	7550	7550	725.7159424	3	2174.124352	2173.124159	1.000192596	K	K	-	2	18	1	0
				882	906	24	R	SNFSKPDLMASLLPQLTGAENVLK	R	0.81%	7493	7493	858.7922974	3	2573.353417	2572.357073	0.996344058	R	R	-	5	24	1	0
				907	918	11	R	MTIIGVILSFR	A	0.81%	9657	9657	625.3682251	2	1248.7208	1248.726412	-0.005612037	R	S	-	5	11	0	0

P55286	Cadherin-8	1	1.38%	698	709	11	K	DIKPDLQFMPR	Q	5.89%	1150	1150	454.2241821	3	1359.649071	1358.701654	0.947417259	K	Q	-	1	11	1	0
P56937	3-keto-steroid reductase	3	18.77%	102	111	9	K	ALFFGLFSR	K	3.65%	7190	7190	530.2975464	2	1058.579443	1056.575647	2.003795237	K	K	-	2	9	2	0
				129	151	22	K	ITADGLQEVFETNVFGHFILIR	E	3.54%	8636	8636	840.7816162	3	2519.321374	2519.306007	0.015366721	K	E	Q7:+0.984	1	22	0	0
				251	284	33	R	FFANAFTLTPYNGTEALVWLFHQKPESLNPLIK	Y	4.67%	9211	9211	952.5013428	4	3805.974071	3806.971202	-0.997131482	R	Y	Q23:+0.984	1	33	-1	0
P59190	Ras-related protein Rab-15	2	10.38%	10	21	11	R	LLLIGDSGVGK	T	0.81%	3675	3675	536.3205566	2	1070.625463	1070.633556	-0.008093215	K	T	-	3	11	0	0
				58	69	11	R	IQIWDTAGQER	Y	5.10%	3162	3162	658.83	2	1315.64435	1315.65206	-0.007710216	R	Y	-	1	11	0	0
P60953	Cell division control protein 42 homolog	6	48.17%	16	27	11	K	TCLLISYTTNK	F	0.81%	3406	3406	657.3388672	2	1312.662084	1312.669221	-0.007137129	K	F	C2:+57.021	2	11	0	0
				45	66	21	M	IGGEPYTLGLFDTAGQEDYDR	L	4.66%	5782	5782	1159.535278	2	2317.054907	2316.054618	1.000288441	M	L	-	1	21	1	0
				66	94	28	R	LRPLSYPQTDVFLVCFSVVSPSSFENVK	E	0.81%	7474	7474	1072.879883	3	3215.616173	3214.636807	0.979366125	R	E	C15:+57.021	5	28	1	0
				96	107	11	K	WVPEITHHCPK	T	1.93%	822	822	702.3458252	2	1402.676	1402.681123	-0.005123145	K	T	C9:+57.021	4	11	0	0
				107	120	13	K	TPFLLVGTQIDLR	D	0.81%	6265	6265	736.9247437	2	1471.833837	1471.839861	-0.006023871	K	D	-	5	13	0	0
				107	128	21	K	TPFLLVGTQIDLRDDPSTIEK	L	0.81%	5385	5385	787.0923462	3	2358.253563	2357.247839	1.005724686	K	L	-	3	21	1	1
P61006	Ras-related protein Rab-8A	8	42.51%	10	21	11	K	LLLIGDSGVGK	T	0.81%	3675	3675	536.3205566	2	1070.625463	1070.633556	-0.008093215	K	T	-	3	11	0	0
				46	55	9	K	IRTIELDGK	R	5.51%	3105	3105	523.2884521	2	1044.561254	1043.597505	0.963748993	K	T	-	1	9	1	1
				58	69	11	K	LQIWDTAGQER	F	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				71	79	8	R	TITTAYYR	G	0.81%	822	822	494.7568359	2	987.4980218	987.5025421	-0.004520293	R	G	-	3	8	0	0
				79	94	15	R	GAMGIMLVYDITNEK	S	0.81%	6716	6716	827.9124146	2	1653.809179	1653.810614	-0.001434474	R	S	-	5	15	0	0
				104	116	12	R	NIEEHASADVEK	M	0.81%	626	626	671.3170776	2	1340.618505	1340.62082	-0.002314455	R	M	-	5	12	0	0
				138	146	8	K	LALDYGIK	F	3.69%	2742	2742	446.7595215	2	891.5033929	891.5065648	-0.003171903	K	F	-	2	8	0	0
				153	167	14	K	ANINVENAFFTLAR	D	0.81%	6387	6387	790.4140625	2	1578.812475	1578.815437	-0.00296236	K	D	-	5	14	0	0
P61020	Ras-related protein Rab-5B	5	27.91%	22	33	11	K	LVLLGESAVGK	S	0.81%	3455	3455	543.3295898	2	1084.64353	1084.649207	-0.005676888	K	S	-	3	11	0	0
				70	81	11	K	FEIWDTAGQER	Y	0.81%	3794	3794	676.3134766	2	1350.611303	1350.620426	-0.009122603	K	Y	-	5	11	0	0
				81	91	10	R	YHSLAPMYYR	G	0.81%	1956	1956	650.8092651	2	1299.60288	1299.607025	-0.004145007	R	G	-	5	10	0	0
				120	134	14	R	QASPSIVIALAGNK	A	0.81%	3938	3938	684.8927002	2	1367.76975	1367.777261	-0.007510465	R	A	-	5	14	0	0
				165	179	14	K	TAMNVNDLFLAIAK	K	0.81%	6864	6864	760.9066772	2	1519.797704	1519.806848	-0.009143124	K	K	-	5	14	0	0
P61026	Ras-related protein Rab-10	12	54.50%	3	11	8	K	KTYDLLFK	L	0.81%	3138	3138	514.2924805	2	1026.569311	1026.574979	-0.005667942	K	L	-	2	8	0	1
				4	11	7	K	TYDLLFK	L	0.81%	3995	3995	450.2456055	2	898.4755609	898.4800157	-0.004454807	K	L	-	5	7	0	0
				11	22	11	K	LLLIGDSGVGK	T	0.81%	3675	3675	536.3205566	2	1070.625463	1070.633556	-0.008093215	K	T	-	3	11	0	0
				28	47	19	R	FSDDAFNTTFISTIGIDFK	I	0.81%	7558	7558	1070.012939	2	2138.010229	2138.020799	-0.010569822	R	I	-	3	19	0	0
				59	70	11	K	LQIWDTAGQER	F	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				70	80	10	R	FHTITTSYYR	G	0.81%	1142	1142	644.8171997	2	1287.618749	1287.624783	-0.006033346	R	G	-	3	10	0	0
				74	95	21	I	TTSYYRGAMGIMLVYDITNGK	S	5.01%	3258	3258	1187.589844	2	2373.164037	2369.139638	4.024399292	I	S	M12:+15.995	1	21	4	1
				80	95	15	R	GAMGIMLVYDITNGK	S	0.81%	6805	6805	791.8963623	2	1581.777075	1581.789484	-0.012409527	R	S	-	5	15	0	0
				161	172	11	K	AFLTLAEDILR	K	0.81%	7214	7214	631.3625488	2	1260.709448	1260.707784	0.001663464	K	K	-	5	11	0	0
				172	196	24	R	KTPVKEPNSENVDISSGGGVTGWK	S	4.12%	2317	2317	829.7478027	3	2486.219933	2485.244879	0.975054363	R	S	-	1	24	1	2
				173	196	23	K	TPVKEPNSENVDISSGGGVTGWK	S	0.81%	2690	2690	1179.586548	2	2357.157446	2357.149916	0.007530039	K	S	-	4	23	0	1
				177	196	19	K	EPNSENVDISSGGGVTGWK	S	0.81%	2891	2891	967.4490967	2	1932.882543	1931.886096	0.996447335	K	S	-	3	19	1	0
P61077	Ubiquitin-conjugating enzyme E2 D3	2	19.73%	72	90	18	R	IYHPNINSNGSICLDILR	S	1.93%	5018	5018	700.6885376	3	2099.042138	2099.046492	-0.004354655	R	S	N9:+0.984,C13:+57.021	3	18	0	0
				90	101	11	R	SQWSPALTISK	V	0.81%	3318	3318	610.3658447	2	1218.716039	1216.645184	2.070855581	R	V	-	2	11	2	0
P61106	Ras-related protein Rab-14	12	70.23%	13	24	11	K	YIIIGDMGVGK	S	4.62%	2749	2749	591.3146973	2	1180.613744	1180.615278	-0.001533845	K	S	M7:+15.994	2	11	0	0
				24	34	10	K	SCLLHQFTEK	K	6.00%	1875	1875	631.8093262	2	1261.603002	1261.612041	-0.009038528	K	K	C2:+57.021	2	10	0	0
				35	51	16	K	FMADCPHTIGVEFGTR	I	7.32%	3529	3529	613.2768555	3	1836.807091	1836.828259	-0.021168162	K	I	C5:+57.021	2	16	0	0
				61	72	11	K	LQIWDTAGQER	F	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				82	95	13	R	GAAGALMVYDITR	R	0.81%	4444	4444	669.3467407	2	1336.677831	1336.680919	-0.003087203	R	R	-	3	13	0	0
				96	110	14	R	STYNHLSSWLTDAR	N	0.81%	4108	4108	826.3980103	2	1650.78037	1649.77978	1.00059034	R	N	-	5	14	1	0
				110	125	15	R	NLTNPNTVIILIGNK	A	0.81%	5145	5145	812.4741211	2	1622.932592	1622.935553	-0.002960453	R	A	-	5	15	0	0
				140	156	16	K	QFAEENGLLFLEASAK	T	0.81%	5936	5936	883.9491577	2	1765.882665	1765.888662	-0.005996642	K	T	-	4	16	0	0
				156	170	14	K	TGENVEDAFLEAAK	K	0.81%	4674	4674	747.3502197	2	1492.684789	1493.688549	-1.003760035	K	K	N4:+0.984	4	14	-1	0
				156	171	15	K	TGENVEDAFLEAAKK	I	0.81%	3960	3960	541.2700806	3	1620.786767	1620.799513	-0.012745965	K	I	-	1	15	0	1
				170	201	31	K	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	L	2.26%	2942	2942	820.6668091	4	3278.635936	3278.627963	0.007972856	K	L	Q28:+0.984	1	31	0	1
				171	201	30	K	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	L	0.81%	3183	3183	788.89	4	3151.5287	3150.533	0.995699664	K	L	Q27:+0.984	3	30	1	0
P61158	Actin-related protein 3	1	2.63%	198	209	11	R	DITYFIQQLLR	D	0.81%	9047	9047	705.3956909	2	1408.775732	1408.771447	0.004284668	R	E	-	4	11	0	0
P61224	Ras-related protein Rap-1b	10	58.70%	5	16	11	K	LVVLGSGGVGK	S	2.26%	1930	1930	493.3021851	2	984.58872	984.5967769	-0.008056859	K	S	-	3	11	0	0
				16	31	15	K	SALTVQFVQGIFVEK	Y	0.81%	6590	6590	555.9800415	3	1664.916649	1664.913754	0.002894928	K	Y	-	4	15	0	0
				31	41	10	K	YDPTIEDSYR	K	0.81%	1352	1352	629.7790527	2	1257.542455	1257.551343	-0.008887595	E	K	-	5	10	0	0
				31	42	11	K	YDPTIEDSYRK	Q	4.45%	733	733	462.8866272	3	1385.636406	1385.646306	-0.009899648	E	Q	-	1	11	0	1
				73	102	29	K	NGQGFALVYSITAQSTFNDLQDLREQILR	V	3.69%	9232	9232	1100.231201	3	3297.670128	3296.678952	0.991176548	K	V	-	2	29	1	1
				102	117	15	R	VKDTDDVPMILVGNK	C	0.81%	3705	3705	822.4366455	2	1642.857641	1642.860005	-0.002364528	R	C	-	5	15	0	1
				108	117	9	D	VPMILVGNK	C	0.81%	2873	2873	485.7896423	2	969.5636346	969.5681204	-0.00448578	D	C	-	5	9	0	0
				136	149	13	R	QWNNCAFLESSAK	S	0.81%	3461	3461	777.8513184	2	1553.686987	1553.692811	-0.005823865	R	S	C5:+57.021	5	13	0	0
				149	163	14	K	SKINVNEIFYDLVR	Q	0.81%	6817	6817	570.9821777	3	1709.923058	1708.914817	1.008240963	K	Q	-	5	14	1	1
				151	163	12	K	INVNEIFYDLVR	Q	0.81%	7387	7387	748.399292	2	1494.782934	1493.787826	0.995108408	K	Q	-	5	12	1	0
P61421	V-type proton ATPase subunit d 1	3	9.12%	75	83	8	K	EKMVVEFR	H	3.96%	6255	6255	519.2562256	2	1036.496801	1036.537549	-0.040747444	K	H	-	3	8	0	1
				246	257	11	R	LYPEGLAQLAR	A	4.57%	4120	4120	615.843689	2	1229.671728	1229.676818	-0.00509043	R	A	-	2	11	0	0
				275	288	13	K	LLFEGAGSNPGDK	T	0.81%	2290	2290	653.3271484	2	1304.638647	1303.640827	0.997820035	K	T	-	5	13	1	0
P61586	Transforming protein RhoA	7	46.63%	18	27	9	K	TCLLIVFSK	D	0.81%	5235	5235	540.8076172	2	1079.599584	1079.604436	-0.004851825	K	D	C2:+57.021	5	9	0	0
				51	68	17	K	QVELALWDTAGQEDYDR	L	0.81%	5128	5128	1004.963501	2	2007.911352	2007.917396	-0.006044231	K	L	-	5	17	0	0
				68	98	30	R	LRPLSYPDTDVILMCFSIDSPDSLENIPEK	W	2.26%	7364	7364	1155.904541	3	3464.690148	3463.688646	1.001502207	R	W	C15:+57.021	5	30	1	0
				104	118	14	K	HFCPNVPIILVGNK	K	0.81%	4369	4369	804.4395142	2	1606.863378	1606.864902	-0.001523472	K	K	C3:+57.021	3	14	0	0
				109	118	9	N	VPIILVGNK	K	0.81%	2947	2947	476.8119507	2	951.6082513	951.6116986	-0.003447361	N	K	-	4	9	0	0
				150	162	12	R	IGAFGYMECSAK	T	0.81%	3295	3295	667.2940674	2	1332.572485	1332.583778	-0.011293578	R	T	C9:+57.021	5	12	0	0
				168	176	8	R	EVFEMATR	A	2.61%	1898	1898	491.734436	2	981.453222	981.4589638	-0.005741818	R	A	-	2	8	0	0
P61769	Beta-2-microglobulin	3	40.34%	39	61	22	K	SNFLNCYVSGFHPSDIEVDLLK	N	0.81%	6526	6526	852.4122925	3	2554.213402	2553.220509	0.992892865	K	N	C6:+57.021	2	22	1	0
				68	78	10	K	VEHSDLSFSK	D	0.81%	801	801	574.7797852	2	1147.54392	1147.550949	-0.007028751	K	D	-	3	10	0	0
				95	111	16	K	DEYACRVNHVTLSQPK	I	5.76%	4055	4055	640.3375244	3	1917.989098	1917.888579	0.10051917	K	I	C5:+57.021,N8:+0.984,Q1	1	16	0	1
P62330	ADP-ribosylation factor 6	5	44.57%	15	26	11	R	ILMLGLDAAGK	T	0.81%	4321	4321	551.3184204	2	1100.621191	1100.626364	-0.005172916	R	T	-	5	11	0	0
				34	55	21	K	LGQSVTTIPTVGFNVETVTYK	N	0.81%	5384	5384	752.4038696	3	2254.188134	2253.189261	0.998872615	K	N	-	4	21	1	0
				58	69	11	K	FNVWDVGGQDK	I	0.81%	3989	3989	632.7995605	2	1263.583471	1263.588397	-0.004926146	K	I	-	4	11	0	0
				75	95	20	R	HYYTGTQGLIFVVDCADRDR	I	2.88%	4837	4837	796.3744507	3	2386.099877	2386.100713	-0.000835981	R	I	Q7:+0.984,C15:+57.021	3	20	0	1
				123	138	15	K	QDLPDAMKPHEIQEK	L	4.76%	987	987	593.9597778	3	1778.855858	1778.850882	0.004976568	K	L	Q1:+0.984	1	15	0	0
P62491	Ras-related protein Rab-11A	10	57.87%	13	24	11	K	VVLIGDSGVGK	S	0.81%	2094	2094	523.2819824	2	1044.548315	1042.602256	1.946058508	K	S	-	3	11	2	0
				41	51	10	K	STIGVEFATR	S	0.81%	2531	2531	541.77	2	1081.52435	1079.56112	1.963230216	K	S	-	5	10	2	0
				61	72	11	K	AQIWDTAGQER	Y	0.81%	1882	1882	639.2866211	2	1276.557592	1273.60511	2.952482212	K	Y	-	2	11	3	0
				74	82	8	R	AITSAYYR	G	0.81%	767	767	472.7441711	2	943.4726922	943.4763273	-0.003635083	R	G	-	4	8	0	0
				82	95	13	R	GAVGALLVYDIAK	H	0.81%	5299	5299	645.8803101	2	1289.74497	1288.739084	1.005885765	R	H	-	4	13	1	0
				107	125	18	K	ELRDHADSNIVIMLVGNK	S	0.81%	4711	4711	675.3575439	3	2023.049157	2023.052057	-0.002900332	K	S	-	4	18	0	1
				110	125	15	R	DHADSNIVIMLVGNK	S	0.81%	5099	5099	813.43	2	1624.84435	1624.824289	0.02006132	R	S	-	5	15	0	0
				145	174	29	K	NGLSFIETSALDSTNVEAAFQTILTEIYR	I	0.81%	10362	10362	1068.878662	3	3203.612511	3202.603387	1.009124368	K	I	-	4	29	1	0
				184	209	25	R	RENDMSPSNNVVPIHVPPTTENKPK	V	3.66%	1842	1842	701.3562622	4	2801.393749	2799.397375	1.99637394	R	V	-	3	25	2	1
				185	209	24	R	ENDMSPSNNVVPIHVPPTTENKPK	V	1.98%	3279	3279	882.7716064	3	2645.291344	2644.280264	1.01108064	R	V	N8:+0.984	1	24	1	0
P62834	Ras-related protein Rap-1A	9	55.43%	5	16	11	K	LVVLGSGGVGK	S	2.26%	1930	1930	493.3021851	2	984.58872	984.5967769	-0.008056859	K	S	-	3	11	0	0
				16	31	15	K	SALTVQFVQGIFVEK	Y	0.81%	6590	6590	555.9800415	3	1664.916649	1664.913754	0.002894928	K	Y	-	4	15	0	0
				31	41	10	K	YDPTIEDSYR	K	0.81%	1352	1352	629.7790527	2	1257.542455	1257.551343	-0.008887595	E	K	-	5	10	0	0
				31	42	11	K	YDPTIEDSYRK	Q	4.45%	733	733	462.8866272	3	1385.636406	1385.646306	-0.009899648	E	Q	-	1	11	0	1
				73	102	29	K	NGQGFALVYSITAQSTFNDLQDLREQILR	V	3.69%	9232	9232	1100.231201	3	3297.670128	3296.678952	0.991176548	K	V	-	2	29	1	1
				108	117	9	D	VPMILVGNK	C	0.81%	2873	2873	485.7896423	2	969.5636346	969.5681204	-0.00448578	D	C	-	5	9	0	0
				136	149	13	R	QWCNCAFLESSAK	S	0.81%	3574	3574	800.8513794	2	1599.687109	1599.680069	0.007040093	R	S	C3:+57.021,C5:+57.021	2	13	0	0
				149	163	14	K	SKINVNEIFYDLVR	Q	0.81%	6817	6817	570.9821777	3	1709.923058	1708.914817	1.008240963	K	Q	-	5	14	1	1
				151	163	12	K	INVNEIFYDLVR	Q	0.81%	7387	7387	748.399292	2	1494.782934	1493.787826	0.995108408	K	Q	-	5	12	1	0
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	8	18.53%	32	43	11	Q	ITNNIDPVGRI	Q	7.91%	3809	3809	606.3389893	2	1210.662328	1210.666982	-0.004653452	Q	Q	-	1	11	0	1
				57	68	11	K	IYAMHWGTDSR	L	0.81%	2297	2297	668.8023682	2	1335.589086	1335.603003	-0.013916248	K	L	-	5	11	0	0
				78	89	11	K	LIIWDSYTTNK	V	0.81%	4214	4214	677.3544312	2	1352.693212	1352.697613	-0.004401167	K	V	-	5	11	0	0
				197	209	12	R	LFVSGACDASAK	L	3.83%	854	854	614.3261719	2	1226.636694	1224.580406	2.056287366	R	L	C7:+57.021	2	12	2	0
				283	301	18	R	LLLAGYDDFNCNVWDALK	A	3.96%	7208	7208	1065.008545	2	2128.00144	2126.013811	1.987628988	R	A	C11:+57.021	2	18	2	0
				57	68	11	K	IYAMHWGTDSR	L	0.81%	2297	2297	668.8023682	2	1335.589086	1335.603003	-0.013916248	K	L	-	5	11	0	0
				78	89	11	K	LIIWDSYTTNK	V	0.81%	4214	4214	677.3544312	2	1352.693212	1352.697613	-0.004401167	K	V	-	5	11	0	0
				256	280	24	R	ADQELLMYSHDNIICGITSVAFSR	S	0.81%	7243	7243	914.7720337	3	2741.292626	2739.299172	1.993454186	R	S	C15:+57.021	3	24	2	0
P63000	Ras-related C3 botulinum toxin substrate 1	10	61.46%	44	66	22	V	MVDGKPVNLGLWDTAGQEDYDR	L	5.08%	3603	3603	624.8286743	4	2495.283397	2496.110537	-0.827139406	V	L	M1:+15.994,N8:+0.984,Q1	1	22	-1	0
				49	66	17	K	PVNLGLWDTAGQEDYDR	L	4.29%	4948	4948	974.9525146	2	1947.889379	1947.896267	-0.006887447	K	L	-	1	17	0	0
				66	94	28	R	LRPLSYPQTDVFLICFSLVSPASFENVR	A	2.61%	8360	8360	1086.562134	3	3256.662926	3254.679341	1.983585519	R	A	C15:+57.021	3	28	2	0
				102	116	14	R	HHCPNTPIILVGTK	L	0.81%	1456	1456	793.9242554	2	1585.832861	1585.839415	-0.006554578	R	L	C3:+57.021	2	14	0	0
				116	128	12	K	LDLRDDKDTIEK	L	4.17%	747	747	730.8804321	2	1459.745214	1459.751834	-0.006619798	K	L	-	1	12	0	2
				132	147	15	K	KLTPITYPQGLAMAK	E	0.81%	3735	3735	544.6420288	3	1630.902611	1630.911647	-0.009035758	K	E	-	5	15	0	1
				133	147	14	K	LTPITYPQGLAMAK	E	0.81%	4149	4149	752.4129028	2	1502.810156	1502.816684	-0.006528344	K	E	-	5	14	0	0
				153	163	10	K	YLECSALTQR	G	0.81%	1586	1586	620.8023682	2	1239.589086	1239.591305	-0.002219104	K	G	C4:+57.021	5	10	0	0
				166	174	8	K	TVFDEAIR	A	0.81%	2550	2550	475.7470398	2	949.4784295	949.486892	-0.008462498	K	A	-	3	8	0	0
				174	183	9	R	AVLCPPPVK	K	0.81%	980	980	490.7819824	2	979.5483148	979.5520065	-0.003691756	R	K	C4:+57.021	5	9	0	0
P63010	AP-2 complex subunit beta	8	10.89%	11	19	8	K	KGEIFELK	A	3.64%	2157	2157	482.2801209	2	962.5445916	962.5436786	0.000912979	K	A	-	2	8	0	1
				67	78	11	K	LVYLYLMNYAK	S	0.81%	6046	6046	696.3780518	2	1390.740453	1389.736643	1.003810892	K	S	-	5	11	1	0
				247	261	14	R	LSHANSAVVLSAVK	V	1.93%	1334	1334	698.4037476	2	1394.791845	1394.78816	0.003685213	R	V	-	5	14	0	0
				283	304	21	K	LAPPLVTLLSGEPEVQYVALR	N	2.32%	8285	8285	756.4393311	3	2266.294518	2264.278017	2.016501444	K	N	-	2	21	2	0
				327	335	8	K	YNDPIYVK	L	0.81%	1314	1314	506.7606812	2	1011.505712	1010.507293	0.998419105	K	L	-	5	8	1	0
				344	359	15	R	LASQANIAQVLAELK	E	0.81%	6305	6305	784.9517212	2	1567.887792	1567.893353	-0.005561049	R	E	-	4	15	0	0
				390	402	12	R	CVSTLLDLIQTK	V	0.81%	6239	6239	695.8815308	2	1389.747411	1389.753286	-0.005874069	R	V	C1:+57.021	5	12	0	0
				879	892	13	R	NVEGQDMLYQSLK	L	1.97%	3731	3731	763.37146	2	1524.72727	1523.728991	0.998278706	R	L	-	4	13	1	0
P63027	Vesicle-associated membrane protein 2	3	46.55%	0	30	30	-	MSATAATAPPAAPAGEGGPPAPPPNLTSNR	R	5.37%	5855	5855	697.8602905	4	2787.409862	2786.317176	1.092686429	-	R	M1:+15.994,N25:+0.984,N	1	30	1	0
				59	83	24	K	LSELDDRADALQAGASQFETSAAK	L	0.81%	3712	3712	832.4003906	3	2494.177697	2494.182322	-0.004625725	K	L	Q12:+0.984	3	24	0	1
				66	83	17	R	ADALQAGASQFETSAAK	L	0.81%	2591	2591	833.4085693	2	1664.801489	1664.800575	0.000913392	R	L	-	5	17	0	0
P63167	Dynein light chain 1, cytoplasmic	2	24.72%	49	60	11	K	YNPTWHCIVGR	N	2.26%	2792	2792	701.8335571	2	1401.651464	1401.660722	-0.009258166	K	N	C7:+57.021	5	11	0	0
				60	71	11	R	NFGSYVTHETK	H	0.81%	978	978	641.8040771	2	1281.592504	1281.598962	-0.006457663	R	H	-	5	11	0	0
P63241	Eukaryotic translation initiation factor 5A-1	9	66.23%	6	26	20	D	FETGDAGASATFPMQCSALR	K	4.65%	3939	3939	1058.973022	2	2115.930395	2115.93491	-0.00451479	D	K	C16:+57.021	1	20	0	0
				39	50	11	K	IVEMSTSKTGK	H	5.35%	3534	3534	598.2988281	2	1194.582006	1195.610921	-1.028915094	K	H	M4:+15.994	1	11	-1	1
				55	67	12	K	VHLVGIDIFTGK	K	0.81%	4711	4711	433.5852966	3	1297.732415	1297.739419	-0.007003827	K	K	-	5	12	0	0
				67	85	18	K	KYEDICPSTHNMDVPNIK	R	0.81%	2512	2512	721.0045776	3	2159.990258	2160.98151	-0.991252162	K	R	C6:+57.021,N11:+0.984	4	18	-1	1
				68	85	17	K	YEDICPSTHNMDVPNIK	R	2.80%	3060	3060	678.6389771	3	2032.893456	2032.886547	0.006909216	K	R	C5:+57.021,N10:+0.984	2	17	0	0
				85	109	24	K	RNDFQLIGIQDGYLSLLQDSGEVR	E	0.81%	7131	7131	912.7977905	3	2735.369896	2735.387855	-0.01795829	K	E	-	3	24	0	1
				86	109	23	R	NDFQLIGIQDGYLSLLQDSGEVR	E	0.81%	7567	7567	1291.659058	2	2581.302465	2579.286744	2.015721554	R	E	-	2	23	2	0
				109	121	12	R	EDLRLPEGDLGK	E	0.81%	2673	2673	671.3496704	2	1340.683691	1340.693591	-0.009899948	R	E	-	5	12	0	1
				109	126	17	R	EDLRLPEGDLGKEIEQK	Y	5.51%	3490	3490	657.010376	3	1968.007653	1968.016382	-0.008729134	R	Y	-	1	17	0	2
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	22	87.70%	12	36	24	K	GHNGWVTQIATTPQFPDMILSASR	D	0.81%	6320	6320	877.4382324	3	2629.291222	2627.280204	2.011018242	K	D	N3:+0.984	1	24	2	0
				36	44	8	R	DKTIIMWK	L	1.93%	2559	2559	517.7861328	2	1033.556616	1033.563035	-0.006419463	R	L	-	5	8	0	1
				44	57	13	K	LTRDETNYGIPQR	A	1.93%	777	777	781.9024048	2	1561.789159	1561.784865	0.004294042	K	A	-	4	13	0	1

				47	57	10	R	DETNYGIPQR	A	1.97%	962	962	596.7799072	2	1191.544164	1191.552012	-0.007847267	R	A	-	4	10	0	0
				60	88	28	R	GHSHFVSDVVISSDGQFALSGSWDGTLR	L	4.72%	8041	8041	989.824707	3	2966.450646	2961.389296	5.061350158	R	L	Q16:+0.984	2	28	5	0
				87	99	12	L	RLWDLTTGTTTR	R	5.63%	2797	2797	710.8781738	2	1419.740698	1419.747023	-0.006325696	L	R	-	1	12	0	1
				88	99	11	R	LWDLTTGTTTR	R	0.81%	3567	3567	632.8261108	2	1263.636572	1263.645912	-0.00934052	R	R	-	2	11	0	0
				106	118	12	K	DVLSVAFSSDNR	Q	0.81%	4046	4046	655.3170776	2	1308.618505	1308.63099	-0.012485175	K	Q	-	5	12	0	0
				130	139	9	K	LWNTLGVCK	Y	0.81%	3221	3221	546.29	2	1090.56435	1089.563634	1.000716024	K	Y	C8:+57.021	5	9	1	0
				139	155	16	K	YTVQDESHSEWVSCVR	F	0.81%	2541	2541	661.6239014	3	1981.848229	1981.847124	0.001105318	K	F	Q4:+0.984,C14:+57.021	3	16	0	0
				155	172	17	R	FSPNSSNPIIVSCGWDK	L	0.81%	4200	4200	954.4483032	2	1906.880956	1906.887882	-0.006925443	R	L	C13:+57.021	3	17	0	0
				159	172	13	N	SSNPIIVSCGWDK	L	3.69%	3299	3299	731.8519287	2	1461.688207	1461.691748	-0.003540506	N	L	C9:+57.021	1	13	0	0
				175	183	8	K	VWNLANCK	L	0.81%	1712	1712	502.7505493	2	1003.485449	1003.490469	-0.005020303	K	L	C7:+57.021	5	8	0	0
				185	212	27	K	TNHIGHTGYLNTVTVSPDGSLCASGGK	D	0.81%	2808	2808	686.8320313	4	2743.296825	2743.286676	0.010148688	K	D	N2:+0.984,C22:+57.021	2	27	0	0
				212	225	13	K	DGQAMLWDLNEGK	H	0.81%	4580	4580	739.88	2	1477.74435	1475.671476	2.072873744	K	H	-	2	13	2	0
				225	245	20	K	HLYTLDGGDIINALCFSPNR	Y	0.81%	6304	6304	760.0108032	3	2277.008935	2276.089086	0.919849012	K	Y	N12:+0.984,C15:+57.021	1	20	1	0
				245	257	12	R	YWLCAATGPSIK	I	0.81%	3970	3970	683.84375	2	1365.67185	1365.674641	-0.002791192	R	I	C4:+57.021	5	12	0	0
				257	264	7	K	IWDLEGK	I	0.81%	2885	2885	430.7284546	2	859.4412591	859.4439645	-0.002705372	K	I	-	3	7	0	0
				264	271	7	K	IIVDELK	Q	2.64%	1855	1855	415.2544861	2	828.4933221	828.4956657	-0.002343656	K	Q	-	2	7	0	0
				264	280	16	K	IIVDELKQEVISTSSK	A	0.81%	3998	3998	895.006897	2	1787.998144	1787.988042	0.010102033	K	A	-	5	16	0	1
				280	308	28	K	AEPPQCTSLAWSADGQTLFAGYTDNLVR	V	0.81%	6718	6718	1535.218872	2	3068.422094	3067.434084	0.988009581	K	V	C6:+57.021	3	28	1	0
				308	317	9	R	VWQVTIGTR	-	0.81%	3263	3263	531.2803955	2	1060.545141	1058.587275	1.957866104	R	-	-	5	9	2	0
P68400	Casein kinase II subunit alpha	1	4.86%	172	191	19	R	LIDWGLAEFYHPGQEYNVR	V	1.97%	6231	6231	770.3760986	3	2308.104821	2306.112014	1.992807042	R	V	-	1	19	2	0
P82279	Crumbs homolog 1	2	2.35%	513	526	13	R	FQTVQPMALLLFR	S	9.21%	3823	3823	527.2857666	3	1578.833825	1578.859303	-0.025478139	R	S	M7:+15.995	2	13	0	0
				647	667	20	K	IDWNHITLENISSGSSLNVK	A	3.73%	4493	4493	1113.060425	2	2224.1052	2226.128058	-2.022858287	K	A	-	1	20	-1	0
P84085	ADP-ribosylation factor 5	6	42.78%	19	30	11	R	ILMVGLDAAGK	T	0.81%	3622	3622	544.3093262	2	1086.603002	1086.610714	-0.007711312	R	T	-	4	11	0	0
				38	59	21	K	LGEIVTTIPTIGFNVETVEYK	N	0.81%	6313	6313	775.4179077	3	2323.230248	2322.235877	0.994370961	K	N	-	5	21	1	0
				79	97	18	R	HYFQNTQGLIFVVDSNDR	E	0.81%	4864	4864	1077.521851	2	2153.028051	2152.033763	0.994287756	R	E	-	4	18	1	0
				79	99	20	R	HYFQNTQGLIFVVDSNDRER	V	0.81%	3881	3881	813.7289429	3	2438.163353	2438.161468	0.001885797	R	V	N5:+0.984	1	20	0	1
				117	127	10	R	DAVLLVFANK	Q	0.81%	5024	5024	545.3164673	2	1088.617284	1088.622992	-0.005707206	R	Q	-	2	10	0	0
				127	142	15	K	QDMPNAMPVSELTDK	L	3.54%	3546	3546	838.8827515	2	1675.749853	1674.759306	0.990546626	K	L	-	4	15	1	0
P84095	Rho-related GTP-binding protein RhoG	6	40.84%	30	49	19	K	EYIPTVFDNYSAQSAVDGR	T	0.81%	4828	4828	1066.999512	2	2131.983373	2130.98581	0.997563246	K	T	-	4	19	1	0
				49	66	17	R	TVNLNLWDTAGQEEYDR	L	0.81%	4952	4952	1012.471619	2	2022.927587	2022.928295	-0.000707927	R	L	-	5	17	0	0
				128	147	19	R	LKEQGQAPITPQQGQALAK	Q	0.81%	792	792	1003.55	2	2005.08435	2005.095635	-0.011285408	R	Q	-	4	19	0	1
				130	147	17	K	EQGQAPITPQQGQALAK	Q	0.81%	806	806	882.9607544	2	1763.905859	1763.916608	-0.010749395	K	Q	-	5	17	0	0
				153	166	13	R	YLECSALQQDGVK	E	0.81%	1993	1993	756.355957	2	1510.696264	1509.712877	0.983386695	R	E	C4:+57.021	5	13	1	0
				174	184	10	R	AVLNPTPIKR	G	1.93%	745	745	554.8425903	2	1107.669531	1107.676424	-0.006893696	R	G	-	5	10	0	1
Q00325	Phosphate carrier protein, mitochondrial	15	54.42%	101	112	11	K	GIFNGFSVTLK	E	0.81%	5849	5849	592.3196411	2	1182.623632	1182.628455	-0.004823317	K	E	N4:+0.984	1	11	0	0
				101	117	16	K	GIFNGFSVTLKEDGVR	G	0.81%	5744	5744	870.9577026	2	1739.899755	1738.888981	1.010774465	K	G	N4:+0.984	5	16	1	1
				121	137	16	K	GWAPTFLGYSMQGLCK	F	0.81%	6465	6465	606.2871704	3	1815.838036	1815.831932	0.006103878	K	F	Q12:+0.984,C15:+57.021	2	16	0	0
				137	145	8	K	FGFYEVFK	V	0.81%	5681	5681	518.7591553	2	1035.50266	1035.506565	-0.003904325	K	V	-	1	8	0	0
				145	161	16	K	VLYSNMLGEENTYLWR	T	0.81%	6048	6048	994.4777222	2	1986.939794	1986.950946	-0.01115164	K	T	-	4	16	0	0
				161	187	26	R	TSLYLAASASAEFFADIALAPMEAAK	V	4.03%	10047	10047	888.1117554	3	2661.311791	2658.325104	2.986686897	R	V	-	2	26	3	0
				189	201	12	R	IQTQPGYANTLR	D	0.81%	949	949	681.3612061	2	1360.706762	1360.709909	-0.003147395	R	D	-	5	12	0	0
				218	226	8	K	GVAPLWMR	Q	0.81%	3980	3980	465.2540894	2	928.4925286	928.4952897	-0.002761025	K	Q	-	5	8	0	0
				226	234	8	R	QIPYTMMK	F	3.06%	2515	2515	506.2528687	2	1010.490087	1010.492908	-0.002820375	R	F	-	1	8	0	0
				240	247	7	R	TVEALYK	F	4.00%	814	814	412.2307129	2	822.4457757	822.4487155	-0.002939803	R	F	-	1	7	0	0
				247	254	7	K	FVVPKPR	S	3.70%	773	773	421.7651978	2	841.5147454	841.5174042	-0.00265874	K	S	-	3	7	0	0
				254	293	39	R	SECSKPEQLVVTFVAGYIAGVFCAIVSHPADSVVSVLNK	E	3.78%	11690	11690	1045.539551	4	4178.126903	4179.089861	-0.962958115	R	E	C3:+57.021,Q8:+0.984,C2	3	39	-1	0
				318	337	19	R	IIMIGTLTALQWFIYDSVK	V	1.93%	9119	9119	1115.114502	2	2228.213354	2227.196347	1.01700665	R	V	M3:+15.995	3	19	1	0
				341	355	14	R	LPRPPPPEMPESLK	K	0.81%	2915	2915	529.9559326	3	1586.844323	1586.849047	-0.004724012	R	K	-	5	14	0	0
				341	356	15	R	LPRPPPPEMPESLKK	K	0.81%	2164	2164	429.7431641	4	1714.941356	1714.94401	-0.00265379	R	K	-	4	15	0	1
Q00341	Vigilin	1	0.87%	349	360	11	K	LGQALTEVYAK	A	3.00%	1932	1932	597.8532104	2	1193.690771	1191.649935	2.040835994	K	A	-	2	11	2	0
Q00610	Clathrin heavy chain 1	69	50.75%	43	63	20	K	VGEQAQVVIIDMNDPSNPIR	R	0.81%	5064	5064	1098.560913	2	2195.106176	2194.105215	1.000961116	K	R	-	4	20	1	0
				63	78	15	R	RPISADSAIMNPASK	V	0.81%	827	827	779.406311	2	1556.796972	1556.798074	-0.00110181	R	V	-	4	15	0	0
				86	96	10	K	TLQIFNIEMK	S	0.81%	5468	5468	618.8364258	2	1235.657201	1235.658392	-0.001190661	K	S	-	4	10	0	0
				100	112	12	K	AHTMTDDVTFWK	W	0.81%	3853	3853	726.3334351	2	1450.65122	1450.655098	-0.003877731	K	W	-	2	12	0	0
				112	140	28	K	WISLNTVALVTDNAVYHWSMEGESQPVK	M	4.17%	8552	8552	1059.194214	3	3174.559166	3174.533184	0.025982314	K	M	N5:+0.984	1	28	0	0
				144	157	13	R	HSSLAGCQIINYR	T	0.81%	2141	2141	760.3813477	2	1518.747045	1517.740429	1.006615833	R	T	C7:+57.021	4	13	1	0
				163	176	13	K	WLLLTGISAQQNR	V	0.81%	5479	5479	750.4211426	2	1498.826635	1498.825608	0.001027076	K	V	-	5	13	0	0
				176	188	12	R	VVGAMQLYSVDR	K	0.81%	3133	3133	669.3261719	2	1336.636694	1336.680919	-0.044224898	R	K	-	5	12	0	0
				188	205	17	R	KVSQPIEGHAASFAQFK	M	0.81%	1677	1677	615.6582031	3	1843.951134	1843.958079	-0.006944729	R	M	-	4	17	0	1
				189	205	16	K	VSQPIEGHAASFAQFK	M	0.81%	2923	2923	858.9360962	2	1715.856542	1715.863116	-0.006573545	K	M	-	4	16	0	0
				227	245	18	K	LHIIEVGTPPTGNQPFPK	K	0.81%	3704	3704	973.5387573	2	1945.061865	1944.046894	1.014970464	K	K	-	5	18	1	0
				246	269	23	K	AVDVFFPPEAQNDFPVAMQISEK	H	0.81%	6939	6939	1290.62439	2	2579.233129	2578.241374	0.991754881	K	H	-	5	23	1	0
				269	278	9	K	HDVVFLITK	Y	0.81%	2902	2902	536.3111572	2	1070.606664	1070.612427	-0.005762603	K	Y	-	5	9	0	0
				297	320	23	R	ISGETIFVTAPHEATAGIIGVNR	K	0.81%	4875	4875	1177.629395	2	2353.243139	2352.243756	0.99938259	R	K	-	4	23	1	0
				350	366	16	R	MAVRNNLAGAEELFAR	K	4.90%	7703	7703	589.2664795	3	1764.775963	1762.867185	1.908778405	R	K	N5:+0.984,N6:+0.984	1	16	2	1
				354	366	12	R	NNLAGAEELFAR	K	0.81%	4286	4286	652.8325195	2	1303.649389	1303.65206	-0.002671153	R	K	-	5	12	0	0
				366	382	16	R	KFNALFAQGNYSEAAK	V	0.81%	2806	2806	586.9623413	3	1757.863549	1757.873681	-0.010131762	R	V	-	3	16	0	1
				367	382	15	K	FNALFAQGNYSEAAK	V	7.05%	3768	3768	816.402771	2	1630.789892	1629.778717	1.01117448	K	V	-	1	15	1	0
				400	429	29	R	FQSVPAQPGQTSPLLQYFGILLDQGQLNK	Y	0.81%	9022	9022	1063.22998	3	3186.666466	3186.671347	-0.00488089	R	Y	-	2	29	0	0
				468	481	13	K	SVDPTLALSVYLR	A	0.81%	6127	6127	717.4106445	2	1432.805639	1432.792577	0.013062455	K	A	-	2	13	0	0
				487	500	13	K	VIQCFAETGQVQK	I	0.81%	859	859	754.3804932	2	1506.745336	1506.749597	-0.004260888	K	I	C4:+57.021	5	13	0	0
				487	506	19	K	VIQCFAETGQVQKIVLYAK	K	5.40%	5675	5675	1099.047363	2	2196.079076	2196.149545	-0.07046847	K	K	Q3:+0.984,C4:+57.021,Q1	1	19	0	1
				506	519	13	K	KVGYTPDWIFLLR	N	0.81%	7132	7132	536.6356812	3	1606.883568	1606.887146	-0.003577327	K	N	-	2	13	0	1
				507	519	12	K	VGYTPDWIFLLR	N	0.81%	7858	7858	740.4071045	2	1478.798559	1478.792183	0.006376376	K	N	-	5	12	0	0
				583	610	27	R	LLEMNLMHAPQVADAILGNQMFTHYDR	A	0.81%	7589	7589	1043.834961	3	3128.481408	3128.488167	-0.006759452	R	A	Q11:+0.984	2	27	0	0
				625	637	12	R	ALEHFTDLYDIK	R	0.81%	4313	4313	733.8688965	2	1465.722143	1463.729642	1.992501009	R	R	-	2	12	2	0
				625	638	13	R	ALEHFTDLYDIKR	A	0.81%	3685	3685	540.9490356	3	1619.823632	1619.830753	-0.007121218	R	A	-	5	13	0	1
				668	676	8	R	AMLSANIR	Q	3.19%	1119	1119	438.2419128	2	874.4681756	874.4694689	-0.001293252	R	Q	-	2	8	0	0
				676	688	12	R	QNLQICVQVASK	Y	5.30%	2732	2732	696.8884888	2	1391.761327	1389.680468	2.080859763	R	Y	Q1:+0.984,Q4:+0.984,C6:	1	12	2	0
				688	706	18	K	YHEQLSTQSLIELFESFK	S	0.81%	8406	8406	1101.056274	2	2200.096899	2198.089547	2.007351764	K	S	-	2	18	2	0
				798	806	8	K	YIEIYVQK	V	2.46%	2581	2581	528.2912598	2	1054.566869	1054.569893	-0.003023989	K	V	-	2	8	0	0
				811	830	19	R	LPVVIGGLLDVDCSEDVIK	N	0.81%	6989	6989	1021.046875	2	2040.0781	2040.080828	-0.00272788	R	N	C13:+57.021	5	19	0	0
				830	837	7	K	NLILVVR	G	0.81%	3395	3395	413.7784729	2	825.5412957	825.543619	-0.002323247	K	G	-	5	7	0	0
				837	851	14	R	GQFSTDELVAEVEK	R	0.81%	4690	4690	776.3807373	2	1550.745825	1550.746414	-0.000589759	R	R	-	5	14	0	0
				837	852	15	R	GQFSTDELVAEVEKR	N	0.81%	4526	4526	854.932373	2	1707.849096	1706.847525	1.001570574	R	N	-	5	15	1	1
				856	865	9	K	LLLPWLEAR	I	0.81%	6635	6635	555.8360596	2	1109.656469	1109.659712	-0.003242483	K	I	-	5	9	0	0
				865	881	16	R	IHEGCEEPATHNALAK	I	4.50%	612	612	594.2863159	3	1779.835473	1775.825616	4.009856818	R	I	C5:+57.021	1	16	4	0
				881	892	11	K	IYIDSNNNPER	F	0.81%	676	676	667.8201294	2	1333.624609	1333.626239	-0.001630627	K	F	-	3	11	0	0
				949	967	18	R	RKDPELWGSVLLESNPYR	R	4.79%	5362	5362	720.7139893	3	2159.118493	2158.117099	1.001393557	R	R	-	1	18	1	2
				950	967	17	R	KDPELWGSVLLESNPYR	R	0.81%	5980	5980	668.3439941	3	2002.008507	2002.015988	-0.007480642	R	R	-	3	17	0	1
				967	984	17	R	RPLIDQVVQTALSETQD	P	3.23%	6476	6476	957.5019531	2	1912.988256	1911.990167	0.998089026	R	P	-	1	17	1	0
				967	993	26	R	RPLIDQVVQTALSETQDPEEVSVTVK	A	0.81%	6855	6855	961.8459473	3	2882.514367	2881.49203	1.022336973	R	A	Q9:+0.984	4	26	1	0
				993	1010	17	K	AFMTADLPNELIELLEK	I	0.81%	9070	9070	974.0108032	2	1946.005956	1946.007064	-0.001107507	K	I	-	4	17	0	0
				1010	1022	12	K	IVLDNSVFSEHR	N	0.81%	2904	2904	709.3913574	2	1416.767065	1414.720474	2.04659062	K	N	-	2	12	2	0
				1022	1034	12	R	NLQNLLILTAIK	A	0.81%	6965	6965	677.427063	2	1352.838476	1352.839133	-0.000656871	R	A	-	5	12	0	0
				1039	1046	7	R	VMEYINR	L	0.81%	894	894	463.7330627	2	925.4504754	923.4534844	1.99699096	R	L	-	5	7	2	0
				1073	1094	21	R	KFDVNTSAVQVLIEHIGNLDR	A	0.81%	7586	7586	790.0918579	3	2367.252099	2367.254655	-0.00255683	R	A	-	3	21	0	1
				1074	1094	20	K	FDVNTSAVQVLIEHIGNLDR	A	0.81%	8108	8108	747.725708	3	2240.153649	2239.159692	0.993956599	K	A	-	4	20	1	0
				1101	1113	12	R	CNEPAVWSQLAK	A	3.82%	3791	3791	702.3659058	2	1402.716161	1401.670618	1.045543035	R	A	C1:+57.021	3	12	1	0
				1122	1130	8	K	EAIDSYIK	A	3.06%	1725	1725	469.7440796	2	937.4725091	937.4756586	-0.003149532	K	A	-	2	8	0	0
				1130	1155	25	K	ADDPSSYMEVVQAANTSGNWEELVK	Y	0.81%	6505	6505	914.4189453	3	2740.233361	2740.217389	0.015972217	K	Y	N15:+0.984	3	25	0	0
				1165	1179	14	R	ESYVETELIFALAK	T	0.81%	6863	6863	807.4250488	2	1612.834448	1611.839586	0.994861136	R	T	-	5	14	1	0
				1182	1204	22	R	LAELEEFINGPNNAHIQQVGDR	C	0.81%	4624	4624	822.065979	3	2463.174462	2463.214247	-0.039785324	R	C	-	2	22	0	0
				1215	1226	11	K	LLYNNVSNFGR	L	0.81%	3043	3043	648.8380127	2	1295.660375	1295.662231	-0.001855545	K	L	-	4	11	0	0
				1226	1245	19	R	LASTLVHLGEYQAAVDGAR	K	0.81%	3861	3861	986.5202026	2	1971.024755	1970.022136	1.002619233	R	K	-	5	19	1	0
				1311	1326	15	R	AHMGMFTELAILYSK	F	2.46%	6761	6761	571.2886353	3	1710.842431	1710.847333	-0.004902702	R	F	-	4	15	0	0
				1331	1342	11	K	MREHLELFWSR	V	0.81%	4199	4199	501.9185791	3	1502.732262	1502.74525	-0.012988015	K	V	-	5	11	0	1
				1333	1342	9	R	EHLELFWSR	V	2.90%	4265	4265	610.355896	2	1218.696142	1215.603653	3.092488672	L	V	-	1	9	3	0
				1397	1406	9	K	VANVELYYR	A	0.81%	2171	2171	563.7970581	2	1125.578466	1125.581855	-0.003389013	K	A	-	5	9	0	0
				1443	1453	10	K	QLPLVKPYLR	S	4.33%	3377	3377	613.8841553	2	1225.75266	1225.754675	-0.002014213	G	S	-	1	10	0	0
				1461	1481	20	K	SVNESLNNLFITEEDYQALR	T	0.81%	6086	6086	786.0530396	3	2355.135644	2355.123017	0.012626996	K	T	N8:+0.984	1	20	0	0
				1481	1498	17	R	TSIDAYDNFDNISLAQR	L	0.81%	4581	4581	970.9675903	2	1939.919531	1941.906831	-1.9873008	R	L	-	4	17	-1	0
				1498	1508	10	R	LEKHELIEFR	R	2.59%	1790	1790	438.5791931	3	1312.714104	1312.713932	0.000172098	R	R	-	2	10	0	1
				1501	1508	7	K	HELIEFR	R	3.38%	1571	1571	473.2715454	2	944.5274407	942.4923117	2.035129044	K	R	-	1	7	2	0
				1509	1516	7	R	IAAYLFK	G	0.81%	2906	2906	413.2455139	2	824.4753778	824.4796217	-0.004243912	R	G	-	5	7	0	0
				1545	1562	17	K	DTELAEELLQWFLQEEK	R	2.26%	9434	9434	1061.02771	2	2120.03977	2120.031363	0.008406474	K	R	-	5	17	0	0
				1545	1563	18	K	DTELAEELLQWFLQEEKR	E	0.81%	8824	8824	759.7191772	3	2276.134057	2277.116475	-0.982417902	K	E	Q14:+0.984	3	18	-1	1
				1588	1604	16	R	HNIMDFAMPYFIQVMK	E	0.81%	8293	8293	992.9781494	2	1983.940649	1983.940917	-0.00026866	R	E	-	4	16	0	0
				1609	1620	11	K	VDKLDASESLR	K	0.81%	665	665	411.5536804	3	1231.637566	1231.640827	-0.00326062	K	K	-	5	11	0	1
Q00839	Heterogeneous nuclear ribonucleoprotein U	23	37.70%	37	69	32	R	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	S	0.81%	3642	3642	1043.151367	3	3126.430626	3126.415982	0.014644242	R	S	N20:+0.984	3	32	0	0
				186	204	18	K	SSGPTSLFAVTVAPPGAR	Q	0.81%	5086	5086	857.9588623	2	1713.902075	1713.904981	-0.002906199	K	Q	-	5	18	0	0
				255	268	13	R	GYFEYIEENKYSR	A	1.93%	3617	3617	849.3953857	2	1696.775121	1696.773298	0.00182366	R	A	-	4	13	0	1
				303	324	21	R	DRLSASSLTMESFAFLWAGGR	A	0.81%	7844	7844	768.3811035	3	2302.119835	2301.121199	0.998636043	R	A	-	3	21	1	1
				305	324	19	R	LSASSLTMESFAFLWAGGR	A	0.81%	8219	8219	1017.015564	2	2032.015478	2029.993145	2.022332746	R	A	-	2	19	2	0
				352	360	8	K	DIDIHEVR	I	0.81%	763	763	498.7576904	2	995.4997308	995.5036047	-0.003873965	K	I	-	5	8	0	0
				423	433	10	K	NGQDLGVAFK	I	0.81%	2752	2752	525.7639771	2	1049.512304	1048.518905	0.993399118	K	I	N1:+0.984	4	10	1	0
				436	462	26	K	EVLAGRPLFPHVLCHNCAVEFNFGQK	E	2.83%	4921	4921	1014.511169	3	3040.510033	3039.483808	1.026225205	K	E	C14:+57.021,N16:+0.984,	4	26	1	0
				462	484	22	K	EKPYFPIPEEYTFIQNVPLEDR	V	0.81%	6438	6438	908.7891846	3	2723.344079	2723.348281	-0.004202673	K	V	-	4	22	0	0
				462	486	24	K	EKPYFPIPEEYTFIQNVPLEDRVR	G	0.81%	6259	6259	995.51	3	2983.506525	2979.501806	4.004718456	K	G	N16:+0.984	1	24	4	1
				489	510	21	K	GPEEKKDCEVVMMIGLPGAGK	T	3.91%	3927	3927	749.3758545	3	2245.104088	2244.094782	1.009305965	K	T	C8:+57.021	1	21	1	2
				516	536	20	K	HAAENPGKYNILGTNTIMDK	M	0.81%	2848	2848	729.6991577	3	2186.073998	2186.079	-0.005002151	K	M	-	2	20	0	1
				524	536	12	K	YNILGTNTIMDK	M	0.81%	3922	3922	691.8528442	2	1381.690038	1381.691149	-0.001110563	K	M	-	4	12	0	0
				544	558	14	K	QMADTGKLNTLLQR	A	0.81%	4084	4084	786.4193115	2	1570.822973	1570.813273	0.009699959	K	A	Q1:-17.027	2	14	0	1
				565	572	7	K	FIEIAAR	K	0.81%	1663	1663	410.2390137	2	818.4623773	818.4650342	-0.002656976	K	K	-	3	7	0	0
				574	590	16	K	RNFILDQTNVSAAAQR	R	0.81%	2573	2573	902.4803467	2	1802.945043	1802.938741	0.006302751	K	R	-	3	16	0	1
				575	590	15	R	NFILDQTNVSAAAQR	R	0.81%	3418	3418	824.4259644	2	1646.836279	1646.837629	-0.001350745	R	R	-	5	15	0	0
				592	601	9	K	MCLFAGFQR	K	0.81%	4691	4691	565.265686	2	1128.515722	1128.52039	-0.004667954	K	K	C2:+57.021	5	9	0	0
				619	635	16	K	KAEVEGKDLPEHAVLK	M	3.64%	745	745	588.3269043	3	1761.957238	1761.962496	-0.005257917	K	M	-	1	16	0	2
				620	635	15	K	AEVEGKDLPEHAVLK	M	0.81%	837	837	817.9385376	2	1633.861425	1633.867533	-0.006107437	K	M	-	5	15	0	1
				626	635	9	K	DLPEHAVLK	M	0.81%	830	830	511.2826538	2	1020.549658	1020.560391	-0.010733839	K	M	-	2	9	0	0
				637	664	27	K	GNFTLPEVAECFDEITYVELQKEEAQK	L	4.45%	7892	7892	1063.510132	3	3187.50692	3186.506247	1.000673852	K	L	C11:+57.021	1	27	1	1
				796	825	29	K	NQSQGYNQWQQGQFWGQKPWSQHYHQGYY	-	4.41%	4582	4582	915.9061279	4	3659.593212	3659.566744	0.026467175	K	-	Q11:+0.984,Q17:+0.984	1	29	0	0

Q01082	Spectrin beta chain, brain 1	23	15.02%	329	348	19	K	FANSLVGVQQQLQAFNTYR	T	2.34%	6193	6193	1093.063721	2	2184.111791	2183.112348	0.999443262	K	T	-	3	19	1	0
				359	372	13	K	GNLEVLLFTIQSK	M	1.93%	6832	6832	731.4186401	2	1460.82163	1460.823877	-0.002246495	K	M	-	4	13	0	0
				384	394	10	R	EGKLISDINK	A	5.64%	4865	4865	558.5801392	2	1115.144628	1116.602635	-1.458006424	R	A	N9:+0.984	1	10	-1	1
				443	462	19	R	LVSQDNFGFDLPAVEAATK	K	0.81%	6036	6036	1012.007019	2	2021.998388	2021.010568	0.98781975	R	K	-	3	19	1	0
				462	477	15	K	KHEAIETDIAAYEER	V	2.26%	2439	2439	592.6248779	3	1774.851159	1773.853339	0.997819541	K	V	-	4	15	1	1
				523	532	9	R	LEMNLGLQK	I	2.31%	3226	3226	524.2955933	2	1046.575536	1044.563763	2.011773107	R	I	-	1	9	2	0
				558	569	11	K	HLLGVEDLLQK	H	0.81%	4616	4616	632.8649292	2	1263.714208	1263.718683	-0.004474842	K	H	-	1	11	0	0
				723	736	13	R	EQWANLEQLSAIR	K	0.81%	5347	5347	779.9006348	2	1557.785619	1556.794702	0.990917611	R	K	-	5	13	1	0
				765	784	19	K	IVSSSDVGHDEYSTQSLVK	K	3.73%	2072	2072	684.3375244	3	2049.989098	2050.969476	-0.980377662	K	K	Q15:+0.984	2	19	-1	0
				787	821	34	K	DVAEEIANYRPTLDTLHEQASALPQEHAESPDVR	G	4.41%	5192	5192	951.96	4	3803.8087	3801.808173	2.000527304	K	G	N8:+0.984	1	34	2	0
				821	830	9	R	GRLSGIEER	Y	5.14%	12883	12883	507.3354187	2	1012.655187	1015.541053	-2.885865598	R	Y	-	1	9	-1	1
				832	839	7	K	EVAELTR	L	5.21%	2110	2110	410.6195374	2	819.2234246	816.4341281	2.789296547	K	L	-	1	7	3	0
				842	853	11	K	QALQDTLALYK	M	8.11%	3869	3869	632.3509521	2	1262.686254	1262.687049	-0.000794455	K	M	-	1	11	0	0
				904	913	9	R	VAVVNQIAR	Q	0.81%	902	902	485.2937317	2	968.5718133	968.5767101	-0.004896813	R	Q	-	5	9	0	0
				964	972	8	C	NETKSWIR	E	4.97%	2378	2378	518.7675171	2	1035.519384	1033.535239	1.984144868	C	E	K4:+1.000	1	8	2	1
				976	996	20	K	VIESTQDLGNDLAGVMALQR	K	0.81%	5964	5964	710.697876	3	2129.070153	2129.078666	-0.008513038	K	K	-	4	20	0	0
				1036	1048	12	R	LAEISDVWEEMK	T	0.81%	5604	5604	725.8487549	2	1449.68186	1448.685729	0.996130414	R	T	-	5	12	1	0
				1069	1080	11	R	DLDDFQSWLSR	T	0.81%	6207	6207	691.3201904	2	1380.624731	1380.63099	-0.006259589	R	T	-	5	11	0	0
				1080	1099	19	R	TQTAIASEDMPNTLTEAEK	L	1.93%	3127	3127	1025.497803	2	2048.979955	2048.957213	0.022742133	R	L	-	5	19	0	0
				1099	1120	21	K	LLTQHENIKNEIDNYEEDYQK	M	0.81%	3540	3540	879.7510376	3	2636.229638	2636.224187	0.005450313	K	M	N10:+0.984	3	21	0	1
				1179	1209	30	K	QAEAFLNNQEYVLAHTEMPTTLEGAEAAIK	K	4.65%	6298	6298	1097.542969	3	3289.605431	3289.581257	0.024174394	K	K	N7:+0.984	1	30	0	0
				1633	1653	20	K	HQILEQAVEDYAETVHQLSK	T	2.26%	6381	6381	780.3978882	3	2338.170189	2338.144086	0.026103127	K	T	Q6:+0.984	5	20	0	0
				1941	1957	16	R	DVSSVELLMNNHQGIK	A	6.30%	6499	6499	894.8606567	2	1787.705663	1785.845431	1.860232461	R	A	N10:+0.984,N11:+0.984,Q	1	16	2	0
Q01484	Ankyrin-2	1	0.54%	52	73	21	K	GGIDINTCNQNGLNALHLAAK	E	8.94%	3998	3998	733.0444336	3	2196.109826	2194.079583	2.030242189	K	E	C8:+57.021,Q10:+0.984	1	21	2	0
Q01518	Adenylyl cyclase-associated protein 1	2	6.53%	100	113	13	K	LSDLLAPISEQIK	E	0.81%	5032	5032	713.9098511	2	1425.804052	1425.807892	-0.003840212	K	E	-	4	13	0	0
				330	348	18	R	VENQENVSNLVIEDTELK	Q	2.46%	4494	4494	1037.520386	2	2073.025121	2072.027341	0.99778074	R	Q	-	3	18	1	0
Q01650	Large neutral amino acids transporter small subunit 1	3	8.09%	30	48	18	K	SADGSAPAGEGEGVTLQR	N	0.81%	741	741	851.4043579	2	1700.793066	1700.796553	-0.003486756	K	N	-	5	18	0	0
				221	237	16	K	GDVSNLDPNFSFEGTK	L	0.81%	4039	4039	864.4003906	2	1726.785131	1725.784591	1.000540378	K	L	-	5	16	1	0
				348	355	7	R	LFFVGSR	E	0.81%	3657	3657	413.2332764	2	824.4509027	824.4544695	-0.003566866	R	E	-	4	7	0	0
Q01844	RNA-binding protein EWS	1	2.13%	410	424	14	K	GDATVSYEDPPTAK	A	2.59%	736	736	725.8440552	2	1449.67246	1449.66235	0.010110072	K	A	-	4	14	0	0
Q02750	Dual specificity mitogen-activated protein kinase kinase 1	3	12.72%	160	168	8	R	IPEQILGK	V	1.97%	1429	1429	449.272583	2	896.5295159	896.5331139	-0.003597984	R	V	-	4	8	0	0
				234	260	26	R	LQGTHYSVQSDIWSMGLSLVEMAVGR	Y	0.81%	10162	10162	956.1384888	3	2865.391991	2863.399684	1.992307157	R	Y	-	1	26	2	0
				324	340	16	K	LPSGVFSLEFQDFVNK	C	0.81%	6551	6551	914.4659424	2	1826.916235	1825.925048	0.991187174	K	C	-	5	16	1	0
Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein	12	47.77%	24	46	22	K	FLFGGLAGMGATVFVQPLDLVK	N	0.81%	9007	9007	1140.634888	2	2279.254125	2279.238795	0.015329959	K	N	-	4	22	0	0
				32	48	16	G	MGATVFVQPLDLVKNR	M	5.62%	645	645	602.28	3	1803.816525	1803.954373	-0.137847816	K	M	M1:+15.994,N15:+0.984	1	16	0	1
				62	73	11	K	TSFHALTSILK	A	0.81%	3995	3995	609.3459473	2	1216.676244	1216.681569	-0.005324861	K	A	-	5	11	0	0
				98	108	10	R	LGIYTVLFER	L	3.42%	6272	6272	607.3299561	2	1212.644262	1209.675756	2.968506405	R	L	-	2	10	3	0
				108	122	14	R	LTGADGTPPGFLLK	A	0.81%	4011	4011	693.8832397	2	1385.750829	1385.755463	-0.004633268	R	A	-	5	14	0	0
				122	146	24	K	AVIGMTAGATGAFVGTPAEVALIR	M	0.81%	6175	6175	1137.121826	2	2272.228002	2272.224936	0.003066008	K	M	-	5	24	0	0
				162	170	8	K	NVFNALIR	I	0.81%	4219	4219	473.7766418	2	945.5376336	945.5395963	-0.001962653	K	I	-	2	8	0	0
				173	182	9	R	EEGVLTLWR	G	0.81%	4987	4987	551.7957153	2	1101.575781	1101.581855	-0.00607456	R	G	-	5	9	0	0
				190	206	16	R	AVVVNAAQLASYSQSK	Q	0.81%	3166	3166	818.4396362	2	1634.863622	1634.862782	0.000840861	R	Q	-	5	16	0	0
				260	268	8	K	NGLDVLFK	V	0.81%	4350	4350	453.2555542	2	904.4954583	904.5018138	-0.006355442	K	V	-	5	8	0	0
				271	280	9	R	YEGFFSLWK	G	0.81%	6731	6731	589.281189	2	1176.546728	1175.565142	0.981585442	R	G	-	5	9	1	0
				288	305	17	R	LGPHTVLTFIFLEQMNK	A	0.81%	7151	7151	663.3568115	3	1987.046959	1987.060102	-0.013143006	R	A	-	5	17	0	0
Q03113	Guanine nucleotide-binding protein subunit alpha-12	1	2.89%	59	70	11	K	ILLLGAGESGK	S	0.81%	3405	3405	529.3126831	2	1056.609716	1056.617906	-0.008190205	K	S	-	2	11	0	0
Q03135	Caveolin-1	1	11.80%	65	86	21	K	IDFEDVIAEPEGTHSFDGIWK	A	0.81%	6574	6574	802.7133179	3	2405.116478	2404.122304	0.994174693	K	A	-	5	21	1	0
Q03518	Antigen peptide transporter 1	10	22.28%	102	116	14	R	IFSLLVPTALPLLR	V	0.81%	8487	8487	776.9942017	2	1551.972753	1551.975232	-0.002479216	R	V	-	5	14	0	0
				174	189	15	R	ELISWGAPGSADSTR	L	0.81%	8225	8225	509.6509399	3	1525.929345	1527.731332	-1.801987208	R	L	E1:-18.011	1	15	-1	0
				216	234	18	K	LGSLWVPGGQGGSGNPVR	R	0.81%	3977	3977	869.9573975	2	1737.899145	1736.895813	1.00333185	K	R	-	4	18	1	0
				407	417	10	K	WYQLLEVQVR	E	4.37%	5520	5520	667.8671875	2	1333.718725	1332.719017	0.999707432	K	E	-	3	10	1	0
				422	438	16	K	SSQVAIEALSAMPTVR	S	0.81%	5049	5049	831.4454346	2	1660.875219	1658.866153	2.009065581	K	S	-	1	16	2	0
				537	544	7	K	IFEYLDR	T	1.93%	3241	3241	478.2477722	2	954.4798944	954.4810783	-0.001183966	K	T	-	4	7	0	0
				604	635	31	K	STVAALLQNLYQPTGGQLLLDGKPLPQYEHR	Y	1.93%	7155	7155	856.2132568	4	3420.821727	3420.804137	0.017590288	K	Y	Q17:+0.984	1	31	0	0
				639	653	14	R	QVAAVGQEPQVFGR	S	0.81%	2502	2502	743.3934937	2	1484.771337	1484.773572	-0.002235175	R	S	-	5	14	0	0
				653	678	25	R	SLQENIAYGLTQKPTMEEITAAAVK	S	0.81%	5688	5688	903.1271973	3	2706.358117	2705.394581	0.963535917	R	S	-	3	25	1	0
				678	708	30	K	SGAHSFISGLPQGYDTEVDEAGSQLSGGQR	Q	1.93%	4896	4896	1017.470093	3	3049.386803	3049.401333	-0.014529584	K	Q	-	2	30	0	0
Q03519	Antigen peptide transporter 2	7	16.03%	45	54	9	R	LGGLWGLLK	L	0.81%	6522	6522	478.7980347	2	955.5804193	955.5854838	-0.005064592	R	L	-	5	9	0	0
				291	308	17	R	LTLLSLLHMPFTIAAEK	V	0.81%	8959	8959	950.0427856	2	1898.069921	1897.07469	0.995231329	R	V	-	5	17	1	0
				333	343	10	R	EAVGGLQTVR	S	3.55%	716	716	515.2872314	2	1028.558813	1028.561454	-0.002641221	R	S	-	3	10	0	0
				449	469	20	R	QPNLPSPGTLAPTTLQGVVK	F	1.93%	4955	4955	1010.067017	2	2018.118383	2017.120787	0.997595651	R	F	-	2	20	1	0
				469	487	18	K	FQDVSFAYPNRPDRPVLK	G	4.12%	3397	3397	717.3804321	3	2149.117821	2149.09562	0.022201531	K	G	N10:+0.984	1	18	0	0
				626	651	25	R	VLILDEATSALDVQCEQALQDWNSR	G	2.83%	7430	7430	959.4738159	3	2875.397973	2873.386072	2.01190105	R	G	C15:+57.021	2	25	2	0
				668	679	11	R	AHQILVLQEGK	L	0.81%	1398	1398	618.3570557	2	1234.698461	1234.703367	-0.00490616	R	L	-	5	11	0	0
Q04656	Copper-transporting ATPase 1	1	1.13%	616	633	17	R	DIIHTIESLGFEASLVK	K	0.81%	8235	8235	624.6784058	3	1871.011742	1871.004026	0.007715925	R	K	-	5	17	0	0
Q04721	Neurogenic locus notch homolog protein 2	1	0.32%	1622	1630	8	K	VFLEIDNR	Q	7.51%	2598	2598	503.2875671	2	1004.559484	1004.529091	0.030392981	K	Q	-	2	8	0	0
Q04941	Proteolipid protein 2	2	18.42%	6	21	15	R	LSAPGCWAACTNFSR	T	0.81%	3811	3811	849.3775635	2	1696.739477	1696.744066	-0.004589047	R	T	C6:+57.021,C10:+57.021	5	15	0	0
				139	152	13	R	HTAAPTDPADGPV	-	3.51%	725	725	624.7945557	2	1247.573461	1247.578226	-0.004765192	R	-	-	4	13	0	0
Q05655	Protein kinase C delta type	1	1.33%	576	585	9	K	DILEKLFER	E	9.23%	3914	3914	581.8197021	2	1161.623754	1161.63937	-0.015615887	K	E	-	1	9	0	1
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	1	4.96%	80	94	14	K	AFVDFLSDEIKEER	K	9.20%	5573	5573	566.6137695	3	1696.817833	1696.830813	-0.01297923	K	K	-	2	14	0	1
Q07837	Neutral and basic amino acid transport protein rBAT	2	4.82%	181	203	22	R	EVDPIFGTMEDFENLVAAIHDK	G	5.25%	8015	8015	829.7341919	3	2486.179101	2489.17844	-2.999339124	R	G	-	1	22	-1	0
				306	317	11	K	GVDGFSLDAVK	F	6.52%	2586	2586	554.3048706	2	1106.594091	1106.560785	0.033305755	K	F	-	3	11	0	0
Q08722	Leukocyte surface antigen CD47	3	8.67%	74	85	11	K	STVPTDFSSAK	I	3.69%	794	794	570.2810059	2	1138.546362	1138.550615	-0.004253017	K	I	-	3	11	0	0
				85	93	8	K	IEVSQLLK	G	0.81%	3750	3750	465.2867737	2	928.5578973	928.5593287	-0.001431437	K	G	-	3	8	0	0
				121	130	9	R	EGETIIELK	Y	4.04%	2846	2846	516.2834473	2	1030.551244	1030.554637	-0.003392909	R	Y	-	2	9	0	0
Q0VF96	Cingulin-like protein 1	1	0.77%	736	746	10	K	QDLQDLLIAK	E	4.46%	2667	2667	578.824585	2	1155.63352	1155.649935	-0.016414982	K	E	-	3	10	0	0
Q10589	Bone marrow stromal antigen 2	1	8.33%	111	126	15	K	KVEELEGEITTLNHK	L	0.81%	2016	2016	580.6412964	3	1738.900414	1738.910126	-0.00971172	K	L	-	4	15	0	1
Q12816	Trophinin	1	0.77%	549	560	11	K	ASEAVIWEVLR	K	4.24%	884	884	636.8291016	2	1271.642553	1271.687383	-0.044829955	K	K	-	4	11	0	0
Q12860	Contactin-1	2	1.57%	468	476	8	S	LEINNITR	N	6.36%	1687	1687	487.7715454	2	973.5274407	972.5239903	1.003450476	S	N	N5:+0.984	1	8	1	0
				775	783	8	S	PSTAFQVK	V	7.95%	3777	3777	439.2401733	2	876.4646966	876.4705136	-0.005817	S	V	-	1	8	0	0
Q12879	Glutamate [NMDA] receptor subunit epsilon-1	1	0.55%	360	368	8	R	LVVIVLNK	D	6.15%	1927	1927	449.7879944	2	897.5603387	897.589885	-0.02954627	R	D	N7:+0.984	2	8	0	0
Q12912	Lymphoid-restricted membrane protein	1	1.44%	373	381	8	R	VTIASLPR	N	9.69%	1637	1637	428.7657776	2	855.5159051	855.5177982	-0.001893072	R	N	-	1	8	0	0
Q12974	Protein tyrosine phosphatase type IVA 2	4	27.54%	15	29	14	R	FLITHNPTNATLNK	F	0.81%	1881	1881	792.9294434	2	1583.843237	1582.846737	0.996499199	R	F	-	4	14	1	0
				36	44	8	K	YGVTTLVR	V	5.94%	1976	1976	454.7638245	2	907.5119988	907.5127128	-0.000713962	K	V	-	1	8	0	0
				107	122	15	R	APVLVALALIECGMK	Y	0.81%	8374	8374	528.9674072	3	1583.878747	1583.877441	0.001305152	R	Y	C12:+57.021	5	15	0	0
				122	131	9	K	YEDAVQFIR	Q	2.46%	3404	3404	570.7839355	2	1139.552221	1139.56112	-0.00889869	K	Q	-	5	9	0	0
Q13322	Growth factor receptor-bound protein 10	1	2.02%	508	520	12	K	QQGLVDGLFLLR	D	6.94%	7044	7044	681.8214722	2	1361.627294	1359.739781	1.88751284	K	D	Q1:+0.984,Q2:+0.984	2	12	2	0
Q13402	Myosin-VIIa	2	1.17%	72	88	16	R	LGDLNEAGILRNLLIR	Y	6.80%	5125	5125	593.99	3	1778.946525	1780.020664	-1.074138832	R	Y	N12:+0.984	1	16	-1	1
				378	388	10	R	GETVSTPLSR	E	4.27%	3779	3779	523.7941895	2	1045.572729	1045.540384	0.032344562	R	E	-	3	10	0	0
Q13425	Beta-2-syntrophin	1	1.85%	327	337	10	K	HIAWLAEQAK	L	2.90%	1526	1526	583.8191528	2	1165.622656	1165.624389	-0.001733096	K	L	-	1	10	0	0
Q13444	Disintegrin and metalloproteinase domain-containing protein 15	2	3.71%	256	268	12	R	VALVGLEAWTQR	D	0.81%	5430	5430	671.8792725	2	1341.742895	1341.740481	0.002413586	R	D	-	5	12	0	0
				268	288	20	R	DLVEISPNPAVTLENFLHWR	R	0.81%	9162	9162	784.7388306	3	2351.193017	2350.195728	0.997288675	R	R	N15:+0.984	3	20	1	0
Q13488	V-type proton ATPase 116 kDa subunit a isoform 3	3	3.98%	28	38	10	R	LGELGLVEFR	D	0.81%	4967	4967	566.8209229	2	1131.626196	1131.628805	-0.002609761	R	D	-	5	10	0	0
				151	166	15	R	TPLLQAPGGPHQDLR	V	4.36%	2022	2022	533.9564209	3	1598.845788	1598.852885	-0.007097881	R	V	-	2	15	0	0
				276	284	8	R	FLSQVLGR	V	0.81%	2769	2769	460.2546692	2	918.4936883	918.5286972	-0.035008917	R	V	-	2	8	0	0
Q13564	NEDD8-activating enzyme E1 regulatory subunit	1	1.69%	338	347	9	K	YIKLQNVYR	E	8.50%	3634	3634	599.3314819	2	1196.647314	1196.655339	-0.008025133	K	E	Q5:+0.984	2	9	0	1
Q14108	Lysosome membrane protein 2	8	22.18%	82	92	10	R	VEEVGPYTYR	E	0.81%	1416	1416	606.7971191	2	1211.578588	1211.582249	-0.003660943	R	S	-	5	10	0	0
				134	153	19	R	TLNIPVLTVIEWSQVHFLR	E	0.81%	9495	9495	1134.139893	2	2266.264135	2264.268121	1.99601454	R	E	-	4	19	2	0
				153	161	8	R	EIIEAMLK	A	4.82%	3688	3688	473.7641296	2	945.5126092	945.5205015	-0.007892275	R	A	-	1	8	0	0
				330	348	18	K	NGAPIIMSFPHFYQADER	F	4.79%	5817	5817	698.6646118	3	2092.97036	2091.983643	0.986717289	K	F	-	1	18	1	0
				348	378	30	R	FVSAIEGMHPNQEDHETFVDINPLTGIILK	A	1.97%	7122	7122	841.925415	4	3363.67036	3363.680927	-0.010566828	R	A	-	2	30	0	0
				381	390	9	K	RFQINIYVK	K	2.61%	3647	3647	590.8447876	2	1179.673925	1179.676424	-0.002499165	K	K	-	3	9	0	1
				382	390	8	R	FQINIYVK	K	4.12%	4264	4264	512.7940674	2	1023.572485	1023.575313	-0.002828442	R	K	-	1	8	0	0
				390	402	12	K	KLDDFVETGDIR	T	0.81%	3143	3143	704.3571167	2	1406.698583	1406.704155	-0.00557209	K	T	-	5	12	0	1
Q14145	Kelch-like ECH-associated protein 1	2	2.88%	326	336	10	R	LIYTAGGYFR	Q	2.59%	3505	3505	582.3171997	2	1162.618749	1159.602591	3.01615875	R	Q	-	2	10	3	0
				354	362	8	R	LADLQVPR	S	2.90%	1489	1489	457.2752991	2	912.5349481	910.5236119	2.011336209	R	S	-	2	8	2	0
Q14160	Protein scribble homolog	2	1.60%	105	119	14	K	ALEIADFSGNPLSR	L	4.40%	3463	3463	497.2592163	3	1488.754174	1488.757254	-0.003079858	K	L	-	1	14	0	0
				721	733	12	R	IEEEELTLTILR	Q	3.76%	8569	8569	729.9146729	2	1457.813696	1457.797722	0.015974063	R	Q	-	2	12	0	0
Q14232	Translation initiation factor eIF-2B subunit alpha	4	16.39%	36	46	10	R	DKGETIQGLR	A	6.12%	1820	1820	559.3	2	1116.58435	1115.593483	0.9908674	R	A	-	1	10	1	1
				74	88	14	R	FISLASLEYSDYSK	C	0.81%	5432	5432	811.894104	2	1621.772558	1621.787551	-0.014992912	R	C	-	5	14	0	0
				120	132	12	K	DGATILTHAYSR	V	0.81%	1539	1539	652.8321533	2	1303.648657	1303.65206	-0.003403575	K	V	-	5	12	0	0
				220	234	14	K	AQNKPFYVVAESFK	F	0.81%	4080	4080	814.9251099	2	1627.83457	1626.840589	0.993980223	K	F	-	5	14	1	0
Q14258	E3 ubiquitin/ISG15 ligase TRIM25	5	9.37%	249	261	12	K	ALLDASETTSTR	K	0.81%	805	805	632.8220215	2	1263.628393	1263.630656	-0.002263151	K	K	-	5	12	0	0
				273	283	10	K	FDTIYQILLK	K	3.04%	6667	6667	629.5426636	2	1257.069677	1253.690721	3.378955612	K	K	Q6:+0.984	2	10	3	0
				301	310	9	K	RDEFEFLEK	A	2.46%	3289	3289	606.7997437	2	1211.583837	1211.582249	0.001588081	K	A	-	4	9	0	1
				315	332	17	R	GISTKPVYIPEVELNHK	L	0.81%	3171	3171	642.0178223	3	1923.029992	1923.04656	-0.016568099	R	L	-	2	17	0	0
				447	458	11	K	SRPELLEYYIK	V	0.81%	3954	3954	705.8809814	2	1409.746313	1409.755463	-0.009149869	K	V	-	3	11	0	0
Q14444	Caprin-1	1	1.69%	98	110	12	K	YQEVTNNLEFAK	E	1.97%	2717	2717	728.3624878	2	1454.709326	1454.704155	0.005170098	K	E	-	5	12	0	0
Q14517	Protocadherin Fat 1	2	0.31%	209	216	7	R	LDYLETK	L	5.24%	2654	2654	441.7248535	2	881.434057	880.4541949	0.979862087	R	L	-	4	7	1	0
				3731	3738	7	R	ILNVFQK	L	9.88%	5993	5993	432.2605591	2	862.5054681	861.4959845	1.009483604	R	L	Q6:+0.984	2	7	1	0
Q14654	ATP-sensitive inward rectifier potassium channel 11	1	3.33%	301	314	13	R	TSYLADEILWGQR	F	3.81%	3762	3762	518.5819702	3	1552.722436	1551.756904	0.965531781	R	F	Q12:+0.984	3	13	1	0
Q14676	Mediator of DNA damage checkpoint protein 1	14	13.79%	619	642	23	R	AHEVGAQGGPPVAQVEQDLPISR	E	4.72%	3916	3916	786.4146729	3	2356.220543	2354.197869	2.022674627	R	E	-	1	23	2	0
				807	818	11	R	QTVDKVMGIPK	E	4.94%	2476	2476	608.8179932	2	1215.620336	1214.669291	0.951045056	R	E	-	1	11	1	1
				876	885	9	K	NGESASPER	D	5.46%	5029	5029	473.7467651	2	945.4778802	945.4151836	0.062696569	K	D	-	1	9	0	0
				1059	1079	20	K	HLAPPPLLSPLLPSIKPTVR	K	0.81%	6003	6003	716.4437866	3	2146.307885	2145.303778	1.004107015	K	K	-	4	20	1	0
				1197	1229	32	K	TPETVVPTALELQPSTSTDRPVTSEPTSQATR	G	4.46%	3789	3789	1133.580566	3	3397.718224	3396.68962	1.028603779	K	G	Q13:+0.984	2	32	1	0
				1320	1349	29	K	TPETVVPTAPELQISTSTDQPVTPKPTSR	T	0.81%	3920	3920	1026.867676	3	3077.579552	3076.592822	0.986730104	K	T	-	3	29	1	0
				1402	1413	11	K	TPETLVPTAPK	L	0.81%	1674	1674	578.7960205	2	1155.576391	1152.639036	2.93735516	K	L	-	2	11	3	0
				1607	1632	25	K	TPEPVVPTAPEPHPTTSTDQPVTPK	L	2.26%	2170	2170	875.4561768	3	2623.345055	2622.317709	1.027345721	K	L	-	2	25	1	0
				1648	1682	34	K	TPKPVEPAASDLEPFTPTDQSVTPEAIAQGGQSK	T	0.81%	4567	4567	1165.574585	3	3493.70028	3493.710021	-0.009741669	K	T	Q20:+0.984	4	34	0	0
				1762	1790	28	R	AAESLTAIPEPASPQLLETPIHASQIQK	V	5.41%	5135	5135	981.1928711	3	2940.555138	2939.5604	0.994738529	R	V	-	2	28	1	0
				1907	1930	23	R	AVLALGGSLAGSAAEASHLVTDR	I	0.81%	5925	5925	723.3866577	3	2167.136498	2165.144042	1.992455801	R	I	-	5	23	2	0
				1943	1957	14	R	GIPILSLDWLHQSR	K	5.48%	7034	7034	545.6358643	3	1633.884118	1633.894022	-0.009904355	R	K	-	1	14	0	0
				1977	1989	12	K	NFGFSLQDALSR	A	0.81%	5542	5542	678.3516846	2	1354.687719	1353.66771	1.020008845	K	A	-	5	12	1	0
				2054	2071	17	R	VGLPLLSPEFLLTGVLK	Q	0.81%	9451	9451	899.0532837	2	1796.090917	1795.085905	1.005011959	R	Q	-	5	17	1	0
Q14BN4	Sarcolemmal membrane-associated protein	1	1.33%	543	554	11	K	QIQVLQAQLQR	L	7.33%	5591	5591	664.8554688	2	1327.695287	1327.698279	-0.002991932	K	L	Q1:+0.984,Q6:+0.984,Q8:	1	11	0	0
Q15019	Septin-2	1	2.49%	174	183	9	K	VNIVPVIAK	A	2.32%	2683	2683	476.8110962	2	951.6065423	951.6116986	-0.005156345	V	A	-	4	9	0	0
Q15046	Lysyl-tRNA synthetase	7	13.23%	111	127	16	K	YSHLQPGDHLTDITLK	V	4.73%	2663	2663	460.2362366	4	1836.913646	1836.937009	-0.023363087	K	V	-	1	16	0	0
				230	241	11	R	YLDLILNDFVR	Q	0.81%	7221	7221	690.8794556	2	1379.743261	1379.744898	-0.001636907	R	Q	-	5	11	0	0
				305	314	9	K	MLVVGGIDR	V	0.81%	2233	2233	480.7578125	2	959.4999749	958.5269838	0.972991104	K	V	-	4	9	1	0
				370	392	22	K	VTYHPDGPEGQAYDVDFTPPFR	R	0.81%	4683	4683	836.7189331	3	2507.133324	2507.139351	-0.006026668	K	R	-	4	22	0	0
				407	420	13	K	LPETNLFETEETR	K	0.81%	3665	3665	790.3847656	2	1578.753881	1577.757313	0.996567834	K	K	-	5	13	1	0

				407	421	14	K	LPETNLFETEETRK	I	1.93%	2885	2885	854.9306641	2	1707.845678	1705.852276	1.993401573	K	I	-	5	14	2	1
				485	492	7	R	FELFVMK	K	4.11%	5066	5066	457.2449951	2	912.4743402	912.4779083	-0.00356811	R	K	-	1	7	0	0
Q15047	Histone-lysine N-methyltransferase SETDB1	1	0.93%	59	71	12	K	QLAELETWVIQK	E	5.24%	3663	3663	729.9052734	2	1457.794897	1456.792577	1.002320267	K	E	-	1	12	1	0
Q15084	Protein disulfide-isomerase A6	4	15.23%	118	132	14	R	TGEAIVDAALSALR	Q	0.81%	6522	6522	693.8835449	2	1385.75144	1385.75144	-2.1225E-07	R	Q	-	5	14	0	0
				216	231	15	K	LAAVDATVNQVLASR	Y	0.81%	4723	4723	764.9313354	2	1527.847021	1526.841652	1.005368738	K	Y	-	5	15	1	0
				264	289	25	R	ALDLFSDNAPPPELLEIINEDIAKR	T	3.19%	8408	8408	932.4956055	3	2794.463341	2792.459623	2.003718478	R	T	-	2	25	2	1
				373	386	13	K	GSFSEQGINEFLR	E	0.81%	4757	4757	742.8632813	2	1483.710912	1482.710303	1.000608996	K	E	-	5	13	1	0
Q15125	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	1	10.43%	147	171	24	R	FILQLVVSVGQIYGDVLYFLTEHR	D	3.98%	12763	12763	703.64	4	2810.5287	2808.521435	2.007264712	R	D	-	1	24	2	0
Q15139	Serine/threonine-protein kinase D1	1	1.75%	530	546	16	R	MWEIAIQHALMPVIPK	G	5.01%	6626	6626	632.668335	3	1894.98153	1892.989316	1.992213275	R	G	M1:+15.995,Q7:+0.984	2	16	2	0
Q15149	Plectin	108	28.91%	236	248	12	K	LQNVQIALDYLR	H	0.81%	5493	5493	723.9146118	2	1445.813574	1444.80381	1.009763649	K	H	-	5	12	1	0
				328	336	8	R	LFNAIIHR	H	1.97%	2630	2630	492.7966309	2	983.5776116	982.5712308	1.006380887	R	H	-	5	8	1	0
				336	346	10	R	HKPLLIDMNK	V	3.49%	987	987	403.5647278	3	1207.670708	1207.674711	-0.00400265	R	V	-	2	10	0	0
				349	365	16	R	QTNLENLDQAFSVAER	D	0.81%	5114	5114	918.458313	2	1834.900976	1833.885702	1.015273953	R	D	-	4	16	1	0
				371	386	15	R	LLDPEDVDVPQPDEK	S	0.81%	3589	3589	854.9178467	2	1707.820043	1707.820308	-0.000264377	R	S	-	5	15	0	0
				460	469	9	K	FKEMELPAK	E	5.75%	5723	5723	546.3117676	2	1090.607885	1091.568514	-0.960629292	K	E	-	1	9	-1	1
				477	493	16	K	GIYQSLEGAVQAGQLK	V	0.81%	13211	13211	833.0440674	2	1664.072485	1662.846432	1.226053086	K	V	Q4:+0.984,Q14:+0.984	1	16	1	0
				509	517	8	K	LHVAILER	E	0.81%	1811	1811	476.2903137	2	950.5649774	949.5708964	0.994080937	K	E	-	3	8	1	0
				587	597	10	R	LLFNDVQTLK	D	0.81%	4327	4327	595.8416748	2	1189.6677	1189.67067	-0.002970735	R	D	-	2	10	0	0
				630	650	20	K	AGVAAPATQVAQVTLQSVQR	R	0.81%	4331	4331	666.0054321	3	1994.992821	1995.074884	-0.082063029	K	R	Q12:+0.984	3	20	0	0
				660	675	15	R	YLQDLLAWVEENQHR	V	0.81%	7049	7049	957.9761963	2	1913.936743	1912.943157	0.993585266	R	V	-	4	15	1	0
				675	696	21	R	VDGAEWGVDLPSVEAQLGSHR	G	0.81%	5621	5621	741.6991577	3	2222.073998	2222.060357	0.013641481	R	G	Q16:+0.984	3	21	0	0
				696	706	10	R	GLHQSIEEFR	A	0.81%	1476	1476	608.810791	2	1215.605932	1214.604382	1.001550383	R	A	-	4	10	1	0
				750	764	14	R	SLESLHSFVAAATK	E	0.81%	4404	4404	730.8986206	2	1459.781591	1459.76709	0.014501075	R	E	-	5	14	0	0
				896	915	19	R	LEDLLQDAQDEKEQLNEYK	G	0.81%	4840	4840	774.3760376	3	2320.104638	2321.091048	-0.986410047	R	G	Q14:+0.984	2	19	-1	1
				1044	1052	8	R	SWSLATFR	T	0.81%	4504	4504	484.2527466	2	966.4898431	966.4923117	-0.002468612	R	T	-	4	8	0	0
				1060	1075	15	R	QALHSLELHYQAFLR	D	0.81%	4716	4716	457.2474976	4	1824.95869	1824.963499	-0.004808598	R	D	-	2	15	0	0
				1186	1201	15	K	VLALPEPSPAAPTLR	S	0.81%	3915	3915	766.9424438	2	1531.869238	1530.876975	0.992262671	K	S	-	5	15	1	0
				1201	1210	9	R	SELELTLGK	L	0.81%	3119	3119	495.2784119	2	988.5411737	988.5440726	-0.00289899	R	L	-	5	9	0	0
				1233	1243	10	R	GTQGAEEVLR	A	5.14%	739	739	530.2728882	2	1058.530126	1058.535633	-0.005506945	R	A	-	1	10	0	0
				1250	1266	16	K	EAQAVPATLPELEATK	A	0.81%	3764	3764	834.4451904	2	1666.874731	1666.877763	-0.003032165	K	A	-	5	16	0	0
				1273	1291	18	R	AQAEAQQPTFDALRDELR	G	0.81%	4241	4241	687.0140991	3	2058.018822	2058.013028	0.005794347	R	G	-	1	18	0	1
				1315	1324	9	R	ERVAQLLER	W	5.51%	828	828	557.3116455	2	1112.607641	1112.630202	-0.022561432	R	W	-	1	9	0	1
				1317	1324	7	R	VAQLLER	W	0.81%	923	923	414.7500916	2	827.484533	827.486498	-0.001964983	R	W	-	4	7	0	0
				1324	1335	11	R	WQAVLAQTDVR	Q	0.81%	2995	2995	644.3414917	2	1286.667333	1285.677881	0.989452382	R	Q	-	5	11	1	0
				1350	1364	14	R	ESADPLGAWLQDAR	R	0.81%	6055	6055	764.8717041	2	1527.727758	1527.731767	-0.004009069	R	R	-	5	14	0	0
				1366	1382	16	R	QEQIQAMPLADSQAVR	E	0.81%	3088	3088	892.9549561	2	1783.894262	1783.88868	0.005582125	R	E	-	4	16	0	0
				1377	1386	9	D	SQAVREQLR	Q	6.30%	1514	1514	545.2792358	2	1088.542822	1086.578151	1.964670424	D	Q	Q7:+0.984	1	9	2	1
				1410	1427	17	K	QYINAIKDYELQLVTYK	A	0.81%	5606	5606	1052.565674	2	2103.115698	2101.109554	2.00614348	K	A	-	2	17	2	1
				1427	1438	11	K	AQLEPVASPAK	K	2.88%	694	694	555.8075562	2	1109.599462	1109.60807	-0.008607719	K	K	-	3	11	0	0
				1441	1457	16	K	VQSGSESVIQEYVDLR	T	0.81%	5195	5195	904.9525146	2	1807.889379	1807.895204	-0.005824791	K	T	-	5	16	0	0
				1459	1472	13	H	YSELTTLTSQYIK	F	3.80%	4944	4944	774.4120483	2	1546.808447	1545.792636	1.0158104	H	F	-	1	13	1	0
				1498	1508	10	R	LAEVEAALEK	Q	1.93%	2063	2063	536.7979126	2	1071.580175	1071.581186	-0.001011373	R	Q	-	2	10	0	0
				1584	1592	8	R	LRIEEEIR	V	6.38%	1127	1127	530.7543335	2	1059.493017	1056.592754	2.90026272	R	V	-	2	8	3	1
				1605	1616	11	R	GGAEGELQALR	A	6.90%	1935	1935	551.7920532	2	1101.568456	1099.562182	2.006274005	R	A	-	1	11	2	0
				1698	1709	11	R	QVQVALETAQR	S	3.08%	952	952	620.3441772	2	1238.672704	1241.672796	-3.000091164	R	S	-	2	11	-1	0
				1731	1744	13	R	SLQEEHVAVAQLR	E	0.81%	1819	1819	740.4005127	2	1478.785375	1478.784137	0.001238191	R	E	-	5	13	0	0
				1792	1808	16	K	SLAQAEAEKQKEEAER	E	4.06%	626	626	606.3084717	3	1815.90194	1815.896267	0.005673255	K	E	-	1	16	0	2
				1824	1833	9	R	ELAEQELEK	Q	3.50%	790	790	544.774231	2	1087.532812	1087.539716	-0.006903774	R	Q	-	3	9	0	0
				1845	1854	9	R	LAAEQELIR	L	0.81%	1914	1914	521.7958984	2	1041.576147	1041.581855	-0.005708349	R	L	-	4	9	0	0
				1866	1875	9	R	QLLEEELAR	L	1.93%	2985	2985	550.800354	2	1099.585058	1099.587335	-0.002276576	R	L	-	3	9	0	0
				1886	1896	10	K	RQELEAELAK	V	4.23%	747	747	593.8236084	2	1185.631567	1185.635347	-0.003780683	K	V	-	2	10	0	1
				1975	1984	9	K	LAAIGEATR	L	0.81%	732	732	451.2583313	2	900.5010125	900.5028764	-0.001863898	K	L	-	5	9	0	0
				1984	1994	10	R	LKTEAEIALK	E	3.69%	903	903	558.3356934	2	1114.655737	1114.659771	-0.004034577	R	E	-	2	10	0	1
				2047	2055	8	K	GLVEDTLR	Q	1.93%	1880	1880	451.7531128	2	901.4905755	901.486892	0.003683498	K	Q	-	3	8	0	0
				2058	2068	10	R	QVEEEILALK	A	3.50%	3881	3881	586.3319092	2	1170.648168	1170.649601	-0.001432217	R	A	-	4	10	0	0
				2171	2182	11	R	QLQLAQEAAQK	R	0.81%	850	850	614.3377075	2	1226.659765	1226.661897	-0.002131569	R	R	-	5	11	0	0
				2198	2217	19	K	EQELQQTLQQEQSVLDQLR	G	0.81%	6009	6009	1157.585815	2	2313.155981	2312.160815	0.995166147	K	G	-	4	19	1	0
				2318	2329	11	K	AQVEQELTTLR	L	0.81%	2796	2796	645.2883911	2	1288.561132	1286.683026	1.878106179	K	L	-	5	11	2	0
				2339	2348	9	K	NLLDEELQR	L	4.61%	3452	3452	565.2959595	2	1128.576269	1128.577498	-0.001229247	K	L	-	2	9	0	0
				2360	2371	11	R	SQVEEELFSVR	V	0.81%	4231	4231	661.8279419	2	1321.640234	1321.651391	-0.011157771	R	V	-	5	11	0	0
				2461	2473	12	R	LKAEAELLQQQK	E	0.81%	861	861	699.897644	2	1397.779638	1397.787826	-0.00818749	R	E	-	5	12	0	1
				2463	2473	10	K	AEAELLQQQK	E	6.72%	774	774	580.3174438	2	1158.619238	1156.608798	2.010439343	K	E	-	1	10	2	0
				2482	2503	21	R	LQEDKEQMAQQLAEETQGFQR	T	1.93%	3946	3946	837.0684204	3	2508.181786	2506.175814	2.005972142	R	T	-	2	21	2	1
				2564	2575	11	K	VTLVQTLEIQR	Q	0.81%	3275	3275	434.247345	3	1299.71856	1299.739797	-0.021237216	K	Q	Q10:+0.984	2	11	0	0
				2586	2594	8	R	EAIAELER	E	5.96%	1036	1036	465.7488403	2	929.4820306	929.4818066	0.000223936	R	E	-	1	8	0	0
				2609	2636	27	K	SEEMQTVQQEQLLQETQALQQSFLSEK	D	5.14%	6878	6878	1061.188599	3	3180.542321	3179.529237	1.01308405	K	D	-	2	27	1	0
				2650	2663	13	K	AKLEQLFQDEVAK	A	0.81%	4056	4056	760.413147	2	1518.810644	1517.808955	1.001688929	K	A	-	5	13	1	1
				2652	2663	11	K	LEQLFQDEVAK	A	0.81%	3416	3416	660.3469238	2	1318.678198	1318.676878	0.001319624	K	A	-	5	11	0	0
				2730	2743	13	R	LREQLQLLEEQHR	A	0.81%	2343	2343	564.64	3	1690.896525	1690.911463	-0.014938192	R	A	-	2	13	0	1
				2743	2761	18	R	AALAHSEEVTASQVAATK	T	0.81%	860	860	892.4644165	2	1782.913183	1782.911188	0.001994512	R	T	-	5	18	0	0
				2794	2808	14	R	LQEAGILSAEELQR	L	0.81%	3797	3797	778.9156494	2	1555.815649	1555.820582	-0.004933564	R	L	-	5	14	0	0
				2808	2821	13	R	LAQGHTTVDELAR	R	0.81%	13287	13287	471.33	3	1410.966525	1410.710288	0.256237048	R	R	Q3:+0.984	1	13	0	0
				2832	2841	9	R	SSIAGLLLK	A	1.93%	4484	4484	451.2893677	2	900.5630853	900.5644141	-0.001328808	R	A	-	4	9	0	0
				2855	2881	26	R	QLLSPGTALILLEAQAASGFLLDPVR	N	0.81%	10451	10451	898.8460693	3	2693.514733	2692.51635	0.99838312	R	N	-	2	26	1	0
				2941	2960	19	R	LLEAQIATGGVIDPVHSHR	V	0.81%	3549	3549	671.7016602	3	2012.081505	2012.08032	0.001185773	R	V	-	4	19	0	0
				2960	2968	8	R	VPVDVAYR	R	0.81%	777	777	459.7528687	2	917.4900872	917.4970627	-0.006975503	R	R	-	5	8	0	0
				2988	3007	19	K	GFFDPNTHENLTYLQLLER	C	5.31%	6686	6686	769.3876343	3	2305.139428	2307.117143	-1.977715464	K	C	N6:+0.984	3	19	-1	0
				3044	3053	9	K	ATVSAPFGK	F	4.61%	954	954	439.241272	2	876.4668939	876.4705136	-0.003619735	K	F	-	2	9	0	0
				3094	3106	12	K	IIITVVEEQEQK	G	0.81%	3224	3224	714.902832	2	1427.790014	1427.787157	0.002857143	K	G	-	5	12	0	0
				3115	3127	12	R	SLVPAAELLESR	V	0.81%	4663	4663	642.8599243	2	1283.704199	1283.708512	-0.004313887	R	V	-	5	12	0	0
				3145	3154	9	R	DVAEVDTVR	R	4.32%	726	726	503.2527161	2	1004.489782	1002.498185	1.991596993	R	R	-	3	9	2	0
				3158	3174	16	R	GANVIAGVWLEEAGQK	L	0.81%	5458	5458	821.4285278	2	1640.841406	1640.852217	-0.010811216	R	L	-	5	16	0	0
				3183	3212	29	K	DLLPSDMAVALLEAQAGTGHIIDPATSAR	L	6.13%	7870	7870	978.8417358	3	2933.501732	2932.49642	1.00531216	K	L	-	1	29	1	0
				3212	3220	8	R	LTVDEAVR	A	0.81%	890	890	452.7473755	2	903.4791009	901.486892	1.992208889	R	K	-	2	8	2	0
				3269	3285	16	R	LLDAQLSTGGIVDPSK	S	0.81%	3898	3898	807.8999023	2	1613.784155	1612.867198	0.916956384	R	S	-	3	16	1	0
				3316	3335	19	K	AYSDPSTGEPATYGELQQR	C	0.81%	1853	1853	1035.981812	2	2069.947973	2068.933775	1.014198455	K	C	-	5	19	1	0
				3355	3368	13	R	ARQEELYSELQAR	E	3.02%	2301	2301	797.4067383	2	1592.797826	1591.79543	1.002396315	R	E	-	3	13	1	1
				3373	3384	11	K	TPVEVPVGGFK	G	2.46%	3020	3020	565.32	2	1128.62435	1128.617906	0.006443584	K	G	-	5	11	0	0
				3423	3436	13	K	ILITIVEEVETLR	Q	0.81%	7610	7610	764.9526978	2	1527.889745	1526.891956	0.99778906	K	Q	-	5	13	1	0
				3446	3462	16	R	APVPASELLASGVLSR	A	0.81%	4921	4921	783.94	2	1565.86435	1565.877703	-0.013353352	R	A	-	5	16	0	0
				3476	3485	9	K	DLSELGSVR	T	4.10%	2444	2444	488.2549438	2	974.4942376	974.5032704	-0.009032801	K	T	-	2	9	0	0
				3505	3513	8	K	VSIYEAMR	R	1.98%	2612	2612	484.747345	2	967.4790399	967.4796992	-0.000659387	K	R	-	4	8	0	0
				3551	3568	17	K	AGVVGPELHEQLLSAEK	A	0.81%	3367	3367	889.4810181	2	1776.946386	1775.94176	1.004625805	K	A	-	5	17	1	0
				3574	3590	16	R	DPYSGSTISLFQAMQK	G	4.61%	5728	5728	888.6773071	2	1775.338964	1771.845084	3.493880466	R	G	-	2	16	3	0
				3619	3628	9	R	VPVDVAYQR	G	0.81%	912	912	525.781311	2	1049.546972	1045.55564	3.991331646	R	G	-	1	9	4	0
				3628	3637	9	R	GYFSEEMNR	V	5.46%	12821	12821	568.383728	2	1134.751806	1132.449506	2.302300151	R	V	N8:+0.984	1	9	2	0
				3685	3702	17	K	AEVVETTQVYTEEETRR	A	3.70%	1570	1570	681.3345947	3	2040.980309	2039.964725	1.015584308	K	A	Q8:+0.984	4	17	1	1
				3770	3781	11	R	QQGLASYDYVR	R	0.81%	2221	2221	650.3166504	2	1298.617651	1298.625511	-0.007860307	R	R	-	4	11	0	0
				3783	3793	10	R	LTAEDLFEAR	I	0.81%	4562	4562	582.7966309	2	1163.577612	1163.582249	-0.004637505	R	I	-	5	10	0	0
				3793	3804	11	R	IISLETYNLLR	E	0.81%	5467	5467	667.8861694	2	1333.756689	1333.760548	-0.003859253	R	E	-	5	11	0	0
				3849	3858	9	K	GLLSAEVAR	L	0.81%	1345	1345	458.2663574	2	914.5170648	914.5185265	-0.001461732	K	L	-	4	9	0	0
				3858	3878	20	R	LLLEAQAATGFLLDPVKGER	L	5.56%	6453	6453	715.0565796	3	2142.146264	2140.189201	1.95706217	R	L	-	1	20	2	1
				3935	3950	15	R	LLDAQLATGGIVDPR	L	0.81%	4053	4053	770.4325562	2	1538.849462	1537.846403	1.003059113	R	L	-	5	15	1	0
				3950	3963	13	R	LGFHLPLEVAYQR	G	0.81%	5209	5209	514.951416	3	1541.830773	1541.835444	-0.004671465	R	G	-	5	13	0	0
				3968	3981	13	K	DTHDQLSEPSEVR	S	0.81%	699	699	757.3530273	2	1512.690405	1511.685211	1.005193656	K	S	-	3	13	1	0
				3991	3999	8	R	LSYTQLLR	R	0.81%	3667	3667	497.2894287	2	992.5632073	992.5654767	-0.002269394	R	R	-	5	8	0	0
				4003	4018	15	R	DDGTGQLLLPLSDAR	K	6.68%	4954	4954	785.9088135	2	1569.801977	1569.799847	0.002130001	R	K	-	1	15	0	0
				4036	4049	13	R	SQVMDEATALQLR	E	2.83%	3597	3597	731.8708496	2	1461.726049	1460.729325	0.996723675	R	E	-	4	13	1	0
				4049	4060	11	R	EGLTSIEEVTK	N	3.94%	2927	2927	603.3148193	2	1204.613989	1204.618694	-0.004705744	R	N	-	3	11	0	0
				4092	4118	26	K	GIIRPGTAFELLEAQAATGYVIDPIK	G	0.81%	7568	7568	915.5004272	3	2743.477807	2742.495614	0.98219229	K	G	-	3	26	1	0
				4121	4129	8	K	LTVEEAVR	M	4.81%	849	849	459.26	2	916.5043499	915.5025421	1.001807832	K	M	-	1	8	1	0
				4129	4138	9	R	MGIVGPEFK	D	3.76%	3141	3141	490.2671204	2	978.5185906	976.5051857	2.013404923	R	D	-	2	9	2	0
				4158	4167	9	K	LISLFQAMK	K	0.81%	5583	5583	525.8027954	2	1049.589941	1049.594335	-0.004394428	K	K	-	5	9	0	0
				4178	4197	19	R	LLEAQIATGGIIDPEESHR	L	0.81%	4192	4192	684.024231	3	2049.049218	2048.05383	0.995387631	R	L	-	4	19	1	0
				4197	4205	8	R	LPVEVAYK	R	0.81%	1732	1732	459.7680054	2	917.5203607	917.5222149	-0.00185421	R	R	-	3	8	0	0
				4466	4475	9	R	FPVTDAVNK	G	0.81%	938	938	495.765564	2	989.5154779	989.5181922	-0.002714318	R	G	-	3	9	0	0
				4542	4551	9	R	VPLDEALQR	G	0.81%	1773	1773	520.7871094	2	1039.558569	1039.566205	-0.007636394	R	G	-	5	9	0	0
Q15256	Receptor-type tyrosine-protein phosphatase R	1	3.96%	337	363	26	R	GSNVSLTLDMSSLGNIEPFVSIPTPR	E	5.52%	5085	5085	687.8554077	4	2747.390331	2747.36883	0.021500971	R	E	N3:+0.984,M10:+15.995	2	26	0	0
Q15283	Ras GTPase-activating protein 2	1	2.59%	335	357	22	K	SPDVQPISASAAYILSEICRDK	N	4.10%	5909	5909	807.7439575	3	2420.208397	2419.204859	1.003538063	K	N	C19:+57.021	2	22	1	1
Q15286	Ras-related protein Rab-35	6	42.79%	3	10	7	R	DYDHLFK	L	2.36%	1841	1841	469.2225037	2	936.4293572	936.4341281	-0.004770836	R	L	-	5	7	0	0
				58	69	11	K	LQIWDTAGQER	F	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				79	100	21	R	GTHGVIVVYDVTSAESFVNVK	R	2.36%	5480	5480	1111.573486	2	2221.131323	2220.142645	0.988677336	R	R	-	2	21	1	0
				101	115	14	R	WLHEINQNCDDVCR	I	1.93%	1429	1429	620.602356	3	1858.783593	1857.787722	0.995870967	R	I	C9:+57.021,C13:+57.021	5	14	1	0
				137	152	15	K	FAGQMGIQLFETSAK	E	0.81%	5348	5348	813.4492188	2	1624.882787	1626.807576	-1.924788444	K	E	-	3	15	-1	0
				152	170	18	K	ENVNVEEMFNCITELVLR	A	0.81%	9851	9851	1105.555054	2	2209.094457	2208.055025	1.03943243	K	A	C11:+57.021	4	18	1	0
Q15375	Ephrin type-A receptor 7	1	0.90%	976	985	9	K	IMSSIQTMR	A	9.51%	5106	5106	541.7703247	2	1081.524999	1081.526084	-0.00108477	K	A	M2:+15.995	1	9	0	0
Q15382	GTP-binding protein Rheb	5	25.00%	7	15	8	R	KIAILGYR	S	2.26%	2289	2289	467.2955322	2	932.5754144	932.5807328	-0.005318443	R	S	-	5	8	0	1
				109	120	11	K	VQIPIMLVGNK	K	0.81%	4909	4909	606.3599854	2	1210.704321	1210.710762	-0.006441449	K	K	-	3	11	0	0
				109	121	12	K	VQIPIMLVGNKK	D	1.93%	4070	4070	670.40271	2	1338.78977	1338.805725	-0.015955366	K	D	-	5	12	0	1
				135	151	16	K	ALAESWNAAFLESSAK	E	0.81%	5064	5064	847.9193115	2	1693.822973	1693.831147	-0.008174065	K	E	-	4	16	0	0
				151	161	10	K	ENQTAVDVFR	R	0.81%	2114	2114	590.2971802	2	1178.57871	1177.572747	1.005963192	K	R	-	3	10	1	0
Q15599	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	1	6.53%	195	217	22	R	LIEVNGQNVEGLRHAEVVASIK	A	6.42%	6939	6939	793.4497681	3	2377.325829	2376.264855	1.060974431	R	A	Q7:+0.984,N8:+0.984	1	22	1	1
Q15722	Leukotriene B4 receptor 1	1	2.56%	294	303	9	R	SAGVGFVAK	L	9.04%	743	743	418.24	2	834.4643499	834.4599489	0.00440104	R	L	-	1	9	0	0
Q15758	Neutral amino acid transporter B(0)	8	24.40%	85	98	13	R	LSAFVFPGELLLR	L	0.81%	7945	7945	731.4264526	2	1460.837255	1460.839133	-0.001877575	R	L	-	5	13	0	0
				101	126	25	R	MIILPLVVCSLIGGAASLDPGALGR	L	4.01%	10395	10395	832.1373291	3	2493.388512	2492.385408	1.003104281	R	L	C9:+57.021	2	25	1	0
				178	189	11	K	EVLDSFLDLAR	N	0.81%	6411	6411	639.3406982	2	1276.665746	1276.666313	-0.000566828	K	N	-	5	11	0	0
				189	202	13	R	NIFPSNLVSAAFR	S	0.81%	6584	6584	718.3911743	2	1434.766699	1434.761945	0.004753529	R	S	-	3	13	0	0
				288	301	13	K	IVEMEDVGLLFAR	L	0.81%	6774	6774	746.3948975	2	1490.774145	1490.780298	-0.006153566	K	L	-	5	13	0	0
				335	362	27	R	FLWGIVTPLATAFGTSSSSATLPLMMK	C	0.81%	9404	9404	943.503418	3	2827.486779	2826.469995	1.016783354	R	C	-	3	27	1	0
				492	502	10	R	STEPELIQVK	S	0.81%	2308	2308	572.3140869	2	1142.612524	1142.6183	-0.005776588	R	S	-	2	10	0	0
				502	522	20	K	SELPLDPLPVPTEEGNPLLK	H	0.81%	6580	6580	1080.089844	2	2158.164037	2157.156898	1.007139084	K	H	-	4	20	1	0
Q15771	Ras-related protein Rab-30	3	22.66%	59	70	11	K	LQIWDTAGQER	F	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0

				136	154	18	R	AEEFSEAQDMYYLETSAK	E	0.81%	4718	4718	1056.960205	2	2111.90476	2110.904115	1.000645076	R	E	-	5	18	1	0
				175	192	17	R	QNTLVNNVSSPLPGEGK	S	0.81%	2610	2610	877.9604492	2	1753.905248	1752.900624	1.004624662	R	S	-	5	17	1	0
Q15833	Syntaxin-binding protein 2	1	2.70%	387	403	16	K	LIVPVLLDAAVPAYDK	I	0.81%	6839	6839	849.5023804	2	1696.989111	1695.981106	1.008004846	K	I	-	5	16	1	0
Q15907	Ras-related protein Rab-11B	9	45.87%	13	24	11	K	VVLIGDSGVGK	S	0.81%	2094	2094	523.2819824	2	1044.548315	1042.602256	1.946058508	K	S	-	3	11	2	0
				41	51	10	K	STIGVEFATR	S	0.81%	2531	2531	541.77	2	1081.52435	1079.56112	1.963230216	K	S	-	5	10	2	0
				61	72	11	K	AQIWDTAGQER	Y	0.81%	1882	1882	639.2866211	2	1276.557592	1273.60511	2.952482212	K	Y	-	2	11	3	0
				74	82	8	R	AITSAYYR	G	0.81%	767	767	472.7441711	2	943.4726922	943.4763273	-0.003635083	R	G	-	4	8	0	0
				82	95	13	R	GAVGALLVYDIAK	H	0.81%	5299	5299	645.8803101	2	1289.74497	1288.739084	1.005885765	R	H	-	4	13	1	0
				107	125	18	K	ELRDHADSNIVIMLVGNK	S	0.81%	4711	4711	675.3575439	3	2023.049157	2023.052057	-0.002900332	K	S	-	4	18	0	1
				110	125	15	R	DHADSNIVIMLVGNK	S	0.81%	5099	5099	813.43	2	1624.84435	1624.824289	0.02006132	R	S	-	5	15	0	0
				145	166	21	K	NNLSFIETSALDSTNVEEAFK	N	0.81%	6460	6460	1165.05957	2	2328.103491	2328.112133	-0.008642535	K	N	-	4	21	0	0
				166	174	8	K	NILTEIYR	I	2.34%	4389	4389	511.2798462	2	1020.544042	1020.560391	-0.016349073	K	I	-	5	8	0	0
Q16181	Septin-7	1	5.26%	63	86	23	K	STLINSLFLTDLYSPEYPGPSHR	I	3.64%	6926	6926	870.1109619	3	2607.309411	2606.301665	1.00774527	K	I	-	3	23	1	0
Q16602	Calcitonin gene-related peptide type 1 receptor	3	10.20%	22	38	16	A	ELEESPEDSIQLGVTR	N	3.50%	3520	3520	901.4454956	2	1800.875341	1800.874134	0.001206891	A	N	-	1	16	0	0
				403	417	14	K	IQFGNSFSNSEALR	S	0.81%	3638	3638	785.8858032	2	1569.755956	1568.758316	0.997640045	K	S	-	4	14	1	0
				444	461	17	K	SIHDIENVLLKPENLYN	-	4.85%	5767	5767	671.3609009	3	2011.059228	2010.042203	1.017024773	K	-	-	1	17	1	0
Q16658	Fascin	1	4.26%	1	22	21	M	TANGTAEAVQIQFGLINCGNK	Y	6.29%	4680	4680	736.4007568	3	2206.178795	2206.06835	0.110445292	M	Y	N17:+0.984,C18:+57.021	1	21	0	0
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	5	19.40%	60	73	13	K	VAFITGGGTGLGK	G	0.81%	2788	2788	589.3309326	2	1176.646215	1176.650269	-0.004053998	K	G	-	5	13	0	0
				133	155	22	K	VAGHPNIVINNAAGNFISPTER	L	0.81%	3732	3732	764.3998413	3	2290.176049	2290.181825	-0.005775922	K	L	-	4	22	0	0
				234	244	10	R	FNVIQPGPIK	T	0.81%	2956	2956	556.8253784	2	1111.635107	1111.638976	-0.003869348	R	T	-	3	10	0	0
				251	260	9	R	LDPTGTFEK	E	6.83%	1038	1038	504.250885	2	1006.48612	1006.497122	-0.01100246	R	E	-	1	9	0	0
				319	330	11	K	EQWDTIEELIR	K	2.46%	6081	6081	716.3578491	2	1430.700048	1430.704155	-0.004107246	K	K	-	5	11	0	0
Q16762	Thiosulfate sulfurtransferase	1	6.40%	187	206	19	R	FLGTEPEPDAVGLDSGHIR	G	0.81%	3530	3530	670.6642456	3	2008.969262	2008.985416	-0.016154416	R	G	-	4	19	0	0
Q18PE1	Protein Dok-7	1	3.57%	432	450	18	R	DSGGQTSAGCPSGWLGTR	R	3.78%	4351	4351	897.9089966	2	1793.802343	1792.779394	1.02294918	R	R	C10:+57.021	2	18	1	0
Q1EHB4	Sodium-coupled monocarboxylate transporter 2	1	5.50%	188	222	34	Q	MVVMIVGFLTVLIQGSTHAGGFHNVLEQSTNGSR	L	4.83%	8703	8703	905.43	4	3617.6887	3616.801843	0.88685732	Q	L	M4:+15.995,Q14:+0.984,N	1	34	1	0
Q3SYG4	Protein PTHB1	1	2.59%	124	147	23	K	LMYEHNLQRTACNMTYGSFGGVK	G	7.72%	3732	3732	898.409668	3	2692.205529	2692.219234	-0.01370487	K	G	M2:+15.995,C12:+57.021	1	23	0	1
Q4VCS5	Angiomotin	2	2.77%	535	543	8	K	TISQLFAK	N	4.84%	2472	2472	454.2644959	2	906.5133416	906.5174638	-0.004122221	K	N	-	1	8	0	0
				684	706	22	K	YLEENVMRHFALDAAATVAAQR	D	0.81%	3783	3783	831.7406616	3	2492.19851	2492.211875	-0.013365513	K	D	N5:+0.984,M7:+15.995	2	22	0	1
Q5BJF2	Transmembrane protein 97	5	42.05%	36	44	8	R	ELYPVEFR	N	0.81%	3640	3640	526.7711182	2	1051.526586	1051.533842	-0.007256	R	N	-	1	8	0	0
				52	67	15	K	EFKDPLLQEPPAWFK	S	0.81%	6250	6250	615.9873657	3	1844.938622	1844.934868	0.003753736	K	S	Q8:+0.984	2	15	0	1
				55	67	12	K	DPLLQEPPAWFK	S	0.81%	5730	5730	721.8582153	2	1441.700781	1439.744898	1.955882624	K	S	-	4	12	2	0
				97	125	28	R	TPAIIYSVHTMTTLIPILSTFLFEDFSK	A	1.93%	11123	11123	1063.231323	3	3186.670495	3184.677011	1.993484079	R	A	-	5	28	2	0
				140	163	23	R	LTLVSVYAPYLLIPFILLIFMLR	S	3.91%	13474	13474	903.8765259	3	2708.606103	2707.61546	0.990642589	R	S	-	3	23	1	0
Q5DID0	Uromodulin-like 1	1	1.29%	965	982	17	K	AAFVQGTSPTPQGLPQR	L	4.82%	7593	7593	878.4508057	2	1754.885961	1754.895129	-0.009167496	K	L	Q16:+0.984	2	17	0	0
Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	3	4.44%	667	677	10	K	LIDKQLQDEK	M	5.58%	5126	5126	616.796875	2	1231.5781	1229.650313	1.927786688	K	M	Q7:+0.984	1	10	2	1
				743	770	27	K	EAIETIVAAMSNLVPPVELANPENQFR	V	0.81%	9008	9008	985.1765747	3	2952.506249	2951.506257	0.999992369	K	V	-	2	27	1	0
				908	917	9	R	LQEALNLFK	S	3.60%	4202	4202	539.3046875	2	1076.593725	1074.607342	1.986383304	R	S	-	5	9	2	0
Q5KSL6	Diacylglycerol kinase kappa	2	1.97%	513	526	13	K	QYLNPSQVFDLLK	G	5.88%	3594	3594	783.8180542	2	1565.620458	1565.79769	-0.177232058	K	G	N4:+0.984,Q7:+0.984	3	13	0	0
				694	706	12	K	QNNTAIVSVILK	S	5.33%	3510	3510	650.84	2	1299.66435	1298.755797	0.908552912	K	S	-	3	12	1	0
Q5T2D2	Trem-like transcript 2 protein	1	3.12%	86	96	10	K	VVNITMVALK	L	4.41%	4073	4073	544.8188477	2	1087.622045	1087.631099	-0.009053863	K	L	N3:+0.984	1	10	0	0
Q5T3U5	Multidrug resistance-associated protein 7	1	0.74%	1456	1467	11	R	VVELDSPATLR	N	5.03%	945	945	401.2163696	3	1200.625634	1198.655749	1.969885255	R	N	-	3	11	2	0
Q5TCZ1	SH3 and PX domain-containing protein 2A	1	1.94%	331	353	22	K	KNLAGPVEIIGNIMEISNLLNK	K	4.00%	6487	6487	800.4942017	3	2398.45913	2399.250565	-0.791435204	K	K	N2:+0.984,N12:+0.984,M1	2	22	-1	1
Q5VT25	Serine/threonine-protein kinase MRCK alpha	1	0.81%	101	115	14	K	VFAMKILNKWEMLK	R	9.04%	4967	4967	590.3223267	3	1767.943505	1767.946389	-0.002884092	K	R	M4:+15.995,N8:+0.984,K9	1	14	0	2
Q6IAA8	RhoA activator C11orf59	5	49.69%	47	60	13	R	TDEQALLSSILAK	T	0.81%	5618	5618	694.8838501	2	1387.75205	1387.755857	-0.003806565	R	T	-	5	13	0	0
				60	84	24	K	TASNIIDVSAADSQGMEQHEYMDR	A	3.98%	3690	3690	890.7185669	3	2669.132226	2668.138093	0.994132108	K	A	Q18:+0.984	1	24	1	0
				91	103	12	R	LAVLSSSLTHWK	K	1.97%	4081	4081	671.38	2	1340.74435	1340.745232	-0.000882368	R	K	-	4	12	0	0
				103	134	31	K	KLPPLPSLTSQPHQVLASEPIPFSDLQQVSR	I	3.19%	6026	6026	853.4631958	4	3409.821483	3409.824538	-0.003054965	K	I	Q11:+0.984	2	31	0	1
				104	134	30	K	LPPLPSLTSQPHQVLASEPIPFSDLQQVSR	I	4.01%	6404	6404	1095.266479	3	3282.775963	3282.713575	0.062388485	K	I	Q10:+0.984,Q26:+0.984	3	30	0	0
Q6PHW0	Iodotyrosine dehalogenase 1	1	2.77%	270	278	8	K	EATVPDLK	R	7.56%	1301	1301	435.7724915	2	869.5293328	871.4650939	-1.935761082	K	R	-	3	8	-1	0
Q6RW13	Type-1 angiotensin II receptor-associated protein	1	13.84%	130	152	22	R	SAYQTIDSAEAPADPFAVPEGR	S	0.81%	4464	4464	764.696106	3	2291.064843	2291.070603	-0.005759777	R	S	-	3	22	0	0
Q6YHK3	CD109 antigen	1	1.31%	86	105	19	K	TLTLPSLPLNSADEIYELR	V	0.81%	7040	7040	1073.577637	2	2145.139623	2144.136497	1.003126134	K	V	-	3	19	1	0
Q6ZMI3	Gliomedin	1	1.45%	385	393	8	K	GGSNTLVR	F	6.32%	2918	2918	402.7131958	2	803.4107415	803.4137114	-0.002969854	K	F	N4:+0.984	2	8	0	0
Q6ZRP7	Sulfhydryl oxidase 2	7	17.34%	57	72	15	R	AGEDAVWVLDSGSVR	G	2.32%	4694	4694	780.887146	2	1559.758642	1559.757982	0.00065992	R	G	-	2	15	0	0
				190	206	16	R	LDPIQPSDVLSLLDNR	G	0.81%	7365	7365	599.3227539	3	1794.944787	1793.952325	0.992461631	R	G	-	2	16	1	0
				224	240	16	R	EVILDLIPYESIVVTR	A	3.61%	7655	7655	930.1481323	2	1858.280615	1858.045163	0.235451776	R	A	-	4	16	0	0
				321	336	15	K	LYTVDLESGLHYLLR	V	0.81%	6841	6841	597.9920654	3	1790.952721	1790.956682	-0.003960831	K	V	-	1	15	0	0
				434	467	33	K	LFHTLTVEASTHPDALVGTGFEDDPQAVLQTMR	R	2.46%	6230	6230	900.1940918	4	3596.745067	3596.745697	-0.000629509	K	R	Q26:+0.984	4	33	0	0
				495	506	11	K	TPDQAILWLWK	K	0.81%	7152	7152	685.8753052	2	1369.73496	1369.739419	-0.004458328	K	K	-	5	11	0	0
				544	559	15	K	GLASWDEGHVLTFLK	Q	0.81%	5965	5965	837.4490356	2	1672.882421	1671.862053	1.020368017	K	Q	-	5	15	1	0
Q7L1I2	Synaptic vesicle glycoprotein 2B	1	1.76%	623	635	12	R	ATAFGILNGLCK	F	7.19%	4938	4938	633.3258057	2	1264.635961	1264.648076	-0.012115144	R	F	N8:+0.984,C11:+57.021	1	12	0	0
Q7L576	Cytoplasmic FMR1-interacting protein 1	13	12.61%	49	58	9	R	NAFVTGIAR	Y	0.81%	1938	1938	474.764801	2	947.513952	947.5188608	-0.004908853	R	Y	-	5	9	0	0
				110	121	11	K	TVEVLEPEVTK	L	5.03%	1932	1932	623.3156738	2	1244.615698	1242.67073	1.94496764	K	L	-	2	11	2	0
				150	163	13	K	DFVSEAYLITLGK	F	0.81%	7028	7028	728.8931274	2	1455.770605	1454.765693	1.004911731	K	F	-	5	13	1	0
				163	175	12	K	FINMFAVLDELK	N	0.81%	8746	8746	720.3890381	2	1438.762426	1438.753021	0.00940514	K	N	-	5	12	0	0
				459	467	8	K	GLQVLMGR	M	5.54%	2935	2935	437.249115	2	872.4825799	872.4902043	-0.007624396	K	M	-	1	8	0	0
				550	563	13	R	AVGPSSTQLYMVR	T	1.93%	3160	3160	705.37	2	1408.72435	1407.718032	1.006317504	R	T	-	4	13	1	0
				563	573	10	R	TMLESLIADK	S	0.81%	4851	4851	560.7979126	2	1119.580175	1119.584558	-0.004383333	R	S	-	5	10	0	0
				635	656	21	R	IQFPIEMSMPWILTDHILETK	E	4.92%	9166	9166	848.4423828	3	2542.303673	2541.301139	1.00253439	R	E	-	1	21	1	0
				705	715	10	K	LADQIFAYYK	V	4.79%	4402	4402	617.861145	2	1233.70664	1231.612471	2.094168903	K	A	Q4:+0.984	1	10	2	0
				919	935	16	R	LLGYQGIAVVMEELLK	V	0.81%	9724	9724	888.5065308	2	1774.997411	1774.990291	0.007119979	R	I	-	5	16	0	0
				938	950	12	K	SLLQGTILQYVK	T	0.81%	6274	6274	681.9042358	2	1361.792822	1361.791848	0.0009734	K	T	-	4	12	0	0
				1053	1065	12	K	YAPLHLVPLIER	L	0.81%	5142	5142	474.2787781	3	1419.812859	1419.823817	-0.010957907	K	L	-	2	12	0	0
				1065	1076	11	R	LGTPQQIAIAR	E	0.81%	1819	1819	584.3467407	2	1166.677831	1166.677153	0.000678757	R	E	-	2	11	0	0
Q7Z2W7	Transient receptor potential cation channel subfamily M member 8	1	1.09%	298	310	12	K	IPIVCFAQGGGK	E	8.97%	6496	6496	624.8257446	2	1247.635839	1246.637512	0.998327506	K	E	C5:+57.021,Q8:+0.984	1	12	1	0
Q7Z407	CUB and sushi domain-containing protein 3	1	0.22%	2270	2278	8	R	NWNHPLPR	C	7.92%	2724	2724	517.2670898	2	1032.51853	1032.525343	-0.00681356	R	C	-	1	8	0	0
Q7Z6M3	Probable mast cell antigen 32 homolog	1	4.66%	266	282	16	R	GDTAMEVGIYANILEK	Q	9.79%	7307	7307	863.8933105	2	1725.770971	1723.833835	1.93713627	R	Q	N12:+0.984	2	16	2	0
Q86UE4	Protein LYRIC	6	12.03%	4	20	16	R	SWQDELAQQAEEGSAR	L	0.81%	3772	3772	902.9064941	2	1803.797338	1803.802366	-0.005027983	R	L	-	5	16	0	0
				22	33	11	R	EMLSVGLGFLR	T	2.26%	6265	6265	611.3317261	2	1220.647802	1220.658726	-0.010924404	R	T	-	5	11	0	0
				33	45	12	R	TELGLDLGLEPK	R	0.81%	4616	4616	643.3552246	2	1284.694799	1283.697279	0.997520075	R	R	-	5	12	1	0
				87	107	20	R	KREEAAAVPAAAPDDLALLK	N	4.12%	3755	3755	684.3814697	3	2050.120934	2048.126601	1.9943329	R	N	-	1	20	2	2
				89	107	18	R	EEAAAVPAAAPDDLALLK	N	0.81%	4658	4658	883.4707642	2	1764.925878	1763.930527	0.995351368	R	N	-	5	18	1	0
				131	142	11	R	TVEVAEGEAVR	T	0.81%	697	697	580.3004761	2	1158.585302	1158.588063	-0.002760764	R	T	-	5	11	0	0
Q86UN3	Reticulon-4 receptor-like 2	1	1.90%	132	140	8	R	LQSLHLYR	C	0.81%	1555	1555	515.295166	2	1028.574682	1028.57671	-0.002028161	R	C	-	4	8	0	0
Q86XR7	TIR domain-containing adapter molecule 2	1	6.81%	200	216	16	R	GFPTQVERIFQESVYK	T	5.52%	12919	12919	644.397583	3	1930.169274	1927.967959	2.201314447	R	T	Q5:+0.984	1	16	2	1
Q86YS6	Ras-related protein Rab-43	2	11.79%	68	79	11	K	LQIWDTAGQER	F	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				118	132	14	K	YAGSNIVQLLIGNK	S	0.81%	6751	6751	745.9205933	2	1489.825536	1488.830025	0.995511739	K	S	-	5	14	1	0
Q8IWZ6	Bardet-Biedl syndrome 7 protein	1	1.82%	371	384	13	K	AKSAVPSFGINDK	F	5.24%	5886	5886	668.3543701	2	1334.69309	1332.703761	1.989328746	K	F	-	3	13	2	1
Q8IXI1	Mitochondrial Rho GTPase 2	6	11.33%	6	17	11	R	ILLLGEAQVGK	T	0.81%	3992	3992	570.8505249	2	1139.6854	1139.691406	-0.006005979	R	T	-	4	11	0	0
				36	50	14	R	AEEITIPADVTPEK	V	2.51%	3257	3257	757.3953247	2	1512.774999	1511.771901	1.003098574	R	V	-	5	14	1	0
				110	119	9	R	VPIILVGNK	S	0.81%	2947	2947	476.8119507	2	951.6082513	951.6116986	-0.003447361	N	K	-	4	9	0	0
				153	164	11	R	NISELFYYAQK	A	0.81%	5207	5207	688.3477783	2	1374.679907	1374.681963	-0.002056751	K	A	-	5	11	0	0
				164	179	15	K	AVLHPTAPLYDPEAK	Q	0.81%	2675	2675	811.9326172	2	1621.849584	1620.851154	0.998430151	K	Q	-	5	15	1	0
				429	439	10	K	SAFLQAFLGR	G	5.30%	6233	6233	555.3080444	2	1108.600439	1109.586925	-0.986486125	K	G	Q5:+0.984	3	10	-1	0
Q8IXI2	Mitochondrial Rho GTPase 1	2	3.24%	110	119	9	R	LPLILVGNK	S	0.81%	4138	4138	483.8206787	2	965.6257073	965.6273487	-0.001641386	R	S	-	5	9	0	0
				153	164	11	K	NISELFYYAQK	A	0.81%	5207	5207	688.3477783	2	1374.679907	1374.681963	-0.002056751	K	A	-	5	11	0	0
Q8IY63	Angiomotin-like protein 1	2	2.20%	101	108	7	R	LIQEQLR	Y	4.85%	1657	1657	450.7629089	2	899.5101678	898.5236119	0.986555935	R	Y	-	2	7	1	0
				611	625	14	K	LQQALTQLQSACEK	R	5.14%	4032	4032	540.6025391	3	1618.784142	1618.786739	-0.002597404	K	R	Q3:+0.984,Q7:+0.984,C12	1	14	0	0
Q8IZJ3	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8	1	0.90%	58	75	17	R	EVTVQAQLVAQGEPVVQ	S	9.88%	3698	3698	598.934021	3	1793.778588	1793.952325	-0.1737371	R	S	-	1	17	0	0
Q8N162	Olfactory receptor 8H2	1	2.88%	298	307	9	K	NAVIRVMQR	R	5.97%	1094	1094	544.291626	2	1086.567602	1086.596779	-0.029177343	K	R	Q8:+0.984	4	9	0	1
Q8N1N5	Cysteine-rich PAK1 inhibitor	1	3.59%	188	204	16	R	LITRAHVECSPAHTCR	C	6.11%	685	685	954.4606323	2	1906.905615	1906.92449	-0.01887556	R	C	C9:+57.021,C15:+57.021	3	16	0	1
Q8N3I7	Bardet-Biedl syndrome 5 protein	1	2.64%	47	56	9	R	GRLLVTNLR	I	6.59%	2439	2439	520.8250732	2	1039.634496	1040.645458	-1.010962044	R	I	-	4	9	-1	1
Q8N4V1	Membrane magnesium transporter 1	3	42.75%	7	28	21	K	GLVGIGLFALAHAAFSAAQHR	S	0.81%	7818	7818	703.0529785	3	2106.13546	2106.148674	-0.013213485	K	S	-	5	21	0	0
				85	96	11	R	NHPSFYVFNHR	G	4.46%	1678	1678	473.5619202	3	1417.662285	1416.668713	0.993572178	R	G	-	2	11	1	0
				98	122	24	R	VLFRPSDTANSSNQDALSSNTSLK	L	0.81%	2485	2485	851.4180298	3	2551.230614	2551.251421	-0.020806501	R	L	-	4	24	0	0
Q8N668	COMM domain-containing protein 1	1	9.47%	36	54	18	R	SQLYPEVPPEEFRPFLAK	M	9.61%	5466	5466	716.7090454	3	2147.103661	2146.109888	0.993772686	R	M	-	1	18	1	0
Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	2	3.45%	54	64	10	R	SLGVHLSFIR	S	3.41%	4122	4122	565.7788086	2	1129.541967	1127.645124	1.896842988	R	S	-	5	10	2	0
				305	313	8	R	LGMGLVSR	S	4.76%	1458	1458	417.8	2	833.5843499	831.4636552	2.120694752	R	S	-	2	8	2	0
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	1	4.66%	345	364	19	R	KPANDITSQLEINFGDLGR	P	5.83%	5552	5552	697.0335693	3	2088.077233	2087.064729	1.01250372	R	P	-	1	19	1	0
Q8NCG7	Sn1-specific diacylglycerol lipase beta	1	1.19%	1	9	8	M	PGMVLFGR	R	2.88%	3732	3732	439.2369385	2	876.4582269	875.4687405	0.989486345	M	R	-	3	8	1	0
Q8NFP4	MAM domain-containing glycosylphosphatidylinositol anchor protein 1	1	1.26%	330	342	12	K	NATFQITPDVIK	E	5.29%	5094	5094	673.81427	2	1345.61289	1345.724163	-0.111272561	K	E	-	3	12	0	0
Q8NFP9	Neurobeachin	1	0.44%	2895	2908	13	K	QLYIYPGCDAGIR	A	7.75%	3655	3655	763.3713379	2	1524.727026	1524.739032	-0.012006715	K	A	C8:+57.021	1	13	0	0
Q8NFZ6	Vomeronasal type-1 receptor 2	1	1.77%	163	170	7	K	FLLYAHR	V	3.49%	2520	2520	460.260376	2	918.5051019	918.5075678	-0.002465903	K	V	-	1	7	0	0
Q8NGC3	Olfactory receptor 10G2	1	7.42%	209	232	23	R	VVAASCFMLILLSYANIVHAILK	I	7.78%	7209	7209	850.1572266	3	2547.448205	2546.39998	1.048224832	R	I	C6:+57.021,N16:+0.984	1	23	1	0
Q8NGI2	Olfactory receptor 52N4	1	2.49%	145	153	8	K	VGTATFLR	G	6.00%	1588	1588	432.747406	2	863.4791619	863.486498	-0.007336076	K	G	-	1	8	0	0
Q8NGN1	Olfactory receptor 6T1	1	2.48%	309	317	8	R	LTAVMKLR	V	4.10%	2387	2387	467.2591553	2	932.5026605	930.5684547	1.934205771	R	V	-	3	8	2	1
Q8TAD4	Zinc transporter 5	1	1.31%	705	715	10	R	IVQQVTGILK	D	0.81%	2890	2890	550.7980957	2	1099.580541	1097.680841	1.899700342	R	D	-	5	10	2	0
Q8TAV4	Stomatin-like protein 3	2	5.15%	141	149	8	F	LLAQTTLR	N	0.81%	859	859	458.2843323	2	914.5530145	914.554912	-0.001897545	F	N	-	5	8	0	0
				195	202	7	R	IPVQLQR	S	2.26%	953	953	427.2644653	2	852.5132806	852.5181325	-0.004851912	R	S	-	3	7	0	0
Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	3	4.47%	111	118	7	R	IPTNYLR	R	1.93%	1230	1230	438.7492371	2	875.482824	875.486498	-0.003673967	R	R	-	1	7	0	0
				192	206	14	R	IGIIDGEYVVNPTR	K	0.81%	4216	4216	773.4017944	2	1544.787939	1544.819854	-0.031915197	R	K	-	5	14	0	0
				250	264	14	K	YTQQIIQGIQQLVK	E	0.81%	5970	5970	830.4780273	2	1658.940405	1658.935553	0.004852047	K	E	-	4	14	0	0
Q8TCT9	Minor histocompatibility antigen H13	12	36.60%	61	73	12	K	NASDMPETITSR	D	0.81%	902	902	661.3053589	2	1320.595068	1320.597977	-0.002909115	K	D	-	5	12	0	0
				127	136	9	K	FFPASFPNR	Q	0.81%	3706	3706	541.7731323	2	1081.530615	1081.534511	-0.003896336	K	Q	-	2	9	0	0
				136	150	14	R	QYQLLFTQGSGENK	E	0.81%	3660	3660	806.9013672	2	1611.787084	1611.789282	-0.002197857	R	E	-	5	14	0	0
				136	161	25	R	QYQLLFTQGSGENKEEIINYEFDTK	D	0.81%	5543	5543	999.4876709	3	2995.439538	2994.413445	1.026092599	R	D	N13:+0.984	2	25	1	1
				150	161	11	K	EEIINYEFDTK	D	0.81%	3629	3629	700.8327637	2	1399.649877	1399.650723	-0.00084556	K	D	-	5	11	0	0
				241	251	10	K	LVFPQDLLEK	G	0.81%	5481	5481	601.3436279	2	1200.671606	1200.675421	-0.003815517	K	G	-	3	10	0	0
				251	278	27	K	GLEANNFAMLGLGDVVIPGIFIALLLR	F	0.81%	11787	11787	943.5341797	3	2827.579064	2825.587742	1.991322207	K	F	-	5	27	2	0
				278	285	7	R	FDISLKK	N	4.92%	1671	1671	425.7546997	2	849.4937493	849.4960001	-0.002250738	R	N	-	2	7	0	1
				313	337	24	K	HAQPALLYLVPACIGFPVLVALAK	G	0.81%	9144	9144	854.822937	3	2561.445336	2560.459892	0.985443571	K	G	C13:+57.021	5	24	1	0
				325	337	12	A	CIGFPVLVALAK	G	5.69%	6931	6931	644.3768311	2	1286.738012	1286.741598	-0.003586435	A	G	C1:+57.021	1	12	0	0
				337	352	15	K	GEVTEMFSYEESNPK	D	0.81%	3656	3656	873.880188	2	1745.744726	1745.745429	-0.000703319	K	D	-	5	15	0	0
				337	361	24	K	GEVTEMFSYEESNPKDPAAVTESK	E	0.81%	3731	3731	882.4008179	3	2644.178978	2645.169041	-0.990062883	K	E	N13:+0.984	5	24	-1	1
Q8TD16	Protein bicaudal D homolog 2	1	1.33%	669	680	11	K	EALMEEILKLK	S	7.51%	2400	2400	444.9190369	3	1331.733635	1331.737122	-0.003486428	K	S	M4:+15.995	1	11	0	1
Q8TF72	Protein Shroom3	1	1.60%	1113	1145	32	R	ERAQSAYLQPGPAALEGSGLASASSLSSLREP	S	9.79%	8156	8156	1067.545654	3	3199.613488	3199.610932	0.002555931	R	S	-	1	32	0	2
Q8WTV0	Scavenger receptor class B member 1	11	29.17%	45	57	12	R	IDPSSLSFNMWK	E	0.81%	5875	5875	712.8476563	2	1423.679662	1423.680584	-0.00092182	R	E	-	5	12	0	0
				117	125	8	R	TFQFQPSK	S	0.81%	1068	1068	491.7529907	2	981.4903314	981.4919774	-0.001646003	R	S	-	4	8	0	0
				125	156	31	K	SHGSESDYIVMPNILVLGAAVMMENKPMTLK	L	2.26%	9160	9160	1126.562622	3	3376.664391	3375.658664	1.005726795	K	L	N13:+0.984	3	31	1	0
				156	169	13	K	LIMTLAFTTLGER	A	0.81%	6430	6430	733.4077148	2	1464.79978	1464.801034	-0.00125424	K	A	-	5	13	0	0
				169	184	15	R	AFMNRTVGEIMWGYK	D	5.67%	3678	3678	602.2713623	3	1803.790612	1801.86438	1.926231386	R	D	-	1	15	2	1
				174	193	19	R	TVGEIMWGYKDPLVNLINK	Y	0.81%	6587	6587	731.0611572	3	2190.159997	2189.15546	1.004536968	R	Y	-	2	19	1	1
				193	202	9	K	YFPGMFPFK	D	2.83%	6044	6044	567.2763672	2	1132.537084	1132.541571	-0.004486945	K	D	-	2	9	0	0

				288	300	12	K	ESGVFEGIPTYR	F	0.81%	3971	3971	677.8336182	2	1353.651586	1353.656477	-0.004890592	K	F	-	5	12	0	0
				387	395	8	K	LQLSLYMK	S	0.81%	4235	4235	498.2824097	2	994.5491693	994.552136	-0.002966704	K	S	-	5	8	0	0
				387	405	18	K	LQLSLYMKSVAGIGQTGK	I	5.56%	5615	5615	637.7264404	3	1910.155846	1909.033367	1.122479153	K	I	M7:+15.994	1	18	1	1
				405	439	34	K	IEPVVLPLLWFAESGAMEGETLHTFYTQLVLMPK	V	5.94%	11822	11822	966.0065308	4	3859.994823	3859.982029	0.012794175	K	V	Q28:+0.984	2	34	0	0
Q8WUD1	Ras-related protein Rab-2B	7	44.91%	8	19	11	K	YIIIGDTGVGK	S	0.81%	3189	3189	568.3182983	2	1134.620947	1134.628471	-0.007524456	K	S	-	5	11	0	0
				19	30	11	K	SCLLLQFTDKR	F	0.81%	4093	4093	690.8662109	2	1379.716772	1379.722654	-0.005882213	K	F	C2:+57.021	5	11	0	1
				30	46	16	R	FQPVHDLTIGVEFGAR	M	0.81%	4993	4993	893.4664917	2	1784.917333	1784.920965	-0.003631818	R	M	-	5	16	0	0
				56	69	13	K	LQIWDTAGQESFR	S	0.81%	4385	4385	775.8826904	2	1549.749731	1549.752503	-0.002771853	K	S	-	5	13	0	0
				77	90	13	R	GAAGALLVYDITR	R	0.81%	5037	5037	660.3655396	2	1318.715429	1318.724497	-0.009067826	R	R	-	4	13	0	0
				105	126	21	R	QHSSSNMVIMLIGNKSDLESR	R	5.92%	4806	4806	777.6921997	3	2330.053124	2329.103763	0.949360561	R	R	Q1:-17.027,N14:+0.984	1	21	1	1
				139	151	12	R	EHGLIFMETSAK	T	0.81%	3216	3216	681.8329468	2	1361.650243	1361.664934	-0.014690685	R	T	-	5	12	0	0
Q8WUX1	Sodium-coupled neutral amino acid transporter 5	7	15.68%	7	20	13	K	MNGALPSDAVGYR	Q	0.81%	2341	2341	676.3171387	2	1350.618627	1350.623782	-0.005154752	K	Q	N2:+0.984	5	13	0	0
				23	30	7	R	EGFLPSR	G	4.40%	1667	1667	403.2136536	2	804.411657	804.4129986	-0.001341591	R	G	-	3	7	0	0
				30	47	17	R	GPAPGSKPVQFMDFEGK	T	0.81%	3634	3634	597.9606934	3	1790.858605	1791.850153	-0.991548522	R	T	Q10:+0.984	4	17	-1	0
				37	47	10	K	PVQFMDFEGK	T	3.03%	4112	4112	599.2835693	2	1196.551489	1196.553593	-0.002104024	K	T	-	1	10	0	0
				359	369	10	R	ALQQLLFPGK	A	2.26%	4634	4634	557.8335571	2	1113.651464	1113.654626	-0.003162006	R	A	-	5	10	0	0
				423	437	14	R	IVPSEVEPFLSWPK	I	0.81%	6571	6571	814.4378662	2	1626.860082	1626.865742	-0.005659226	R	I	-	5	14	0	0
				459	472	13	F	ANWATGQSRMSGH	-	5.75%	4415	4415	474.2427979	3	1419.704918	1417.615778	2.089140547	F	-	M10:+15.995	1	13	2	1
Q8WWI5	Choline transporter-like protein 1	1	2.59%	186	203	17	K	FAEALITFVSDNSVLHR	L	3.15%	6642	6642	640.3394165	3	1917.994774	1918.978859	-0.984084112	K	L	N12:+0.984	3	17	-1	0
Q8WXG6	MAP kinase-activating death domain protein	1	0.55%	236	245	9	K	SSALLHDLR	E	4.00%	3563	3563	506.2790222	2	1010.542394	1010.550889	-0.008494958	K	E	-	2	9	0	0
Q8WXG9	G-protein coupled receptor 98	1	0.11%	2253	2260	7	K	VNLPIIR	N	7.95%	1453	1453	412.7531738	2	823.4906976	824.5119689	-1.021271312	K	N	N2:+0.984	2	7	-1	0
Q8WXH0	Nesprin-2	3	0.54%	243	254	11	R	EAFRIAEQELK	I	6.13%	5083	5083	666.8418579	2	1331.668066	1332.703761	-1.035695668	R	I	-	3	11	-1	1
				2992	3000	8	K	CCILQVLK	L	9.00%	889	889	509.2747803	2	1016.53391	1016.502078	0.031832147	K	L	C1:-17.027,C1:+57.021,C	2	8	0	0
				3326	3344	18	K	LQLQYTLQELVSKNSAMK	E	5.30%	10429	10429	704.3775024	3	2110.109032	2110.098074	0.010958132	K	E	Q4:+0.984,M17:+15.995	2	18	0	1
Q92506	Estradiol 17-beta-dehydrogenase 8	1	4.60%	173	185	12	K	AGVIGLTQTAAR	E	2.59%	1636	1636	579.8340454	2	1157.652441	1156.656417	0.996023572	K	E	-	5	12	1	0
Q92536	Y+L amino acid transporter 2	2	2.91%	341	348	7	R	LFFVGSR	E	0.81%	3657	3657	413.2332764	2	824.4509027	824.4544695	-0.003566866	R	E	-	4	7	0	0
				481	489	8	R	NVLAAITR	G	4.41%	2643	2643	429.2646484	2	856.5136468	856.5130471	0.000599659	R	G	-	2	8	0	0
Q92542	Nicastrin	6	11.14%	285	314	29	R	SFFWNVAPGAESAVASFVTQLAAAEALQK	A	5.29%	10009	10009	753.8878784	4	3011.520214	3009.52362	1.9965934	R	A	-	1	29	2	0
				314	323	9	K	APDVTTLPR	N	0.81%	977	977	485.2705078	2	968.5253655	968.5290912	-0.003725671	K	N	-	5	9	0	0
				316	323	7	P	DVTTLPR	N	5.17%	2175	2175	401.7310791	2	801.4465081	800.4392134	1.007294683	P	N	-	1	7	1	0
				349	371	22	K	GKFPVQLENVDSFVELGQVALR	T	0.81%	7358	7358	816.1104736	3	2445.307946	2445.290357	0.017589066	K	T	Q6:+0.984	2	22	0	1
				485	496	11	K	ALADVATVLGR	A	0.81%	3937	3937	544.8195801	2	1087.62351	1084.624054	2.999455724	K	A	-	2	11	3	0
				520	528	8	R	LLYGFLIK	A	3.73%	5834	5834	483.802124	2	965.588598	965.5949859	-0.006387945	R	A	-	1	8	0	0
Q92556	Engulfment and cell motility protein 1	3	7.15%	200	218	18	R	SLAILESMVLNSHDLYQK	V	0.81%	6704	6704	688.0316772	3	2061.071557	2060.061225	1.010331834	R	V	-	4	18	1	0
				284	308	24	R	AINNEMAHQLYVLQVLTFNLLEDR	M	2.46%	9580	9580	949.1653442	3	2844.472558	2843.463998	1.008559843	R	M	-	3	24	1	0
				539	549	10	K	IQPEILELIK	Q	1.97%	6125	6125	598.3623657	2	1194.709081	1194.722372	-0.013290171	K	Q	-	3	10	0	0
Q92797	Symplekin	10	14.60%	241	265	24	K	FMVHPAISSINLTTALGSLANIAR	Q	0.81%	8061	8061	833.4593506	3	2497.354577	2496.352262	1.00231443	K	Q	-	3	24	1	0
				520	533	13	K	RRPEPIIPVTQPR	L	0.81%	796	796	520.3096313	3	1557.905419	1557.910341	-0.004921821	K	L	-	3	13	0	1
				666	683	17	K	VVLEAPLITESALEVVR	K	0.81%	6942	6942	920.0437622	2	1838.071874	1837.056062	1.015812494	K	K	-	5	17	1	0
				751	774	23	K	FALNYLQLLVHPNPPSVLFGADK	D	0.81%	8181	8181	852.4743042	3	2554.399437	2553.363128	1.036309726	K	D	N13:+0.984	3	23	1	0
				924	956	32	R	LLGTQHGEGNSALSPLNPGELLIALHNIDSVK	C	4.01%	8040	8040	828.1985474	4	3308.762889	3306.757202	2.005687045	R	C	-	1	32	2	0
				1011	1022	11	R	LGGFVMNILSR	L	2.26%	6247	6247	603.8370972	2	1205.658544	1205.659061	-0.000516544	R	L	-	3	11	0	0
				1022	1033	11	R	LIMKQVWKYPK	V	5.24%	1035	1035	483.2795715	3	1446.815239	1448.821461	-2.006221168	R	V	M3:+15.995	1	11	-1	2
				1022	1040	18	R	LIMKQVWKYPKVWEGFIK	C	5.02%	7304	7304	1147.425903	2	2292.836157	2292.285686	0.550470641	R	C	-	1	18	1	3
				1040	1067	27	K	CCQRTKPQSFQVILQLPPQQLGAVFDK	C	5.66%	7999	7999	1063.751709	3	3188.231652	3191.550866	-3.319214551	K	C	C1:+57.021,C2:+57.021,Q	1	27	-1	1
				1158	1179	21	K	LKPGGVGAPSSSSPSPSPSAR	P	6.58%	626	626	641.6659546	3	1921.974389	1921.98575	-0.01136179	K	P	-	1	21	0	0
Q92823	Neuronal cell adhesion molecule	1	1.23%	943	959	16	R	VFNTPEGVPSAPSSLK	I	4.73%	3179	3179	815.4281006	2	1628.840551	1628.840983	-0.000432332	R	I	-	2	16	0	0
Q92835	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1	1	1.60%	605	624	19	K	IKQQQYADLLSHDQLLTER	R	3.00%	5585	5585	766.7304688	3	2297.167931	2298.196806	-1.028875022	K	R	-	3	19	-1	1
Q92888	Rho guanine nucleotide exchange factor 1	1	0.88%	684	692	8	R	LLLKSHSR	T	6.40%	5308	5308	477.3020935	2	952.5885369	952.5817955	0.00674146	R	T	-	2	8	0	1
Q92930	Ras-related protein Rab-8B	7	36.71%	10	21	11	K	LLLIGDSGVGK	T	0.81%	3675	3675	536.3205566	2	1070.625463	1070.633556	-0.008093215	K	T	-	3	11	0	0
				46	55	9	K	IRTIELDGK	K	5.51%	3105	3105	523.2884521	2	1044.561254	1043.597505	0.963748993	K	T	-	1	9	1	1
				58	69	11	K	LQIWDTAGQER	F	0.81%	3175	3175	659.33	2	1316.64435	1315.65206	0.992289784	K	F	-	1	11	1	0
				71	79	8	R	TITTAYYR	G	0.81%	822	822	494.7568359	2	987.4980218	987.5025421	-0.004520293	R	G	-	3	8	0	0
				79	94	15	R	GAMGIMLVYDITNEK	S	0.81%	6716	6716	827.9124146	2	1653.809179	1653.810614	-0.001434474	R	S	-	5	15	0	0
				138	146	8	K	LAIDYGIK	F	0.81%	2819	2819	446.7594299	2	891.5032098	891.5065648	-0.003355009	K	F	-	4	8	0	0
				176	190	14	K	MNDSNSAGAGGPVK	I	5.25%	3398	3398	440.8649292	3	1319.571312	1320.560661	-0.989348578	K	I	M1:+15.994,N2:+0.984	1	14	-1	0
Q92974	Rho guanine nucleotide exchange factor 2	7	12.47%	100	111	11	K	NNTALQSVSLR	S	0.81%	1855	1855	602.3306885	2	1202.645727	1201.641495	1.004231457	K	S	-	5	11	1	0
				169	183	14	R	ILSQSTDSLNMRNR	T	5.49%	3375	3375	547.2897339	3	1638.845727	1634.8046	4.041126316	R	T	N10:+0.984	1	14	4	1
				235	252	17	K	QQDVIYELIQTELHHVR	T	3.44%	7124	7124	531.2817383	4	2121.095653	2120.101449	0.994203949	K	T	-	2	17	1	0
				423	438	15	K	ELLSNVDEGIYQLEK	G	0.81%	5346	5346	875.4556885	2	1748.895727	1748.883242	0.012484569	K	G	-	4	15	0	0
				509	529	20	K	YIFPTLDKPSVVSLQNLIVR	D	1.93%	7202	7202	768.1118164	3	2301.311974	2302.293651	-0.981676989	K	D	N16:+0.984	2	20	-1	0
				660	681	21	R	EVEGLKDLLVGPGVELLLTPR	E	4.61%	7926	7926	750.1011963	3	2247.280114	2246.288581	0.991532427	R	E	-	2	21	1	1
				741	766	25	R	LVNLYGLLHGLQAAVAQQDTLMEAR	F	0.81%	9394	9394	908.8265381	3	2723.456139	2723.442868	0.013270826	R	F	-	4	25	0	0
Q93050	V-type proton ATPase 116 kDa subunit a isoform 1	9	17.68%	167	177	10	R	LGFVAGVINR	E	0.81%	3694	3694	523.3106689	2	1044.605688	1044.60801	-0.002322461	R	E	-	5	10	0	0
				198	217	19	R	QAEIENPLEDPVTGDYVHK	S	2.32%	3825	3825	719.0158081	3	2154.023949	2153.027675	0.996274204	R	S	-	2	19	1	0
				217	230	13	K	SVFIIFFQGDQLK	N	7.06%	6464	6464	771.9057007	2	1541.795751	1541.812962	-0.017210761	K	N	Q11:+0.984	2	13	0	0
				264	279	15	R	IDDLQMVLNQTEDHR	Q	6.11%	4518	4518	609.6278076	3	1825.859948	1825.862859	-0.002911372	R	Q	-	1	15	0	0
				317	338	21	K	CLIAEVWCPVTDLDSIQFALR	R	5.66%	9011	9011	836.4674072	3	2506.378747	2505.238674	1.140072832	K	R	C1:+57.021,C8:+57.021	1	21	1	0
				369	387	18	K	FTYGFQNIVDAYGIGTYR	E	0.81%	6691	6691	1043.505981	2	2084.996313	2084.000338	0.995974947	K	E	-	4	18	1	0
				495	528	33	R	GNPVLQLNPALPGVFGGPYPFGIDPIWNIATNK	L	0.81%	8713	8713	1159.952637	3	3476.834435	3475.829245	1.005190076	R	L	-	4	33	1	0
				528	536	8	K	LTFLNSFK	M	0.81%	4473	4473	485.2732849	2	968.5309197	968.5331139	-0.002194176	K	M	-	4	8	0	0
				666	677	11	K	HLGTLNFGGIR	V	0.81%	3432	3432	592.8297729	2	1183.643896	1183.646187	-0.002290958	K	V	-	5	11	0	0
Q93096	Protein tyrosine phosphatase type IVA 1	3	17.92%	18	32	14	R	FLITHNPTNATLNK	F	0.81%	1881	1881	792.9294434	2	1583.843237	1582.846737	0.996499199	R	F	-	4	14	1	0
				39	47	8	K	YGVTTIVR	V	0.81%	1976	1976	454.7617798	2	907.5079095	907.5127128	-0.004803318	K	V	-	5	8	0	0
				125	134	9	K	YEDAVQFIR	Q	2.46%	3404	3404	570.7839355	2	1139.552221	1139.56112	-0.00889869	K	Q	-	5	9	0	0
Q96CW1	AP-2 complex subunit mu	1	1.61%	281	288	7	K	DIILPFR	V	6.11%	2635	2635	437.2373962	2	872.4591424	872.5119845	-0.05284208	K	V	-	2	7	0	0
Q96CX2	BTB/POZ domain-containing protein KCTD12	1	4.62%	128	143	15	R	LGAPQQPGPGPPPSR	R	0.81%	669	669	728.3873291	2	1454.759008	1454.763008	-0.003999557	R	R	-	5	15	0	0
Q96F07	Cytoplasmic FMR1-interacting protein 2	16	16.12%	49	58	9	R	NAFVTGIAR	Y	0.81%	1938	1938	474.764801	2	947.513952	947.5188608	-0.004908853	R	Y	-	5	9	0	0
				110	121	11	K	TVEVLEPEVTK	L	5.03%	1932	1932	623.3156738	2	1244.615698	1242.67073	1.94496764	K	L	-	2	11	2	0
				163	175	12	K	FINMFAVLDELK	N	0.81%	8746	8746	720.3890381	2	1438.762426	1438.753021	0.00940514	K	N	-	5	12	0	0
				331	353	22	K	WTCTQSSISPQYNICEQMVQIR	D	5.10%	6081	6081	687.6322021	4	2746.497508	2745.218814	1.278694466	K	D	C3:+57.021,Q11:+0.984,C	1	22	1	0
				381	395	14	K	SDEEYRELFDLALR	G	0.81%	6206	6206	586.2878418	3	1755.84005	1754.847525	0.992524831	K	G	-	5	14	1	1
				458	466	8	K	GLQVLMGR	M	5.54%	2935	2935	437.249115	2	872.4825799	872.4902043	-0.007624396	K	M	-	1	8	0	0
				503	514	11	K	NVLISVLQAIR	K	0.81%	7501	7501	613.3845825	2	1224.753515	1224.755403	-0.001888049	K	K	-	5	11	0	0
				587	597	10	R	TMLESLIADK	S	0.81%	4851	4851	560.7979126	2	1119.580175	1119.584558	-0.004383333	R	S	-	5	10	0	0
				605	621	16	R	SSLDGPIVLAIEDFHK	Q	2.80%	7012	7012	580.975769	3	1739.903832	1739.909397	-0.005565423	R	Q	-	2	16	0	0
				659	680	21	R	IQFPIEMSMPWILTDHILETK	E	4.92%	9166	9166	848.4423828	3	2542.303673	2541.301139	1.00253439	R	E	-	1	21	1	0
				729	739	10	K	LADQIFAYYK	A	4.79%	4402	4402	617.861145	2	1233.70664	1231.612471	2.094168903	K	A	Q4:+0.984	1	10	2	0
				890	901	11	R	TAIPFTQEPQR	D	0.81%	2178	2178	644.8390503	2	1287.662451	1286.661897	1.000553978	R	D	-	4	11	1	0
				943	959	16	R	LLGYQGIAVVMEELLK	I	0.81%	9724	9724	888.5065308	2	1774.997411	1774.990291	0.007119979	R	I	-	5	16	0	0
				962	974	12	K	SLLQGTILQYVK	T	0.81%	6274	6274	681.9042358	2	1361.792822	1361.791848	0.0009734	K	T	-	4	12	0	0
				1077	1089	12	K	YAPLHLVPLIER	L	0.81%	5142	5142	474.2787781	3	1419.812859	1419.823817	-0.010957907	K	L	-	2	12	0	0
				1089	1100	11	R	LGTPQQIAIAR	E	0.81%	1819	1819	584.3467407	2	1166.677831	1166.677153	0.000678757	R	E	-	2	11	0	0
Q96JP9	Cadherin-related family member 1	1	1.05%	394	403	9	K	FNLQLVGPR	G	6.34%	1708	1708	523.2875977	2	1044.559545	1044.56036	-0.000814959	K	G	N2:+0.984,Q4:+0.984	1	9	0	0
Q96JQ0	Protocadherin-16	1	0.45%	1301	1316	15	R	SASLQLLVQVLPSAR	L	4.36%	2872	2872	527.977356	3	1580.908593	1580.924988	-0.016395089	R	L	-	2	15	0	0
Q96N96	Spermatogenesis-associated protein 13	1	1.38%	237	246	9	K	QQMRTNVIR	E	7.19%	2901	2901	573.3399658	2	1144.664282	1144.613508	0.050774017	K	E	-	3	9	0	1
Q96NY7	Chloride intracellular channel protein 6	1	1.70%	586	598	12	K	DANEIHEKNLLK	A	4.24%	7035	7035	713.3725586	2	1424.729467	1424.714689	0.014778164	K	A	N3:+0.984,N9:+0.984	4	12	0	1
Q96QD8	Sodium-coupled neutral amino acid transporter 2	1	3.16%	170	186	16	K	YELPLVIQALTNIEDK	T	0.81%	8363	8363	930.5189209	2	1859.022192	1858.008777	1.013414445	K	T	-	5	16	1	0
Q96QZ7	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	1	2.28%	1003	1037	34	R	GENEGFGFVIVSSVSRPEAGTTFAGNACVAMPHK	I	8.79%	5574	5574	1175.557373	3	3523.648644	3524.633559	-0.984915195	R	I	N3:+0.984,N26:+0.984,C2	2	34	-1	0
Q96R67	Olfactory receptor 4C12	1	2.91%	78	87	9	K	LIVDSFQEK	K	4.45%	1563	1563	539.7902832	2	1077.564916	1077.570622	-0.005705442	K	K	-	1	9	0	0
Q99439	Calponin-2	2	11.97%	35	52	17	R	TWIEGLTGLSIGPDFQK	G	2.59%	6749	6749	932.4823608	2	1862.949072	1860.962161	1.98691024	R	G	-	4	17	2	0
				194	214	20	K	NHILPPMDHSTISLQMGTNK	C	5.20%	4365	4365	745.031189	3	2232.070092	2233.098357	-1.028264769	K	C	-	1	20	-1	0
Q99572	P2X purinoceptor 7	1	3.70%	441	463	22	R	LPLALHDTPPIPGQPEEIQLLR	K	2.32%	5879	5879	816.7902832	3	2447.347374	2446.358392	0.988982177	R	K	-	2	22	1	0
Q99665	Interleukin-12 receptor subunit beta-2	1	1.04%	265	274	9	R	LWNMVNVTK	A	3.94%	3095	3095	552.7955933	2	1103.575536	1103.579748	-0.004211301	R	A	-	1	9	0	0
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	15	88.51%	9	29	20	K	GLVAVITGGASGLGLATAER	L	0.81%	5869	5869	907.5095215	2	1813.003393	1812.010509	0.992884305	K	L	-	5	20	1	0
				29	52	23	R	LVGQGASAVLLDLPNSGGEAQAK	K	0.81%	4687	4687	732.73	3	2195.166525	2194.159358	1.007166904	R	K	-	2	23	1	0
				53	69	16	K	LGNNCVFAPADVTSEK	D	0.81%	2913	2913	861.4093018	2	1720.802953	1720.808569	-0.005615316	K	D	C5:+57.021	5	16	0	0
				53	79	26	K	LGNNCVFAPADVTSEKDVQTALALAK	G	0.81%	5655	5655	911.4644165	3	2731.369774	2732.368615	-0.998840536	K	G	C5:+57.021,Q19:+0.984	3	26	-1	1
				69	79	10	K	DVQTALALAK	G	0.81%	2726	2726	515.2987061	2	1028.581762	1028.586606	-0.004844147	K	G	-	5	10	0	0
				84	99	15	R	VDVAVNCAGIAVASK	T	0.81%	2591	2591	737.3900757	2	1472.764501	1472.765247	-0.000745929	R	T	C7:+57.021	5	15	0	0
				105	116	11	K	GQTHTLEDFQR	V	0.81%	802	802	666.3164063	2	1330.617162	1330.626574	-0.009411244	K	V	-	4	11	0	0
				116	130	14	R	VLDVNLMGTFNVIR	L	0.81%	6233	6233	795.9403687	2	1589.865087	1589.859946	0.005141433	R	L	-	5	14	0	0
				130	147	17	R	LVAGEMGQNEPDQGGQR	G	0.81%	674	674	893.4074707	2	1784.799291	1784.811158	-0.011866506	R	G	-	4	17	0	0
				147	172	25	R	GVIINTASVAAFEGQVGQAAYSASK	G	0.81%	5857	5857	813.7549438	3	2438.241356	2439.22815	-0.986793969	R	G	Q15:+0.984	2	25	-1	0
				172	184	12	K	GGIVGMTLPIAR	D	0.81%	4726	4726	592.8409424	2	1183.666235	1183.674711	-0.008476194	K	D	-	5	12	0	0
				184	192	8	R	DLAPIGIR	V	2.26%	2665	2665	427.7561035	2	853.496557	853.5021481	-0.005591137	R	V	-	1	8	0	0
				192	212	20	R	VMTIAPGLFGTPLLTSLPEK	V	0.81%	7146	7146	1043.088623	2	2084.161596	2084.159148	0.002448046	R	V	-	5	20	0	0
				212	226	14	K	VCNFLASQVPFPSR	L	0.81%	4915	4915	811.9085083	2	1621.801367	1620.807781	0.99358577	K	L	C2:+57.021	5	14	1	0
				226	252	26	R	LGDPAEYAHLVQAIIENPFLNGEVIR	L	0.81%	9253	9253	961.1754761	3	2880.502953	2877.502491	3.000462431	R	L	-	1	26	3	0
Q99720	Sigma non-opioid intracellular receptor 1	7	48.43%	0	7	7	-	MQWAVGR	R	0.81%	1544	1544	424.2138062	2	846.4119622	846.4170393	-0.005077031	-	R	-	5	7	0	0
				39	47	8	R	EEIAQLAR	Q	2.46%	898	898	465.2543945	2	928.493139	928.4977911	-0.004652073	R	Q	-	3	8	0	0
				47	60	13	R	QYAGLDHELAFSR	L	0.81%	3325	3325	502.9129028	3	1505.715233	1505.726288	-0.011054456	R	L	-	2	13	0	0
				119	137	18	R	YWAEISDTIISGTFHQWR	E	0.81%	6909	6909	1105.536987	2	2209.058325	2209.05925	-0.000925279	R	E	-	4	18	0	0
				142	175	33	K	SEVFYPGETVVHGPGEATAVEWGPNTWMVEYGR	G	2.34%	6513	6513	1217.894409	3	3650.659752	3651.661632	-1.001880029	K	G	N25:+0.984	3	33	-1	0
				175	204	29	R	GVIPSTLAFALADTVFSTQDFLTLFYTLR	S	0.81%	12258	12258	1070.574951	3	3208.701378	3207.674351	1.027027092	R	S	Q19:+0.984	4	29	1	0
				184	204	20	F	ALADTVFSTQDFLTLFYTLR	S	5.65%	9454	9454	775.0730591	3	2322.195702	2321.194347	1.001355614	F	S	-	1	20	1	0
Q99805	Transmembrane 9 superfamily member 2	4	6.49%	90	104	14	K	RPSENLGQVLFGER	I	0.81%	4545	4545	534.614502	3	1600.820031	1600.83215	-0.012119277	K	I	-	4	14	0	0
				91	104	13	R	PSENLGQVLFGER	I	4.41%	5140	5140	723.876709	2	1445.737768	1444.731039	1.006729025	R	I	-	1	13	1	0
				203	215	12	R	DTFYIFNHVDIK	I	0.81%	5166	5166	756.380188	2	1510.744726	1510.745626	-0.000900391	R	I	-	5	12	0	0
				332	349	17	R	YNQMDSTEDAQEEFGWK	L	0.81%	3889	3889	1039.92	2	2077.82435	2076.837098	0.987251944	R	L	-	4	17	1	0
Q99808	Equilibrative nucleoside transporter 1	8	25.88%	239	255	16	K	LEGPGEQETKLDLISK	G	0.81%	2950	2950	879.4667358	2	1756.917822	1755.925442	0.992380088	K	G	-	4	16	1	1
				260	283	23	R	AGKEESGVSVSNSQPTNESHSIK	A	3.82%	644	644	593.7869263	4	2371.116405	2372.109157	-0.992752522	R	A	N17:+0.984	3	23	-1	1
				315	326	11	K	SSIAGSSTWER	Y	2.83%	900	900	590.7816772	2	1179.547704	1179.552012	-0.004307228	K	Y	-	3	11	0	0
				345	356	11	R	SLTAVFMWPGK	D	0.81%	5998	5998	618.8253174	2	1235.634985	1235.637263	-0.002278018	R	D	-	4	11	0	0
				359	368	9	R	WLPSLVLAR	L	0.81%	5648	5648	527.8220825	2	1053.628515	1053.633497	-0.004981785	R	L	-	3	9	0	0
				368	381	13	R	LVFVPLLLLCNIK	P	5.59%	9064	9064	771.9765625	2	1541.937475	1540.941027	0.99644812	R	P	C10:+57.021	1	13	1	0
				368	383	15	R	LVFVPLLLLCNIKPR	R	0.81%	8806	8806	599.0391235	3	1794.093895	1794.094902	-0.001006395	R	R	C10:+57.021	3	15	0	0
				420	453	33	K	KVKPAEAETAGAIMAFFLCLGLALGAVFSFLFR	A	5.83%	6191	6191	886.9378052	4	3543.719921	3544.897397	-1.177476561	K	A	C19:+57.021	1	33	-1	1
Q9BQE4	Selenoprotein S	1	4.76%	11	20	9	R	PALETEGLR	F	3.15%	903	903	493.2663574	2	984.5170648	984.5240059	-0.006941092	R	F	-	1	9	0	0
Q9BRV3	RAG1-activating protein 1	1	8.14%	183	201	18	R	DPYIMVSNFPGIVTSFIR	F	2.80%	8262	8262	686.024292	3	2055.049401	2055.049932	-0.000530879	R	F	-	3	18	0	0
Q9BUL8	Programmed cell death protein 10	1	5.19%	139	150	11	K	ELLDTVNNVFK	K	0.81%	4912	4912	646.847229	2	1291.678808	1290.681963	0.996844616	K	K	-	4	11	1	0
Q9BV40	Vesicle-associated membrane protein 8	2	24.00%	14	24	10	R	NLQSEVEGVK	N	2.61%	1386	1386	551.7866821	2	1101.557714	1101.566599	-0.008884886	R	N	-	5	10	0	0

				45	59	14	R	NKTEDLEATSEHFK	T	1.93%	741	741	550.2630615	3	1647.765709	1647.774026	-0.008316622	R	T	-	3	14	0	1
Q9BX59	Tapasin-related protein	4	15.38%	137	163	26	K	TAAWFMANMQVSGGGPSISLVMKTPR	V	5.73%	7488	7488	918.3044434	3	2751.889855	2753.333983	-1.444128466	K	V	N8:+0.984,M22:+15.995	1	26	-1	1
				251	264	13	K	GATLEPAQLGMAR	D	4.94%	2793	2793	658.8400269	2	1315.664404	1313.676168	1.988236095	K	D	-	1	13	2	0
				291	305	14	R	AQQIIQLNIQASPK	V	9.84%	3664	3664	777.8983154	2	1553.780981	1551.862038	1.918943179	R	V	N8:+0.984	2	14	2	0
				337	356	19	R	EELGGSPAQVSGASFSSLR	Q	0.81%	3572	3572	940.4627686	2	1878.909887	1877.911917	0.997970285	R	Q	-	5	19	1	0
Q9BXS9	Solute carrier family 26 member 6	1	2.24%	66	83	17	R	AYALLLQHLPVLVWLPR	Y	0.81%	8554	8554	668.4021606	3	2002.183007	2001.192771	0.990236302	R	Y	-	5	17	1	0
Q9BZA7	Protocadherin-11 X-linked	1	1.56%	358	379	21	R	YIVNPVNDTVVLSENIPLNTK	I	4.27%	9141	9141	781.0546875	3	2340.140587	2341.252924	-1.112336748	R	I	-	3	21	-1	0
Q9BZQ8	Protein Niban	1	1.72%	494	510	16	K	IFQEALVQITLPTVQK	A	3.40%	5007	5007	915.9767456	2	1829.937841	1830.002582	-0.064741349	K	A	Q3:+0.984,Q8:+0.984,Q1	3	16	0	0
Q9BZZ2	Sialoadhesin	1	0.70%	606	618	12	R	LDLDAAGAGAGR	R	6.47%	2783	2783	543.7799683	2	1085.544286	1085.546532	-0.002245837	R	R	-	1	12	0	0
Q9C037	Tripartite motif-containing protein 4	1	1.60%	248	256	8	K	LILEVGEK	S	3.69%	2547	2547	450.768219	2	899.5207879	899.5327796	-0.011991684	K	S	-	2	8	0	0
Q9C0D5	Protein TANC1	1	0.59%	544	555	11	K	EPQLQSMLSLR	S	6.34%	3533	3533	642.828125	2	1283.6406	1283.653919	-0.013318648	K	S	E1:-18.011,Q3:+0.984	2	11	0	0
Q9GZM5	Protein YIPF3	1	2.57%	132	141	9	R	LLESMIPIK	M	0.81%	4319	4319	522.3102417	2	1042.604833	1042.609651	-0.004817602	R	M	-	4	9	0	0
Q9H0M0	NEDD4-like E3 ubiquitin-protein ligase WWP1	1	2.71%	440	465	25	R	YLYSASMLAAENDPYGPLPPGWEKR	V	4.46%	5896	5896	943.46	3	2827.356525	2824.35305	3.003474672	R	V	-	1	25	3	1
Q9H1V8	Orphan sodium- and chloride-dependent neurotransmitter transporter NTT4	1	2.75%	413	433	20	K	EDQFSALGLDPCLLEDELDK	S	2.51%	5269	5269	1154.091553	2	2306.167455	2306.061943	0.105512373	K	S	C12:+57.021	3	20	0	0
Q9H222	ATP-binding cassette sub-family G member 5	1	1.23%	381	389	8	R	NKLAVITR	L	8.50%	2143	2143	457.2748413	2	912.5340325	913.5708964	-1.036863887	R	L	-	3	8	-1	1
Q9H2H9	Sodium-coupled neutral amino acid transporter 1	2	3.90%	136	147	11	K	LGEQVFGTTGK	F	0.81%	1726	1726	569.31	2	1136.60435	1135.587335	1.017015416	K	F	-	5	11	1	0
				376	384	8	R	SSLFELAK	K	5.14%	3682	3682	447.7503052	2	893.4849603	893.4858294	-0.00086908	R	K	-	1	8	0	0
Q9H2X9	Solute carrier family 12 member 5	1	0.61%	531	538	7	R	LLQAISR	D	6.32%	2685	2685	401.26297	2	800.5102899	799.4915834	1.018706493	R	D	-	2	7	1	0
Q9H307	Pinin	2	3.07%	144	155	11	R	IFGLLMGTLQK	F	0.81%	6015	6015	611.3534546	2	1220.691259	1219.699863	0.991396076	R	F	-	4	11	1	0
				236	247	11	K	TKPHLFYIPGR	M	1.97%	2085	2085	443.5869751	3	1327.73745	1327.740087	-0.002637083	K	M	-	5	11	0	0
Q9H490	Phosphatidylinositol glycan anchor biosynthesis class U protein	1	3.91%	111	128	17	K	LLLELDQYAPDVAELIR	T	2.34%	7573	7573	986.0474243	2	1970.079199	1970.07244	0.006758305	K	T	-	4	17	0	0
Q9H4M9	EH domain-containing protein 1	2	6.74%	13	32	19	K	EPELFQTVAEGLRQLYAQK	L	5.64%	5887	5887	556.5750732	4	2222.268993	2222.11063	0.158363161	K	L	Q6:+0.984,Q14:+0.984,Q1	1	19	0	1
				251	268	17	R	VYIGSFWSHPLLIPDNR	K	4.35%	6410	6410	672.6964722	3	2015.065941	2013.047228	2.018712952	R	K	-	1	17	2	0
Q9HAB3	Riboflavin transporter 3	1	1.80%	267	275	8	K	AYQLLSAR	S	0.81%	1883	1883	461.2598877	2	920.5041253	920.5079618	-0.003836465	K	S	-	4	8	0	0
Q9HBY0	NADPH oxidase 3	1	1.23%	74	81	7	R	NLISFIR	G	4.85%	5819	5819	431.7608643	2	861.5060784	861.5072334	-0.001155012	R	G	-	2	7	0	0
Q9HC29	Nucleotide-binding oligomerization domain-containing protein 2	1	2.50%	870	896	26	R	QNFLALRLGNNYITAAGAQVLAEGLR	G	8.76%	8583	8583	694.6303101	4	2774.48994	2774.471494	0.018446418	R	G	N11:+0.984,Q19:+0.984	2	26	0	1
Q9HDC9	Adipocyte plasma membrane-associated protein	4	19.47%	10	29	19	R	RPLRPQVVTDDDGQAPEAK	D	0.81%	676	676	698.0283203	3	2091.061486	2091.070877	-0.009391367	R	D	-	4	19	0	0
				93	120	27	R	LFENQLVGPESIAHIGDVMFTGTADGR	V	1.93%	7239	7239	959.1378174	3	2874.389977	2873.401791	0.988185596	R	V	-	2	27	1	0
				183	195	12	K	LLLSSETPIEGK	N	0.81%	2885	2885	643.8618164	2	1285.707983	1285.712929	-0.004946411	K	N	-	5	12	0	0
				257	280	23	R	FPNGVQLSPAEDFVLVAETTMAR	I	5.40%	8653	8653	831.7455444	3	2492.213158	2493.209709	-0.996550483	R	I	N3:+0.984,Q6:+0.984	3	23	-1	0
Q9NP72	Ras-related protein Rab-18	5	29.61%	10	21	11	K	ILIIGESGVGK	S	0.81%	2980	2980	543.3290405	2	1084.642431	1084.649207	-0.006775521	K	S	-	4	11	0	0
				58	69	11	K	LAIWDTAGQER	F	0.81%	3246	3246	630.319397	2	1258.623144	1258.630596	-0.007452503	K	F	-	5	11	0	0
				79	92	13	R	GAQGVILVYDVTR	R	0.81%	4417	4417	695.8953247	2	1389.774999	1389.761611	0.013388638	R	R	-	1	13	0	0
				112	123	11	R	NDIVNMLVGNK	I	3.54%	4987	4987	608.8200073	2	1215.624365	1215.628155	-0.003790072	R	I	-	2	11	0	0
				168	183	15	K	IIQTPGLWESENQNK	G	0.81%	3464	3464	878.9456787	2	1755.875707	1755.87916	-0.003452586	K	G	-	5	15	0	0
Q9NQC3	Reticulon-4	6	8.64%	57	91	34	R	KPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPR	G	0.81%	6126	6126	1091.583008	3	3271.725548	3271.669953	0.055595805	R	G	N26:+0.984	3	34	0	0
				91	104	13	R	GPLPAAPPVAPER	Q	0.81%	2120	2120	636.3584595	2	1270.701269	1270.703367	-0.002098543	R	Q	-	5	13	0	0
				1074	1090	16	R	AYLESEVAISEELVQK	Y	0.81%	5147	5147	904.4692383	2	1806.922826	1806.925107	-0.002280701	R	Y	-	5	16	0	0
				1090	1104	14	K	YSNSALGHVNCTIK	E	0.81%	818	818	782.3823242	2	1562.748998	1562.75066	-0.001661434	K	E	C11:+57.021	5	14	0	0
				1108	1120	12	R	LFLVDDLVDSLK	F	0.81%	7550	7550	689.3897095	2	1376.763769	1375.759879	1.003889481	R	F	-	5	12	1	0
		1	0.94%	1157	1171	14	R	HQAQIDHYLGLANK	N	0.81%	2402	2402	536.6107788	3	1606.808861	1606.821585	-0.01272399	R	N	-	1	14	0	0
Q9NQC7	Ubiquitin carboxyl-terminal hydrolase CYLD	2	3.00%	147	156	9	R	FRGPLLAER	T	4.92%	3981	3981	529.8035889	2	1057.591528	1057.603259	-0.011731586	R	T	-	2	9	0	1
Q9NR96	Toll-like receptor 9			348	367	19	R	VSFAHLSLAPSFGSLVALK	E	0.81%	6943	6943	649.0336914	3	1944.077599	1943.088031	0.989568443	R	E	-	4	19	1	0
				678	690	12	K	LEVLDLAGNQLK	A	0.81%	4814	4814	656.8791504	2	1311.742651	1311.739813	0.002838101	K	A	-	5	12	0	0
Q9NRZ7	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	2	5.59%	236	247	11	K	NPSLLGILYGK	K	0.81%	6059	6059	587.8446655	2	1173.673681	1173.675756	-0.002074649	K	K	-	4	11	0	0
				281	291	10	K	DALQEIYNQK	G	0.81%	2960	2960	611.3078003	2	1220.599951	1220.603713	-0.003762406	K	G	-	3	10	0	0
Q9NT99	Leucine-rich repeat-containing protein 4B	1	2.10%	74	89	15	R	RDLAEVPASIPVNTR	Y	3.84%	8470	8470	820.4431152	2	1638.87058	1637.873665	0.996915413	R	Y	N13:+0.984	4	15	1	1
Q9NX77	HERV-K_16p3.3 provirus ancestral Env polyprotein	1	3.73%	76	94	18	K	AVVLQTLAMGIVIDWAPK	G	7.44%	6793	6793	963.0458984	2	1924.076147	1924.085589	-0.009442133	K	G	-	1	18	0	0
Q9NY61	Protein AATF	1	3.21%	246	264	18	K	ALLTTNQLPQPDVFPLFK	D	0.81%	7207	7207	1022.075439	2	2042.135229	2041.12481	1.01041865	K	D	-	5	18	1	0
Q9NZ42	Gamma-secretase subunit PEN-2	1	14.85%	39	54	15	R	EAFLVPAYTEQSQIK	G	0.81%	3811	3811	862.9482422	2	1723.880834	1722.882848	0.997985991	R	G	-	5	15	1	0
Q9NZQ8	Transient receptor potential cation channel subfamily M member 5	1	1.03%	440	452	12	R	LTLAGLGTQQAR	E	8.70%	1056	1056	615.3197021	2	1228.623754	1228.677531	-0.053776799	R	E	Q9:+0.984	2	12	0	0
Q9P0L0	Vesicle-associated membrane protein-associated protein A	7	42.17%	10	24	14	K	HEQILVLDPPTDLK	F	0.81%	4076	4076	809.9442139	2	1617.872778	1616.877369	0.99540871	K	F	-	5	14	1	0
				24	38	14	K	FKGPFTDVVTTNLK	L	0.81%	4140	4140	784.4303589	2	1566.845068	1565.84534	0.999727237	K	L	-	4	14	1	1
				26	38	12	K	GPFTDVVTTNLK	L	0.81%	3803	3803	646.3427734	2	1290.669897	1290.681963	-0.012066517	K	L	-	5	12	0	0
				94	114	20	K	FMVQTIFAPPNTSDMEAVWK	E	0.81%	7074	7074	1157.050293	2	2312.084936	2311.101711	0.983225266	K	E	-	5	20	1	0
				127	146	19	R	CVFEMPNENDKLNDMEPSK	A	5.33%	3727	3727	766.9979858	3	2297.970482	2296.96454	1.005941928	R	A	C1:+57.021,N13:+0.984	1	19	1	1
				181	194	13	R	LQGEMMKLSEENR	H	4.98%	2578	2578	533.6256104	3	1597.853356	1596.712511	1.140844823	R	H	M5:+15.995,M6:+15.995,N	1	13	1	1
				221	246	25	R	DNVTSPLPSLLVVIAAIFIGFFLGK	F	3.76%	14768	14768	878.5133667	3	2632.516625	2630.508745	2.007879882	R	F	-	2	25	2	0
Q9P2M7	Cingulin	1	1.09%	698	711	13	K	MVAEAEATVLGQR	R	9.51%	9461	9461	696.3411865	2	1390.666723	1390.675297	-0.008574009	K	R	M1:+15.994,Q12:+0.984	1	13	0	0
Q9UBS5	Gamma-aminobutyric acid type B receptor subunit 1	1	1.56%	567	582	15	K	WIGGSPPADQTLVIK	T	7.03%	2928	2928	528.3033447	3	1581.886559	1581.84024	0.046319556	K	T	Q10:+0.984	3	15	0	0
Q9UGQ3	Solute carrier family 2, facilitated glucose transporter member 6	1	1.97%	489	499	10	R	SLEQIESFFR	T	0.81%	6269	6269	628.3240967	2	1254.632543	1254.624448	0.008094927	R	T	-	5	10	0	0
Q9UHC6	Contactin-associated protein-like 2	1	0.90%	783	795	12	K	LSVGPLRCQGDR	N	8.66%	804	804	453.8413086	3	1358.500451	1356.692751	1.807699829	K	N	C8:+57.021	2	12	2	1
Q9UHD2	Serine/threonine-protein kinase TBK1	2	4.80%	271	291	20	R	GLQVLLTPVLANILEADQEK	C	0.81%	8618	8618	722.4188232	3	2164.232995	2163.215082	1.017912655	R	C	-	2	20	1	0
				646	661	15	K	YQEYTNELQETLPQK	M	3.50%	3311	3311	942.9588623	2	1883.902075	1882.89487	1.007204849	K	M	-	3	15	1	0
Q9UHG3	Prenylcysteine oxidase 1	4	11.09%	144	151	7	R	YGFQSLR	M	4.58%	1649	1649	435.7722473	2	869.5288445	869.4395478	0.089296781	R	M	-	3	7	0	0
				304	319	15	R	SDFYDIVLVATPLNR	K	3.00%	6766	6766	861.9616699	2	1721.90769	1721.898833	0.008857052	R	K	-	3	15	0	0
				330	349	19	D	PPIEEFHQYYQHIVTTLVK	G	7.03%	6544	6544	781.7381592	3	2342.191002	2342.194665	-0.003662829	D	G	Q11:+0.984	1	19	0	0
				349	364	15	K	GELNTSIFSSRPIDK	F	6.13%	12925	12925	833.0454712	2	1664.075292	1662.857696	1.217596143	K	F	-	1	15	1	0
Q9UIQ6	Leucyl-cystinyl aminopeptidase	18	25.66%	159	167	8	K	LFPWAQIR	L	0.81%	5375	5375	515.7929688	2	1029.570287	1029.575982	-0.005694364	K	L	-	3	8	0	0
				167	176	9	R	LPTAVVPLR	Y	1.93%	3002	3002	483.3092041	2	964.6027581	964.6069476	-0.004189493	R	Y	-	5	9	0	0
				218	230	12	R	VTFMSAVSSQEK	Q	0.81%	2994	2994	657.3256836	2	1312.635717	1312.6333	0.002417436	R	Q	-	5	12	0	0
				318	333	15	K	IIRDEQYTALSNMPK	K	0.81%	2856	2856	890.4597778	2	1778.903906	1777.903267	1.000638256	K	K	-	5	15	1	1
				334	353	19	K	SSVVLDDGLVQDEFSESVK	M	0.81%	5140	5140	1027.004883	2	2051.994116	2051.989892	0.004223057	K	M	-	5	19	0	0
				386	399	13	K	IGQVHYALETTVK	L	0.81%	2139	2139	729.902771	2	1457.789892	1457.787826	0.002066416	K	L	-	5	13	0	0
				460	478	18	K	IIAHELAHQWFGNLVTMK	W	0.81%	5746	5746	703.3753662	3	2107.102624	2107.103699	-0.001075135	K	W	-	3	18	0	0
				503	515	12	K	ELSSYEDFLDAR	F	0.81%	4821	4821	722.8329468	2	1443.650243	1443.651785	-0.001542005	K	F	-	5	12	0	0
				551	560	9	K	GSSLLLMLK	T	1.93%	5235	5235	481.2903442	2	960.5650384	960.567786	-0.002747643	K	T	-	5	9	0	0
				634	663	29	R	FFLNMKPEIQPSDTSYLWHIPLSYVTEGR	N	3.69%	7468	7468	872.4383545	4	3485.722118	3483.717398	2.004720105	R	N	M5:+15.995	1	29	2	0
				667	677	10	K	YQSVSLLDKK	S	3.02%	1055	1055	590.83	2	1179.64435	1179.649935	-0.005584904	K	S	-	3	10	0	1
				728	743	15	R	ANLINNIFELAGLGK	V	0.81%	8585	8585	793.9497681	2	1585.883886	1585.882789	0.001097421	R	V	-	5	15	0	0
				781	790	9	K	LGYMDLASR	L	0.81%	3146	3146	513.2582397	2	1024.500829	1024.501163	-0.000333604	K	L	-	5	9	0	0
				797	817	20	K	LLQNQIQQQTWTDEGTPSMR	E	3.59%	3670	3670	1188.577271	2	2375.138891	2373.138306	2.000584816	K	E	-	2	20	2	0
				869	880	11	K	TDKGWSFLLGK	Y	2.32%	5043	5043	418.07	3	1251.186525	1250.665919	0.520605648	K	Y	-	5	11	1	1
				933	946	13	R	HFPGHLLAWDFVK	E	2.26%	5587	5587	523.2828979	3	1566.825219	1565.814315	1.010903776	R	E	-	5	13	1	0
				955	977	22	K	FPLGSYTIQNIVAGSTYLFSTK	T	0.81%	8852	8852	803.0865479	3	2406.236168	2406.24711	-0.010942005	K	T	-	1	22	0	0
				977	996	19	K	THLSEVQAFFENQSEATFR	L	4.06%	5709	5709	747.6868896	3	2240.037194	2240.049807	-0.012613591	K	L	-	1	19	0	0
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	21	40.15%	29	43	14	K	NGEFFMSPNDFVTR	Y	2.26%	5351	5351	831.3735352	2	1660.73142	1659.735139	0.996281081	K	Y	-	4	14	1	0
				43	56	13	R	YLNIFGESQPNPK	T	0.81%	3968	3968	754.3775635	2	1506.739477	1505.75144	0.988036897	R	T	-	4	13	1	0
				56	69	13	K	TVELLSGVVDQTK	D	1.96%	3829	3829	695.352417	2	1388.689184	1387.755857	0.933327224	K	D	-	2	13	1	0
				177	184	7	R	VTAIDFR	D	4.44%	1369	1369	410.2354431	2	818.4552362	820.4442988	-1.98906265	R	D	-	2	7	-1	0
				245	260	15	K	DVEVTKEEFVLAAQK	F	0.81%	3284	3284	853.4577026	2	1704.899755	1704.893413	0.006342169	K	F	-	5	15	0	1
				284	292	8	R	MTLADIER	I	0.81%	2705	2705	474.7432251	2	947.4708001	947.4746139	-0.003813773	R	I	-	5	8	0	0
				292	310	18	R	IAPLEEGTLPFNLAEAQR	Q	0.81%	5754	5754	985.0231934	2	1968.030737	1968.031638	-0.000901385	R	Q	-	4	18	0	0
				312	331	19	K	ASGDSARPVLLQVAESAYR	F	0.81%	4765	4765	664.0151367	3	1989.021935	1989.02795	-0.006014612	K	F	-	4	19	0	0
				319	331	12	R	PVLLQVAESAYR	F	3.82%	4458	4458	673.3735352	2	1344.73142	1344.740147	-0.008726695	R	F	-	1	12	0	0
				331	353	22	R	FGLGSVAGAVGATAVYPIDLVK	T	0.81%	7364	7364	1053.085205	2	2104.15476	2104.156839	-0.002078588	R	T	-	5	22	0	0
				360	372	12	R	STGSFVGELMYK	N	0.81%	4360	4360	659.8198242	2	1317.623998	1317.627486	-0.003487626	R	N	-	5	12	0	0
				408	416	8	K	LTVNDFVR	D	0.81%	3252	3252	482.2624207	2	962.5091912	962.5185265	-0.009335267	K	D	-	2	8	0	0
				455	467	12	R	LQVAGEITTGPR	V	0.81%	1826	1826	621.8474731	2	1241.679296	1240.677547	1.001749601	R	V	-	5	12	1	0
				467	475	8	R	VSALSVVR	D	0.81%	921	921	415.7589417	2	829.5022332	829.5021481	8.51328E-05	R	D	-	5	8	0	0
				475	484	9	R	DLGFFGIYK	G	0.81%	5871	5871	530.276062	2	1058.536474	1058.543679	-0.007204697	R	G	-	5	9	0	0
				553	567	14	R	AGQTTYSGVIDCFR	K	4.85%	3731	3731	787.86	2	1573.70435	1573.719025	-0.014675384	R	K	C12:+57.021	2	14	0	0
				588	605	17	R	SSPQFGVTLLTYELLQR	W	0.81%	7753	7753	977.0350952	2	1952.05454	1951.041474	1.013065934	R	W	-	5	17	1	0
				605	624	19	R	WFYIDFGGVKPMGSEPVPK	S	0.81%	6169	6169	719.0288696	3	2154.063134	2153.065582	0.997551951	R	S	-	4	19	1	0
				626	641	15	R	INLPAPNPDHVGGYK	L	0.81%	2096	2096	531.2764893	3	1590.805993	1590.815437	-0.009444627	R	L	-	2	15	0	0
				641	653	12	K	LAVATFAGIENK	F	0.81%	3524	3524	617.3442993	2	1232.672949	1232.676484	-0.003535399	K	F	-	4	12	0	0
				653	669	16	K	FGLYLPLFKPSVSTSK	A	0.81%	6474	6474	595.3365479	3	1782.986168	1782.992005	-0.005836429	K	A	-	5	16	0	0
Q9UL26	Ras-related protein Rab-22A	2	16.49%	55	66	11	K	FLIWDTAGQER	F	0.81%	5003	5003	668.3344116	2	1334.653173	1334.661897	-0.008723366	K	F	-	5	11	0	0
				76	97	21	R	GSAAAIIVYDITKEETFSTLK	N	0.81%	7018	7018	753.4025269	3	2257.184105	2256.188927	0.995178622	R	N	-	5	21	1	1
Q9UM54	Myosin-VI	1	1.47%	615	634	19	K	FIRELFESSTNNNKDTKQK	A	9.91%	5261	5261	768.39	3	2302.146525	2299.144421	3.002104248	K	A	Q18:+0.984	1	19	3	3
Q9UN70	Protocadherin gamma-C3	1	1.82%	491	508	17	R	LSFFLLEQGAETGLVGR	Y	4.00%	5188	5188	613.6583252	3	1837.9515	1836.962146	0.989354698	R	Y	Q8:+0.984	2	17	1	0
Q9UN76	Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)	1	3.12%	41	61	20	K	KSDYLLSMIGYAVGLGNVWR	F	7.59%	987	987	749.0438232	3	2244.107995	2242.145608	1.962386999	K	F	N17:+0.984	1	20	2	1
Q9UNQ0	ATP-binding cassette sub-family G member 2	8	13.28%	86	96	10	K	SSLLDVLAAR	K	0.81%	5282	5282	522.8049927	2	1043.594335	1043.597505	-0.003169952	K	K	-	5	10	0	0
				137	147	10	R	ENLQFSAALR	L	4.98%	3250	3250	574.805481	2	1147.595312	1147.598568	-0.003256046	R	L	-	1	10	0	0
				147	160	13	R	LATTMTNHEKNER	I	5.78%	3312	3312	521.5734253	3	1561.696801	1559.735287	1.961513591	R	I	M5:+15.994	1	13	2	1
				163	172	9	R	VIQELGLDK	V	0.81%	1895	1895	507.794281	2	1013.572912	1013.575707	-0.002795196	R	V	-	4	9	0	0
				251	263	12	K	LFDSLTLLASGR	L	0.81%	5791	5791	646.8632813	2	1291.710912	1291.713598	-0.00268538	K	L	-	5	12	0	0
				331	343	12	K	LAEIYVNSSFYK	E	0.81%	3972	3972	717.375061	2	1432.734472	1432.723828	0.010643798	K	E	-	5	12	0	0
				417	426	9	K	NDSTGIQNR	A	5.03%	834	834	504.2428284	2	1006.470007	1006.420282	0.049724778	K	A	N1:+0.984,Q7:+0.984,N8:	1	9	0	0
				616	628	12	K	QGIDLSPWGLWK	N	0.81%	6768	6768	700.3686523	2	1398.721655	1398.729582	-0.0079276	K	N	-	4	12	0	0
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	2	0.59%	1179	1201	22	K	LSQEEVVLADLSALEAHWSTLR	H	0.81%	8687	8687	823.4360352	3	2467.28463	2466.275451	1.009179797	K	H	-	5	22	1	0
				3157	3167	10	R	QEQLELTLGR	V	5.54%	2548	2548	595.8052368	2	1189.594824	1187.603347	1.991476153	R	V	Q1:+0.984,Q3:+0.984	2	10	2	0
Q9UQ52	Contactin-6	1	0.68%	939	946	7	K	ILYRQNR	Q	4.03%	963	963	481.7794495	2	961.5432488	961.5457443	-0.002495434	K	Q	-	3	7	0	1
Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein 2	2	7.25%	239	262	23	R	AVQLMQQVASNGATLPSALSASK	S	5.29%	4584	4584	760.6806641	3	2279.018517	2274.141279	4.877238004	R	S	Q3:+0.984,Q6:+0.984,Q7:	1	23	5	0
				380	397	17	K	AIFSHAAGDNSTLLSFK	E	8.04%	3946	3946	594.3	3	1779.876525	1777.899895	1.976629512	K	E	-	2	17	2	0
Q9UQP3	Tenascin-N	3	3.46%	560	574	14	K	YVVRYTSADDQETR	E	5.66%	4730	4730	851.8798218	2	1701.743993	1701.795824	-0.051830693	K	E	-	3	14	0	1
				611	630	19	K	ADTNAPTDIDSPKNLVTDR	V	4.41%	3052	3052	681.37	3	2041.086525	2042.975624	-1.88909892	K	V	N14:+0.984	2	19	-1	1
				1051	1063	12	R	NVSTTLSTVGAR	F	7.49%	3873	3873	603.3271484	2	1204.638647	1204.641161	-0.002514293	R	F	-	1	12	0	0
Q9Y239	Nucleotide-binding oligomerization domain-containing protein 1	1	0.94%	765	774	9	N	NQITDVGAR	Y	8.75%	1647	1647	488.2640076	2	974.5123651	972.4988537	2.013511345	N	Y	-	1	9	2	0
Q9Y289	Sodium-dependent multivitamin transporter	1	2.05%	555	568	13	R	SLNPATIYPVLPK	L	0.81%	4612	4612	706.91	2	1411.80435	1411.807498	-0.00314836	R	L	-	5	13	0	0
Q9Y2P4	Long-chain fatty acid transport protein 6	1	1.78%	232	243	11	K	AAVISQLQVLR	G	9.79%	2910	2910	400.2389526	3	1197.693383	1197.708103	-0.014720058	K	G	Q6:+0.984	1	11	0	0
Q9Y2T6	G-protein coupled receptor 55	1	3.76%	306	318	12	R	VQLVLQDTTISR	G	7.86%	3539	3539	458.590271	3	1372.747338	1372.756175	-0.008837548	R	G	Q2:+0.984	1	12	0	0
Q9Y2X7	ARF GTPase-activating protein GIT1	1	1.97%	472	487	15	R	QPPGPVPTPPLPSER	A	4.83%	3720	3720	785.4204712	2	1568.825292	1568.819838	0.005453911	R	A	Q1:+0.984	3	15	0	0
Q9Y490	Talin-1	35	23.77%	592	613	21	K	LLAALLEDEGGSGRPLLQAAK	G	0.81%	5313	5313	708.06604	3	2121.174645	2121.179365	-0.004720091	K	G	-	5	21	0	0
				613	624	11	K	GLAGAVSELLR	S	0.81%	5545	5545	543.3182983	2	1084.620947	1084.624054	-0.003107752	K	S	-	5	11	0	0
				765	786	21	R	GVGAAATAVTQALNELLQHVK	A	0.81%	8999	8999	1046.590332	2	2091.165014	2090.148399	1.016614727	R	A	-	4	21	1	0
				797	824	27	R	YDQATDTILTVTENIFSSMGDAGEMVR	Q	3.30%	9938	9938	989.4604492	3	2965.357873	2963.352853	2.0050194	R	Q	-	2	27	2	0
				827	841	14	R	ILAQATSDLVNAIK	A	0.81%	4774	4774	729.420105	2	1456.82456	1455.82969	0.994869505	R	A	-	5	14	1	0
				891	910	19	R	EAAEGLRMATNAAAQNAIK	K	4.83%	626	626	645.7883911	3	1934.341698	1929.957807	4.383891572	R	K	N16:+0.984	1	19	4	1
				922	943	21	K	QAAASATQTIAAAQHAASTPK	A	0.81%	1653	1653	666.0117188	3	1995.011681	1995.986113	-0.974432126	K	A	Q1:+0.984,Q8:+0.984	1	21	-1	0
				957	971	14	K	AVAEQIPLLVQGVR	G	0.81%	5174	5174	747.4451294	2	1492.874609	1491.877309	0.997299437	K	G	-	5	14	1	0
				971	999	28	R	GSQAQPDSPSAQLALIAASQSFLQPGGK	M	0.81%	6852	6852	919.4743652	3	2755.399621	2753.398419	2.001201111	R	M	-	2	28	2	0

				1025	1035	10	K	NLGTALAELR	T	0.81%	4017	4017	529.303894	2	1056.592138	1056.592754	-0.000616186	K	T	-	4	10	0	0
				1096	1122	26	K	AVSSAAQLLGEVAQGNENYAGIAAR	D	2.34%	7797	7797	859.12146	3	2574.340905	2573.308526	1.032378659	K	D	N19:+0.984	2	26	1	0
				1136	1161	25	R	GVAALTSDPAVQAIVLDTASDVLDK	A	0.81%	8073	8073	1235.667358	2	2469.319067	2468.300997	1.018070021	R	A	-	4	25	1	0
				1170	1184	14	K	KAAGHPGDPESQQR	L	5.70%	3304	3304	493.2653503	3	1476.772576	1476.706949	0.065626529	K	L	-	1	14	0	1
				1241	1261	20	R	LNEAAAGLNQAATELVQASR	G	0.81%	5511	5511	1014.530884	2	2027.046118	2026.044328	1.001789442	R	G	-	4	20	1	0
				1320	1332	12	K	ALSTDPAIPNLK	S	0.81%	1003	1003	599.3260498	2	1196.63645	1196.640098	-0.003648903	K	S	-	4	12	0	0
				1401	1415	14	K	VLGEAMTGISQNAK	N	0.81%	2191	2191	710.3682251	2	1418.7208	1417.723512	0.997288339	K	N	-	5	14	1	0
				1559	1593	34	R	AATAPLLEAVDNLSAFASNPEFSSIPAQISPEGR	A	0.81%	8888	8888	868.95	4	3471.7687	3469.736526	2.03217336	R	A	-	1	34	2	0
				1604	1618	14	K	TMLESAGGLIQTAR	A	0.81%	4018	4018	724.8814087	2	1447.747167	1446.750061	0.997106399	K	A	-	5	14	1	0
				1625	1638	13	R	DPPSWSVLAQHSR	T	5.83%	9841	9841	470.9164124	3	1409.725762	1407.689508	2.036253629	R	T	-	1	13	2	0
				1690	1721	31	R	EGISQEALHTGMLTAVQEISHLIEPLANAAR	A	0.81%	9562	9562	1124.912354	3	3371.713585	3370.719088	0.994497691	R	A	Q5:+0.984	3	31	1	0
				1730	1751	21	K	VSQMAQYFEPLTLAAVGAASK	T	0.81%	7147	7147	1092.072266	2	2182.128881	2181.113989	1.014892458	K	T	-	5	21	1	0
				1751	1766	15	K	TLSHPQQMALLDQTK	T	0.81%	2524	2524	855.9447021	2	1709.873754	1709.877053	-0.003298311	K	T	-	3	15	0	0
				1766	1780	14	K	TLAESALQLLYTAK	E	0.81%	6729	6729	761.9317017	2	1521.847753	1520.845006	1.002747112	K	E	-	2	14	1	0
				1862	1874	12	K	AIAVTVQEMVTK	S	0.81%	3784	3784	645.3562012	2	1288.696752	1288.706071	-0.009318448	K	S	-	5	12	0	0
				1895	1917	22	R	LASEAKPAAVAAENEEIGSHIK	H	2.26%	2167	2167	746.0653076	3	2235.172448	2234.154273	1.018175116	R	H	-	5	22	1	0
				1960	1973	13	K	VSHVLAALQAGNIR	G	0.81%	1745	1745	668.8769531	2	1335.738256	1334.741878	0.99637793	K	G	-	5	13	1	0
				2043	2057	14	K	LAQAAQSSVATITR	L	0.81%	806	806	708.8955688	2	1415.775488	1415.773238	0.002249543	K	L	-	5	14	0	0
				2043	2063	20	K	LAQAAQSSVATITRLADVVK	L	5.24%	3083	3083	682.5178223	3	2044.529992	2043.12115	1.408841389	K	L	Q3:+0.984,Q6:+0.984	1	20	1	1
				2089	2099	10	K	ALGDLISATK	A	2.26%	3140	3140	494.7877808	2	987.5599114	987.560057	-0.000145605	K	A	-	3	10	0	0
				2104	2115	11	K	VGDDPAVWQLK	N	0.81%	3679	3679	614.3180542	2	1226.620458	1226.629534	-0.009075394	K	N	-	5	11	0	0
				2119	2130	11	K	VMVTNVTSLLK	T	3.81%	4826	4826	603.3566895	2	1204.697729	1203.689692	1.008036522	K	T	-	3	11	1	0
				2275	2291	16	R	VAGSVTELIQAAEAMK	G	0.81%	6699	6699	809.4378052	2	1616.85996	1616.844355	0.015604888	R	G	-	5	16	0	0
				2291	2321	30	K	GTEWVDFEDPTVAENELLGAAAAIEAAAK	K	0.81%	9595	9595	1018.177388	3	3051.508629	3050.508424	1.000205668	K	K	-	5	30	1	0
				2454	2464	10	K	RLQAAGNAVK	R	5.40%	4498	4498	513.8095703	2	1025.603491	1027.577423	-1.973932303	R	R	Q3:+0.984	1	10	-1	1
				2521	2531	10	K	LAQIRQQQYK	F	5.76%	4514	4514	426.5740356	3	1276.698632	1277.661515	-0.962883361	K	F	Q6:+0.984,Q7:+0.984,Q8:	1	10	-1	1
Q9Y493	Zonadhesin	1	0.89%	1590	1615	25	R	GGILEVSYIKAVHVTVFDLSISLLR	G	9.91%	4926	4926	911.105957	3	2730.294396	2728.552735	1.741660686	R	G	-	1	25	2	1
Q9Y561	Low-density lipoprotein receptor-related protein 12	1	2.21%	153	172	19	R	LAYFSGKSEEFNCACDQFR	C	7.66%	6415	6415	760.6803589	3	2279.017602	2277.977373	1.040228814	R	C	C13:+57.021,C15:+57.021	2	19	1	1
Q9Y566	SH3 and multiple ankyrin repeat domains protein 1	1	0.51%	162	173	11	K	QTNLDEKQLAK	L	5.29%	1630	1630	646.3256836	2	1290.635717	1289.635026	1.00069114	K	L	Q1:+0.984,N3:+0.984,Q8:	1	11	1	1
Q9Y5E8	Protocadherin beta-15	1	3.43%	62	89	27	R	GARVVSEDNEQGLQLDLQTGQLILNEK	L	4.55%	6976	6976	990.8699341	3	2969.586327	2968.49889	1.08743667	R	L	Q14:+0.984,Q21:+0.984	3	27	1	1
Q9Y5U5	Tumor necrosis factor receptor superfamily member 18	1	4.15%	38	48	10	R	LLLGTGTGAR	C	0.81%	1255	1255	508.7890015	2	1015.562353	1015.566205	-0.003852214	R	C	-	5	10	0	0
Q9Y5Y6	Suppressor of tumorigenicity 14 protein	3	5.26%	28	45	17	K	VNGLEEGVEFLPVNNVK	K	0.81%	5251	5251	929.975708	2	1857.935766	1856.951975	0.983790888	K	K	N2:+0.984	3	17	1	0
				125	139	14	K	LLYSGVPFLGPYHK	E	0.81%	5314	5314	795.9334717	2	1589.851293	1589.860597	-0.009303257	K	E	-	3	14	0	0
				322	336	14	R	RHPGFEATFFQLPR	M	3.69%	4670	4670	569.6486816	3	1705.92257	1701.873955	4.048614578	R	M	-	2	14	4	1
Q9Y624	Junctional adhesion molecule A	1	7.69%	125	148	23	K	LIVLVPPSKPTVNIPSSATIGNR	A	0.81%	4625	4625	792.1351318	3	2373.38192	2372.379128	1.002792636	K	A	-	4	23	1	0
Q9Y639	Neuroplastin	1	2.51%	149	159	10	R	IVTSEEVIIR	D	0.81%	2335	2335	579.8364258	2	1157.657201	1157.665585	-0.008383421	R	D	-	5	10	0	0
Q9Y666	Solute carrier family 12 member 7	2	3.14%	88	109	21	K	LANYTNLSQGVVEHEEDEESR	R	2.32%	3168	3168	807.0363159	3	2418.085473	2419.077523	-0.992050318	K	R	Q9:+0.984	4	21	-1	0
				816	829	13	R	DTTAAHQALLVAK	N	0.81%	890	890	699.8689575	2	1337.722265	1337.730311	-0.008045577	R	N	-	4	13	0	0
Q9Y6V0	Protein piccolo	1	0.27%	980	994	14	K	SLTAEPQKAVLPTK	L	6.78%	3933	3933	495.2435303	3	1482.707116	1482.82934	-0.122224756	K	L	Q7:+0.984	2	14	0	1
Q9Y6X8	Zinc fingers and homeoboxes protein 2	1	1.08%	471	480	9	R	LIEVTGLAR	S	3.04%	821	821	486.274231	2	970.5328118	970.5811268	-0.048314982	R	S	-	5	9	0	0

Digestion method : In-solution
File conversion : PepArML batch uploader
Search engine : PepArML
Database : IPI Human
Specific cleavage : trypsin
Fixed modification : Carbamidomethyl (C)
Variable modification : Oxidation (M), Deamidation (NQ)
Data Processing : In-house tool - Coverage Table 1.7 with Parsimony
FDR < 10%

UniProt Accession number	Description	Number of peptides	Sequence Coverage	Start	End	Length	Left AA	peptide	Right AA	FDR	start_scan	end_scan	precursor_mz	assumed_charge	precursor_neutral_mass	calc_neutral_pep_mass	massdiff	leftaa	rightaa	mods	number of agreed search engines	peptide_length	c13peak	missclevages
A4UGR9	Xin actin-binding repeat-containing protein 2	1	0.53%	3314	3332	18	R	VFKGLGYATADASATEMR	T	6.00%	3672	3672	636.3189087	3	1905.933251	1902.914646	3.018605218	R	T	M17:+15.995	1	18	3	1
A6NMY6	Putative annexin A2-like protein	1	4.72%	88	104	16	K	SALSGHLETVILGLLK	T	0.23%	7786	7786	551.3311768	3	1650.970055	1649.971604	0.998451401	K	T	-	6	16	1	0
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal	2	4.41%	389	406	17	K	YGSVAFPNFEQGVACLR	E	0.23%	5653	5653	958.4471436	2	1914.878637	1913.908952	0.969685453	K	E	C15:+57.021	6	17	1	0
				628	640	12	K	ESISDVGFGMLK	S	6.81%	4892	4892	642.32	2	1282.62435	1281.627486	0.996863936	K	S	-	1	12	1	0
O00299	Chloride intracellular channel protein 1	1	7.47%	95	113	18	K	LAALNPESNTAGLDIFAK	F	0.23%	5268	5268	923.4866943	2	1844.957739	1843.967975	0.989763544	K	F	-	6	18	1	0
O00555	Voltage-dependent P/Q-type calcium channel subunit alpha-1A	1	1.12%	2166	2194	28	R	SLGRYTDVDTGLGTDLSMTTQSGDLPSK	E	1.04%	9860	9860	978.4685059	3	2932.382042	2931.365595	1.016447434	R	E	M18:+15.995,Q21:+0.984	1	28	1	1
O14522	Receptor-type tyrosine-protein phosphatase T	1	1.57%	995	1018	23	R	MIWQENSASIVMVTNLVEVGRVK	C	0.69%	8006	8006	1311.1875	2	2620.35935	2619.340114	1.019236392	R	C	M12:+15.995,N15:+0.984	2	23	1	1
O14610	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-T2	1	24.64%	34	51	17	K	EIKEYVEAQAGNDPFLK	G	3.67%	2165	2165	652.00354	3	1952.987145	1949.973454	3.013690589	K	G	-	1	17	3	1
O14654	Insulin receptor substrate 4	1	1.03%	671	684	13	K	EVKDAEIPEGAAR	G	6.69%	1099	1099	456.2357178	3	1365.683678	1365.688404	-0.004726176	K	G	E1:-18.011	1	13	0	1
O14672	Disintegrin and metalloproteinase domain-containing protein 10	2	4.14%	30	45	15	R	HYEGLSYNVDSLHQK	H	0.23%	1635	1635	597.2860718	3	1788.83474	1788.843109	-0.008368524	R	H	-	3	15	0	0
				410	426	16	K	ENGNYIMYARATSGDK	L	8.25%	1008	1008	448.4566345	4	1789.795238	1789.794095	0.00114275	K	L	N2:+0.984	1	16	0	1
O15083	ERC protein 2	1	1.36%	236	249	13	R	DLNHLLQQESGNR	G	5.72%	4178	4178	509.6109924	3	1525.809502	1525.700814	0.108687919	R	G	N3:+0.984,Q7:+0.984,Q8:	3	13	0	0
O15357	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2	2	1.91%	882	893	11	R	ERLYEWISIDK	D	1.81%	4075	4075	484.5866089	3	1450.736352	1450.745626	-0.009274748	R	D	-	1	11	0	1
				917	930	13	R	KPAFTEASCPLSR	L	9.25%	4043	4043	489.2661438	3	1464.774956	1462.723382	2.05157394	R	L	C9:+57.021	2	13	2	0
O43609	Protein sprouty homolog 1	1	9.72%	107	138	31	R	GPILSRSTSTGSAASSGSNSSASSEQGLLGR	S	0.94%	3349	3349	728.397644	4	2909.559276	2910.380232	-0.82095582	R	S	N19:+0.984,Q26:+0.984	3	31	-1	1
O43847	Nardilysin	1	0.87%	341	351	10	K	FFWGNAETLK	H	7.24%	4154	4154	608.3427734	2	1214.669897	1212.581505	2.088391571	K	H	N5:+0.984	1	10	2	0
O60241	Brain-specific angiogenesis inhibitor 2	1	0.88%	1447	1461	14	R	TVPGSTMKMGSLER	K	0.88%	5150	5150	747.3708496	2	1492.726049	1492.737783	-0.011733645	R	K	-	2	14	0	1
O60299	ProSAP-interacting protein 1	1	4.01%	544	571	27	R	RQAGVAAAASLVSVDGEAEAGGESGTR	A	1.81%	10398	10398	839.4631348	3	2515.365929	2515.226269	0.139660585	R	A	-	1	27	0	1
O60437	Periplakin	1	1.14%	1498	1518	20	K	VVLSESVQVEKGDTEQEIQR	L	2.95%	7725	7725	1138.083252	2	2274.150854	2274.122667	0.02818721	K	L	Q8:+0.984,Q19:+0.984	1	20	0	1
O75122	CLIP-associating protein 2	1	0.85%	671	682	11	K	EGLLGLQNLLK	N	1.82%	5767	5767	599.3624268	2	1196.709203	1196.712869	-0.003666036	K	N	-	2	11	0	0
O75330	Hyaluronan mediated motility receptor	1	1.80%	251	264	13	K	LDIAQLEENLKEK	N	6.04%	1034	1034	771.8699341	2	1541.724218	1541.830084	-0.105866292	K	N	-	2	13	0	1
O75923	Dysferlin	1	1.30%	1345	1372	27	K	SYQLANISSPSLVVECGGQTVQSCVIR	N	6.27%	4218	4218	740.1176147	4	2956.439159	2953.415163	3.023995432	K	N	Q3:+0.984,C16:+57.021,C	1	27	3	0
O75955	Flotillin-1	2	8.67%	91	109	18	K	TEAEIAHIALETLEGHQR	A	0.23%	4942	4942	673.6502686	3	2017.927331	2017.022864	0.904466256	K	A	-	4	18	1	0
				133	152	19	K	VASSDLVNMGISVVSYTLK	D	0.23%	8147	8147	993.2946777	2	1984.573705	1982.039427	2.534278701	K	D	-	2	19	3	0
O76094	Signal recognition particle 72 kDa protein	2	5.96%	254	275	21	K	LKPTDVGLLAVIANNIITINK	D	0.23%	9157	9157	741.1151733	3	2220.322045	2219.325301	0.996743732	K	D	-	5	21	1	0
				479	498	19	K	DIHTLAQLISAYSLVDPEK	A	6.36%	8245	8245	705.3755493	3	2113.103173	2113.094282	0.008890405	K	A	Q7:+0.984	1	19	0	0
O94905	Erlin-2	1	3.83%	240	253	13	K	KISEIEDAAFLAR	E	0.23%	3166	3166	731.9003906	2	1461.785131	1461.78274	0.002391034	K	E	-	3	13	0	1
O94985	Calsyntenin-1	1	1.83%	147	165	18	K	ATVHIQVNDVNEYAPVFK	E	3.34%	9450	9450	682.6715698	3	2044.991234	2045.010537	-0.019302719	K	E	Q6:+0.984,N8:+0.984	1	18	0	0
O95232	Luc7-like protein 3	1	3.70%	36	52	16	K	YYLCGFCPAELFTNTR	S	3.42%	7026	7026	1006.674255	2	2011.332861	2010.895875	0.436985302	K	S	C4:+57.021,C7:+57.021	2	16	0	0
O95294	RasGAP-activating-like protein 1	1	1.62%	174	187	13	K	TRFPHWDEVLELR	E	0.23%	4638	4638	567.64	3	1699.896525	1696.868536	3.027989344	K	E	-	3	13	3	1
O95342	Bile salt export pump	1	1.82%	977	1001	24	K	ANIYGFCFAFAQCIMFIANSASYR	Y	7.89%	9243	9243	946.1026001	3	2835.284325	2839.243557	-3.959231347	K	Y	N2:+0.984,C7:+57.021,Q1	1	24	-1	0
O95622	Adenylate cyclase type 5	1	0.95%	1145	1157	12	K	THIKALADFAMK	L	5.29%	4177	4177	449.243866	3	1344.708123	1344.722389	-0.014266668	K	L	-	1	12	0	1
O95907	Monocarboxylate transporter 3	1	3.57%	212	230	18	R	AGDAPGEAEADGAGLQLR	E	9.20%	2282	2282	425.7	4	1698.7687	1697.785638	0.983061984	R	E	Q16:+0.984	2	18	1	0
O96005	Cleft lip and palate transmembrane protein 1	1	4.78%	634	666	32	R	EEASTSLPTKPTQGASSASEPQEAPPKPAEDK	K	0.28%	1148	1148	1089.867432	3	3266.57882	3264.563373	2.015447186	R	K	-	2	32	2	0
O96019	Actin-like protein 6A	2	11.19%	112	130	18	K	SEASLHPVLMSEAPWNTR	A	9.74%	2319	2319	511.4968262	4	2041.956005	2040.956558	0.999446848	K	A	M10:+15.994,N16:+0.984	1	18	1	0
				164	194	30	R	STGLILDSGATHTTAIPVHDGYVLQQGIVK	S	1.82%	4363	4363	1031.55835	3	3091.651574	3090.634962	1.016612052	R	S	-	2	30	1	0
P00505	Aspartate aminotransferase, mitochondrial	2	9.07%	309	325	16	K	ILIRPMYSNPPLNGAR	I	1.66%	3046	3046	605.991394	3	1814.950707	1812.955606	1.995100937	K	I	N9:+0.984,N13:+0.984	2	16	2	0
				407	430	23	R	ISVAGVTSSNVGYLAHAIHQVTK	-	0.23%	5203	5203	785.0930176	3	2352.255578	2352.243741	0.011836814	R	-	Q20:+0.984	2	23	0	0
P00734	Prothrombin	2	4.98%	384	399	15	K	SPQELLCGASLISDR	W	0.36%	4526	4526	824.4586792	2	1646.901708	1644.813654	2.088054206	K	W	C7:+57.021	3	15	2	0
				399	415	16	R	WVLTAAHCLLYPPWDK	N	0.23%	6258	6258	985.4997559	2	1968.983862	1968.991559	-0.007697369	R	N	C8:+57.021	6	16	0	0
P02786	Transferrin receptor protein 1	15	27.76%	6	22	16	R	SAFSNLFGGEPLSYTR	F	0.23%	6065	6065	873.9246826	2	1745.833715	1744.842046	0.991669074	R	F	-	6	16	1	0
				39	53	14	K	LAVDEEENADNNTK	A	0.23%	898	898	781.3465576	2	1560.677465	1560.690356	-0.01289083	K	A	-	7	14	0	0
				120	128	8	R	RLYWDDLK	R	5.69%	2444	2444	554.7879639	2	1107.560278	1107.57129	-0.01101277	R	R	-	1	8	0	1
				155	174	19	R	EAGSQKDENLALYVENQFR	E	0.23%	5048	5048	1106.530396	2	2211.045141	2210.060372	0.9847688	R	E	-	3	19	1	1
				193	205	12	K	DSAQNSVIIVDK	N	3.03%	1516	1516	645.0917969	2	1288.167944	1287.667042	0.50090211	K	N	-	1	12	0	0
				208	224	16	R	LVYLVENPGGYVAYSK	A	0.23%	4318	4318	886.9671021	2	1771.918554	1770.919234	0.999320198	R	A	-	7	16	1	0
				325	339	14	R	SSGLPNIPVQTISR	A	0.23%	3275	3275	734.9064941	2	1467.797338	1467.804538	-0.007200031	R	A	-	6	14	0	0
				344	358	14	K	LFGNMEGDCPSDWK	T	0.23%	3873	3873	828.3452759	2	1654.674902	1654.675113	-0.000211018	K	T	C9:+57.021	4	14	0	0
				394	409	15	K	GFVEPDHYVVVGAQR	D	0.23%	2589	2589	836.9280396	2	1671.840429	1671.836901	0.003527974	K	D	-	6	15	0	0
				428	439	11	K	LAQMFSDMVLK	D	0.23%	4776	4776	641.8265991	2	1281.637548	1281.646114	-0.008565862	K	D	-	6	11	0	0
				495	508	13	K	VSASPLLYTLIEK	T	0.23%	5649	5649	717.4115601	2	1432.80747	1432.817729	-0.010258635	K	T	-	7	13	0	0
				514	531	17	K	HPVTGQFLYQDSNWASK	V	0.23%	2978	2978	989.47229	2	1976.92893	1976.938072	-0.009141874	K	V	-	6	17	0	0
				613	623	10	R	YNSQLLSFVR	D	0.23%	4193	4193	613.83	2	1225.64435	1225.645518	-0.0011682	R	D	-	5	10	0	0
				680	693	13	R	VEYHFLSPYVSPK	E	0.23%	3363	3363	522.6011963	3	1564.780114	1564.792577	-0.012462781	R	E	-	1	13	0	0
				698	717	19	R	HVFWGSGSHTLPALLENLK	L	0.23%	5389	5389	1054.058838	2	2106.102026	2105.105806	0.996219653	R	L	-	6	19	1	0
P04004	Vitronectin	1	3.14%	197	212	15	R	DVWGIEGPIDAAFTR	I	0.23%	7050	7050	823.9102173	2	1645.804784	1645.810018	-0.005233102	R	I	-	7	15	0	0
P04222	HLA class I histocompatibility antigen, Cw-3 alpha chain	7	29.78%	41	59	18	R	GEPHFIAVGYVDDTQFVR	F	2.75%	4600	4600	1027.528198	2	2053.040746	2049.979587	3.061159572	R	F	Q15:+0.984	1	18	3	0
				121	132	11	R	MYGCDVGPDGR	L	0.49%	1133	1133	613.7481079	2	1225.480566	1225.485127	-0.004561012	R	L	C4:+57.021	6	11	0	0
				155	169	14	R	SWTAADTAAQITQR	K	0.28%	2769	2769	760.9244385	2	1519.833227	1518.742666	1.090560633	R	K	-	4	14	1	0
				181	193	12	R	AYLEGLCVEWLR	R	0.92%	6367	6367	754.144043	2	1506.272436	1507.748869	-1.476432951	R	R	C7:+57.021	5	12	-1	0
				243	267	24	W	DGEDQTQDTELVETRPAGDGTFQK	W	0.23%	2135	2135	1320.095581	2	2638.175512	2636.183795	1.991717301	R	W	-	2	24	2	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.23%	2358	2358	714.3626709	2	1426.709692	1426.720474	-0.010782427	K	Y	-	4	13	0	0
				280	297	17	R	YTCHVQHEGLPEPLTLR	W	0.23%	2352	2352	684.0063477	3	2048.995568	2049.993728	-0.998160551	R	W	C3:+57.021,Q6:+0.984	3	17	-1	0
P04233	HLA class II histocompatibility antigen gamma chain	1	4.73%	80	94	14	K	LTVTSQNLQLENLR	M	0.23%	3539	3539	814.9476318	2	1627.879614	1627.889331	-0.009717056	K	M	-	6	14	0	0
P04264	Keratin, type II cytoskeletal 1	2	4.35%	199	211	12	R	FLEQQNQVLQTK	W	1.63%	1699	1699	738.8948364	2	1475.774023	1475.761989	0.012033668	R	W	Q4:+0.984	3	12	0	0
				223	239	16	R	THNLEPYFESFINNLR	R	0.23%	7085	7085	666.6635742	3	1996.967248	1994.937372	2.029875504	R	R	N3:+0.984,N13:+0.984	1	16	2	0
P04792	Heat shock protein beta-1	6	55.61%	27	37	10	R	LFDQAFGLPR	L	0.23%	4654	4654	582.312439	2	1162.609228	1162.61349	-0.004261782	R	L	-	7	10	0	0
				37	75	38	R	LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR	A	0.28%	7681	7681	1365.353638	3	4093.037438	4093.037385	5.32619E-05	R	A	Q7:+0.984	6	38	0	0
				96	112	16	R	VSLDVNHFAPDELTVK	T	0.23%	4114	4114	892.4622192	2	1782.908788	1782.915211	-0.006422723	R	T	-	6	16	0	0
				96	114	18	R	VSLDVNHFAPDELTVKTK	D	2.18%	5369	5369	671.9907837	3	2012.948876	2012.057853	0.89102313	R	D	-	1	18	1	1
				140	171	31	R	KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	L	0.23%	5265	5265	1076.888794	3	3227.642907	3226.631895	1.011011364	R	L	Q12:+0.984	7	31	1	1
				171	188	17	K	LATQSNEITIPVTFESR	A	0.23%	4469	4469	953.99646	2	1905.97727	1904.984353	0.992916386	K	A	-	6	17	1	0
P04839	Cytochrome b-245 heavy chain	2	4.74%	318	328	10	K	MEVGQYIFVK	C	0.49%	4135	4135	608.3373413	2	1214.659033	1212.621278	2.037754241	K	C	-	3	10	2	0
				531	548	17	R	IGVFLCGPEALAETLSK	Q	0.23%	7065	7065	903.4860229	2	1804.956396	1803.943606	1.012790034	R	Q	C6:+57.021	7	17	1	0
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	6	24.51%	70	86	16	R	AVVYSNTIQSIMAIVK	A	0.58%	7237	7237	869.480896	2	1736.946142	1735.95424	0.99190164	R	A	-	5	16	1	0
				129	143	14	R	RLWADHGVQACFGR	S	0.29%	1928	1928	558.6231689	3	1672.846032	1671.804761	1.041270684	R	S	C11:+57.021	4	14	1	1
				130	143	13	R	LWADHGVQACFGR	S	0.56%	2420	2420	758.864624	2	1515.713598	1515.70365	0.009948087	R	S	C10:+57.021	4	13	0	0
				162	177	15	R	IAQSDYIPTQQDVLR	T	0.23%	3234	3234	874.4498901	2	1746.88413	1745.89481	0.989320185	R	T	-	7	15	1	0
				278	307	29	K	ITHSPLTICFPEYTGANKYDEAASYIQSK	F	0.23%	4888	4888	1102.526367	3	3304.555626	3304.559329	-0.003702757	K	F	C9:+57.021,N17:+0.984	5	29	0	1
				318	331	13	K	EIYTHFTCATDTK	N	0.28%	1494	1494	793.8578491	2	1585.700048	1585.707792	-0.007743766	K	N	C8:+57.021	5	13	0	0
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	8	11.83%	162	173	11	K	NMVPQQALVIR	N	0.74%	2750	2750	634.8573608	2	1267.699072	1267.707074	-0.008002096	K	E	-	3	11	0	0
				204	227	23	R	IISANGCKVDNSSLTGESEPQTR	S	2.65%	9081	9081	823.26	3	2466.756525	2465.122265	1.63426004	R	S	N5:+0.984,C7:+57.021,N1	1	23	2	1
				430	444	14	R	AVFQANQENLPILK	R	0.23%	4051	4051	792.9361572	2	1583.856664	1583.867139	-0.010474179	R	R	-	4	14	0	0
				526	551	25	K	EQPLDEELKDAFQNAYLELGGLGER	V	1.82%	8995	8995	946.1176758	3	2835.329552	2834.361015	0.968536848	K	V	Q13:+0.984	3	25	1	1
				535	551	16	K	DAFQNAYLELGGLGER	V	0.28%	6329	6329	876.9255371	2	1751.835424	1751.84786	-0.012435629	K	V	-	4	16	0	0
				629	647	18	K	GVGIISEGNETVEDIAAR	L	0.23%	4306	4306	915.4597168	2	1828.903784	1828.916668	-0.012884262	K	L	-	6	18	0	0
				647	658	11	R	LNIPVSQVNPR	D	0.23%	2065	2065	618.8537598	2	1235.691869	1235.698616	-0.006746925	R	D	-	6	11	0	0
				707	726	19	R	QGAIVAVTGDGVNDSPALK	K	0.23%	2670	2670	906.4716187	2	1810.927587	1810.942489	-0.014901351	R	K	-	4	19	0	0
P05120	Plasminogen activator inhibitor 2	1	2.89%	238	250	12	R	EKLNIGYIEDLK	A	9.72%	11881	11881	718.1538086	2	1434.291967	1434.760592	-0.468625013	R	A	N4:+0.984	4	12	0	1
P05141	ADP/ATP translocase 2	5	25.50%	10	23	13	K	DFLAGGVAAAISK	T	0.28%	5231	5231	610.3364258	2	1218.657201	1218.660834	-0.003632389	K	T	-	3	13	0	0
				63	72	9	K	EQGVLSFWR	G	0.23%	4916	4916	561.2879639	2	1120.560278	1120.566539	-0.006261738	K	G	-	7	9	0	0
				80	92	12	R	YFPTQALNFAFK	D	0.23%	6264	6264	724.3772583	2	1446.738867	1445.734333	1.004533282	R	D	-	6	12	1	0
				111	138	27	R	YFAGNLASGGAAGATSLCFVYPLDFAR	T	0.23%	9927	9927	1399.197998	2	2796.380346	2796.321271	0.059075326	R	T	N5:+0.984,C18:+57.021	3	27	0	0
				244	259	15	R	KGTDIMYTGTLDCWR	K	0.23%	3707	3707	908.9190674	2	1815.822485	1815.827925	-0.005440434	R	K	C13:+57.021	5	15	0	1
P05362	Intercellular adhesion molecule 1	5	14.10%	56	66	10	K	LLGIETPLPK	K	0.23%	3908	3908	540.8338013	2	1079.651952	1079.659043	-0.007090429	K	K	-	6	10	0	0
				115	129	14	R	VELAPLPSWQPVGK	N	0.23%	4702	4702	761.4303589	2	1520.845068	1519.839861	1.005206597	R	N	-	5	14	1	0
				158	176	18	K	REPAVGEPAEVTTTVLVR	R	0.23%	2618	2618	962.5239868	2	1923.032324	1923.042537	-0.010213519	K	R	-	6	18	0	1
				273	287	14	K	ASVSVTAEDEGTQR	L	0.23%	921	921	725.3427734	2	1448.669897	1448.674312	-0.004415109	K	L	-	7	14	0	0
				430	449	19	K	CLKDGTFPLPIGESVTVTR	D	3.09%	5988	5988	698.7112427	3	2093.110253	2089.08731	4.022942763	K	D	C1:+57.021	1	19	4	1
P06576	ATP synthase subunit beta, mitochondrial	23	72.21%	18	34	16	R	RLTPSASLPPAQLLLR	A	3.47%	11581	11581	867.9326782	2	1733.849706	1733.019935	0.829770981	R	A	Q12:+0.984	1	16	1	1
				94	109	15	R	LVLEVAQHLGESTVR	T	0.23%	3662	3662	826.4622803	2	1650.90891	1649.910066	0.998844379	R	T	-	4	15	1	0
				109	121	12	R	TIAMDGTEGLVR	G	0.23%	2357	2357	631.8214722	2	1261.627294	1261.633634	-0.006339744	R	G	-	6	12	0	0
				133	143	10	K	IPVGPETLGR	I	0.23%	1703	1703	519.7979736	2	1037.580297	1037.586941	-0.006643318	K	I	-	7	10	0	0
				143	155	12	R	IMNVIGEPIDER	G	0.23%	3106	3106	693.3565674	2	1384.697485	1384.702048	-0.004563322	R	G	-	6	12	0	0
				143	159	16	R	IMNVIGEPIDERGPIK	T	0.23%	3152	3152	890.9788818	2	1779.942114	1779.955303	-0.013189336	R	T	-	7	16	0	1
				161	188	27	K	QFAPIHAEAPEFMEMSVEQEILVTGIK	V	0.23%	7539	7539	1015.835205	3	3044.48214	3044.487481	-0.005340462	K	V	Q1:+0.984	2	27	0	0
				188	198	10	K	VVDLLAPYAK	G	0.28%	3600	3600	544.8175049	2	1087.61936	1087.627743	-0.008383042	K	G	-	1	10	0	0
				201	212	11	K	IGLFGGAGVGK	T	0.28%	2777	2777	488.2835083	2	974.5513665	974.554912	-0.003545494	K	T	-	6	11	0	0
				212	225	13	K	TVLIMELINNVAK	A	0.23%	7933	7933	729.4182129	2	1456.820776	1456.832334	-0.011558307	K	A	-	7	13	0	0
				225	239	14	K	AHGGYSVFAGVGER	T	0.23%	1897	1897	703.8341675	2	1405.652685	1405.673858	-0.021173351	K	T	-	7	14	0	0
				239	259	20	R	TREGNDLYHEMIESGVINLK	D	0.23%	4920	4920	775.4	3	2323.176525	2318.121243	5.055281416	R	D	N5:+0.984	2	20	5	1
				264	279	15	K	VALVYGQMNEPPGAR	A	0.23%	2412	2412	801.4082031	2	1600.800756	1600.803159	-0.00240299	K	A	-	6	15	0	0
				281	294	13	R	VALTGLTVAEYFR	D	0.23%	5917	5917	720.3931274	2	1438.770605	1438.782012	-0.011407005	R	D	-	7	13	0	0
				294	310	16	R	DQEGQDVLLFIDNIFR	F	0.23%	10409	10409	961.9823608	2	1921.949072	1920.958139	0.990932944	R	F	-	7	16	1	0
				310	324	14	R	FTQAGSEVSALLGR	I	0.23%	4246	4246	718.38	2	1434.74435	1434.746689	-0.002339024	R	I	-	6	14	0	0
				324	345	21	R	IPSAVGYQPTLATDMGTMQER	I	0.23%	4248	4248	1133.54248	2	2265.069311	2265.076952	-0.007641591	R	I	-	5	21	0	0
				350	387	37	K	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	A	0.23%	6269	6269	961.7446289	4	3842.947215	3841.973797	0.973418473	K	A	-	3	37	1	1
				387	406	19	R	AIAELGIYPAVDPLDSTSR	I	0.23%	5696	5696	994.5182495	2	1987.020849	1987.026218	-0.005369393	R	I	-	6	19	0	0
				406	422	16	R	IMDPNIVGSEHYDVAR	G	0.23%	2560	2560	908.4326782	2	1814.849706	1814.862131	-0.012424411	R	G	-	4	16	0	0
				432	451	19	K	SLQDIIAILGMDELSEEDK	L	0.46%	9200	9200	1060.543213	2	2119.070776	2118.040215	1.030561013	K	L	-	4	19	1	0
				462	480	18	R	FLSQPFQVAEVFTGHMGK	L	0.23%	6319	6319	1012.003296	2	2021.990942	2022.003316	-0.012374107	R	L	-	2	18	0	0
				489	519	30	K	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	A	0.23%	8983	8983	1117.547729	3	3349.619713	3350.616914	-0.997200571	K	A	Q16:+0.984	3	30	-1	0
P06733	Alpha-enolase	15	53.69%	80	92	12	K	KLNVTEQEKIDK	L	0.58%	884	884	482.6045227	3	1444.790093	1444.777305	0.012788139	K	L	N3:+0.984	1	12	0	2
				92	103	11	K	LMIEMDGTENK	S	0.23%	2283	2283	640.7961426	2	1279.576635	1279.578822	-0.002187268	K	S	-	6	11	0	0
				105	120	15	K	FGANAILGVSLAVCK	A	0.23%	9261	9261	760.4189453	2	1518.822241	1518.822368	-0.000127631	K	A	C14:+57.021	5	15	0	0
				132	162	30	R	HIADLAGNSEVILPVPAFNVINGGSHAGNK	L	0.23%	9247	9247	754.6567993	4	3014.595897	3012.530465	2.065431834	R	L	N22:+0.984,N29:+0.984	1	30	2	0
				162	179	17	K	LAMQEFMILPVGAANFR	E	0.23%	7852	7852	954.987793	2	1907.959936	1906.979745	0.980191202	K	E	-	6	17	1	0
				202	221	19	K	DATNVGDEGGFAPNILENK	E	0.23%	4395	4395	980.9629517	2	1959.910253	1959.917396	-0.007142864	K	E	-	6	19	0	0
				202	228	26	K	DATNVGDEGGFAPNILENKEGLELLK	T	0.23%	6048	6048	915.128418	3	2742.361779	2743.355202	-0.993422902	K	T	N18:+0.984	3	26	-1	1

				239	253	14	K	VVIGMDVAASEFFR	S	0.23%	9589	9589	771.3977661	2	1540.779882	1539.775547	1.004334771	K	S	-	6	14	1	0
				269	281	12	R	YISPDQLADLYK	S	0.23%	5117	5117	713.3720703	2	1424.728491	1424.718743	0.009747713	R	S	-	1	12	0	0
				281	306	25	K	SFIKDYPVVSIEDPFDQDDWGAWQK	F	0.23%	7245	7245	1494.198364	2	2986.381078	2984.386852	1.994226668	K	F	-	3	25	2	1
				285	306	21	K	DYPVVSIEDPFDQDDWGAWQK	F	0.23%	7753	7753	839.1293945	3	2514.364708	2510.091382	4.273326426	K	F	Q13:+0.984	1	21	4	0
				306	326	20	K	FTASAGIQVVGDDLTVTNPK	R	0.23%	6093	6093	1017.540894	2	2033.066137	2032.047682	1.018454925	K	R	-	4	20	1	0
				343	358	15	K	VNQIGSVTESLQACK	L	0.23%	2448	2448	817.4099121	2	1632.804174	1632.813654	-0.009479973	K	L	C14:+57.021	4	15	0	0
				358	372	14	K	LAQANGWGVMVSHR	S	0.23%	2532	2532	763.8789673	2	1525.742284	1525.745963	-0.003678446	K	S	N5:+0.984	7	14	0	0
				372	394	22	R	SGETEDTFIADLVVGLCTGQIK	T	0.23%	11027	11027	785.7141113	3	2354.118859	2352.151427	1.967432072	R	T	C17:+57.021	5	22	2	0
P06744	Glucose-6-phosphate isomerase	2	5.73%	194	211	17	K	TLAQLNPESSLFIIASK	T	0.95%	6310	6310	917.9595947	2	1833.903539	1831.009112	2.894427773	K	T	-	2	17	3	0
				423	438	15	K	ILLANFLAQTEALMR	G	0.23%	9303	9303	852.48	2	1702.94435	1702.94401	0.00034004	K	G	-	4	15	0	0
P06858	Lipoprotein lipase	1	6.53%	219	250	31	R	SIGIQKPVGHVDIYPNGGTFQPGCNIGEAIR	V	8.81%	2026	2026	824.6697388	4	3294.647655	3293.661065	0.98658999	R	V	C24:+57.021	1	31	1	0
P07237	Protein disulfide-isomerase	6	23.43%	81	97	16	K	VDATEESDLAQQYGVR	G	0.47%	3116	3116	890.9680786	2	1779.920507	1779.827518	0.092988819	K	G	-	3	16	0	0
				132	162	30	R	TGPAATTLPDGAAAESLVESSEVAVIGFFK	D	0.23%	10175	10175	979.4981079	3	2935.470849	2934.486232	0.984617002	R	D	-	5	30	1	0
				170	195	25	K	QFLQAAEAIDDIPFGITSNSDVFSK	Y	0.23%	7894	7894	1358.163696	2	2714.311743	2712.328274	1.983468346	K	Y	-	1	25	2	0
				230	247	17	K	HNQLPLVIEFTEQTAPK	I	0.23%	4968	4968	983.0279541	2	1964.040258	1964.036723	0.003534739	K	I	-	6	17	0	0
				350	366	16	K	IKPHLMSQELPEDWDK	Q	0.23%	2792	2792	655.9923096	3	1964.953454	1964.966596	-0.013142385	K	Q	-	2	16	0	0
				409	424	15	K	LGETYKDHENIVIAK	M	0.23%	1414	1414	433.2326355	4	1728.899242	1729.888646	-0.989404568	K	M	N10:+0.984	4	15	-1	1
P07858	Cathepsin B	1	5.31%	263	281	18	K	SGVYQHVTGEMMGGHAIR	I	0.23%	1991	1991	644.3045654	3	1929.890221	1928.898534	0.991686961	K	I	-	3	18	1	0
P07900	Heat shock protein HSP 90-alpha	7	12.98%	100	112	12	K	ADLINNLGTIAK	S	0.23%	3697	3697	621.8533325	2	1241.691015	1241.697948	-0.006932761	K	S	-	6	12	0	0
				185	201	16	K	VILHLKEDQTEYLEER	R	0.23%	2494	2494	1008.02478	2	2014.03391	2014.037117	-0.003206917	K	R	-	7	16	0	1
				269	283	14	K	KDGDKKKKKKIKEK	Y	3.67%	1166	1166	853.39	2	1704.76435	1701.067236	3.697114376	K	Y	K12:+1.000	1	14	4	8
				314	327	13	K	SLTNDWEDHLAVK	H	0.23%	3116	3116	764.3719482	2	1526.728246	1526.736518	-0.00827182	K	H	-	5	13	0	0
				327	338	11	K	HFSVEGQLEFR	A	1.57%	5451	5451	674.3340454	2	1346.652441	1347.657146	-1.004704756	K	A	-	1	11	-1	0
				386	400	14	R	GVVDSEDLPLNISR	E	0.23%	3955	3955	757.3928223	2	1512.769994	1512.778383	-0.008388653	R	E	-	4	14	0	0
				632	647	15	K	HLEINPDHSIIETLR	Q	0.23%	3198	3198	893.9760742	2	1785.936498	1785.937344	-0.000845186	K	Q	-	6	15	0	0
P07954	Fumarate hydratase, mitochondrial	7	32.16%	131	160	29	K	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	A	2.44%	5849	5849	1091.197388	3	3270.568688	3270.572758	-0.00406969	K	A	Q17:+0.984	2	29	0	0
				183	213	30	K	SQSSNDTFPTAMHIAAAIEVHEVLLPGLQK	L	2.03%	7154	7154	802.4188843	4	3205.644237	3204.612497	1.031739725	K	L	Q29:+0.984	1	30	1	0
				233	256	23	R	THTQDAVPLTLGQEFSGYVQQVK	Y	0.23%	5557	5557	849.430603	3	2545.268334	2546.265264	-0.996930278	R	Y	Q13:+0.984	4	23	-1	0
				296	337	41	K	VAALTGLPFVTAPNKFEALAAHDALVELSGAMNTTACSLMK	I	0.48%	10185	10185	1058.543457	4	4230.142528	4231.136246	-0.993717971	K	I	N14:+0.984,C37:+57.021	4	41	-1	1
				311	337	26	K	FEALAAHDALVELSGAMNTTACSLMK	I	0.61%	8037	8037	918.4489136	3	2752.323266	2750.307295	2.015970843	K	I	C22:+57.021	2	26	2	0
				447	467	20	K	LMNESLMLVTALNPHIGYDK	A	0.23%	6223	6223	753.7195435	3	2258.135155	2258.14391	-0.008754549	K	A	-	2	20	0	0
				483	504	21	K	ETAIELGYLTAEQFDEWVKPK	D	0.23%	8362	8362	823.0803223	3	2466.217492	2467.215854	-0.998362683	K	D	Q13:+0.984	1	21	-1	0
P08134	Rho-related GTP-binding protein RhoC	1	7.77%	104	119	15	K	HFCPNVPIILVGNKK	D	0.23%	2897	2897	579.326355	3	1734.95559	1734.959865	-0.004275027	K	D	C3:+57.021	2	15	0	1
P08195	4F2 cell-surface antigen heavy chain	8	20.95%	122	145	23	K	QPMNAASGAAMSLAGAEKNGLVK	I	2.76%	8083	8083	740.56	3	2218.656525	2217.076921	1.579603616	K	I	N4:+0.984,N19:+0.984	1	23	2	1
				226	245	19	R	IGDLQAFQGHGAGNLAGLK	G	0.23%	3415	3415	933.9943848	2	1865.973119	1865.974792	-0.001672269	R	G	-	6	19	0	0
				245	255	10	K	GRLDYLSSLK	V	0.70%	2267	2267	576.321106	2	1150.626562	1150.634619	-0.008057238	K	V	-	4	10	0	1
				439	451	12	R	LLTSFLPAQLLR	L	0.23%	6824	6824	686.4196167	2	1370.823583	1370.828568	-0.00498473	R	L	-	7	12	0	0
				510	524	14	K	GQSEDPGSLLSLFR	R	0.23%	6586	6586	753.3806152	2	1504.74558	1504.752168	-0.006587915	K	R	-	7	14	0	0
				534	555	21	R	SLLHGDFHAFSAGPGLFSYIR	H	0.23%	6201	6201	574.2902222	4	2293.129589	2291.148734	1.980854928	R	H	-	2	21	2	0
				592	613	21	K	ADLLLSTQPGREEGSPLELER	L	0.23%	4082	4082	1155.596313	2	2309.176977	2309.186301	-0.009324231	K	L	-	4	21	0	1
				613	625	12	R	LKLEPHEGLLLR	F	0.23%	2322	2322	709.9259644	2	1417.836279	1416.845281	0.990997847	R	F	-	6	12	1	1
P08237	6-phosphofructokinase, muscle type	6	14.62%	184	201	17	R	IMEIVDAITTTAQSHQR	T	0.23%	4433	4433	958.4902954	2	1914.964941	1912.967659	1.997282108	R	T	-	6	17	2	0
				315	345	30	R	MGVEAVMALLEGTPDTPACVVSLSGNQAVR	L	6.10%	8596	8596	1025.519043	3	3073.533654	3071.508514	2.025139706	R	L	C19:+57.021	1	30	2	0
				397	420	23	K	SGSHTVAVMNVGAPAAGMNAAVR	S	2.59%	2456	2456	723.3535767	3	2167.037255	2167.06264	-0.02538482	K	S	-	1	23	0	0
				603	615	12	R	DLQANVEHLVQK	M	0.28%	3126	3126	697.3668823	2	1392.718115	1392.736124	-0.018009656	R	M	-	4	12	0	0
				656	673	17	K	NVLGHMQQGGSPTPFDR	N	0.23%	2127	2127	921.4386597	2	1840.861669	1839.868613	0.993056136	K	N	-	4	17	1	0
				699	714	15	R	IFANTPDSGCVLGMR	K	0.23%	3649	3649	551.3085938	3	1650.902306	1652.764682	-1.862375702	R	K	C10:+57.021,M14:+15.99	1	15	-1	0
P08574	Cytochrome c1, heme protein, mitochondrial	7	49.23%	84	99	15	A	SDLELHPPSYPWSHR	G	6.52%	3177	3177	911.4404297	2	1820.865209	1819.864179	1.001030791	A	G	-	1	15	1	0
				99	111	12	R	GLLSSLDHTSIR	R	0.67%	2844	2844	433.5717468	3	1297.691765	1297.69901	-0.007245017	R	R	-	1	12	0	0
				133	170	37	R	HLVGVCYTEDEAKELAAEVEVQDGPNEDGEMFMRPGK	L	0.69%	5717	5717	1038.715698	4	4150.831493	4150.844084	-0.012590719	R	L	C6:+57.021,Q22:+0.984,N	2	37	0	1
				170	186	16	K	LFDYFPKPYPNSEAAR	A	0.23%	3887	3887	958.4682007	2	1914.920751	1913.931196	0.989555759	K	A	-	5	16	1	0
				186	202	16	R	AANNGALPPDLSYIVR	A	2.05%	4960	4960	836.9422607	2	1671.868871	1670.862766	1.006105476	R	A	N4:+0.984	2	16	1	0
				204	228	24	R	HGGEDYVFSLLTGYCEPPTGVSLR	E	0.23%	6889	6889	885.4173584	3	2653.2286	2653.247787	-0.019186837	R	E	C15:+57.021	7	24	0	0
				228	268	40	R	EGLYFNPYFPGQAIAMAPPIYTDVLEFDDGTPATMSQIAK	D	1.27%	9820	9820	1096.026611	4	4380.075145	4378.0854	1.989745041	R	D	-	2	40	2	0
P08758	Annexin A5	1	3.44%	260	271	11	K	GAGTDDHTLIR	V	6.75%	3251	3251	578.288269	2	1154.560888	1154.567996	-0.007108042	K	V	-	1	11	0	0
P08865	40S ribosomal protein SA	3	20.00%	63	80	17	R	AIVAIENPADVSVISSR	N	0.23%	4245	4245	870.9767456	2	1739.937841	1739.94176	-0.003919117	R	N	-	5	17	0	0
				102	117	15	R	FTPGTFTNQIQAAFR	E	1.04%	5644	5644	849.4081421	2	1696.800634	1697.852551	-1.051917028	R	E	-	4	15	-1	0
				128	155	27	R	ADHQPLTEASYVNLPTIALCNTDSPLR	Y	0.23%	5736	5736	1000.171936	3	2997.492333	2995.47047	2.021862985	R	Y	C20:+57.021	2	27	2	0
P08F94	Fibrocystin	1	0.29%	2149	2161	12	R	EKLLVSCQEANA	P	3.32%	2798	2798	682.3278809	2	1362.640112	1362.633199	0.006912919	R	P	C7:+57.021,Q8:+0.984,N1	1	12	0	1
P09429	High mobility group protein B1	1	7.44%	96	112	16	K	RPPSAFFLFCSEYRPK	I	0.23%	4162	4162	667.9985962	3	2000.972313	2000.992622	-0.02030821	K	I	C10:+57.021	5	16	0	0
P09601	Heme oxygenase 1	1	8.33%	153	177	24	K	ALDLPSSGEGLAFFTFPNIASATK	F	1.27%	8233	8233	1228.634277	2	2455.252905	2453.247839	2.00506584	K	F	-	3	24	2	0
P09603	Macrophage colony-stimulating factor 1	1	2.17%	136	148	12	R	TFYETPLQLLEK	V	7.24%	3232	3232	494.934021	3	1481.778588	1480.781343	0.997244716	R	V	-	1	12	1	0
P0CG47	Polyubiquitin-B	2	50.94%	11	27	16	K	TITLEVEPSDTIENVK	A	0.23%	3897	3897	894.4616089	2	1786.907568	1786.920022	-0.012454131	K	A	-	4	16	0	0
				63	72	9	K	ESTLHLVLR	L	0.23%	1972	1972	534.3114624	2	1066.607275	1066.61349	-0.006214907	K	L	-	7	9	0	0
P11142	Heat shock cognate 71 kDa protein	19	39.32%	3	25	22	K	GPAVGIDLGTTYSCVGVFQHGK	V	0.23%	4522	4522	1132.056274	2	2262.096899	2262.109837	-0.01293782	K	V	C14:+57.021	6	22	0	0
				36	49	13	R	TTPSYVAFTDTER	L	0.23%	2480	2480	744.3519897	2	1486.688329	1486.693985	-0.005655276	R	L	-	7	13	0	0
				56	71	15	K	NQVAMNPTNTVFDAK	R	0.23%	2582	2582	825.3974609	2	1648.779272	1648.787903	-0.008631285	K	R	-	7	15	0	0
				76	88	12	R	RFDDAVVQSDMK	H	0.23%	1453	1453	705.8343506	2	1409.653051	1409.660911	-0.007860364	R	H	-	6	12	0	1
				88	102	14	K	HWPFMVVNDAGRPK	V	0.23%	2892	2892	551.9450073	3	1652.811547	1652.824563	-0.013016403	K	V	-	3	14	0	0
				112	126	14	K	SFYPEEVSSMVLTK	M	0.23%	5096	5096	808.8970947	2	1615.778539	1615.780358	-0.001818707	K	M	-	7	14	0	0
				128	137	9	K	EIAEAYLGK	T	0.36%	1598	1598	497.265686	2	992.515722	992.5178578	-0.00213585	K	T	-	5	9	0	0
				137	155	18	K	TVTNAVVTVPAYFNDSQR	Q	0.23%	4200	4200	994.01	2	1986.00435	1982.958501	3.045848448	K	Q	N4:+0.984,Q17:+0.984	1	18	3	0
				170	187	17	L	RIINEPTAAAIAYGLDK	K	2.22%	3574	3574	909.0011597	2	1815.986669	1814.989045	0.99762444	L	K	-	1	17	1	1
				171	187	16	R	IINEPTAAAIAYGLDK	K	0.23%	4617	4617	830.9378052	2	1659.85996	1658.887934	0.972026608	R	K	-	4	16	1	0
				171	188	17	R	IINEPTAAAIAYGLDKK	V	0.23%	3448	3448	895.4403076	2	1788.864965	1786.982897	1.882068354	R	V	-	4	17	2	1
				220	236	16	K	STAGDTHLGGEDFDNR	M	0.23%	1244	1244	846.3626709	2	1690.709692	1690.718302	-0.008610379	K	M	-	6	16	0	0
				236	246	10	R	MVNHFIAEFK	R	0.23%	2700	2700	412.8953552	3	1235.662591	1234.616862	1.045728962	R	R	-	2	10	1	0
				299	311	12	R	ARFEELNADLFR	G	0.23%	3968	3968	740.8769531	2	1479.738256	1479.747023	-0.008767102	R	G	-	5	12	0	1
				328	342	14	K	SQIHDIVLVGGSTR	I	0.23%	1885	1885	741.4036865	2	1480.791723	1480.799787	-0.008064233	K	I	-	7	14	0	0
				361	384	23	K	SINPDEAVAYGAAVQAAILSGDK	S	0.23%	7238	7238	1130.574585	2	2259.13352	2259.138288	-0.004768366	K	S	-	5	23	0	0
				539	550	11	K	NSLESYAFNMK	A	0.23%	3542	3542	652.2980957	2	1302.580541	1302.591435	-0.010893466	K	A	-	6	11	0	0
				573	583	10	K	CNEIINWLDK	N	0.23%	4927	4927	652.8181152	2	1303.62058	1303.622606	-0.002025123	K	N	C1:+57.021	6	10	0	0
				609	632	23	K	LYQSAGGMPGGMPGGFPGGGAPP	S	2.86%	1710	1710	524.0194092	4	2092.046337	2090.917166	1.129170847	K	S	M8:+15.994,M12:+15.994	1	23	1	0
P11166	Solute carrier family 2, facilitated glucose transporter member 1	1	3.46%	232	249	17	R	GTADVTHDLQEMKEESR	Q	0.23%	1964	1964	649.3001099	3	1944.876854	1944.884717	-0.007862402	R	Q	-	5	17	0	1
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	2	8.91%	129	145	16	K	TYYMSGGLQPVPIVFR	G	0.36%	5706	5706	914.980896	2	1827.946142	1826.938925	1.007217392	K	G	-	5	16	1	0
				269	285	16	R	TIRPMDMETIEASVMK	T	0.23%	4828	4828	926.4453125	2	1850.874975	1850.894027	-0.01905192	R	T	-	4	16	0	0
P11277	Spectrin beta chain, erythrocyte	1	0.51%	1458	1469	11	K	RFLDLLEPLGR	R	4.90%	1349	1349	664.8586426	2	1327.701635	1327.761217	-0.05958162	K	R	-	2	11	0	1
P11413	Glucose-6-phosphate 1-dehydrogenase	1	6.02%	257	288	31	R	DVMQNHLLQMLCLVAMEKPASTNSDDVRDEK	V	6.06%	8828	8828	1197.887207	3	3590.638146	3589.640347	0.997798758	R	V	Q4:+0.984,N5:+0.984,Q9:	1	31	1	1
P11717	Cation-independent mannose-6-phosphate receptor	1	0.52%	1052	1065	13	K	FLHQDIDSGQGIR	N	1.62%	1428	1428	496.2505188	3	1485.728081	1485.721187	0.006894396	K	N	Q4:+0.984	2	13	0	0
P12259	Coagulation factor V	1	0.63%	513	527	14	R	DIASGLIGLLLICK	S	0.23%	9852	9852	744.4378052	2	1486.85996	1484.86317	1.996789872	R	S	C13:+57.021	5	14	2	0
P13473	Lysosome-associated membrane glycoprotein 2	1	1.95%	144	152	8	R	IPLNDLFR	C	0.46%	4425	4425	495.2895203	2	988.5633904	986.554912	2.008478431	R	C	-	3	8	2	0
P13498	Cytochrome b-245 light chain	1	15.90%	164	195	31	R	KKPSEEEAAVAAGGPPGGPQVNPIPVTDEVV	-	0.48%	3945	3945	1014.190918	3	3039.549279	3039.540043	0.009236186	R	-	N22:+0.984	3	31	0	1
P13591	Neural cell adhesion molecule 1	1	1.28%	37	48	11	K	FFLCQVAGDAK	D	1.19%	3395	3395	629.364502	2	1256.713354	1254.606227	2.107126722	K	D	C4:+57.021	3	11	2	0
P13796	Plastin-2	1	3.99%	545	570	25	K	ISTSLPVLDLIDAIQPGSINYDLLK	T	0.23%	10301	10301	1350.747192	2	2699.478735	2697.484047	1.994688062	K	T	-	5	25	2	0
P13866	Sodium/glucose cotransporter 1	1	3.01%	479	499	20	R	VNEPGAFWGLILGLLIGISR	M	8.04%	4337	4337	532.27	4	2125.0487	2124.209543	0.83915692	R	M	-	2	20	1	0
P13987	CD59 glycoprotein	2	18.75%	66	78	12	K	FEHCNFNDVTTR	L	0.23%	1344	1344	770.33	2	1538.64435	1538.656759	-0.012409392	K	L	C4:+57.021	6	12	0	0
				78	90	12	R	LRENELTYYCCK	K	0.23%	1537	1537	825.37323	2	1648.73081	1647.737584	0.993226305	R	K	C10:+57.021,C11:+57.021	4	12	1	1
P14174	Macrophage migration inhibitory factor	5	85.22%	1	12	11	M	PMFIVNTNVPR	A	0.48%	3308	3308	644.34	2	1286.66435	1286.680525	-0.016174648	M	A	-	3	11	0	0
				12	67	55	R	ASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSLHSIGK	I	1.08%	9220	9220	1453.476563	4	5809.87495	5808.846803	1.028146792	R	I	Q24:+0.984,Q34:+0.984,C	2	55	1	0
				78	87	9	K	LLCGLLAER	L	0.23%	3564	3564	523.7999878	2	1045.584326	1043.579284	2.00504153	K	L	C3:+57.021	3	9	2	0
				78	89	11	K	LLCGLLAERLR	I	3.01%	1689	1689	438.5575867	3	1312.649285	1312.764459	-0.115174326	K	I	C3:+57.021	1	11	0	1
				94	115	21	R	VYINYYDMNAANVGWNNSTFA	-	2.99%	5885	5885	611.7923584	4	2443.138133	2443.041744	0.096389338	R	-	N4:+0.984,M8:+15.994	1	21	0	0
P14373	Zinc finger protein RFP	1	3.31%	353	370	17	R	FNLFPCVLGSPCFIAGR	H	1.16%	7475	7475	978.4989624	2	1954.982275	1953.958416	1.023858717	R	H	C6:+57.021,C12:+57.021	3	17	1	0
P14550	Alcohol dehydrogenase [NADP+]	1	6.77%	218	240	22	R	AWRDPDEPVLLEEPVVLALAEK	Y	0.48%	7177	7177	830.4495239	3	2488.325097	2488.321338	0.003758521	R	Y	-	2	22	0	1
P14618	Pyruvate kinase isozymes M1/M2	28	61.77%	32	43	11	R	LDIDSPPITAR	N	0.23%	2649	2649	600.3510132	2	1198.686376	1196.640098	2.046277855	R	N	-	3	11	2	0
				43	56	13	R	NTGIICTIGPASR	S	0.23%	2006	2006	680.3520508	2	1358.688451	1358.697168	-0.008716053	R	S	C6:+57.021	7	13	0	0
				73	89	16	R	LNFSHGTHEYHAETIK	N	0.23%	1228	1228	628.9710083	3	1883.88955	1883.880207	0.00934279	R	N	N2:+0.984	2	16	0	0
				92	115	23	R	TATESFASDPILYRPVAVALDTK	G	0.23%	5599	5599	822.4331055	3	2464.275841	2464.284953	-0.00911133	R	G	-	5	23	0	0
				125	135	10	K	GSGTAEVELK	K	0.48%	1013	1013	495.757019	2	989.498388	989.5029361	-0.004548082	K	K	-	6	10	0	0
				125	136	11	K	GSGTAEVELKK	G	4.84%	832	832	560.63	2	1119.24435	1117.597899	1.646450696	K	G	-	4	11	2	1
				151	162	11	K	CDENILWLDYK	N	0.23%	5233	5233	734.8339844	2	1467.652319	1467.66995	-0.017631082	K	N	C1:+57.021	4	11	0	0
				173	186	13	K	IYVDDGLISLQVK	Q	0.23%	5151	5151	732.3994751	2	1462.7833	1461.807892	0.975407835	K	Q	-	5	13	1	0
				188	206	18	K	GADFLVTEVENGGSLGSK	K	0.23%	5144	5144	891.4342651	2	1780.85288	1779.852655	1.000225313	K	K	N11:+0.984	7	18	1	0
				188	207	19	K	GADFLVTEVENGGSLGSKK	G	2.81%	3375	3375	636.9971924	3	1907.968102	1907.947618	0.020484012	K	G	N11:+0.984	2	19	0	1
				206	224	18	K	KGVNLPGAAVDLPAVSEK	D	0.23%	3268	3268	588.9970703	3	1763.967736	1763.978146	-0.01040995	K	D	-	5	18	0	1
				206	230	24	K	KGVNLPGAAVDLPAVSEKDIQDLK	F	0.74%	4634	4634	826.7896729	3	2477.345543	2476.353701	0.991842483	K	F	-	1	24	1	2
				207	224	17	K	GVNLPGAAVDLPAVSEK	D	0.23%	4168	4168	818.9477539	2	1635.879858	1635.883183	-0.003324899	K	D	-	6	17	0	0
				230	246	16	K	FGVEQDVDMVFASFIR	K	0.23%	9873	9873	930.9490356	2	1859.882421	1858.892368	0.990052929	K	K	-	7	16	1	0
				278	294	16	R	RFDEILEASDGIMVAR	G	0.23%	6321	6321	911.4020386	2	1820.788427	1820.909081	-0.120653948	R	G	-	3	16	0	1
				294	305	11	R	GDLGIEIPAEK	V	0.23%	2913	2913	571.3059082	2	1140.596166	1140.60265	-0.00648393	R	V	-	6	11	0	0
				319	336	17	R	AGKPVICATQMLESMIK	K	0.23%	5937	5937	626.3245239	3	1875.950097	1876.945583	-0.995486423	R	K	C7:+57.021,Q10:+0.984	7	17	-1	0
				322	336	14	K	PVICATQMLESMIK	K	0.94%	6703	6703	811.4147949	2	1620.81394	1619.808042	1.005897436	K	K	C4:+57.021	2	14	1	0
				342	367	25	R	AEGSDVANAVLDGADCIMLSGETAK	G	0.23%	6987	6987	1247.569336	2	2493.123022	2494.119854	-0.996832501	R	G	N8:+0.984,C16:+57.021	4	25	-1	0
				342	376	34	R	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	M	0.23%	7350	7350	875.1629639	4	3496.620555	3493.63365	2.986905237	R	M	C16:+57.021	1	34	3	1
				367	376	9	K	GDYPLEAVR	M	0.23%	1798	1798	510.2575073	2	1018.499365	1018.508356	-0.008991208	K	M	-	1	9	0	0
				383	400	17	R	EAEAAIYHLQLFEELRR	L	0.28%	5061	5061	696.6983032	3	2087.071435	2087.079985	-0.0085507	R	L	-	1	17	0	1
				400	422	22	R	LAPITSDPTEATAVGAVEASFK	C	0.23%	6557	6557	1088.560303	2	2175.104955	2174.110676	0.994278965	R	C	-	7	22	1	0
				422	433	11	K	CCSGAIIVLTK	S	0.23%	2194	2194	611.32	2	1220.62435	1220.624785	-0.000435456	K	S	C1:+57.021,C2:+57.021	1	11	0	0
				467	475	8	R	GIFPVLCK	D	0.23%	3733	3733	467.2639771	2	932.512304	932.5148927	-0.00258865	R	D	C7:+57.021	1	8	0	0
				467	489	22	R	GIFPVLCKDPVQEAWAEDVDLR	V	0.23%	6628	6628	853.09375	3	2556.257775	2557.251794	-0.994019144	R	V	C7:+57.021,Q12:+0.984	5	22	-1	1
				475	489	14	K	DPVQEAWAEDVDLR	V	0.23%	5059	5059	821.8842163	2	1641.752783	1641.763461	-0.010678815	K	V	-	7	14	0	0
				504	526	22	K	KGDVVIVLTGWRPGSGFTNTMR	V	0.23%	4865	4865	1196.130493	2	2390.245336	2390.252882	-0.00754612	K	V	-	2	22	0	1
P14625	Endoplasmin	6	9.84%	102	114	12	R	ELISNASDALDK	I	0.23%	1974	1974	638.3184204	2	1274.621191	1274.635407	-0.014216332	R	I	-	6	12	0	0
				142	156	14	K	NLLHVTDTGVGMTR	E	0.23%	2243	2243	757.3970337	2	1512.778417	1512.771859	0.006558303	K	E	-	7	14	0	0
				142	161	19	K	NLLHVTDTGVGMTREELVK	N	0.23%	3170	3170	705.0404663	3	2112.097924	2111.104487	0.993437158	K	N	-	5	19	1	1
				270	285	15	K	YSQFINFPIYVWSSK	T	1.27%	7515	7515	940.4262695	2	1878.836889	1878.919218	-0.082329249	K	T	N6:+0.984	1	15	0	0
				414	428	14	R	RVFITDDFHDMMPK	Y	0.23%	3982	3982	585.3078613	3	1752.900109	1750.817096	2.083013024	R	Y	-	3	14	2	1
				511	530	19	R	FQSSHHPTDITSLDQYVER	M	0.23%	2868	2868	754.0217285	3	2259.04171	2259.055621	-0.013910677	R	M	-	3	19	0	0
P14778	Interleukin-1 receptor type 1	1	1.23%	535	542	7	R	YHMPVQR	R	2.14%	4439	4439	474.2486572	2	946.4816644	945.4491531	1.032511269	R	R	M3:+15.995	4	7	1	0
P14868	Aspartyl-tRNA synthetase, cytoplasmic	2	5.99%	126	141	15	K	IGSCTQQDVELHVQK	I	0.23%	1298	1298	581.2866211	3	1740.836388	1740.846017	-0.009628767	K	I	C4:+57.021	2	15	0	0
				460	475	15	R	FGAPPHAGGGIGLER	V	0.23%	1608	1608	479.2506714	3	1434.728539	1434.736793	-0.00825384	R	V	-	6	15	0	0
P15153	Ras-related C3 botulinum toxin substrate 2	2	13.02%	132	147	15	K	KLAPITYPQGLALAK	E	0.23%	3325	3325	792.4758301	2	1582.93601	1582.944661	-0.008650548	K	E	-	5	15	0	1

				153	163	10	K	YLECSALTQR	G	0.52%	1482	1482	620.7967529	2	1239.577856	1239.591305	-0.013449573	K	G	C4:+57.021	3	10	0	0
P15498	Proto-oncogene vav	1	2.37%	38	58	20	R	DGVLLCQLLNNLLPHAINLR	E	0.23%	10365	10365	763.7338867	3	2288.178185	2286.25134	1.926844684	R	E	C6:+57.021,Q7:+0.984	4	20	2	0
P15924	Desmoplakin	20	10.76%	44	64	20	R	RGVITDQNSDGYCQTGTMSR	H	1.20%	1202	1202	749.3372803	3	2244.988366	2245.968714	-0.980347812	R	H	C13:+57.021,Q14:+0.984	5	20	-1	1
				45	64	19	R	GVITDQNSDGYCQTGTMSR	H	2.86%	2566	2566	524.02	4	2092.0487	2090.851602	1.19709748	R	H	N7:+0.984,C12:+57.021,Q	1	19	1	0
				103	126	23	R	SRELDECFAQANDQMEILDSLIR	E	0.23%	7204	7204	918.7630615	3	2753.265709	2752.279165	0.986544794	R	E	C7:+57.021	4	23	1	1
				126	140	14	R	EMRQMGQPCDAYQK	R	2.49%	14570	14570	872.409668	2	1742.803686	1741.721731	1.08195493	R	R	Q4:+0.984,C9:+57.021	1	14	1	1
				129	140	11	R	QMGQPCDAYQK	R	3.09%	750	750	450.1594543	3	1347.454888	1342.516541	4.938347157	R	R	Q1:+0.984,M2:+15.995,Q4	1	11	5	0
				245	260	15	K	SAIYQLEEEYENLLK	A	0.23%	7464	7464	922.472229	2	1842.928808	1840.909457	2.019350824	K	A	-	3	15	2	0
				407	419	12	K	NMPLQHLLEQIK	E	2.86%	5083	5083	732.3973999	2	1462.77915	1463.780617	-1.001467419	K	E	N1:+0.984	1	12	-1	0
				738	752	14	K	YCYLQNEVFGLFQK	L	3.04%	6927	6927	905.4811401	2	1808.94663	1807.859876	1.086754169	K	L	C2:+57.021	2	14	1	0
				771	785	14	R	ALLQAILQTEDMLK	V	0.23%	7774	7774	793.9398193	2	1585.863989	1585.874927	-0.010938624	R	V	-	6	14	0	0
				1173	1184	11	R	LRVLLQEEGTR	K	2.75%	642	642	439.2544861	3	1314.739983	1313.730295	1.009688188	R	K	Q6:+0.984	1	11	1	1
				1611	1626	15	K	ITNLTQQLEQASIVK	K	0.23%	4347	4347	843.4696045	2	1684.923559	1684.935947	-0.012387656	K	K	-	6	15	0	0
				1802	1818	16	K	NQCTQVVQERESLLVK	I	2.83%	3397	3397	643.9909058	3	1928.949242	1931.961744	-3.012501827	K	I	C3:+57.021,Q5:+0.984,Q	1	16	-1	1
				2038	2066	28	K	LISPESTVMLLEAQAATGGIIDPHRNEK	L	0.23%	6803	6803	748.89	4	2991.5287	2990.53827	0.990430312	K	L	N26:+0.984	3	28	1	1
				2279	2309	30	K	IGLVRPGTALELLEAQAATGFIVDPVSNLR	L	0.23%	8974	8974	1041.254639	3	3120.740441	3120.718282	0.022159072	K	L	Q16:+0.984	3	30	0	0
				2334	2356	22	R	AVTGYNDPETGNIISLFQAMNK	E	0.23%	7408	7408	1192.082153	2	2382.148657	2382.152559	-0.003902655	R	E	-	6	22	0	0
				2381	2393	12	K	ESHRLPVDIAYK	R	1.59%	1648	1648	476.931488	3	1427.770989	1426.75686	1.014129327	K	R	-	1	12	1	1
				2548	2564	16	R	SGSLSLTQFADMISLK	N	1.62%	7334	7334	849.440979	2	1696.866308	1696.87057	-0.004262256	R	N	-	4	16	0	0
				2630	2639	9	K	ISITEGIER	G	0.74%	1849	1849	510.2597046	2	1018.503759	1016.550221	1.953538444	K	G	-	4	9	2	0
				2649	2668	19	R	LLEAQACTGGIIHPTTGQK	L	0.28%	1859	1859	665.6791992	3	1994.014123	1994.025044	-0.010921616	R	L	C7:+57.021	2	19	0	0
				2725	2744	19	R	FLEFQYLTGGLVDPEVHGR	I	0.23%	6408	6408	726.3710327	3	2176.089623	2176.095301	-0.005677975	R	I	-	3	19	0	0
P16188	HLA class I histocompatibility antigen, A-30 alpha chain	6	26.58%	72	89	17	R	APWIEQERPEYWDQETR	N	0.36%	3684	3684	1117.014526	2	2232.013403	2232.023593	-0.010189962	R	N	-	3	17	0	0
				155	169	14	R	SWTAADMAAQITQR	K	0.23%	4483	4483	775.8775635	2	1549.739477	1548.735473	1.004003393	R	K	-	4	14	1	0
				181	193	12	R	AYLEGTCVEWLR	R	0.23%	4716	4716	748.8579102	2	1495.70017	1495.712483	-0.012313055	R	R	C7:+57.021	6	12	0	0
				243	267	24	R	DGEDQTQDTELVETRPAGDGTFQK	W	0.23%	2135	2135	1320.095581	2	2638.175512	2636.183795	1.991717301	R	W	-	2	24	2	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.23%	2358	2358	714.3626709	2	1426.709692	1426.720474	-0.010782427	K	Y	-	4	13	0	0
				280	297	17	R	YTCHVQHEGLPKPLTLR	W	0.23%	1682	1682	683.6915283	3	2048.05111	2049.046098	-0.994988487	R	W	C3:+57.021,Q6:+0.984	1	17	-1	0
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	7	10.94%	7	31	24	K	TVEEVLGHFGVNESTGLSLEQVKK	L	0.23%	4973	4973	867.7893066	3	2600.344445	2600.333344	0.011100882	K	L	N12:+0.984	4	24	0	1
				174	189	15	R	VDQSILTGESVSVIK	H	0.40%	3757	3757	788.4289551	2	1574.84226	1573.856299	0.9859609	R	H	-	5	15	1	0
				334	352	18	R	SLPSVETLGCTSVICSDK	T	0.23%	4085	4085	977.4741821	2	1952.932714	1951.92215	1.010564346	R	T	C10:+57.021,C15:+57.021	7	18	1	0
				436	451	15	K	VGEATETALTCLVEK	M	0.23%	3978	3978	810.90979	2	1619.80393	1619.807172	-0.00324177	K	M	C11:+57.021	7	15	0	0
				572	585	13	R	EEMHLEDSANFIK	Y	9.56%	2785	2785	781.8571777	2	1561.698705	1561.708256	-0.009550307	R	Y	-	1	13	0	0
				711	727	16	K	KAEIGIAMGSGTAVAK	T	0.23%	1535	1535	501.9421082	3	1502.802849	1502.812661	-0.009811881	K	T	-	3	16	0	1
				863	876	13	R	VSFYQLSHFLQCK	E	0.70%	5456	5456	552.9418945	3	1655.802208	1655.812532	-0.01032331	R	E	C12:+57.021	1	13	0	0
P17987	T-complex protein 1 subunit alpha	8	28.78%	0	18	18	-	MEGPLSVFGDRSTGETIR	S	2.18%	6765	6765	651.7224121	3	1952.143761	1950.946923	1.196838016	-	S	-	1	18	1	1
				18	33	15	R	SQNVMAAASIANIVK	S	0.23%	4227	4227	758.9141235	2	1515.812597	1515.80791	0.004686798	R	S	-	6	15	0	0
				84	102	18	K	EVGDGTTSVVIIAAELLK	N	0.37%	8609	8609	908.01	2	1814.00435	1814.003692	0.000658008	K	N	-	5	18	0	0
				321	355	34	K	ASGATILSTLANLEGEETFEAAMLGQAEEVVQER	I	0.28%	10245	10245	1190.557495	3	3568.64901	3566.682122	1.966888512	K	I	N12:+0.984,Q26:+0.984,C	3	34	2	0
				406	433	27	K	SVVPGGGAVEAALSIYLENYATSMGSR	E	0.95%	9240	9240	901.4460449	3	2701.31466	2699.311229	2.003430238	K	E	N19:+0.984	2	27	2	0
				433	443	10	R	EQLAIAEFAR	S	0.84%	3527	3527	574.3076782	2	1146.599706	1146.603319	-0.003612547	R	S	-	1	10	0	0
				443	466	23	R	SLLVIPNTLAVNAAQDSTDLVAK	L	0.54%	6601	6601	785.1	3	2352.276525	2352.290038	-0.013513096	R	L	-	1	23	0	0
				541	556	15	K	HGSYEDAVHSGALND	-	1.06%	1223	1223	786.3371582	2	1570.658666	1570.66481	-0.006143514	K	-	-	4	15	0	0
P18084	Integrin beta-5	1	1.13%	176	185	9	R	LGFGSFVDK	D	0.23%	3281	3281	485.2533569	2	968.4910638	968.4967284	-0.005664613	R	D	-	3	9	0	0
P18463	HLA class I histocompatibility antigen, B-37 alpha chain	8	30.39%	45	59	14	R	FISVGYVDDTQFVR	F	0.23%	4784	4784	823.4142456	2	1644.812841	1644.814769	-0.001927493	R	F	-	7	14	0	0
				72	86	14	R	APWIEQEGPEYWDR	E	0.23%	4687	4687	888.3942871	2	1774.772924	1774.795096	-0.022171701	R	N	-	5	14	0	0
				72	92	20	R	APWIEQEGPEYWDRETQISK	T	0.46%	4421	4421	822.0592651	3	2463.15432	2462.139001	1.015319346	R	T	Q6:+0.984	2	20	1	1
				155	169	14	S	SWTAADTAAQITQR	K	0.28%	2769	2769	760.9244385	2	1519.833227	1518.742666	1.090560633	R	K	-	4	14	1	0
				181	193	12	R	AYLEGTCVEWLR	R	0.23%	4716	4716	748.8579102	2	1495.70017	1495.712483	-0.012313055	R	R	C7:+57.021	6	12	0	0
				243	263	20	R	DGEDQTQDTELVETRPAGDR	T	0.37%	1286	1286	744.6651611	3	2230.972008	2230.993809	-0.021800506	R	T	-	2	20	0	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.23%	2358	2358	714.3626709	2	1426.709692	1426.720474	-0.010782427	K	Y	-	4	13	0	0
				280	297	17	R	YTCHVQHEGLPKPLTLR	W	0.23%	1682	1682	683.6915283	3	2048.05111	2049.046098	-0.994988487	R	W	C3:+57.021,Q6:+0.984	1	17	-1	0
P18827	Syndecan-1	1	6.45%	230	250	20	R	NQSPVDQGATGASQGLLDRK	E	0.99%	10766	10766	681.0321045	3	2040.072838	2042.986842	-2.914003227	R	E	N1:+0.984,Q14:+0.984	1	20	-1	1
P20936	Ras GTPase-activating protein 1	1	1.43%	267	282	15	K	LLYPVAPPEPVEDRR	R	6.00%	3484	3484	584.3178711	3	1749.930138	1749.941366	-0.011228087	K	R	-	1	15	0	1
P20963	T-cell surface glycoprotein CD3 zeta chain	1	15.85%	4	30	26	K	ALFTAAILQAQLPITEAQSFGLLDPK	L	5.38%	7937	7937	920.4805298	3	2758.418114	2757.484015	0.934098795	K	L	Q11:+0.984,Q18:+0.984	2	26	1	0
P21333	Filamin-A	1	0.60%	1071	1087	16	K	AFGPGLQGGSAGSPAR	F	1.47%	2177	2177	478.8911438	3	1433.649956	1429.694972	3.954984196	K	F	Q7:+0.984	2	16	4	0
P21796	Voltage-dependent anion-selective channel protein 1	12	55.48%	20	28	8	K	GYGFGLIK	L	0.48%	3272	3272	427.7400818	2	853.4645135	853.4697853	-0.005271778	K	L	-	1	8	0	0
				32	53	21	K	TKSENGLEFTSSGSANTETTK	V	0.23%	1272	1272	730.3405762	3	2187.998253	2188.013147	-0.014893844	K	V	-	2	21	0	1
				63	74	11	R	WTEYGLTFTEK	W	0.23%	4206	4206	687.8288574	2	1373.642065	1373.650329	-0.00826406	R	W	-	6	11	0	0
				74	93	19	K	WNTDNTLGTEITVEDQLAR	G	0.23%	5296	5296	1089.029053	2	2176.042455	2175.044388	0.998067661	K	G	-	4	19	1	0
				96	109	13	K	LTFDSSFSPNTGK	K	0.23%	2874	2874	700.8379517	2	1399.660253	1399.661956	-0.00170296	K	K	-	3	13	0	0
				96	110	14	K	LTFDSSFSPNTGKK	N	0.23%	1986	1986	510.2564087	3	1527.745751	1527.756919	-0.011168382	K	N	-	3	14	0	1
				139	163	24	R	GALVLGYEGWLAGYQMNFETAKSR	V	2.67%	18760	18760	893.409729	3	2677.205712	2677.283706	-0.077994076	R	V	Q15:+0.984,M16:+15.994	1	24	0	1
				200	218	18	K	KLETAVNLAWTAGNSNTR	F	0.23%	2994	2994	973.508667	2	1945.001684	1945.001735	-5.09436E-05	K	F	-	4	18	0	1
				224	236	12	K	YQIDPDACFSAK	V	0.23%	2668	2668	707.8164673	2	1413.617284	1413.623	-0.005715022	K	V	C8:+57.021	5	12	0	0
				236	252	16	K	VNNSSLIGLGYTQTLK	P	2.83%	5437	5437	853.7472534	2	1705.478857	1707.904296	-2.425439724	K	P	N3:+0.984	1	16	-1	0
				236	256	20	K	VNNSSLIGLGYTQTLKPGIK	L	0.23%	4128	4128	702.0611572	3	2103.159997	2103.157551	0.00244516	K	L	Q13:+0.984	2	20	0	0
				256	266	10	K	LTLSALLDGK	N	0.23%	17556	17556	515.390564	2	1028.765478	1029.607007	-0.841529438	K	N	-	2	10	-1	0
P21926	CD9 antigen	1	10.96%	144	169	25	K	AIHYALNCCGLAGGVEQFISDICPK	K	0.23%	9458	9458	933.4434204	3	2797.306786	2793.291036	4.01575023	K	K	C8:+57.021,C9:+57.021,Q	1	25	4	0
P22460	Potassium voltage-gated channel subfamily A member 5	1	2.12%	201	214	13	R	FYQLGDEAMERFR	E	3.72%	3842	3842	840.9713745	2	1679.927099	1677.745774	2.181325303	R	E	Q3:+0.984,M9:+15.995	2	13	2	1
P22607	Fibroblast growth factor receptor 3	1	1.36%	485	496	11	Q	VVMAEAIGIDK	D	1.57%	954	954	581.3081665	2	1160.600683	1160.611193	-0.010510008	Q	D	M3:+15.995	1	11	0	0
P23396	40S ribosomal protein S3	6	39.09%	18	27	9	K	AELNEFLTR	E	0.23%	3098	3098	548.3276367	2	1094.639623	1091.56112	3.078503654	K	E	-	3	9	3	0
				94	106	12	R	GLCAIAQAESLR	Y	0.23%	2970	2970	644.8336182	2	1287.651586	1287.660054	-0.00846744	R	Y	C3:+57.021	6	12	0	0
				151	173	22	K	FVDGLMIHSGDPVNYYVDTAVR	H	0.23%	5424	5424	1234.594727	2	2467.173803	2467.184194	-0.010390659	K	H	-	6	22	0	0
				187	197	10	K	IMLPWDPTGK	I	0.23%	5148	5148	579.3044434	2	1156.593237	1156.595064	-0.001826857	K	I	-	3	10	0	0
				201	227	26	K	KPLPDHVSIVEPKDEILPTTPISEQK	G	0.23%	3310	3310	971.1954956	3	2910.563012	2909.574987	0.98802464	K	G	-	4	26	1	1
				227	243	16	K	GGKPEPPAMPQPVPTA	-	0.23%	1989	1989	787.4016113	2	1572.787573	1572.797011	-0.009438568	K	-	-	6	16	0	0
P23471	Receptor-type tyrosine-protein phosphatase zeta	1	1.30%	2108	2138	30	R	MIWDHNAQLVVMIPDGQNMAEDEFVYWPNK	D	9.00%	9900	9900	903.4215088	4	3609.654735	3606.625869	3.028866476	R	D	N6:+0.984,M19:+15.995	1	30	3	0
P24043	Laminin subunit alpha-2	1	0.45%	355	369	14	Y	DENVARRNLSLNIR	G	9.62%	9334	9334	836.4442139	2	1670.872778	1669.885961	0.986816646	Y	G	N12:+0.984	1	14	1	2
P25705	ATP synthase subunit alpha, mitochondrial	21	48.64%	45	58	13	K	TGTAEMSSILEER	I	0.23%	3164	3164	712.331604	2	1422.647558	1422.666056	-0.01849856	K	I	-	6	13	0	0
				58	73	15	R	ILGADTSVDLEETGR	V	0.23%	3354	3354	788.390625	2	1574.7656	1574.778777	-0.013177184	R	V	-	7	15	0	0
				73	83	10	R	VLSIGDGIAR	V	0.23%	2195	2195	501.29	2	1000.56435	999.5712904	0.993059496	R	V	-	7	10	1	0
				88	103	15	R	NVQAEEMVEFSSGLK	G	0.28%	4543	4543	834.9042969	2	1667.792944	1667.771234	0.021709246	R	G	N1:+0.984	3	15	0	0
				103	123	20	K	GMSLNLEPDNVGVVVFGNDK	L	0.23%	6333	6333	1052.522583	2	2103.029516	2103.030653	-0.001137016	K	L	-	6	20	0	0
				132	149	17	K	RTGAIVDVPVGEELLGR	V	0.23%	4339	4339	890.9953003	2	1779.974951	1779.984294	-0.009343278	K	V	-	7	17	0	1
				133	149	16	R	TGAIVDVPVGEELLGR	V	0.23%	5297	5297	812.9463501	2	1623.87705	1623.883183	-0.006132517	R	V	-	7	16	0	0
				149	161	12	R	VVDALGNAIDGK	G	0.23%	2016	2016	586.3168335	2	1170.618017	1170.624448	-0.00643144	R	G	-	6	12	0	0
				149	167	18	R	VVDALGNAIDGKGPIGSK	T	1.32%	2064	2064	570.98	3	1709.916525	1709.931196	-0.014670648	R	T	-	1	18	0	1
				194	204	10	K	AVDSLVPIGR	G	0.23%	2556	2556	513.7977905	2	1025.579931	1025.586941	-0.007009529	K	G	-	3	10	0	0
				218	230	12	K	TSIAIDTIINQK	R	0.23%	3764	3764	658.8728638	2	1315.730077	1315.734727	-0.004649781	K	R	-	6	12	0	0
				305	316	11	K	HALIIYDDLSK	Q	0.23%	2820	2820	644.3477173	2	1286.679784	1286.687049	-0.007264182	K	Q	-	4	11	0	0
				334	347	13	R	EAYPGDVFYLHSR	L	0.23%	3147	3147	777.3713379	2	1552.727026	1552.731039	-0.004013163	R	L	-	6	13	0	0
				402	416	14	K	GIRPAINVGLSVSR	V	0.23%	2782	2782	719.9212036	2	1437.826757	1437.841592	-0.014835261	K	V	-	4	14	0	0
				441	463	22	R	EVAAFAQFGSDLDAATQQLLSR	G	0.23%	9561	9561	1169.585327	2	2337.155004	2337.160086	-0.005082087	R	G	-	5	22	0	0
				472	493	21	K	QGQYSPMAIEEQVAVIYAGVR	G	0.23%	7476	7476	1155.083618	2	2308.151586	2309.136165	-0.984578968	K	G	Q12:+0.984	6	21	-1	0
				493	503	10	R	GYLDKLEPSK	I	0.23%	1695	1695	575.3085327	2	1148.601415	1148.607736	-0.006320266	R	I	-	6	10	0	1
				503	527	24	K	ITKFENAFLSHVVSQHQALLGTIR	A	0.23%	5198	5198	903.8328857	3	2708.475182	2708.476216	-0.001034093	K	A	-	2	24	0	1
				506	527	21	K	FENAFLSHVVSQHQALLGTIR	A	0.23%	5713	5713	790.7424316	3	2369.20382	2368.21751	0.986309394	K	A	N3:+0.984,Q14:+0.984	4	21	1	0
				527	539	12	R	ADGKISEQSDAK	L	2.15%	14633	14633	416.6	3	1246.776525	1248.583356	-1.806831	R	L	Q8:+0.984	1	12	-1	1
				541	553	12	K	EIVTNFLAGFEA	-	0.23%	8333	8333	655.828186	2	1309.640722	1309.655414	-0.014692194	K	-	-	4	12	0	0
P26010	Integrin beta-7	10	30.33%	24	35	11	K	IPSTGDATEWR	N	0.54%	1631	1631	617.2980347	2	1232.580419	1231.583312	0.997107456	K	N	-	1	11	1	0
				89	116	27	R	GCPLEELEEPRGQQEVLQDQPLSQGAR	G	0.23%	4170	4170	1021.828613	3	3062.462365	3063.456261	-0.99389626	R	G	C2:+57.021,Q13:+0.984	2	27	-1	1
				129	143	14	R	VTLRPGEPQQLQVR	F	0.23%	1638	1638	810.9621582	2	1619.908666	1619.910735	-0.002068418	R	F	-	6	14	0	0
				190	199	9	R	IGFGSFVDK	T	0.29%	3378	3378	485.25177	2	968.48789	968.4967284	-0.008838441	R	T	-	2	9	0	0
				199	211	12	K	TVLPFVSTVPSK	L	0.23%	3762	3762	637.8693237	2	1273.722997	1273.728185	-0.005187843	K	L	-	5	12	0	0
				222	244	22	R	CQSPFSFHHVLSLTGDAQAFER	E	0.23%	4984	4984	845.729187	3	2534.164086	2533.180376	0.983710027	R	E	C1:+57.021	4	22	1	0
				248	278	30	R	QSVSGNLDSPEGGFDAILQAALCQEQIGWR	N	0.23%	9300	9300	1083.187256	3	3246.538292	3245.540675	0.997617466	R	N	C23:+57.021	3	30	1	0
				321	361	40	R	STEFDYPSVGQVAQALSAANIQPIFAVTSAALPVYQELSK	L	0.23%	10927	10927	1405.072754	3	4212.194787	4211.131405	1.063382071	R	L	N20:+0.984	5	40	1	0
				365	418	53	K	SAVGELSEDSSNVVQLIMDAYNSLSSTVTLEHSSLPPGVHISYESQCEGPEKR	E	1.46%	11265	11265	1435.17	4	5736.6487	5735.661343	0.98735716	K	E	N12:+0.984,N22:+0.984,Q	1	53	1	1
				594	618	24	R	ACECSGDMDSCISPEGGLCSGHGR	C	0.23%	1621	1621	867.6592407	3	2599.954247	2597.964323	1.989924136	R	C	C2:+57.021,C4:+57.021,C	7	24	2	0
P26715	NKG2-A/NKG2-B type II integral membrane protein	1	7.73%	0	18	18	-	MDNQGVIYSDLNLPPNPK	R	5.32%	8526	8526	679.0420532	3	2034.102685	2033.913974	0.188710164	-	R	M1:+15.995,N3:+0.984,Q4	2	18	0	0
P27105	Erythrocyte band 7 integral membrane protein	6	39.24%	77	93	16	K	GPGLFFILPCTDSFIK	V	0.23%	8295	8295	906.96875	2	1811.92185	1810.932313	0.989537184	K	V	C10:+57.021	7	16	1	0
				125	144	19	R	VQNATLAVANITNADSATR	L	0.40%	2812	2812	967.4553833	2	1932.895117	1928.991564	3.903552394	R	L	-	3	19	4	0
				158	188	30	K	NLSQILSDREEIAHNMQSTLDDATDAWGIK	V	0.23%	7663	7663	1125.543945	3	3373.608361	3370.609947	2.99841405	K	V	-	2	30	3	1
				220	232	12	K	VIAAEGEMNASR	A	0.23%	1073	1073	624.3031616	2	1246.590673	1246.597583	-0.006909646	K	A	-	7	12	0	0
				235	251	16	K	EASMVITESPAALQLR	Y	0.46%	4261	4261	858.44	2	1714.86435	1714.892368	-0.02801836	K	Y	-	2	16	0	0
				263	283	20	K	NSTIVFPLPIDMLQGIIGAK	H	0.23%	10406	10406	1064.603516	2	2127.191381	2126.180946	1.010435106	K	H	-	5	20	1	0
P27797	Calreticulin	1	3.60%	207	222	15	K	IKDPDASKPEDWDER	A	0.23%	1229	1229	600.9489746	3	1799.823449	1799.832604	-0.00915498	K	A	-	5	15	0	1
P28907	ADP-ribosyl cyclase 1	2	8.33%	78	90	12	R	HVDCQSVWDAFK	G	0.74%	3744	3744	746.3352051	2	1490.65476	1490.660782	-0.00602194	R	G	C4:+57.021	3	12	0	0
				234	247	13	K	VQTLEAWVIHGGR	E	0.23%	3995	3995	733.3999023	2	1464.784155	1464.783743	0.000411488	K	E	-	5	13	0	0
P29965	CD40 ligand	1	8.05%	1	22	21	M	IETYNQTSPRSAATGLPISMK	I	9.49%	5075	5075	761.7301636	3	2282.167016	2281.12608	1.040935747	M	I	Q6:+0.984,M20:+15.995	1	21	1	1
P30519	Heme oxygenase 2	4	19.30%	16	24	8	K	KNSGALEK	E	3.26%	1982	1982	425.2133484	2	848.4110467	846.4446772	1.966369489	K	E	N2:+0.984	1	8	2	1
				137	156	19	R	IHYIGQNEPELLVAHAYTR	Y	0.23%	3429	3429	742.3824463	3	2224.123864	2223.143648	0.980215523	R	Y	-	3	19	1	0
				176	199	23	K	LPSTGEGTQFYLFENVDNAQQFK	Q	0.62%	6050	6050	1318.118774	2	2634.221899	2632.244544	1.977354356	K	Q	-	5	23	2	0
				203	214	11	R	ARMNALDLNMK	T	2.92%	1222	1222	646.664856	2	1291.314062	1291.63676	-0.322698142	R	T	M10:+15.994	1	11	0	1
P31146	Coronin-1A	5	26.25%	29	45	16	R	VSQTTWDSGFCAVNPK	F	0.23%	3139	3139	899.416687	2	1796.817724	1795.819468	0.998256143	R	F	C11:+57.021	5	16	1	0
				253	287	34	K	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK	G	0.23%	9160	9160	1283.308838	3	3846.903039	3845.906894	0.99614436	K	G	C32:+57.021	3	34	1	0
				293	313	20	R	YFEITSEAPFLHYLSMFSSK	E	0.23%	8794	8794	800.0498047	3	2397.125939	2396.139869	0.986069759	R	E	-	6	20	1	0
				354	383	29	R	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	D	0.23%	7322	7322	1058.510254	3	3172.507287	3173.519307	-1.012020561	R	D	Q6:+0.984	5	29	-1	1
				416	438	22	R	AAPEASGTPSSDAVSRLEEEMR	K	2.82%	3951	3951	764.0192261	3	2289.034203	2289.054302	-0.020098601	R	K	-	1	22	0	1
P31785	Cytokine receptor common subunit gamma	1	6.50%	140	164	24	R	QATQMLKLQNLVIPWAPENLTLHK	L	0.61%	3565	3565	930.1339111	3	2787.378258	2785.531289	1.846968846	R	L	-	2	24	2	1
P32926	Desmoglein-3	1	2.00%	855	875	20	K	LAEISLGVDGEGKEVQPPSK	D	6.64%	12037	12037	1027.005859	2	2051.996069	2052.073897	-0.077828234	K	D	-	3	20	0	1
P32942	Intercellular adhesion molecule 3	1	1.83%	214	224	10	R	TFVLPVTPPR	L	0.83%	3518	3518	564.3320313	2	1126.648412	1125.654626	0.993786236	R	L	-	4	10	1	0
P33527	Multidrug resistance-associated protein 1	1	1.76%	867	894	27	R	TYASTEQEQDAEENGVTGVSGPGKEAK	Q	9.30%	6431	6431	696.6106567	4	2782.411327	2783.225688	-0.814361303	R	Q	Q7:+0.984,Q9:+0.984	2	27	-1	1
P33681	T-lymphocyte activation antigen CD80	1	5.90%	71	88	17	K	MVLTMMSGDMNIWPEYK	N	1.00%	5480	5480	1023.487244	2	2044.958837	2044.913049	0.045788345	K	N	-	2	17	0	0
P35221	Catenin alpha-1	1	3.20%	496	525	29	R	VLTDAVDDITSIDDFLAVSENHILEDVNK	C	0.23%	10042	10042	1068.196533	3	3201.566124	3200.561232	1.004892777	R	C	N21:+0.984	4	29	1	0
P35232	Prohibitin	11	65.07%	11	35	24	K	FGLALAVAGGVVNSALYNVDAGHR	A	0.23%	11700	11700	791.4202881	3	2371.237389	2371.228425	0.00896409	K	A	N13:+0.984	4	24	0	0
				43	70	27	R	GVQDIVVGEGTHFLIPWVQKPIIFDCR	S	0.23%	7994	7994	1043.55	3	3127.626525	3123.621082	4.005443032	R	S	Q19:+0.984,C26:+57.021	2	27	4	0
				83	93	10	K	DLQNVNITLR	I	0.70%	3041	3041	592.3278809	2	1182.640112	1184.651332	-2.011220169	K	I	-	2	10	-1	0
				93	105	12	R	ILFRPVASQLPR	I	0.23%	2789	2789	698.9226074	2	1395.829565	1395.83505	-0.005485628	R	I	-	5	12	0	0
				105	117	12	R	IFTSIGEDYDER	V	0.23%	2797	2797	722.8287964	2	1443.641943	1443.651785	-0.009842787	R	V	-	6	12	0	0
				117	128	11	R	VLPSITTEILK	S	0.23%	4331	4331	607.369751	2	1212.723852	1212.732936	-0.009084383	R	S	-	4	11	0	0

				133	143	10	R	FDAGELITQR	E	0.23%	3148	3148	575.2980957	2	1148.580541	1148.582583	-0.002042146	R	E	-	6	10	0	0
				157	177	20	R	AATFGLILDDVSLTHLTFGK	E	4.75%	7913	7913	707.0529785	3	2118.13546	2118.136103	-0.000642797	R	E	-	1	20	0	0
				219	239	20	K	AAELIANSLATAGDGLIELR	K	0.23%	6764	6764	999.5446167	2	1997.073583	1997.079317	-0.005733274	K	K	-	7	20	0	0
				239	253	14	R	KLEAAEDIAYQLSR	S	0.23%	3678	3678	803.9210205	2	1605.826391	1605.836232	-0.009841456	R	S	-	5	14	0	1
				255	272	17	R	NITYLPAGQSVLLQLPQ	-	0.23%	6972	6972	928.0184326	2	1854.021215	1854.025096	-0.003880854	R	-	-	3	17	0	0
P35579	Myosin-9	62	40.71%	14	29	15	K	NFINNPLAQADWAAK	K	0.23%	5030	5030	836.925293	2	1671.834936	1671.836901	-0.00196519	K	K	-	5	15	0	0
				79	102	23	K	FSKVEDMAELTCLNEASVLHNLK	E	0.23%	5316	5316	883.7720947	3	2648.292809	2648.282109	0.010699948	K	D	C12:+57.021,N14:+0.984	2	23	0	1
				82	102	20	K	VEDMAELTCLNEASVLHNLK	E	0.23%	5433	5433	762.0525513	3	2283.134179	2285.102703	-1.968524791	K	D	C9:+57.021	2	20	-1	0
				125	139	14	K	NLPIYSEEIVEMYK	G	0.23%	5698	5698	864.9282837	2	1727.840917	1726.848772	0.992145215	K	G	-	5	14	1	0
				143	159	16	R	HEMPPHIYAITDTAYR	S	0.23%	2222	2222	638.97	3	1913.886525	1913.909415	-0.022890464	R	S	-	6	16	0	0
				159	180	21	R	SMMQDREDQSILCTGESGAGK	T	0.23%	1976	1976	767.9969482	3	2300.96737	2299.971417	0.995952791	R	T	Q9:+0.984,C13:+57.021	1	21	1	1
				185	199	14	K	KVIQYLAYVASSHK	S	0.23%	2562	2562	536.3001099	3	1605.876854	1605.887874	-0.011019522	K	S	-	5	14	0	1
				186	199	13	K	VIQYLAYVASSHK	S	0.23%	2982	2982	739.8977661	2	1477.779882	1477.792911	-0.013028709	K	S	-	5	13	0	0
				209	225	16	R	QLLQANPILEAFGNAK	T	0.23%	6475	6475	863.9747314	2	1725.933813	1725.941366	-0.007553437	R	T	-	5	16	0	0
				301	316	15	R	FLSNGHVTIPGQQDK	D	0.28%	1780	1780	547.6152954	3	1639.822411	1639.831816	-0.009404578	R	D	-	1	15	0	0
				316	327	11	K	DMFQETMEAMR	I	0.23%	5454	5454	694.7843018	2	1387.552953	1387.557042	-0.004088724	K	I	-	5	11	0	0
				327	341	14	R	IMGIPEEEQMGLLR	V	0.28%	4993	4993	808.8956909	2	1615.775732	1614.810948	0.964783932	R	V	-	4	14	1	0
				341	356	15	R	VISGVLQLGNIVFKK	E	0.23%	5523	5523	807.9945068	2	1613.973364	1613.98686	-0.01349624	R	E	-	5	15	0	1
				373	387	14	K	VSHLLGINVTDFTR	G	0.23%	4447	4447	524.6205444	3	1570.838158	1570.846737	-0.008579259	K	G	-	4	14	0	0
				424	441	17	R	MFRWLVLRINKALDKTK	R	2.82%	7822	7822	1076.172363	2	2150.329076	2148.224218	2.104858459	R	R	M1:+15.995,N10:+0.984	1	17	2	4
				587	606	19	K	NMDPLNDNIATLLHQSSDK	F	0.23%	5191	5191	1064.004883	2	2125.994116	2125.01098	0.983135377	K	F	-	7	19	1	0
				617	637	20	R	IIGLDQVAGMSETALPGAFK	T	0.23%	6751	6751	1007.986877	2	2013.958105	2017.055411	-3.097306293	R	T	-	2	20	-1	0
				679	693	14	K	AGKLDPHLVLDQLR	C	0.59%	3456	3456	789.45	2	1576.88435	1573.894022	2.990327912	R	C	-	2	14	3	1
				682	693	11	K	LDPHLVLDQLR	C	0.23%	4260	4260	659.8765869	2	1317.737524	1317.740481	-0.002957508	K	C	-	6	11	0	0
				718	731	13	R	QRYEILTPNSIPK	G	0.23%	2437	2437	779.9342041	2	1557.852758	1557.851488	0.001269651	R	G	-	5	13	0	1
				745	755	10	K	ALELDSNLYR	I	0.29%	2938	2938	598.8171997	2	1195.618749	1192.608798	3.009951062	K	I	-	3	10	3	0
				764	778	14	R	AGVLAHLEEERDLK	I	0.23%	2050	2050	790.4246216	2	1578.833593	1578.836567	-0.002973636	R	I	-	6	14	0	1
				842	856	14	R	QEEEMMAKEEELVK	V	0.23%	2069	2069	861.8944702	2	1721.77329	1721.785187	-0.011896346	R	V	-	6	14	0	1
				867	882	15	R	LTEMETLQSQLMAEK	L	0.23%	4830	4830	876.4266357	2	1750.837621	1750.848121	-0.01049994	R	L	-	6	15	0	0
				882	903	21	K	LQLQEQLQAETELCAEAEELR	A	1.62%	10718	10718	1252.606079	2	2503.196508	2500.211067	2.985441059	K	A	C14:+57.021	1	21	3	0
				909	923	14	K	KQELEEICHDLEAR	V	0.23%	2617	2617	885.4237061	2	1768.831762	1768.840932	-0.009169539	K	V	C8:+57.021	6	14	0	1
				939	959	20	K	KMQQNIQELEEQLEEEESAR	Q	2.70%	1252	1252	827.3671265	3	2479.077904	2478.106845	0.971059123	K	Q	M2:+15.995,N5:+0.984,Q1	1	20	1	1
				940	959	19	K	MQQNIQELEEQLEEEESAR	Q	0.23%	5240	5240	1168.032715	2	2334.04978	2332.048882	2.000897592	K	Q	-	3	19	2	0
				974	989	15	K	KLEEEQIILEDQNCK	L	0.23%	2092	2092	945.4837036	2	1888.951757	1887.924327	1.027430147	K	L	C14:+57.021	2	15	1	1
				1000	1014	14	R	IAEFTTNLTEEEEK	S	0.69%	2857	2857	827.925354	2	1653.835058	1652.778108	1.05694948	R	S	-	4	14	1	0
				1024	1035	11	K	HEAMITDLEER	L	0.23%	1705	1705	672.3170166	2	1342.618383	1342.618712	-0.000329125	K	L	-	6	11	0	0
				1050	1075	25	R	RKLEGDSTDLSDQIAELQAQIAELK	M	1.00%	6829	6829	924.8115234	3	2771.411095	2770.434865	0.976230528	R	M	-	1	25	1	2
				1051	1075	24	R	KLEGDSTDLSDQIAELQAQIAELK	M	0.23%	7480	7480	1308.667725	2	2615.319799	2614.333754	0.986045627	R	M	-	4	24	1	1
				1105	1124	19	K	IRELESQISELQEDLESER	A	0.23%	5535	5535	769.0442505	3	2304.109276	2302.128846	1.980430529	K	A	-	4	19	2	1
				1107	1124	17	R	ELESQISELQEDLESER	A	0.23%	5857	5857	1017.469177	2	2032.922704	2032.943671	-0.020966164	R	A	-	6	17	0	0
				1135	1162	27	R	DLGEELEALKTELEDTLDSTAAQQELR	S	0.23%	10042	10042	1510.232666	2	3018.449682	3016.472432	1.977249767	R	S	-	5	27	2	1
				1174	1191	17	K	TLEEEAKTHEAQIQEMR	Q	0.23%	2306	2306	681.6605835	3	2041.958275	2041.973866	-0.015590952	K	Q	-	2	17	0	1
				1193	1209	16	K	HSQAVEELAEQLEQTK	R	0.23%	3809	3809	920.4517212	2	1838.887792	1838.901018	-0.013225393	K	R	-	5	16	0	0
				1193	1210	17	K	HSQAVEELAEQLEQTKR	V	0.28%	3046	3046	666.3406372	3	1995.998437	1995.986129	0.012307653	K	V	Q11:+0.984	2	17	0	1
				1219	1234	15	K	QTLENERGELANEVK	V	0.23%	1491	1491	865.4342651	2	1728.85288	1728.864238	-0.011357983	K	V	-	5	15	0	1
				1234	1246	12	K	VLLQGKGDSEHK	R	2.71%	2336	2336	656.5322266	2	1311.048803	1309.69901	1.349792669	K	R	-	1	12	1	1
				1248	1260	12	K	KVEAQLQELQVK	F	0.23%	1648	1648	706.8856812	2	1411.755712	1411.803476	-0.047763351	K	F	-	6	12	0	1
				1301	1322	21	K	DFSALESQLQDTQELLQEENR	Q	0.23%	7316	7316	1248.079468	2	2494.143285	2492.166688	1.976597475	K	Q	-	6	21	2	0
				1342	1357	15	R	EQLEEEEEAKHNLEK	Q	4.31%	1100	1100	618.9581299	3	1853.850915	1853.864298	-0.01338332	R	Q	-	1	15	0	1
				1371	1388	17	K	KMEDSVGCLETAEEVKR	K	0.76%	1585	1585	661.3161011	3	1980.924828	1979.928762	0.996066487	K	K	C8:+57.021	1	17	1	2
				1415	1433	18	K	TRLQQELDDLLVDLDHQR	Q	0.23%	6947	6947	736.3818359	3	2206.122033	2206.134206	-0.01217314	K	Q	-	7	18	0	1
				1417	1433	16	R	LQQELDDLLVDLDHQR	Q	0.23%	6117	6117	650.6655884	3	1948.97329	1949.969416	-0.996126095	R	Q	Q3:+0.984	3	16	-1	0
				1527	1555	28	K	RALEQQVEEMKTQLEELEDELQATEDAK	L	1.87%	7635	7635	1102.202026	3	3303.582604	3302.582395	1.000209326	K	L	-	1	28	1	2
				1528	1555	27	R	ALEQQVEEMKTQLEELEDELQATEDAK	L	0.36%	8534	8534	1050.162842	3	3147.46505	3146.481284	0.983766767	R	L	-	2	27	1	1
				1538	1555	17	K	TQLEELEDELQATEDAK	L	0.23%	5712	5712	981.9658813	2	1961.916113	1960.911308	1.004804855	K	L	-	6	17	1	0
				1566	1576	10	K	AQFERDLQGR	D	2.31%	4488	4488	610.3187866	2	1218.621923	1219.59453	-0.972606422	K	D	Q2:+0.984	1	10	-1	1
				1603	1612	9	K	QRSMAVAAR	K	2.90%	4800	4800	495.7938232	2	989.5719964	988.5236298	1.048366636	K	K	-	1	9	1	1
				1676	1694	18	K	SMEAEMIQLQEELAAAER	A	0.23%	7213	7213	1024.980347	2	2047.945043	2047.95544	-0.010396905	K	A	-	5	18	0	0
				1696	1716	20	K	RQAQQERDELADEIANSSGK	G	0.56%	1554	1554	749.0266724	3	2244.056542	2244.073062	-0.016520198	K	G	-	1	20	0	2
				1697	1716	19	R	QAQQERDELADEIANSSGK	G	0.23%	1866	1866	1044.987427	2	2087.959203	2087.971951	-0.01274758	R	G	-	3	19	0	1
				1730	1751	21	R	IAQLEEELEEEQGNTELINDR	L	0.23%	4842	4842	1237.084229	2	2472.152807	2471.166354	0.986453287	R	L	-	6	21	1	0
				1754	1770	16	K	ANLQIDQINTDLNLER	S	0.23%	4691	4691	935.9863892	2	1869.957128	1868.959201	0.997926928	K	S	-	6	16	1	0
				1815	1828	13	K	IAQLEEQLDNETK	E	0.23%	2199	2199	765.881897	2	1529.748144	1529.757313	-0.009169471	K	E	-	7	13	0	0
				1815	1830	15	K	IAQLEEQLDNETKER	Q	4.40%	1992	1992	605.9691772	3	1814.884057	1814.901018	-0.016961078	K	Q	-	1	15	0	1
				1839	1855	16	R	TEKKLKDVLLQVDDER	R	3.42%	3522	3522	643.9932861	3	1928.956383	1929.041853	-0.085469546	R	R	Q11:+0.984	1	16	0	3
				1845	1856	11	K	DVLLQVDDERR	N	1.21%	1733	1733	679.3536377	2	1356.691625	1356.699739	-0.008113393	K	N	-	2	11	0	1
				1922	1932	10	R	RGDLPFVVPR	R	0.23%	2606	2606	578.3320313	2	1154.648412	1154.656023	-0.007610748	R	R	-	6	10	0	1
P35580	Myosin-10	7	4.10%	83	106	23	K	FSKVEDMAELTCLNEASVLHNLK	D	0.23%	5316	5316	883.7720947	3	2648.292809	2648.282109	0.010699948	K	D	C12:+57.021,N14:+0.984	2	23	0	1
				86	106	20	K	VEDMAELTCLNEASVLHNLK	D	0.23%	5433	5433	762.0525513	3	2283.134179	2285.102703	-1.968524791	K	D	C9:+57.021	2	20	-1	0
				686	700	14	R	AGKLDPHLVLDQLR	C	0.59%	3456	3456	789.45	2	1576.88435	1573.894022	2.990327912	R	C	-	2	14	3	1
				689	700	11	K	LDPHLVLDQLR	C	0.23%	4260	4260	659.8765869	2	1317.737524	1317.740481	-0.002957508	K	C	-	6	11	0	0
				749	762	13	R	MIRALELDPNLYR	I	5.74%	926	926	535.2890015	3	1602.843529	1602.855195	-0.011665485	R	I	-	1	13	0	1
				771	785	14	R	AGVLAHLEEERDLK	I	0.23%	2050	2050	790.4246216	2	1578.833593	1578.836567	-0.002973636	R	I	-	6	14	0	1
				1545	1562	17	R	TQLEELEDELQATEDAK	L	0.23%	5712	5712	981.9658813	2	1961.916113	1960.911308	1.004804855	K	L	-	6	17	1	0
P35611	Alpha-adducin	1	2.04%	452	467	15	R	GDEASEEGQNGSSPK	S	9.87%	5209	5209	498.5817261	3	1492.721703	1492.580106	0.141597519	R	S	Q9:+0.984,N10:+0.984	2	15	0	0
P35613	Basigin	4	17.14%	227	243	16	K	SSEHINEGETAMLVCK	S	0.23%	1640	1640	903.413208	2	1804.810766	1803.812669	0.998096896	K	S	C15:+57.021	5	16	1	0
				243	257	14	K	SESVPPVTDWAWYK	I	1.14%	5235	5235	833.4031372	2	1664.790624	1663.78822	1.002404838	K	I	-	4	14	1	0
				282	300	18	R	SELHIENLNMEADPGQYR	C	0.23%	3425	3425	1059.497925	2	2116.9802	2114.969115	2.011084241	R	C	-	2	18	2	0
				348	366	18	R	RKPEDVLDDDDAGSAPLK	S	0.23%	1590	1590	648.3248901	3	1941.951195	1939.948696	2.002499026	R	S	-	1	18	2	1
P35670	Copper-transporting ATPase 2	2	3.55%	725	755	30	R	SANMDVLIVLATSIAYVYSLVILVVAVAEK	A	4.70%	5892	5892	1060.470215	3	3178.387169	3179.77581	-1.388640645	R	A	M4:+15.994	2	30	-1	0
				794	816	22	K	LMSLQATEATVVTLGEDNLIIR	E	2.92%	5915	5915	797.7678833	3	2390.280175	2387.26176	3.018414926	K	E	N18:+0.984	1	22	3	0
P37802	Transgelin-2	3	20.10%	57	78	21	K	DGTVLCELINALYPEGQAPVK	K	0.23%	9297	9297	763.3961792	3	2287.165062	2286.156118	1.008944326	K	K	C6:+57.021	3	21	1	0
				57	79	22	K	DGTVLCELINALYPEGQAPVKK	I	1.61%	8413	8413	807.0731201	3	2418.195885	2415.235081	2.960803944	K	I	C6:+57.021,N10:+0.984	1	22	3	1
				102	120	18	R	YGINTTDIFQTVDLWEGK	N	0.23%	7971	7971	1051.514404	2	2101.013159	2099.021133	1.992025538	R	N	-	5	18	2	0
P38570	Integrin alpha-E	1	0.93%	1155	1166	11	K	YQQLNLESIRK	A	1.46%	2003	2003	464.92453	3	1391.750115	1391.74086	0.009255304	K	A	N5:+0.984	1	11	0	1
P38606	V-type proton ATPase catalytic subunit A	1	1.94%	44	56	12	R	VGHSELVGEIIR	L	0.23%	2269	2269	437.2308655	3	1308.669121	1307.719746	0.9493755	R	L	-	1	12	1	0
P38646	Stress-70 protein, mitochondrial	9	19.88%	85	99	14	R	TTPSVVAFTADGER	L	0.23%	2498	2498	725.8587036	2	1449.701757	1449.709969	-0.008211949	R	L	-	6	14	0	0
				159	173	14	K	LYSPSQIGAFVLMK	M	0.23%	6253	6253	777.4196777	2	1552.823705	1552.832334	-0.008628619	K	M	-	5	14	0	0
				187	202	15	K	NAVITVPAYFNDSQR	Q	0.23%	4104	4104	847.9277954	2	1693.839941	1693.84238	-0.002439668	T	Q	-	5	15	0	0
				218	234	16	R	VINEPTAAALAYGLDK	S	0.23%	4213	4213	823.44104	2	1644.86643	1644.872284	-0.005853586	R	S	-	7	16	0	0
				265	284	19	K	STNGDTFLGGEDFDQALLR	H	0.23%	6406	6406	1029.476563	2	2056.937475	2055.93851	0.998964968	K	H	N3:+0.984	4	19	1	0
				348	360	12	R	AQFEGIVTDLIR	R	0.23%	5746	5746	681.3738403	2	1360.732031	1360.735062	-0.003030984	R	R	-	6	12	0	0
				394	405	11	K	VQQTVQDLFGR	A	0.23%	3155	3155	646.3428345	2	1290.670019	1289.672796	0.997223289	K	A	-	6	11	1	0
				498	513	15	K	LLGQFTLIGIPPAPR	G	0.23%	6470	6470	797.4686279	2	1592.921606	1591.944995	0.976610827	K	G	-	3	15	1	0
				576	595	19	K	ERVEAVNMAEGIIHDTETK	M	0.23%	4173	4173	714.6746826	3	2141.000573	2141.04228	-0.041707596	K	M	-	4	19	0	1
P40763	Signal transducer and activator of transcription 3	1	3.38%	114	140	26	R	LLQTAATAAQQGGQANHPTAAVVTEK	Q	0.23%	1503	1503	859.7843018	3	2576.32943	2576.319425	0.010005001	R	Q	N16:+0.984	3	26	0	0
P40926	Malate dehydrogenase, mitochondrial	4	19.53%	26	45	19	K	VAVLGASGGIGQPLSLLLK	N	0.23%	7029	7029	897.0438232	2	1792.071996	1792.082217	-0.010220564	K	N	-	7	19	0	0
				52	74	22	R	LTLYDIAHTPGVAADLSHIETK	A	0.96%	5435	5435	789.76	3	2366.256525	2364.232523	2.024001864	R	A	-	2	22	2	0
				91	104	13	K	GCDVVVIPAGVPR	K	0.23%	3093	3093	669.8630981	2	1337.710546	1337.712089	-0.001543079	K	K	C2:+57.021	4	13	0	0
				203	215	12	K	TIIPLISQCTPK	V	0.48%	3661	3661	686.3918457	2	1370.768041	1369.763456	1.004585094	K	V	C9:+57.021	4	12	1	0
P41146	Nociceptin receptor	1	7.84%	302	331	29	R	FCTALGYVNSCLNPILYAFLDENFKACFR	K	9.08%	1569	1569	877.1654053	4	3504.630321	3504.617834	0.012486686	R	K	C2:+57.021,C11:+57.021,I	1	29	0	1
P42261	Glutamate receptor 1	1	2.32%	221	242	21	K	NGIGYHYILANLGFMDIDLNK	F	3.06%	10823	10823	794.727478	3	2381.158959	2380.188551	0.970408226	K	F	-	1	21	1	0
P42701	Interleukin-12 receptor subunit beta-1	1	1.06%	521	528	7	R	ADTAWLR	G	6.48%	11514	11514	417.04	2	832.0643499	831.4238977	0.640452232	R	G	-	3	7	1	0
P43007	Neutral amino acid transporter A	5	22.18%	138	175	37	I	IKPGSGAQTLQSSDLGLEDSGPPPVPKETVDSFLDLA	R	2.76%	3406	3406	1257.306885	3	3768.897179	3764.899629	3.997550209	I	R	-	1	37	4	1
				176	189	13	R	NLFPSNLVVAAFR	T	0.94%	6801	6801	724.409668	2	1446.803686	1446.798331	0.005355314	R	T	-	1	13	0	0
				457	480	23	R	TTTVVNVEGDALGAGILHHLNQK	A	1.91%	4478	4478	796.7556763	3	2387.243554	2387.244469	-0.000915439	R	A	N21:+0.984	1	23	0	0
				483	501	18	K	KGEQELAEVKVEAIPNCK	S	1.66%	1814	1814	681.69104	3	2042.049645	2042.034925	0.014720373	K	S	Q4:+0.984,C17:+57.021	1	18	0	2
				501	528	27	K	SEEETSPLVTHQNPAGPVASAPELESK	E	0.23%	2586	2586	935.7892456	3	2804.344262	2803.351195	0.99306712	K	E	-	2	27	1	0
P43403	Tyrosine-protein kinase ZAP-70	2	3.55%	186	193	7	K	FLLRPRK	E	3.04%	3490	3490	465.2911987	2	928.5667474	928.5970516	-0.030304171	K	E	-	3	7	0	1
				385	400	15	R	EAQIMHQLDNPYIVR	L	8.18%	3526	3526	616.2982788	3	1845.871361	1841.909501	3.961860602	R	L	M5:+15.995	1	15	4	0
P43489	Tumor necrosis factor receptor superfamily member 4	1	5.78%	260	276	16	R	TPIQEEQADAHSTLAK	I	6.36%	2241	2241	580.6151733	3	1738.822045	1738.837339	-0.015294228	R	I	Q4:+0.984	1	16	0	0
P45844	ATP-binding cassette sub-family G member 1	1	2.51%	107	124	17	K	FNSGELVAIMGPSGAGK	S	5.38%	6560	6560	817.909729	2	1633.803808	1633.81339	-0.009581624	K	S	-	1	17	0	0
P46934	E3 ubiquitin-protein ligase NEDD4	1	1.06%	40	54	14	R	ISTSNVVQMKLTPR	Q	4.47%	1516	1516	525.281189	3	1572.820092	1573.849759	-1.029667705	R	Q	Q8:+0.984	2	14	-1	1
P46940	Ras GTPase-activating-like protein IQGAP1	9	10.44%	111	130	19	R	HTDNVIQWLNAMDEIGLPK	I	0.23%	7771	7771	732.7053223	3	2195.092492	2194.072837	1.019655109	R	I	Q7:+0.984	2	19	1	0
				191	230	39	K	YGIQMPAFSKIGGILANELSVDEAALHAAVIAINEAIDR	R	2.45%	7594	7594	1024.77	4	4095.0487	4096.129401	-1.080701224	K	R	M5:+15.994	1	39	-1	1
				201	230	29	K	IGGILANELSVDEAALHAAVIAINEAIDR	R	0.23%	11991	11991	987.5368042	3	2959.586937	2957.582198	2.00473975	K	R	-	1	29	2	0
				241	266	25	K	NPNAMLVNLEEPLASTYQDILYQAK	Q	0.23%	8603	8603	1418.711914	2	2835.408178	2834.416045	0.992133517	K	Q	-	5	25	1	0
				406	431	25	K	TVLELMNPEAQLPQVYPFAADLYQK	E	0.23%	8200	8200	1440.239624	2	2878.463598	2877.462266	1.001331527	K	E	-	3	25	1	0
				538	556	18	R	ILAIGLINEALDEGDAQK	T	0.23%	7111	7111	628.6715698	3	1882.991234	1882.004755	0.986479785	G	T	-	4	18	1	0
				567	585	18	K	LEGVLAEVAQHYQDTLIR	A	0.23%	6292	6292	1028.543823	2	2055.071996	2054.079651	0.992345484	K	A	-	4	18	1	0
				1111	1128	17	K	LPYDVTPEQALAHEEVK	T	0.92%	3410	3410	647.3278809	3	1938.960167	1937.973454	0.98671305	K	T	-	2	17	1	0
				1465	1477	12	K	LTELGTVDPKNK	Y	2.09%	1927	1927	438.9049377	3	1313.691338	1313.719077	-0.027739048	K	Y	-	2	12	0	1
P48047	ATP synthase subunit O, mitochondrial	8	50.23%	26	40	14	K	LVRPPVQVYGIEGR	Y	0.23%	2625	2625	791.9558105	2	1581.895971	1581.899107	-0.003136354	K	Y	-	4	14	0	0
				73	84	11	K	VAASVLNPYVK	R	0.23%	2149	2149	580.8369751	2	1159.6583	1159.660106	-0.001805429	K	R	-	1	11	0	0
				98	117	19	K	ERFSPLTTNLINLLAENGR	L	0.23%	6926	6926	720.3978271	3	2158.170006	2157.154213	1.015793381	K	L	-	3	19	1	1
				100	117	17	R	FSPLTTNLINLLAENGR	L	0.23%	8009	8009	937.5064697	2	1872.997289	1872.994509	0.002780789	R	L	N15:+0.984	6	17	0	0
				117	136	19	R	LSNTQGVVSAFSTMMSVHR	G	0.23%	5317	5317	1026.999756	2	2051.983862	2050.992829	0.991032951	R	G	-	3	19	1	0
				136	158	22	R	GEVPCTVTSASPLEEATLSELK	T	0.23%	5236	5236	773.38	3	2317.116525	2317.135442	-0.018917504	R	T	C5:+57.021	2	22	0	0
				162	172	10	K	SFLSQGQVLK	L	0.28%	2266	2266	553.8112793	2	1105.606909	1105.613155	-0.00624679	K	L	-	4	10	0	0
				176	188	12	K	TDPSILGGMIVR	I	0.23%	4418	4418	629.8388062	2	1257.661962	1257.675105	-0.013142655	K	I	-	6	12	0	0
P48549	G protein-activated inward rectifier potassium channel 1	1	2.59%	287	300	13	S	MQTEQFEIVVILE	G	4.09%	10288	10288	798.392334	2	1594.769018	1594.780094	-0.011075631	S	G	M1:+15.995,Q2:+0.984	1	13	0	0
P48764	Sodium/hydrogen exchanger 3	1	1.56%	575	588	13	R	SSTVEASVSYLLR	E	7.77%	1670	1670	471.2509766	3	1410.729455	1410.735456	-0.006001001	R	E	-	1	13	0	0
P49327	Fatty acid synthase	30	24.97%	12	39	27	K	LPESENLQEFWDNLIGGVDMVTDDDRR	W	0.23%	10076	10076	1055.817871	3	3164.430138	3162.456406	1.973732145	K	W	-	3	27	2	1
				274	298	24	R	SLYQSAGVAPESFEYIEAHGTGTK	V	0.23%	4233	4233	848.0700073	3	2541.186547	2541.202345	-0.015798331	R	V	-	3	24	0	0
				326	343	17	K	SNMGHPEPASGLAALAK	V	0.28%	1961	1961	826.4197998	2	1650.82395	1649.819538	1.004411961	K	V	-	6	17	1	0
				343	373	30	K	VLLSLEHGLWAPNLHFHSPNPEIPALLDGR	L	0.68%	6640	6640	836.95	4	3343.7687	3342.751313	1.017386544	K	L	N13:+0.984	1	30	1	0
				373	384	11	R	LQVVDQPLPVR	G	0.23%	2538	2538	633.87	2	1265.72435	1262.734668	2.989682352	R	G	-	3	11	3	0
				384	422	38	R	GGNVGINSFGFGGSNVHIILRPNTQPPPAPAPHATLPR	L	1.28%	4373	4373	965.513855	4	3858.02412	3858.991756	-0.967636422	R	L	N15:+0.984,N23:+0.984	1	38	-1	0
				405	425	20	R	PNTQPPPAPAPHATLPRLLR	A	3.24%	1183	1183	717.0787354	3	2148.212731	2143.201438	5.011293095	R	A	-	1	20	5	1
				443	468	25	R	HSQDLAFLSMLNDIAAVPATAMPFR	G	0.23%	9567	9567	906.117981	3	2715.330468	2716.335277	-1.004809385	R	G	N12:+0.984	3	25	-1	0
				611	633	22	K	EAHLPPGAMAAVGLSWEECKQR	C	1.84%	5094	5094	812.7033081	3	2435.086449	2436.167369	-1.080920244	K	C	C19:+57.021	1	22	-1	1
				646	667	21	K	DTVTISGPQAPVFEFVEQLRK	E	0.48%	7425	7425	788.0915527	3	2361.251183	2361.221608	0.029574707	K	E	Q18:+0.984	2	21	0	1

				711	728	17	R	WLSTSIPEAQWHSSLAR	T	0.23%	4099	4099	985.0055542	2	1967.995458	1967.985356	0.010101878	R	T	-	5	17	0	0
				790	802	12	R	DNLEFFLAGIGR	L	1.04%	7203	7203	677.3567505	2	1352.697851	1351.677197	1.020654209	R	L	N2:+0.984	1	12	1	0
				802	825	23	R	LHLSGIDANPNALFPPVEFPAPR	G	0.23%	6299	6299	825.1087646	3	2472.302819	2471.296126	1.006692505	R	G	-	2	23	1	0
				901	927	26	R	ALGLGVEQLPVVFEDVVLHQATILPK	T	0.23%	9991	9991	929.5319824	3	2785.572472	2785.56295	0.009522058	R	T	Q20:+0.984	3	26	0	0
				967	992	25	R	LFDHPESPTPNPTEPLFLAQAEVYK	E	0.23%	5794	5794	947.8044434	3	2840.389855	2840.390859	-0.001003922	R	E	N11:+0.984	7	25	0	0
				1023	1051	28	K	DNWVSFMDTMLQMSILGSAKHGLYLPTR	V	1.82%	6134	6134	1076.208496	3	3225.602013	3226.561433	-0.959419975	K	V	M13:+15.995	2	28	-1	1
				1116	1131	15	K	FCFTPHTEEGCLSER	A	0.54%	2313	2313	623.9309692	3	1868.769433	1868.781239	-0.011806845	K	A	C2:+57.021,C11:+57.021	2	15	0	0
				1187	1208	21	R	LQLNGNLQLELAQVLAQERPK	L	0.49%	6919	6919	793.1134644	3	2376.316918	2375.31724	0.999677778	R	L	Q13:+0.984	1	21	1	0
				1208	1225	17	K	LPEDPLLSGLLDSPALK	A	0.23%	7460	7460	889.5	2	1776.98435	1776.987314	-0.002963584	K	A	-	7	17	0	0
				1404	1423	19	R	RPTPQDSPIFLPVDDTSFR	W	0.36%	4662	4662	730.3677368	3	2188.079735	2187.096029	0.983706001	R	W	-	3	19	1	0
				1444	1461	17	K	AINCATSGVVGLVNCLR	R	0.28%	5126	5126	901.4769287	2	1800.938207	1802.912194	-1.973986754	K	R	C4:+57.021,C15:+57.021	4	17	-1	0
				1470	1495	25	R	CVLLSNLSSTSHVPEVDPGSAELQK	V	0.23%	4162	4162	890.1159668	3	2667.324425	2666.32168	1.002744991	R	V	C1:+57.021	3	25	1	0
				1515	1538	23	R	HFLLEEDKPEEPTAHAFVSTLTR	G	0.23%	3976	3976	667.84	4	2667.3287	2666.334028	0.994671672	R	G	-	5	23	1	0
				1851	1866	15	K	VVVQVLAEEPEAVLK	G	0.23%	4796	4796	811.9671631	2	1621.918676	1621.92907	-0.010394124	K	G	-	4	15	0	0
				2125	2138	13	R	DLVEAVAHILGIR	D	0.23%	9997	9997	703.90979	2	1405.80393	1404.808895	0.995034734	R	D	-	7	13	1	0
				2220	2233	13	R	SLLVNPEGPTLMR	L	0.23%	3858	3858	714.3911743	2	1426.766699	1425.764983	1.001715897	R	L	-	6	13	1	0
				2233	2263	30	R	LNSVQSSERPLFLVHPIEGSTTVFHSLASR	L	0.23%	4982	4982	1103.914185	3	3308.719079	3307.731322	0.987756815	R	L	-	3	30	1	0
				2275	2294	19	R	AAPLDSIHSLAAYYIDCIR	Q	0.23%	7673	7673	717.3557129	3	2149.043664	2148.066909	0.97675452	R	Q	C17:+57.021	6	19	1	0
				2354	2382	28	K	LTPGCEAEAETEAICFFVQQFTDMEHNR	V	0.56%	9754	9754	1111.492065	3	3331.452721	3330.425821	1.026899881	K	V	C5:+57.021,C15:+57.021,	2	28	1	0
				2482	2505	23	R	TLLEGSGLESIISIIHSSLAEPR	V	0.23%	9734	9734	808.7749023	3	2423.301232	2421.311502	1.989730167	R	V	-	2	23	2	0
P49368	T-complex protein 1 subunit gamma	18	52.84%	46	68	22	M	MKMLLDPMGGIVMTNDGNAILR	E	1.51%	1564	1564	804.0717773	3	2409.191857	2406.178001	3.013855967	M	E	M13:+15.995,N15:+0.984	1	22	3	1
				48	68	20	K	MLLDPMGGIVMTNDGNAILR	E	0.23%	6997	6997	1066.547485	2	2131.079321	2130.063552	1.015768623	K	E	-	6	20	1	0
				85	127	42	R	TQDEEVGDGTTSVIILAGEMLSVAEHFLEQQMHPTVVISAYR	K	1.20%	13304	13304	1151.82	4	4603.2487	4602.214546	1.034154304	R	K	Q2:+0.984,Q30:+0.984	1	42	1	0
				138	163	25	K	KISIPVDISDSDMMLNIINSSITTK	A	0.23%	7837	7837	1368.716797	2	2735.417944	2734.413268	1.004675198	K	A	-	5	25	1	1
				139	163	24	K	ISIPVDISDSDMMLNIINSSITTK	A	0.23%	8718	8718	1304.66272	2	2607.309789	2606.318305	0.991484037	K	A	-	6	24	1	0
				167	181	14	R	WSSLACNIALDAVK	M	0.23%	4795	4795	774.3936157	2	1546.771581	1546.780897	-0.009315931	R	M	C6:+57.021	6	14	0	0
				203	216	13	K	IPGGIIEDSCVLR	G	0.23%	3676	3676	714.8773804	2	1427.739111	1427.743783	-0.004672786	K	G	C10:+57.021	6	13	0	0
				237	248	11	R	IVLLDSSLEYK	K	0.53%	4199	4199	640.8635864	2	1279.711523	1278.707115	1.004407316	R	K	-	4	11	1	0
				248	266	18	K	KGESQTDIEITREEDFTR	I	0.74%	1752	1752	718.6777954	3	2153.009911	2153.023652	-0.013741178	K	I	-	1	18	0	2
				266	294	28	R	ILQMEEEYIQQLCEDIIQLKPDVVITEK	G	0.23%	9392	9392	1139.942383	3	3416.803673	3417.729432	-0.925759035	R	G	C13:+57.021,Q18:+0.984	4	28	-1	0
				294	306	12	K	GISDLAQHYLMR	A	0.23%	4287	4287	702.3637085	2	1402.711767	1402.702717	0.009050248	K	A	-	6	12	0	0
				330	353	23	R	IVSRPEELREDDVGTGAGLLEIK	K	0.23%	3657	3657	833.45	3	2497.326525	2495.323129	2.00339576	R	K	-	1	23	2	1
				353	367	14	K	KIGDEYFTFITDCK	D	0.23%	4785	4785	868.9107056	2	1735.805761	1735.812257	-0.006496075	K	D	C13:+57.021	7	14	0	1
				381	389	8	K	EILSEVER	N	1.27%	1497	1497	487.7570496	2	973.498449	973.5080214	-0.009572407	K	N	-	1	8	0	0
				389	399	10	R	NLQDAMQVCR	N	2.99%	15185	15185	417.12	3	1248.336525	1250.53796	-2.201435568	R	N	N1:+0.984,M6:+15.995,C	1	10	-1	0
				399	425	26	R	NVLLDPQLVPGGGASEMAVAHALTEK	S	0.23%	6146	6146	873.1235352	3	2616.34713	2616.358136	-0.011005219	R	S	-	4	26	0	0
				438	449	11	R	AVAQALEVIPR	T	0.23%	3005	3005	583.8445435	2	1165.673437	1165.681904	-0.008466806	R	T	-	6	11	0	0
				491	502	11	K	ELGIWEPLAVK	L	0.23%	5346	5346	627.8547363	2	1253.693823	1253.70197	-0.008147848	K	L	-	7	11	0	0
P50281	Matrix metalloproteinase-14	1	2.06%	414	426	12	K	IDAALFWMPNGK	T	3.45%	2765	2765	455.2214661	3	1362.640923	1362.66419	-0.023267167	K	T	N10:+0.984	1	12	0	0
P50395	Rab GDP dissociation inhibitor beta	1	4.27%	118	137	19	K	VPSTEAEALASSLMGLFEK	R	0.23%	9568	9568	991.0045776	2	1979.993505	1978.992142	1.001363073	K	R	-	7	19	1	0
P51148	Ras-related protein Rab-5C	3	19.44%	121	135	14	R	QASPNIVIALAGNK	A	0.30%	3484	3484	698.8998413	2	1395.784033	1395.77216	0.011872713	R	A	Q1:+0.984	2	14	0	0
				166	180	14	K	TAMNVNEIFMAIAK	K	0.23%	6813	6813	776.8928223	2	1551.769994	1551.778919	-0.008924885	K	K	-	7	14	0	0
				184	198	14	K	NEPQNATGAPGRNR	G	3.45%	1127	1127	741.6132813	2	1481.210912	1482.681097	-1.470184972	K	G	N1:+0.984,N13:+0.984	1	14	-1	1
P51151	Ras-related protein Rab-9A	1	7.96%	31	47	16	K	FDTQLFHTIGVEFLNK	D	0.61%	6740	6740	954.9952393	2	1907.974828	1907.978146	-0.003317332	K	D	-	2	16	0	0
P51159	Ras-related protein Rab-27A	2	10.86%	69	80	11	H	LQLWDTAGQER	F	2.42%	2729	2729	660.79	2	1319.56435	1316.63606	2.928289784	S	F	Q2:+0.984	2	11	3	0
				141	154	13	R	VVKEEEAIALAEK	Y	1.33%	1592	1592	476.9342346	3	1427.779229	1427.787157	-0.007928103	R	Y	-	2	13	0	1
P51170	Amiloride-sensitive sodium channel subunit gamma	1	2.62%	13	30	17	K	NLPVTGPQAPTIKELMR	W	2.00%	800	800	627.9437256	3	1880.807702	1881.987051	-1.179349626	K	W	N1:+0.984,Q8:+0.984,M1	1	17	-1	1
P51572	B-cell receptor-associated protein 31	1	6.50%	79	95	16	K	VNLQNNPGAMEHFHMK	L	0.23%	1862	1862	933.9404297	2	1865.865209	1865.866506	-0.001296425	K	L	-	6	16	0	0
P51617	Interleukin-1 receptor-associated kinase 1	1	2.11%	79	94	15	R	VADLVHILTHLQLLR	A	0.23%	7399	7399	580.9802246	3	1739.917199	1740.041021	-0.123822036	R	A	-	4	15	0	0
P51677	C-C chemokine receptor type 3	1	8.45%	277	307	30	K	HLDLVMLVTEVIAYSHCCMNPVIYAFVGER	F	9.25%	11675	11675	885.4265747	4	3537.674999	3536.695519	0.979479404	K	F	C17:+57.021,C18:+57.021	1	30	1	0
P51805	Plexin-A3	1	0.69%	1305	1318	13	R	VLFPGIEAHPVLK	E	7.77%	1181	1181	711.32	2	1420.62435	1418.828568	1.795781872	R	E	-	1	13	2	0
P52272	Heterogeneous nuclear ribonucleoprotein M	21	49.32%	17	48	31	K	MEEESGAPGVPSGNGAPGPKGEGERPAQNEK	R	3.03%	1054	1054	767.35	4	3065.3687	3064.367954	1.000746128	K	R	Q28:+0.984,N29:+0.984	2	31	1	1
				72	83	11	R	AFITNIPFDVK	W	0.23%	5155	5155	632.8480835	2	1263.680517	1263.68632	-0.005803432	R	W	-	6	11	0	0
				94	110	16	K	VGEVTYVELLMDAEGK	S	0.23%	7949	7949	877.8563843	2	1753.697118	1751.865151	1.831967979	K	S	-	3	16	2	0
				159	201	42	K	VMATTGGMGMGPGGPGMITIPPSILNNPNIPNEIIHALQAGR	L	0.53%	9312	9312	1399.375488	3	4195.10299	4195.105033	-0.002043732	K	L	N26:+0.984	2	42	0	0
				201	214	13	R	LGSTVFVANLDYK	V	0.28%	4050	4050	713.8744507	2	1425.733251	1425.750377	-0.017126033	R	V	-	4	13	0	0
				244	277	33	R	GIGTVTFEQSIEAVQAISMFNGQLLFDRPMHVK	M	0.37%	9718	9718	917.48	4	3665.8887	3664.826909	1.061790536	R	M	Q9:+0.984,Q23:+0.984	2	33	1	0
				285	322	37	K	GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLNK	G	0.48%	5162	5162	955.979187	4	3819.885448	3819.879095	0.006352647	K	G	Q10:+0.984,N33:+0.984	2	37	0	0
				322	345	23	K	GIGMGNIGPAGMGMEGIGFGINK	M	0.23%	6231	6231	1089.521606	2	2177.027563	2177.043151	-0.015588077	K	M	-	4	23	0	0
				322	362	40	K	GIGMGNIGPAGMGMEGIGFGINKMGGMEGPFGGGMENMGR	F	2.88%	11517	11517	973.505188	4	3889.989452	3891.651744	-1.662291743	K	F	N6:+0.984,N22:+0.984,M2	1	40	-1	1
				345	362	17	K	MGGMEGPFGGGMENMGR	F	0.23%	3969	3969	857.8389282	2	1713.662206	1713.673153	-0.010946283	K	F	-	6	17	0	0
				371	381	10	R	INEILSNALK	R	0.23%	2839	2839	557.8231201	2	1113.63059	1113.63937	-0.00877995	R	R	-	6	10	0	0
				456	471	15	R	MGPLGLDHMASSIER	M	0.23%	3725	3725	807.3948975	2	1612.774145	1612.770146	0.003999242	R	M	-	3	15	0	0
				485	496	11	R	MGAGMGFGLER	M	0.23%	3023	3023	564.333313	2	1126.650976	1124.510683	2.140292905	R	M	-	3	11	2	0
				565	578	13	R	MGLERMGANSLER	M	3.34%	5243	5243	489.6025696	3	1465.784234	1462.702066	3.0821677	R	M	-	1	13	3	1
				583	606	23	R	MGANSLERMGPAMGPALGAGIER	M	2.49%	4870	4870	580.5430908	4	2318.141063	2317.097877	1.043186601	R	M	M1:+15.995,M9:+15.995	1	23	1	1
				591	606	15	R	MGPAMGPALGAGIER	M	0.23%	2964	2964	714.3547363	2	1426.693823	1426.706089	-0.012266048	R	M	-	6	15	0	0
				591	621	30	R	MGPAMGPALGAGIERMGLAMGGGGGASFDR	A	2.46%	7343	7343	706.6146851	4	2822.42744	2823.290631	-0.863191334	R	A	M1:+15.994,M5:+15.994	1	30	-1	1
				627	650	23	R	GNFGGSFAGSFGGAGGHAPGVAR	K	0.23%	2910	2910	1017.9729	2	2033.930151	2033.945617	-0.015466171	R	K	-	4	23	0	0
				658	667	9	R	NLPFDFTWK	M	1.28%	6126	6126	584.2928467	2	1166.570043	1166.576041	-0.005998177	R	M	-	1	9	0	0
				672	685	13	K	FNECGHVLYADIK	M	0.23%	2131	2131	783.3718872	2	1564.728124	1564.733947	-0.005822722	K	M	C4:+57.021	4	13	0	0
				672	690	18	K	FNECGHVLYADIKMENGK	S	2.20%	10496	10496	708.5404663	3	2122.597924	2123.976381	-1.378456706	K	S	C4:+57.021	1	18	-1	1
P53618	Coatomer subunit beta	7	14.59%	164	185	21	R	NFEHLIPDAPELIHDFLVNEK	D	0.23%	8256	8256	830.7583618	3	2489.25161	2489.259072	-0.007461815	R	D	-	4	21	0	0
				261	279	18	K	YEAAGTLVTLSSAPTAIK	A	0.23%	4028	4028	897.9292603	2	1793.84287	1791.961827	1.881043396	K	A	-	5	18	2	0
				316	327	11	R	VLQDLVMDILR	V	0.23%	7574	7574	657.8728638	2	1313.730077	1313.737705	-0.007627741	R	V	-	6	11	0	0
				495	513	18	K	EAGELKPEEEITVGPVQK	L	0.23%	2211	2211	977.5059204	2	1952.996191	1952.010234	0.985956812	K	L	-	6	18	1	0
				513	535	22	K	LVTEMGTYATQSALSSSRPTKK	E	1.10%	2053	2053	786.7390137	3	2357.193566	2356.194409	0.999157392	K	E	Q11:+0.984	1	22	1	1
				767	786	19	K	LVEKPSPLTLAPHDFANIK	A	0.23%	3528	3528	697.7247314	3	2090.150719	2089.157173	0.993546224	K	A	-	3	19	1	0
				898	928	30	R	SIFGEDALANVSIEKPIHQGPDAAVTGHIR	I	0.23%	4267	4267	1048.871948	3	3143.59237	3142.604709	0.987661047	R	I	Q19:+0.984	3	30	1	0
P53985	Monocarboxylate transporter 1	1	4.00%	459	479	20	K	ESKEEETSIDVAGKPNEVTK	A	0.23%	1136	1136	730.6952515	3	2189.062279	2189.069934	-0.007654597	K	A	-	4	20	0	1
P54709	Sodium/potassium-transporting ATPase subunit beta-3	4	19.71%	17	31	14	K	LFIYNPTTGEFLGR	T	0.23%	5834	5834	814.9367065	2	1627.857763	1627.824589	0.033173582	K	T	N5:+0.984	4	14	0	0
				71	97	26	K	YRDQIPSPGLMVFPKPVTALEYTFSR	S	0.23%	6802	6802	754.3995972	4	3013.567089	3012.541898	1.02519028	K	S	Q4:+0.984	3	26	1	1
				73	97	24	R	DQIPSPGLMVFPKPVTALEYTFSR	S	0.23%	7621	7621	1347.205444	2	2692.395239	2693.377458	-0.98221984	R	S	Q2:+0.984	4	24	-1	0
				97	112	15	R	SDPTSYAGYIEDLKK	F	0.23%	3603	3603	844.4107056	2	1686.805761	1685.814828	0.990932757	R	F	-	6	15	1	1
P55196	Afadin	1	2.52%	728	774	46	K	YLVHCLQSELNNYMPAFLDDPEENSLQRPKIDDVLHTLTGAMSLLR	R	6.57%	9310	9310	1348.659546	4	5390.606883	5389.592183	1.014700818	K	R	C5:+57.021,N11:+0.984,M	1	46	1	1
P61006	Ras-related protein Rab-8A	5	29.95%	10	21	11	K	LLLIGDSGVGK	T	0.23%	3109	3109	536.3213501	2	1070.62705	1070.633556	-0.006506301	K	T	-	3	11	0	0
				58	69	11	K	LQIWDTAGQER	F	0.23%	2690	2690	658.8308105	2	1315.645971	1315.65206	-0.006089122	K	F	-	3	11	0	0
				104	116	12	R	NIEEHASADVEK	M	0.23%	859	859	671.3129883	2	1340.610326	1340.62082	-0.010493165	R	M	-	7	12	0	0
				153	167	14	K	ANINVENAFFTLAR	D	1.34%	6184	6184	790.41	2	1578.80435	1578.815437	-0.01108736	K	D	-	2	14	0	0
				176	190	14	K	LEGNSPQGSNQGVK	I	3.01%	6731	6731	708.3706665	2	1414.725683	1415.652817	-0.927134024	K	I	N4:+0.984,Q7:+0.984	1	14	-1	0
P61026	Ras-related protein Rab-10	5	28.50%	11	22	11	K	LLLIGDSGVGK	T	0.23%	3109	3109	536.3213501	2	1070.62705	1070.633556	-0.006506301	K	T	-	3	11	0	0
				59	70	11	K	LQIWDTAGQER	F	0.23%	2690	2690	658.8308105	2	1315.645971	1315.65206	-0.006089122	K	F	-	3	11	0	0
				161	172	11	K	AFLTLAEDILR	K	0.23%	7237	7237	631.3589478	2	1260.702245	1260.707784	-0.005538684	K	K	-	7	11	0	0
				161	173	12	K	AFLTLAEDILRK	T	1.26%	5955	5955	463.940033	3	1388.796624	1388.802747	-0.006123491	K	T	-	2	12	0	1
				173	196	23	K	TPVKEPNSENVDISSGGGVTGWK	S	0.23%	2363	2363	787.3887939	3	2359.142907	2357.149916	1.992991132	K	S	-	4	23	2	1
P61077	Ubiquitin-conjugating enzyme E2 D3	1	16.33%	101	125	24	K	VLLSICSLLCDPNPDDPLVPEIAR	I	0.23%	8498	8498	1354.183838	2	2706.352026	2705.375896	0.976129957	K	I	C6:+57.021,C10:+57.021	6	24	1	0
P61106	Ras-related protein Rab-14	5	33.02%	61	72	11	K	LQIWDTAGQER	F	0.23%	2690	2690	658.8308105	2	1315.645971	1315.65206	-0.006089122	K	F	-	3	11	0	0
				110	125	15	R	NLTNPNTVIILIGNK	A	0.23%	4866	4866	812.4698486	2	1622.924047	1622.935553	-0.011505374	R	A	-	6	15	0	0
				156	171	15	K	TGENVEDAFLEAAKK	I	2.81%	3455	3455	540.630188	3	1618.867089	1620.799513	-1.932423699	K	I	-	1	15	-1	1
				170	201	31	K	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	L	0.23%	2338	2338	820.6669312	4	3278.636424	3277.643963	0.992461137	K	L	-	2	31	1	1
				171	201	30	K	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	L	0.23%	2683	2683	1051.526123	3	3151.554894	3150.533	1.021893845	K	L	Q20:+0.984	6	30	1	0
P61158	Actin-related protein 3	3	18.66%	161	191	30	R	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	H	0.23%	6286	6286	1020.194153	3	3057.558983	3057.568787	-0.009803808	R	H	C28:+57.021	6	30	0	0
				198	209	11	R	DITYFIQQLLR	D	0.23%	9717	9717	705.3891602	2	1408.76267	1408.771447	-0.008776855	R	E	-	6	11	0	0
				275	312	37	R	FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	R	0.83%	10934	10934	1080.522583	4	4318.059032	4316.077132	1.981899783	R	R	Q19:+0.984,C32:+57.021	3	37	2	0
P61224	Ras-related protein Rap-1b	1	6.52%	151	163	12	K	INVNEIFYDLVR	Q	0.23%	8043	8043	748.4017944	2	1494.787939	1493.787826	1.000113291	K	Q	-	7	12	1	0
P61421	V-type proton ATPase subunit d 1	1	2.28%	75	83	8	K	EKMVVEFR	H	1.01%	6361	6361	519.2548218	2	1036.493993	1036.537549	-0.043555061	K	H	-	1	8	0	1
P61769	Beta-2-microglobulin	1	18.49%	39	61	22	K	SNFLNCYVSGFHPSDIEVDLLK	N	0.23%	7017	7017	852.0770874	3	2553.207787	2553.220509	-0.012722369	K	N	C6:+57.021	3	22	0	0
P62491	Ras-related protein Rab-11A	1	6.02%	82	95	13	R	GAVGALLVYDIAK	H	0.23%	5097	5097	645.8735962	2	1289.731542	1288.739084	0.992458031	R	H	-	7	13	1	0
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	1	3.53%	197	209	12	R	TFVSGACDASIK	L	2.40%	1408	1408	629.0848389	2	1256.154028	1254.590971	1.56305663	R	L	C7:+57.021	3	12	2	0
P63000	Ras-related C3 botulinum toxin substrate 1	2	13.02%	132	147	15	K	KLTPITYPQGLAMAK	E	0.23%	3029	3029	816.458313	2	1630.900976	1630.911647	-0.010671167	K	E	-	5	15	0	1
				153	163	10	K	YLECSALTQR	G	0.52%	1482	1482	620.7967529	2	1239.577856	1239.591305	-0.013449573	K	G	C4:+57.021	3	10	0	0
P63010	AP-2 complex subunit beta	1	1.60%	344	359	15	R	LASQANIAQVLAELK	E	0.23%	6208	6208	785.4585571	2	1568.901464	1567.893353	1.008110826	R	E	-	6	15	1	0
P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	4	22.08%	58	81	23	K	QMRILHVNGFNGEGGEEDPQAAR	S	2.62%	10002	10002	843.4373779	3	2527.288659	2526.155716	1.132942669	K	S	Q1:+0.984,Q20:+0.984	1	23	1	1
				100	127	27	K	EAIETIVAAMSNLVPPVELANPENQFR	V	0.23%	9965	9965	739.64	4	2954.5287	2952.490257	2.038443208	K	V	N21:+0.984	1	27	2	0
				165	186	21	R	SNEYQLIDCAQYFLDKIDVIK	Q	0.28%	8904	8904	859.4215698	3	2575.241234	2574.267125	0.974108985	R	Q	C9:+57.021	2	21	1	1
				317	333	16	R	YTTPEDATPEPGEDPR	V	2.63%	1124	1124	888.7368774	2	1775.458105	1773.769335	1.688770091	R	V	-	2	16	2	0
P63167	Dynein light chain 1, cytoplasmic	1	24.72%	9	31	22	K	NADMSEEMQQDSVECATQALEK	Y	0.23%	4496	4496	1258.52124	2	2515.02683	2513.035155	1.991675333	K	Y	C15:+57.021	6	22	2	0
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	7	40.06%	12	36	24	K	GHNGWVTQIATTPQFPDMILSASR	D	0.23%	6792	6792	1315.139282	2	2628.262914	2627.280204	0.982710469	K	D	N3:+0.984	4	24	1	0
				88	99	11	R	LWDLTTGTTTR	R	0.23%	3162	3162	632.8294067	2	1263.643163	1263.645912	-0.002748723	R	R	-	3	11	0	0
				155	172	17	R	FSPNSSNPIIVSCGWDK	L	0.23%	3987	3987	954.442749	2	1906.869848	1906.887882	-0.018033841	R	L	C13:+57.021	4	17	0	0
				185	212	27	K	TNHIGHTGYLNTVTVSPDGSLCASGGK	D	0.23%	2404	2404	1373.155884	2	2744.296118	2742.302676	1.993441346	K	D	C22:+57.021	4	27	2	0
				225	245	20	K	HLYTLDGGDIINALCFSPNR	Y	0.23%	6275	6275	759.37677	3	2275.106835	2275.105086	0.001749403	K	Y	C15:+57.021	3	20	0	0
				245	257	12	R	YWLCAATGPSIK	I	0.23%	3431	3431	683.8421021	2	1365.668554	1365.674641	-0.00608709	R	I	C4:+57.021	6	12	0	0
				264	280	16	K	IIVDELKQEVISTSSK	A	0.23%	3855	3855	596.9996948	3	1787.975609	1787.988042	-0.012432479	K	A	-	3	16	0	1
P68400	Casein kinase II subunit alpha	1	4.60%	89	107	18	R	GGPNIITLADIVKDPVSR	T	0.31%	5711	5711	622.3497314	3	1864.025719	1864.041809	-0.016089528	R	T	-	2	18	0	1
P78325	Disintegrin and metalloproteinase domain-containing protein 8	1	6.43%	128	181	53	R	GFFQVGSDLHLIEPLDEGGEGGRHAVYQAEHLLQTAGTCGVSDDSLGSLLGPR	T	1.75%	8134	8134	1391.220947	4	5560.852489	5561.690536	-0.838046722	R	T	C39:+57.021	2	53	-1	1
P82279	Crumbs homolog 1	1	1.42%	647	667	20	K	IDWNHITLENISSGSSLNVK	A	2.67%	4201	4201	1113.060669	2	2224.105688	2226.128058	-2.022370005	K	A	-	2	20	-1	0
P98171	Rho GTPase-activating protein 4	3	RHG04_HUMAN	54	65	11	R	RRAEVELEYSR	G	1.13%	1151	1151	469.9151001	3	1406.721825	1406.726622	-0.004796987	R	G	-	1	11	0	2
				145	168	23	K	SRDLEQQLQDELLEVVSELQTAK	K	1.24%	10248	10248	891.4624023	3	2671.363732	2671.355202	0.008530223	K	K	Q20:+0.984	2	23	0	1
				147	168	21	R	DLEQQLQDELLEVVSELQTAK	K	0.23%	11125	11125	810.42	3	2428.236525	2427.238062	0.998462832	R	K	-	4	21	1	0
Q00325	Phosphate carrier protein, mitochondrial	7	19.34%	101	112	11	K	GIFNGFSVTLK	E	0.23%	5909	5909	592.8137817	2	1183.611913	1182.628455	0.983457933	K	E	N4:+0.984	6	11	1	0
				137	145	8	K	FGFYEVFK	V	0.23%	5185	5185	519.256958	2	1036.498266	1035.506565	0.991701144	K	V	-	7	8	1	0
				145	161	16	K	VLYSNMLGEENTYLWR	T	0.23%	5852	5852	994.9692993	2	1987.922949	1986.950946	0.972002657	K	T	-	5	16	1	0
				189	201	12	R	IQTQPGYANTLR	D	2.46%	1803	1803	455.5762024	3	1363.705132	1362.677909	1.027222634	R	D	Q2:+0.984,N9:+0.984	2	12	1	0
				218	226	8	K	GVAPLWMR	Q	0.40%	2998	2998	465.2533569	2	928.4910638	928.4952897	-0.004225869	K	Q	-	3	8	0	0
				341	355	14	R	LPRPPPPEMPESLK	K	0.23%	2285	2285	529.9541016	3	1586.83883	1586.849047	-0.010217176	R	K	-	7	14	0	0
				341	356	15	R	LPRPPPPEMPESLKK	K	0.23%	1738	1738	429.7410584	4	1714.932933	1714.94401	-0.011076642	R	K	-	4	15	0	1
Q00610	Clathrin heavy chain 1	28	31.22%	8	36	28	R	FQEHLQLQNLGINPANIGFSTLTMESDK	F	0.23%	6784	6784	1049.858154	3	3146.550988	3144.554998	1.995989915	R	F	-	3	28	2	0
				227	245	18	K	LHIIEVGTPPTGNQPFPK	K	0.23%	3353	3353	973.0301514	2	1944.044653	1944.046894	-0.00224145	K	K	-	5	18	0	0
				297	320	23	R	ISGETIFVTAPHEATAGIIGVNR	K	0.23%	4704	4704	785.4249268	3	2353.251305	2352.243756	1.007548761	R	K	-	3	23	1	0
				320	350	30	R	KGQVLSVCVEEENIIPYITNVLQNPDLALR	M	0.28%	9183	9183	1142.935669	3	3425.783532	3423.806726	1.976805364	R	M	C8:+57.021	5	30	2	1
				366	382	16	R	KFNALFAQGNYSEAAK	V	0.84%	2312	2312	587.9680176	3	1760.880578	1758.857681	2.022897046	R	V	Q8:+0.984	1	16	2	1

				400	429	29	R	FQSVPAQPGQTSPLLQYFGILLDQGQLNK	Y	0.23%	9610	9610	1063.894531	3	3188.660119	3187.655347	1.004771454	R	Y	Q16:+0.984	5	29	1	0
				429	444	15	K	YESLELCRPVLQQGR	K	0.94%	2658	2658	924.9750366	2	1847.934423	1846.935501	0.998922458	K	K	C7:+57.021	3	15	1	0
				450	468	18	K	WLKEDKLECSEELGDLVK	S	2.79%	3771	3771	731.0372314	3	2190.088219	2190.08737	0.0008494	K	T	C9:+57.021	1	18	0	2
				487	500	13	K	VIQCFAETGQVQK	I	0.23%	1461	1461	754.3793335	2	1506.743017	1506.749597	-0.006580224	K	I	C4:+57.021	6	13	0	0
				571	583	12	K	NNRPSEGPLQTR	L	3.01%	1505	1505	457.0647888	3	1368.170891	1369.658571	-1.487679633	K	L	N1:+0.984,N2:+0.984	1	12	-1	0
				583	610	27	R	LLEMNLMHAPQVADAILGNQMFTHYDR	A	0.23%	7494	7494	782.8823853	4	3127.498241	3127.504167	-0.005926288	R	A	-	2	27	0	0
				668	688	20	R	AMLSANIRQNLQICVQVASK	Y	3.06%	11959	11959	749.0808105	3	2244.218957	2246.139377	-1.920420031	R	Y	N6:+0.984,Q9:+0.984,N10	1	20	-1	1
				688	706	18	K	YHEQLSTQSLIELFESFK	S	0.23%	8518	8518	734.0354614	3	2199.082909	2198.089547	0.993362173	K	S	-	5	18	1	0
				856	865	9	K	LLLPWLEAR	I	0.23%	6551	6551	555.8348999	2	1109.65415	1109.659712	-0.005561819	K	I	-	7	9	0	0
				881	892	11	K	IYIDSNNNPER	F	2.76%	794	794	668.2946777	2	1334.573705	1334.610239	-0.036533947	K	F	N8:+0.984	1	11	0	0
				923	941	18	R	GQCDLELINVCNENSLFK	S	0.23%	5671	5671	1077.997192	2	2153.978735	2151.991961	1.986773862	R	S	C3:+57.021,C11:+57.021	3	18	2	0
				967	993	26	R	RPLIDQVVQTALSETQDPEEVSVTVK	A	0.23%	6989	6989	961.5112915	3	2881.510399	2880.50803	1.002369688	R	A	-	4	26	1	0
				993	1010	17	K	AFMTADLPNELIELLEK	I	0.23%	9620	9620	974.5087891	2	1947.001928	1946.007064	0.994864173	K	I	-	7	17	1	0
				1010	1022	12	K	IVLDNSVFSEHR	N	0.23%	2595	2595	708.3638306	2	1414.712011	1414.720474	-0.008463091	K	N	-	4	12	0	0
				1022	1034	12	R	NLQNLLILTAIK	A	0.23%	6571	6571	677.4243164	2	1352.832983	1352.839133	-0.006150036	R	A	-	6	12	0	0
				1046	1074	28	R	LDNYDAPDIANIAISNELFEEAFAIFRK	F	2.77%	4889	4889	801.16	4	3200.6087	3201.539343	-0.93064292	R	F	N3:+0.984,N11:+0.984,N1	1	28	-1	1
				1073	1094	21	R	KFDVNTSAVQVLIEHIGNLDR	A	0.23%	7339	7339	791.088562	3	2370.242211	2368.238655	2.003555475	R	A	Q10:+0.984	2	21	2	1
				1182	1204	22	R	LAELEEFINGPNNAHIQQVGDR	C	0.23%	4497	4497	822.4099731	3	2464.206444	2464.198247	0.008197098	R	C	N13:+0.984	1	22	0	0
				1226	1245	19	R	LASTLVHLGEYQAAVDGAR	K	0.23%	3655	3655	986.5119019	2	1971.008154	1970.022136	0.986017671	R	K	-	7	19	1	0
				1235	1254	19	G	EYQAAVDGARKANSTRTWK	E	3.09%	9079	9079	1078.146484	2	2154.277319	2152.066111	2.21120811	G	E	N13:+0.984	1	19	2	3
				1461	1481	20	K	SVNESLNNLFITEEDYQALR	T	0.23%	6243	6243	1179.075317	2	2356.134985	2354.139017	1.99596815	K	T	-	3	20	2	0
				1481	1498	17	R	TSIDAYDNFDNISLAQR	L	0.23%	4678	4678	971.9596558	2	1941.903661	1941.906831	-0.003169941	R	L	-	5	17	0	0
				1588	1604	16	R	HNIMDFAMPYFIQVMK	E	0.23%	8630	8630	993.4995117	2	1984.983373	1983.940917	1.04245595	R	E	-	4	16	1	0
Q00839	Heterogeneous nuclear ribonucleoprotein U	12	23.76%	37	69	32	R	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	S	0.36%	3587	3587	1043.474609	3	3127.400353	3126.415982	0.984370805	R	S	N20:+0.984	4	32	1	0
				186	204	18	K	SSGPTSLFAVTVAPPGAR	Q	0.23%	4633	4633	857.9575195	2	1713.899389	1713.904981	-0.005591745	K	Q	-	7	18	0	0
				436	462	26	K	EVLAGRPLFPHVLCHNCAVEFNFGQK	E	0.23%	4624	4624	1014.171814	3	3039.491967	3038.499808	0.992158799	K	E	C14:+57.021,C17:+57.021	3	26	1	0
				442	462	20	R	PLFPHVLCHNCAVEFNFGQK	E	0.58%	4539	4539	1208.078125	2	2414.1406	2413.145048	0.995552016	R	E	C8:+57.021,C11:+57.021	2	20	1	0
				462	484	22	K	EKPYFPIPEEYTFIQNVPLEDR	V	0.23%	6509	6509	1362.681885	2	2723.348119	2723.348281	-0.000161813	K	V	-	5	22	0	0
				494	510	16	K	KDCEVVMMIGLPGAGK	T	0.23%	4146	4146	854.0127563	2	1706.009863	1703.840405	2.169457471	K	T	C3:+57.021	3	16	2	1
				524	536	12	K	YNILGTNTIMDK	M	0.23%	3789	3789	691.850708	2	1381.685766	1381.691149	-0.005383024	K	M	-	4	12	0	0
				574	590	16	K	RNFILDQTNVSAAAQR	R	0.23%	2341	2341	902.9758301	2	1803.93601	1802.938741	0.997269548	K	R	-	3	16	1	1
				575	590	15	R	NFILDQTNVSAAAQR	R	0.23%	3231	3231	824.4233398	2	1646.83103	1646.837629	-0.006599768	R	R	-	6	15	0	0
				592	601	9	K	MCLFAGFQR	K	0.23%	6639	6639	565.7868652	2	1129.55808	1128.52039	1.037690445	K	K	C2:+57.021	1	9	1	0
				637	664	27	K	GNFTLPEVAECFDEITYVELQKEEAQK	L	0.23%	8215	8215	1595.248169	2	3188.480688	3186.506247	1.974441275	K	L	C11:+57.021	5	27	2	1
				796	814	18	K	NQSQGYNQWQQGQFWGQK	P	1.02%	3694	3694	1107.495483	2	2212.975317	2210.98821	1.987106637	K	P	-	2	18	2	0
Q00975	Voltage-dependent N-type calcium channel subunit alpha-1B	1	0.47%	1639	1650	11	R	TFLQALMLLFR	S	8.25%	1915	1915	456.9236145	3	1367.747368	1367.763611	-0.016242974	R	S	M7:+15.995	1	11	0	0
Q01082	Spectrin beta chain, brain 1	2	0.97%	1143	1156	13	R	LQALDTGWNELHK	M	9.02%	2971	2971	762.9215698	2	1523.82749	1523.773238	0.054251496	R	M	-	3	13	0	0
				1622	1632	10	K	DEQSAVSMLK	K	5.66%	2431	2431	554.7862549	2	1107.55686	1107.511772	0.04508787	K	K	Q3:+0.984	3	10	0	0
Q01518	Adenylyl cyclase-associated protein 1	1	4.84%	37	60	23	K	AGAAPYVQAFDSLLAGPVAEYLK	I	0.49%	9552	9552	1177.57	2	2353.12435	2350.220896	2.90345428	K	I	-	2	23	3	0
Q01718	Adrenocorticotropic hormone receptor	1	9.43%	23	51	28	R	VVLPEEIFFTISIVGVLENLIVLLAVFK	N	4.26%	6882	6882	1558.852905	2	3115.69016	3113.839582	1.850578707	R	N	-	2	28	2	0
Q03001	Bullous pemphigoid antigen 1	1	0.29%	1553	1575	22	K	VIAGTIDQTTGEVLSVFQAVLR	G	4.37%	1001	1001	774.5320435	3	2320.572655	2317.252909	3.319746715	K	G	Q18:+0.984	1	22	3	0
Q03518	Antigen peptide transporter 1	1	3.71%	678	708	30	K	SGAHSFISGLPQGYDTEVDEAGSQLSGGQR	Q	0.23%	4596	4596	1018.136475	3	3051.385949	3050.385333	1.000615924	K	Q	Q12:+0.984	2	30	1	0
Q03519	Antigen peptide transporter 2	2	6.71%	469	487	18	K	FQDVSFAYPNRPDRPVLK	G	7.53%	2735	2735	717.3777466	3	2149.109765	2149.09562	0.01414489	K	G	N10:+0.984	1	18	0	0
				575	603	28	K	VMAAAQAAHADDFIQEMEHGIYTDVGEK	G	1.08%	6316	6316	762.8512573	4	3047.373729	3047.364071	0.009658217	K	G	Q6:+0.984	1	28	0	0
Q04941	Proteolipid protein 2	1	9.87%	6	21	15	R	LSAPGCWAACTNFSR	T	0.23%	3506	3506	849.3739624	2	1696.732275	1696.744066	-0.011791195	R	T	C6:+57.021,C10:+57.021	5	15	0	0
Q05469	Hormone-sensitive lipase	1	2.32%	498	523	25	R	NETGLSVAASSLFTSGRFAIDPELR	G	1.38%	5074	5074	880.27	3	2637.786525	2637.339842	0.446683024	R	G	-	2	25	0	1
Q05586	Glutamate [NMDA] receptor subunit zeta-1	1	1.49%	846	860	14	K	QMQLAFAAVNVWRK	N	2.60%	7890	7890	832.4226685	2	1662.829687	1662.855164	-0.025476742	K	N	Q1:+0.984,N10:+0.984	2	14	0	1
Q07001	Acetylcholine receptor subunit delta	1	6.38%	244	277	33	R	KPLFYIINILVPCVLISFMVNLVFYLPADSGEK	T	1.33%	8049	8049	958.19	4	3828.7287	3828.064608	0.664092184	R	T	C13:+57.021,M19:+15.995	2	33	1	0
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	1	4.96%	80	94	14	K	AFVDFLSDEIKEER	K	0.48%	5449	5449	566.617981	3	1696.830468	1696.830813	-0.000344953	K	K	-	4	14	0	1
Q08722	Leukocyte surface antigen CD47	1	2.48%	85	93	8	K	IEVSQLLK	G	0.77%	3104	3104	465.2846985	2	928.5537469	928.5593287	-0.005581827	K	G	-	1	8	0	0
Q10589	Bone marrow stromal antigen 2	1	8.33%	111	126	15	K	KVEELEGEITTLNHK	L	0.23%	1962	1962	870.4579468	2	1738.900243	1738.910126	-0.009882285	K	L	-	7	15	0	1
Q12846	Syntaxin-4	1	6.40%	102	121	19	K	AIEPQKEEADENYNSVNTR	M	0.75%	1071	1071	736.3449097	3	2206.011254	2206.997816	-0.986562012	K	M	N12:+0.984	5	19	-1	1
Q12852	Mitogen-activated protein kinase kinase kinase 12	1	1.63%	692	706	14	R	AGSQHLTPAALLYR	A	0.36%	3600	3600	749.3928833	2	1496.770117	1496.809958	-0.039841398	R	A	-	2	14	0	0
Q12913	Receptor-type tyrosine-protein phosphatase eta	1	1.05%	945	959	14	K	GLIDGAESYVSFSR	Y	1.68%	2673	2673	502.9130859	3	1505.715783	1499.725619	5.990163517	K	Y	-	1	14	6	0
Q13009	T-lymphoma invasion and metastasis-inducing protein 1	1	0.94%	622	637	15	R	CYLASLQGGELPNPK	R	8.65%	1277	1277	549.609436	3	1645.804833	1645.812926	-0.008092799	R	S	C1:+57.021	1	15	0	0
Q13283	Ras GTPase-activating protein-binding protein 1	1	3.86%	335	353	18	R	HPDSHQLFIGNLPHEVDK	S	2.92%	2319	2319	522.27	4	2085.0487	2083.012284	2.036415864	R	S	N11:+0.984	2	18	2	0
Q13308	Tyrosine-protein kinase-like 7	1	1.40%	845	860	15	R	ELEMFGKLNHANVVR	L	7.39%	5014	5014	879.0995483	2	1756.183447	1756.893021	-0.709574744	R	L	N9:+0.984	2	15	-1	1
Q13444	Disintegrin and metalloproteinase domain-containing protein 15	1	2.32%	268	288	20	R	DLVEISPNPAVTLENFLHWR	R	2.10%	9601	9601	784.4093018	3	2350.20443	2349.211728	0.992702249	R	R	-	1	20	1	0
Q13563	Polycystin-2	1	2.27%	28	50	22	R	LMAGCAAVGASLAAPGGLCEQR	G	2.61%	1998	1998	720.6237183	3	2158.84768	2159.027636	-0.179956263	R	G	C5:+57.021,C19:+57.021	1	22	0	0
Q13635	Protein patched homolog 1	1	2.42%	205	240	35	K	SGELITETGYMDQIIEYLYPCLIITPLDCFWEGAK	L	8.06%	7491	7491	1040.75769	4	4158.999462	4153.960604	5.038857615	K	L	M11:+15.995,C21:+57.021	1	35	5	0
Q13740	CD166 antigen	1	1.72%	362	372	10	A	TVVWMKDNIR	L	7.71%	2474	2474	421.2223206	3	1260.643487	1260.664874	-0.021387938	A	L	-	1	10	0	1
Q14108	Lysosome membrane protein 2	1	6.28%	348	378	30	R	FVSAIEGMHPNQEDHETFVDINPLTGIILK	A	0.23%	6709	6709	1122.570801	3	3364.688927	3364.664927	0.0240004	R	A	N22:+0.984	2	30	0	0
Q14254	Flotillin-2	2	7.24%	100	112	12	K	NVVLQTLEGHLR	S	2.98%	3926	3926	688.3684692	2	1374.721288	1377.772844	-3.051555675	K	S	-	2	12	-1	0
				397	416	19	R	LLAELPASVHALTGVDLSK	I	0.49%	5521	5521	645.7011108	3	1934.079857	1933.088425	0.991432744	R	I	-	3	19	1	0
Q14258	E3 ubiquitin/ISG15 ligase TRIM25	6	17.94%	65	83	18	K	NTVLCNVVEQFLQADLAR	E	0.23%	9626	9626	698.0253296	3	2091.052514	2089.062158	1.99035565	K	E	C5:+57.021	5	18	2	0
				117	150	33	K	TCLVCMASFCQEHLQPHFDSPAFQDHPLQPPVR	D	1.64%	5023	5023	988.4434814	4	3949.742626	3949.778285	-0.035659227	K	D	C2:+57.021,C5:+57.021,C	2	33	0	0
				226	236	10	R	QQDVRMTANR	K	3.33%	2971	2971	603.3161011	2	1204.616552	1203.5185	1.098051636	R	K	Q1:-17.027,Q1:+0.984,Q2	1	10	1	1
				236	249	13	R	KVEQLQQEYTEMK	A	0.28%	1424	1424	827.4088135	2	1652.801977	1652.80797	-0.005992991	R	A	-	5	13	0	1
				402	416	14	K	LPTFGAPEQLVDLK	Q	0.23%	5370	5370	764.9180298	2	1527.820409	1526.834441	0.985968082	K	Q	-	5	14	1	0
				469	494	25	K	VALSECYTVASVAEMPQNYRPHPQR	F	3.69%	3715	3715	727.0990601	4	2904.36494	2903.368967	0.995972906	K	F	C6:+57.021,N18:+0.984	2	25	1	0
Q14444	Caprin-1	1	5.92%	13	55	42	K	SSGPPPPSGSSGSEAAAGAGAAAPASQHPATGTGAVQTEAMK	Q	0.30%	1356	1356	1235.905396	3	3704.692711	3703.701994	0.990717467	K	Q	Q27:+0.984	3	42	1	0
Q14574	Desmocollin-3	1	1.79%	429	445	16	R	QVNLEIGVNNEAPFAR	D	3.03%	1133	1133	591.3223267	3	1770.943505	1771.874043	-0.930538524	R	D	Q1:+0.984,N3:+0.984	2	16	-1	0
Q14676	Mediator of DNA damage checkpoint protein 1	4	4.45%	1059	1079	20	K	HLAPPPLLSPLLPSIKPTVR	K	0.48%	5074	5074	716.4416504	3	2146.301476	2145.303778	0.997698324	K	K	-	3	20	1	0
				1114	1147	33	R	MTPFPATSAAPEPHPSTSTAQPVTPKPTSQATR	S	8.06%	1927	1927	848.4231567	4	3389.661327	3389.656153	0.005173705	R	S	Q21:+0.984	2	33	0	0
				1907	1930	23	R	AVLALGGSLAGSAAEASHLVTDR	I	0.93%	5528	5528	723.3936768	3	2167.157555	2165.144042	2.013512929	R	I	-	2	23	2	0
				2037	2054	17	R	VVITCPQDFPHCSIPLR	V	0.23%	3674	3674	680.3426514	3	2038.004479	2038.011908	-0.007429282	R	V	C5:+57.021,C12:+57.021	2	17	0	0
Q14BN4	Sarcolemmal membrane-associated protein	1	1.45%	114	126	12	R	KVTHGCIVSTIK	L	7.86%	582	582	448.2529907	3	1341.735497	1341.743389	-0.0078924	R	L	C6:+57.021	1	12	0	1
Q15046	Lysyl-tRNA synthetase	2	7.37%	111	127	16	K	YSHLQPGDHLTDITLK	V	3.42%	2349	2349	460.49	4	1837.9287	1836.937009	0.991690624	K	V	-	1	16	1	0
				446	474	28	K	LVGEFLEVTCINPTFICDHPQIMSPLAK	W	1.04%	7371	7371	1077.536743	3	3229.586754	3229.585222	0.001531908	K	W	C10:+57.021,C17:+57.021	2	28	0	0
Q15080	Neutrophil cytosol factor 4	1	9.44%	0	32	32	-	MAVAQQLRAESDFEQLPDDVAISANIADIEEK	R	6.58%	7781	7781	881.18	4	3520.6887	3517.676992	3.01170756	-	R	Q5:+0.984,Q6:+0.984	1	32	3	1
Q15084	Protein disulfide-isomerase A6	6	21.36%	85	102	17	K	HHSLGGQYGVQGFPTIK	I	0.23%	2354	2354	609.312439	3	1824.913842	1824.927113	-0.013271377	K	I	-	1	17	0	0
				118	132	14	R	TGEAIVDAALSALR	Q	0.23%	6644	6644	693.880249	2	1385.744848	1385.75144	-0.006592009	R	Q	-	6	14	0	0
				194	208	14	K	NLEPEWAAAASEVK	E	0.23%	3848	3848	758.3805542	2	1514.745458	1513.741269	1.004189062	K	E	-	3	14	1	0
				264	288	24	R	ALDLFSDNAPPPELLEIINEDIAK	R	0.23%	9364	9364	881.4453125	3	2641.312462	2637.342512	3.969950724	R	R	N8:+0.984	2	24	4	0
				264	289	25	R	ALDLFSDNAPPPELLEIINEDIAKR	T	0.23%	8800	8800	933.4490967	3	2797.323815	2793.443623	3.880192111	R	T	N19:+0.984	2	25	4	1
				289	313	24	R	TCEEHQLCVVAVLPHILDTGAAGR	N	1.84%	5410	5410	883.4377441	3	2647.289757	2645.304462	1.985295286	R	N	C2:+57.021,C8:+57.021	1	24	2	0
Q15149	Plectin	11	3.80%	630	650	20	K	AGVAAPATQVAQVTLQSVQR	R	0.23%	4111	4111	998.0454102	2	1994.07517	1994.090884	-0.015714064	K	R	-	7	20	0	0
				1186	1201	15	K	VLALPEPSPAAPTLR	S	0.28%	3752	3752	766.4398193	2	1530.863989	1530.876975	-0.012986352	K	S	-	3	15	0	0
				2650	2663	13	K	AKLEQLFQDEVAK	A	1.77%	3278	3278	760.4159546	2	1518.816259	1517.808955	1.007304164	K	A	-	2	13	1	1
				2730	2743	13	R	LREQLQLLEEQHR	A	0.23%	1898	1898	564.64	3	1690.896525	1690.911463	-0.014938192	R	A	-	1	13	0	1
				3183	3212	29	K	DLLPSDMAVALLEAQAGTGHIIDPATSAR	L	0.23%	8185	8185	978.8336792	3	2933.477562	2933.48042	-0.002857762	K	L	Q15:+0.984	4	29	0	0
				3355	3368	13	R	ARQEELYSELQAR	E	0.23%	1774	1774	797.3950195	2	1592.774389	1591.79543	0.978958815	R	E	-	5	13	1	1
				3446	3462	16	R	APVPASELLASGVLSR	A	1.04%	4723	4723	783.9453125	2	1565.874975	1565.877703	-0.002728352	R	A	-	5	16	0	0
				3551	3568	17	K	AGVVGPELHEQLLSAEK	A	0.52%	2701	2701	592.9850464	3	1775.931664	1775.94176	-0.010096208	K	A	-	2	17	0	0
				3950	3963	13	R	LGFHLPLEVAYQR	G	0.23%	4861	4861	514.9481201	3	1541.820885	1541.835444	-0.01455916	R	G	-	6	13	0	0
				3991	3999	8	R	LSYTQLLR	R	8.12%	3309	3309	498.2849426	2	994.5542352	992.5654767	1.988758438	R	R	-	2	8	2	0
				4360	4381	21	R	AGTLSITEFADMLSGNAGGFR	S	0.23%	8328	8328	1058.508789	2	2115.001928	2114.010252	0.991676205	R	S	-	5	21	1	0
Q15262	Receptor-type tyrosine-protein phosphatase kappa	1	1.11%	1382	1398	16	R	SGMFCAIGIVVEMVKR	Q	8.53%	4349	4349	604.975708	3	1811.903649	1811.909239	-0.005589937	R	Q	C5:+57.021,M13:+15.995	1	16	0	1
Q15286	Ras-related protein Rab-35	3	19.90%	10	21	11	K	LLIIGDSGVGK	S	0.84%	3163	3163	536.3201294	2	1070.624609	1070.633556	-0.008947707	K	S	-	1	11	0	0
				58	69	11	K	LQIWDTAGQER	F	0.23%	2690	2690	658.8308105	2	1315.645971	1315.65206	-0.006089122	K	F	-	3	11	0	0
				152	170	18	K	ENVNVEEMFNCITELVLR	A	1.04%	10992	10992	1106.59	2	2211.16435	2208.055025	3.109325008	K	A	C11:+57.021	2	18	3	0
Q15382	GTP-binding protein Rheb	1	5.98%	109	120	11	K	VQIPIMLVGNK	K	0.84%	4318	4318	607.3706055	2	1212.725561	1210.710762	2.014798786	K	K	-	2	11	2	0
Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	2	9.12%	191	207	16	K	NFLTTAIRPHGIFGPR	D	0.23%	4059	4059	600.0005493	3	1796.978173	1795.984568	0.993604389	K	D	-	4	16	1	0
				263	281	18	K	AFHITNDEPIPFWTFLSR	I	3.71%	7714	7714	732.3727417	3	2194.09475	2191.073822	3.020928338	K	I	N6:+0.984	1	18	3	0
Q15758	Neutral amino acid transporter B(0)	2	6.10%	189	202	13	R	NIFPSNLVSAAFR	S	0.23%	6263	6263	718.3879395	2	1434.760229	1434.761945	-0.001716198	R	S	-	5	13	0	0
				502	522	20	K	SELPLDPLPVPTEEGNPLLK	H	0.23%	6439	6439	1080.084351	2	2158.153051	2157.156898	0.996152756	K	H	-	5	20	1	0
Q15833	Syntaxin-binding protein 2	1	2.53%	424	439	15	K	LIQHANVQAHSSLIR	N	0.68%	1251	1251	422.4902954	4	1685.929881	1685.932533	-0.002651359	K	N	-	3	15	0	0
Q16236	Nuclear factor erythroid 2-related factor 2	1	5.62%	237	271	34	K	EVGNCSPHFLNAFEDSFSSILSTEDPNQLTVNSL	N	6.42%	8024	8024	938.9360962	4	3751.713085	3750.698635	1.014449358	K	N	E1:-18.011,C5:+57.021,N1	1	34	1	0
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	1	3.58%	234	246	12	R	FNVIQPGPIKTK	G	9.25%	3627	3627	671.3601685	2	1340.704687	1341.765618	-1.060930974	R	G	Q5:+0.984	2	12	-1	1
Q17RG1	BTB/POZ domain-containing protein KCTD19	1	3.46%	74	106	32	K	LSFSSCAELNLLYEQALGLQLMPLLQTLDNLK	E	9.38%	8345	8345	911.9302979	4	3643.689891	3636.866579	6.823312142	K	E	C6:+57.021,Q15:+0.984,C	1	32	7	0
Q1EHB4	Sodium-coupled monocarboxylate transporter 2	1	2.10%	105	118	13	R	SGITSTYEYLQLR	F	6.27%	12534	12534	765.9401855	2	1529.864721	1529.772569	0.092151598	R	F	-	2	13	0	0
Q3SYG4	Protein PTHB1	1	2.59%	124	147	23	K	LMYEHNLQRTACNMTYGSFGGVK	G	2.73%	18672	18672	893.7442627	3	2678.209313	2676.224234	1.98507931	K	G	C12:+57.021	2	23	2	1
Q4G0N8	Sodium/hydrogen exchanger 10	1	1.95%	750	773	23	K	GYVQGEADIMTIIDQITSSKQIK	Q	1.76%	6819	6819	847.7704468	3	2540.287865	2539.272703	1.015162228	K	Q	Q4:+0.984,Q15:+0.984	1	23	1	1
Q4VCS5	Angiomotin	1	2.03%	684	706	22	K	YLEENVMRHFALDAAATVAAQR	D	0.49%	3149	3149	831.4083252	3	2491.2015	2491.227875	-0.02637479	K	D	M7:+15.995	2	22	0	1
Q53GL0	Pleckstrin homology domain-containing family O member 1	2	8.31%	120	135	15	K	ESWINALNSAITRAK	N	0.84%	9883	9883	838.4238892	2	1674.832128	1673.873665	0.958463264	K	N	N8:+0.984	4	15	1	1
				315	334	19	K	LEETQELLAEVQGLGDGKR	K	0.93%	6015	6015	696.3682251	3	2086.0812	2085.05896	1.022240613	K	K	Q5:+0.984	2	19	1	1
Q5JS13	Ras-specific guanine nucleotide-releasing factor RalGPS1	1	2.15%	84	96	12	K	HSLAPNVVAFTR	R	6.99%	5171	5171	437.9054871	3	1310.692986	1310.709515	-0.016529362	K	R	-	1	12	0	0
Q5TZA2	Rootletin	1	1.24%	801	826	25	R	QGLEGSLRVAEQAQEALEQQLPTLR	H	7.06%	7306	7306	1385.167847	2	2768.320043	2766.403518	1.916525551	R	H	Q1:+0.984,Q19:+0.984,Q2	3	25	2	1
Q685J3	Mucin-17	1	0.53%	2221	2245	24	P	FTSMPVSTMPVVTSEASTLSATPV	D	8.30%	8470	8470	814.4016724	3	2440.181542	2439.191314	0.990228258	P	D	-	1	24	1	0
Q693B1	BTB/POZ domain-containing protein KCTD11	1	6.03%	173	187	14	R	LGLQPLWTGGPGER	R	6.60%	5482	5482	494.2685242	3	1479.782097	1479.783409	-0.001311402	R	R	-	1	14	0	0
Q6PCB7	Long-chain fatty acid transport protein 1	1	3.41%	483	505	22	K	GDSAYLSGDVLVMDELGYMYFR	D	3.69%	10647	10647	1259.17627	2	2516.336889	2516.124048	0.212841263	K	D	M19:+15.995	2	22	0	0
Q6UXD5	Seizure 6-like protein 2	1	0.99%	263	272	9	R	LLLHFQSPR	V	1.46%	6466	6466	555.8339844	2	1109.652319	1110.618559	-0.96624073	R	V	Q6:+0.984	5	9	-1	0
Q6UXK2	Immunoglobulin superfamily containing leucine-rich repeat protein 2	1	3.09%	356	379	23	R	AHNELGANSTSIRVAVAATGPPK	H	7.06%	741	741	754.2298584	3	2259.6661	2261.176389	-1.510289373	R	H	N8:+0.984	2	23	-1	1
Q6V1P9	Protocadherin-23	1	0.96%	2097	2125	28	K	SYNLSLSEDALVGSTLVTFSNIDHDWTR	E	5.82%	8562	8562	787.8716431	4	3147.455272	3139.509821	7.945451418	K	E	-	1	28	8	0
Q6XYQ8	Synaptotagmin-10	1	4.40%	323	346	23	R	FSRHDMIGEVILDNLFEVSDLSR	E	8.33%	8136	8136	903.7844238	3	2708.329796	2708.310649	0.019147268	R	E	M6:+15.994,N14:+0.984	1	23	0	1
Q6XZF7	Dynamin-binding protein	1	0.70%	958	969	11	K	EINVNINEYKR	R	8.80%	49	49	696.8555908	2	1391.695532	1391.704474	-0.008942583	K	R	N5:+0.984	1	11	0	1
Q6ZTQ4	Cadherin-related family member 3	1	0.90%	361	369	8	G	TLLLDLNK	F	6.53%	3177	3177	465.2823486	2	928.5490472	928.5593287	-0.010281534	G	F	-	1	8	0	0
Q76LX8	A disintegrin and metalloproteinase with thrombospondin motifs 13	1	1.61%	102	125	23	R	YVLTNLNIGAELLRDPSLGAQFR	V	2.84%	1613	1613	1281.586304	2	2561.156957	2560.364919	0.792038606	R	V	N5:+0.984	2	23	1	1
Q7L5Y9	Macrophage erythroblast attacher	1	3.03%	264	276	12	R	MLIQQFRYDNYR	L	6.75%	1263	1263	549.6062012	3	1645.795128	1645.803493	-0.008365092	R	L	-	1	12	0	1
Q7RTY8	Transmembrane protease serine 7	1	1.57%	16	29	13	K	ISNISVQVVSAQK	K	2.73%	3970	3970	688.3712769	2	1374.726904	1374.724175	0.002728215	K	K	N3:+0.984,Q7:+0.984,Q12	2	13	0	0
Q7Z444	GTPase ERas	1	7.30%	37	54	17	R	QLPEYKAVVVGASGVGK	S	8.15%	2197	2197	426.24	4	1700.9287	1700.946117	-0.01741744	R	S	-	1	17	0	1
Q86UE4	Protein LYRIC	1	3.44%	87	107	20	R	KREEAAAVPAAAPDDLALLK	N	2.67%	2834	2834	684.0464478	3	2049.115868	2048.126601	0.989266982	R	N	-	1	20	1	2
Q86W92	Liprin-beta-1	1	2.57%	700	726	26	K	LQLALQALGSEEETNHGKLDFNWVTR	W	0.77%	6682	6682	990.5373535	3	2968.588585	2970.472282	-1.883696229	K	W	Q6:+0.984,N22:+0.984	2	26	-1	1
Q86Y22	Collagen alpha-1(XXIII) chain	1	3.15%	77	94	17	R	AGPPGALDAWAEPHLER	L	0.75%	10879	10879	894.4100952	2	1786.80454	1785.879829	0.924711766	R	L	-	2	17	1	0
Q8IV01	Synaptotagmin-12	1	6.18%	343	369	26	R	DDPNPVFNEAMIFSVPAIVLQDLSLR	V	7.89%	9197	9197	973.1576538	3	2916.449486	2916.457979	-0.00849287	R	V	M11:+15.995,Q21:+0.984	1	26	0	0
Q8IV61	Ras guanyl-releasing protein 3	1	1.59%	43	54	11	R	WYLSSTELAEK	L	5.28%	1088	1088	442.8895264	3	1325.645104	1325.650329	-0.005224842	R	L	-	1	11	0	0
Q8IWV2	Contactin-4	1	2.83%	868	897	29	K	GSVLYHLAVKAYNSAGTGPSSATVNVTTR	K	9.87%	8012	8012	974.50177	3	2920.481835	2920.504282	-0.022446717	K	K	-	1	29	0	1
Q8IWV8	E3 ubiquitin-protein ligase UBR2	1	1.82%	568	600	32	K	CLAVLMQCHGGYTDGEQPITLSICGHSVETIR	Y	9.82%	10803	10803	1202.567383	3	3604.678673	3602.661189	2.01748403	K	Y	C1:+57.021,Q7:+0.984,C8	1	32	2	0
Q8IXI1	Mitochondrial Rho GTPase 2	3	12.14%	50	74	24	K	VPTHIVDYSEAEQTDEELREEIHK	A	0.23%	3441	3441	718.35	4	2869.3687	2866.362094	3.006606216	K	A	-	2	24	3	1
				242	261	19	R	EDRLTLDGFLFLNTLFIQR	G	9.11%	4645	4645	579.0674438	4	2312.238475	2310.237214	2.001260855	R	G	-	1	19	2	1
				315	347	32	K	HDQDRDGALSPVELQSLFSVFPAAPWGPELPR	T	2.76%	8789	8789	884.45	4	3533.7687	3532.726265	1.042434936	K	T	Q3:+0.984,Q15:+0.984	3	32	1	1
Q8N4V1	Membrane magnesium transporter 1	1	18.32%	98	122	24	R	VLFRPSDTANSSNQDALSSNTSLK	L	0.28%	2299	2299	851.7507935	3	2552.228905	2551.251421	0.977484515	R	L	-	2	24	1	0

Q8NBS3	Sodium bicarbonate transporter-like protein 11	1	1.80%	302	318	16	R	QLLTMVSHGPVAPRTK	E	4.86%	1272	1272	585.32	3	1752.936525	1749.956057	2.980467936	R	E	M5:+15.995	1	16	3	1
Q8NE09	Regulator of G-protein signaling 22	1	1.03%	578	591	13	K	SPEVKTATQKPWK	R	9.94%	2910	2910	500.2889404	3	1497.843346	1498.814375	-0.971028455	K	R	-	2	13	-1	1
Q8NGK5	Olfactory receptor 52M1	1	3.47%	226	237	11	R	AVMGLATPEAR	L	8.03%	2428	2428	558.2978516	2	1114.580053	1114.580476	-0.000423027	R	L	-	1	11	0	0
Q8NGV7	Olfactory receptor 5H2	1	3.50%	300	311	11	K	QVIDSFTKMVK	R	0.23%	2048	2048	648.3312378	2	1294.646826	1294.695506	-0.048680486	K	R	-	5	11	0	1
Q8NH51	Olfactory receptor 8K3	1	5.13%	64	80	16	R	HLAFMDLGYSTTVGPK	M	1.70%	1640	1640	584.9564819	3	1751.845971	1751.85534	-0.009369111	R	M	M5:+15.995	1	16	0	0
Q8TAB3	Protocadherin-19	1	1.22%	536	550	14	K	DGGLPSLQSNATVR	V	2.78%	6702	6702	708.3587646	2	1414.701879	1414.705202	-0.003323255	K	V	Q8:+0.984	2	14	0	0
Q8TCT9	Minor histocompatibility antigen H13	3	15.38%	241	251	10	K	LVFPQDLLEK	G	0.23%	5230	5230	601.3438721	2	1200.672094	1200.675421	-0.003327235	K	G	-	4	10	0	0
				313	337	24	K	HAQPALLYLVPACIGFPVLVALAK	G	0.23%	10150	10150	855.4954224	3	2563.462792	2560.459892	3.002899626	K	G	C13:+57.021	1	24	3	0
				337	361	24	K	GEVTEMFSYEESNPKDPAAVTESK	E	0.23%	3434	3434	1324.095215	2	2646.17478	2644.185041	1.989738232	K	E	-	4	24	2	1
Q8TD20	Solute carrier family 2, facilitated glucose transporter member 12	1	1.13%	416	423	7	R	SSLMPLR	N	7.39%	1403	1403	402.6149902	2	803.2143304	802.437106	0.777224349	R	N	-	2	7	1	0
Q8TD46	Cell surface glycoprotein CD200 receptor 1	1	5.54%	143	161	18	R	GYHLQVLVTPEVTLFQNR	N	8.04%	3878	3878	530.0090332	4	2116.004833	2114.116021	1.888811805	R	N	Q5:+0.984	2	18	2	0
Q8TDS5	Oxoeicosanoid receptor 1	1	4.02%	176	193	17	R	TASVVFLTAIALNRYLK	V	1.18%	4556	4556	627.9863281	3	1880.935509	1880.077116	0.858393239	R	V	N13:+0.984	2	17	1	1
Q8TDU9	Relaxin-3 receptor 2	1	4.55%	357	374	17	R	ESRPSTLLTNLDRGTPG	-	5.74%	1617	1617	454.983429	4	1815.902416	1812.932987	2.969429148	R	-	-	1	17	3	1
Q8TEU7	Rap guanine nucleotide exchange factor 6	1	1.56%	1540	1565	25	K	MMHNSLSRLPPASLSSNLVACVPSK	I	7.89%	8363	8363	900.7838135	3	2699.327965	2696.344333	2.983631966	K	I	N17:+0.984,C21:+57.021	1	25	3	1
Q8WX93	Palladin	1	2.96%	191	232	41	R	SPNGESSSPDSGYLSPKNQPSALLSASASQSPMEDQGEMER	E	8.57%	1155	1155	1066.224854	4	4260.868114	4253.84884	7.019274223	R	E	N3:+0.984,Q30:+0.984	1	41	7	1
Q8WXG9	G-protein coupled receptor 98	1	0.24%	5674	5689	15	K	ITTEGKIQAFSVASR	T	0.92%	3667	3667	536.2811279	3	1605.819909	1606.867867	-1.047958211	K	T	-	4	15	-1	1
Q8WXH0	Nesprin-2	2	0.36%	1668	1681	13	K	MELHQLTEEDRER	L	8.43%	4168	4168	851.3970947	2	1700.778539	1700.77888	-0.000341003	K	L	M1:+15.995	1	13	0	1
				5974	5986	12	K	QMGDQLIKASNK	S	6.10%	2899	2899	445.2341309	3	1332.678917	1332.670732	0.008185202	K	S	Q1:+0.984	2	12	0	1
Q8WYL5	Protein phosphatase Slingshot homolog 1	1	1.43%	135	150	15	K	SCTIGMVLRLWSDTK	I	8.93%	4066	4066	884.4008179	2	1766.785986	1765.885046	0.900939582	K	I	C2:+57.021	2	15	1	1
Q92542	Nicastrin	2	5.78%	285	314	29	R	SFFWNVAPGAESAVASFVTQLAAAEALQK	A	1.87%	10979	10979	1004.517029	3	3010.527611	3009.52362	1.003991194	R	A	-	2	29	1	0
				391	403	12	R	NQVEDLLATLEK	S	0.23%	6659	6659	687.3643799	2	1372.71311	1371.724557	0.988553166	R	S	-	6	12	1	0
Q92556	Engulfment and cell motility protein 1	1	1.38%	259	269	10	R	QEMANILAQK	Q	3.03%	981	981	581.3062134	2	1160.596777	1160.586041	0.010735886	R	Q	M3:+15.995	2	10	0	0
Q92797	Symplekin	1	2.51%	924	956	32	R	LLGTQHGEGNSALSPLNPGELLIALHNIDSVK	C	6.08%	7725	7725	828.2	4	3308.7687	3307.741202	1.027497592	R	C	Q5:+0.984	1	32	1	0
Q92835	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1	1	1.68%	501	521	20	R	ISHICTDNVKTGIANTLGNK	G	8.53%	13516	13516	1079.076416	2	2156.137182	2156.089086	0.048096415	R	G	C5:+57.021,N19:+0.984	2	20	0	1
Q92888	Rho guanine nucleotide exchange factor 1	5	0.88%	684	692	8	R	LLLKSHSR	T	2.81%	18833	18833	477.3014526	2	952.5872552	952.5817955	0.005459721	R	T	-	3	8	0	1
				262	292	30	R	TGMLEELHLEPGVVQGLFPCVDELSDIHTR	F	0.51%	7932	7932	849.4101563	4	3393.609325	3391.642349	1.966976296	R	F	Q15:+0.984,C20:+57.021	1	30	2	0
				400	423	23	R	ILQHSHGIEEERQDLTTALGLVK	E	0.23%	4063	4063	647.8505249	4	2587.370799	2587.360562	0.010237745	R	E	Q13:+0.984	1	23	0	1
				741	766	25	R	LVNLYGLLHGLQAAVAQQDTLMEAR	F	0.23%	9865	9865	910.4606323	3	2728.358422	2726.394868	1.963553541	R	F	Q12:+0.984,Q17:+0.984,C	2	25	2	0
				858	883	25	R	QLAALGQTEPLPAEAPWARRPVDPR	R	3.63%	4415	4415	1361.611938	2	2721.208227	2722.418629	-1.210401903	R	R	Q1:-17.027,Q7:+0.984	1	25	-1	1
Q96AP7	Endothelial cell-selective adhesion molecule	1	4.87%	206	225	19	R	GSLSLTNLSSSMAGVYVCK	A	2.81%	10075	10075	994.5107422	2	1987.005834	1988.953333	-1.947499153	R	A	M12:+15.994,C18:+57.02	1	19	-1	0
Q96BI1	Solute carrier family 22 member 18	1	2.83%	377	389	12	R	TLGPTVGGLLYR	S	1.63%	18010	18010	417.06	3	1248.156525	1245.708118	2.44840644	R	S	-	1	12	2	0
Q96CW1	AP-2 complex subunit mu	1	4.60%	380	400	20	K	WARPPISMNFEVPFAPSGLK	V	0.23%	6398	6398	748.7293091	3	2243.164452	2243.156128	0.008323878	K	V	-	1	20	0	0
Q96CX2	BTB/POZ domain-containing protein KCTD12	1	3.08%	273	283	10	K	FNFLEQAFDK	L	6.73%	5523	5523	629.0952759	2	1256.174902	1257.602985	-1.428082906	K	L	-	2	10	-1	0
Q96FE5	Leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 1	1	4.84%	515	545	30	R	SYSPDWPHQPNKTFAFISNQPGEGEANSTR	A	9.68%	8592	8592	1121.379883	3	3361.116173	3362.522829	-1.406656139	R	A	Q9:+0.984	2	30	-1	1
Q96JW4	Solute carrier family 41 member 2	1	1.92%	233	244	11	K	WNLIIGNLALK	Q	8.57%	5509	5509	628.592041	2	1255.168432	1254.733589	0.434842631	K	Q	N2:+0.984	2	11	0	0
Q96NL6	Sodium channel and clathrin linker 1	1	1.45%	370	380	10	R	FVQDATIRTK	K	4.21%	2873	2873	590.8101807	2	1179.604711	1177.645518	1.959193128	R	K	-	3	10	2	1
Q96RW7	Hemicentin-1	1	0.41%	926	949	23	K	NSAMLLQNPYITVRSDGSLHIER	V	7.37%	6826	6826	879.1321411	3	2634.372948	2630.312318	4.060630468	K	V	M4:+15.995,Q7:+0.984	1	23	4	1
Q99578	GTP-binding protein Rit2	1	5.99%	121	134	13	R	HTYEIPLVLVGNK	I	4.17%	2200	2200	495.2763977	3	1482.805718	1482.808211	-0.002493021	R	I	N12:+0.984	1	13	0	0
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	11	72.41%	9	29	20	K	GLVAVITGGASGLGLATAER	L	0.23%	6090	6090	605.3412476	3	1813.000268	1812.010509	0.989758972	K	L	-	7	20	1	0
				29	52	23	R	LVGQGASAVLLDLPNSGGEAQAK	K	0.23%	4575	4575	1098.084595	2	2194.153539	2194.159358	-0.005818603	R	K	-	4	23	0	0
				52	69	17	K	KLGNNCVFAPADVTSEK	D	0.23%	1913	1913	925.4603271	2	1848.905004	1848.903532	0.001472329	K	D	C6:+57.021	6	17	0	1
				53	69	16	K	LGNNCVFAPADVTSEK	D	0.30%	2567	2567	861.4038086	2	1720.791967	1720.808569	-0.016601644	K	D	C5:+57.021	4	16	0	0
				84	99	15	R	VDVAVNCAGIAVASK	T	0.23%	2559	2559	737.388855	2	1472.76206	1472.765247	-0.003187335	R	T	C7:+57.021	7	15	0	0
				130	147	17	R	LVAGEMGQNEPDQGGQR	G	0.23%	1052	1052	893.4105835	2	1784.805517	1784.811158	-0.00564092	R	G	-	6	17	0	0
				147	172	25	R	GVIINTASVAAFEGQVGQAAYSASK	G	0.23%	6198	6198	1220.627808	2	2439.239965	2438.24415	0.995814762	R	G	-	5	25	1	0
				172	184	12	K	GGIVGMTLPIAR	D	0.23%	4311	4311	592.84198	2	1183.66831	1183.674711	-0.006400999	K	D	-	7	12	0	0
				192	212	20	R	VMTIAPGLFGTPLLTSLPEK	V	0.23%	7564	7564	1043.084106	2	2084.152563	2084.159148	-0.006585157	R	V	-	7	20	0	0
				212	226	14	K	VCNFLASQVPFPSR	L	0.23%	4621	4621	811.409668	2	1620.803686	1620.807781	-0.004094894	K	L	C2:+57.021	5	14	0	0
				226	252	26	R	LGDPAEYAHLVQAIIENPFLNGEVIR	L	0.23%	10085	10085	719.883728	4	2875.503612	2879.470491	-3.966878723	R	L	Q12:+0.984,N17:+0.984	1	26	-1	0
Q99720	Sigma non-opioid intracellular receptor 1	2	20.63%	47	60	13	R	QYAGLDHELAFSR	L	2.15%	2657	2657	503.601593	3	1507.781304	1506.710288	1.071016101	R	L	Q1:+0.984	2	13	1	0
				142	175	33	K	SEVFYPGETVVHGPGEATAVEWGPNTWMVEYGR	G	0.23%	6602	6602	1218.233154	3	3651.675988	3650.677632	0.998355323	K	G	-	5	33	1	0
Q99805	Transmembrane 9 superfamily member 2	3	6.79%	35	51	16	A	FYLPGLAPVNFCDEEK	K	6.20%	6321	6321	950.4478149	2	1898.87998	1897.89157	0.988409619	A	K	C12:+57.021	1	16	1	0
				90	104	14	K	RPSENLGQVLFGER	I	0.23%	3680	3680	801.4197998	2	1600.82395	1600.83215	-0.008200487	K	I	-	6	14	0	0
				172	187	15	R	FCNPGFPIGCYITDK	G	0.23%	5192	5192	895.4064941	2	1788.797338	1787.800184	0.997154305	R	G	C2:+57.021,C10:+57.021	6	15	1	0
Q99808	Equilibrative nucleoside transporter 1	1	3.29%	368	383	15	R	LVFVPLLLLCNIKPR	R	1.01%	8884	8884	599.3695679	3	1795.085228	1795.078902	0.006326613	R	R	C10:+57.021,N11:+0.984	1	15	0	0
Q9BQE4	Selenoprotein S	1	5.82%	88	99	11	K	MQEELNAQVEK	H	0.23%	1160	1160	659.8173828	2	1317.619116	1317.623463	-0.004347735	K	H	-	6	11	0	0
Q9BQL6	Fermitin family homolog 1	1	2.51%	535	552	17	R	ILEAHQNVAQMPLVEAK	L	3.60%	7416	7416	636.6643677	3	1906.969628	1906.982316	-0.012687917	R	L	Q10:+0.984,M11:+15.995	1	17	0	0
Q9BXC0	G-protein coupled receptor 81	1	4.05%	306	320	14	K	TQRPEEMPISNLGR	R	9.49%	2393	2393	543.6054688	3	1627.792931	1627.798787	-0.005855406	K	R	N11:+0.984	1	14	0	0
Q9BXN2	C-type lectin domain family 7 member A	1	5.26%	98	111	13	S	SLEDSVTPTKAVK	T	6.58%	3918	3918	688.37	2	1374.72435	1373.740207	0.98414332	S	T	-	1	13	1	1
Q9C037	Tripartite motif-containing protein 4	1	2.20%	172	183	11	K	KVMHLQDVEVK	N	2.40%	3930	3930	671.3585205	2	1340.701391	1340.711304	-0.009913152	K	N	M3:+15.994	1	11	0	1
Q9H2B4	Sulfate anion transporter 1	1	3.14%	314	336	22	R	FGSSVAGDIPTGFMPPQVPEPR	L	0.61%	6032	6032	762.7004395	3	2285.077843	2285.115051	-0.037208129	R	L	-	2	22	0	0
Q9H4M9	EH domain-containing protein 1	2	11.05%	87	119	32	R	IGPEPTTDSFIAVMHGPTEGVVPGNALVVDPR	R	0.23%	6168	6168	1092.225098	3	3273.651818	3272.638712	1.013105825	R	R	N25:+0.984	2	32	1	0
				135	162	27	R	FMCAQLPNPVLDSISIIDTPGILSGEK	Q	0.23%	9049	9049	1459.258057	2	2916.500463	2914.481553	2.018910161	R	Q	C3:+57.021	2	27	2	0
Q9H792	Tyrosine-protein kinase SgK269	1	0.97%	625	642	17	K	VPIVINPNAYDNLAIYK	S	8.75%	8022	8022	960.9891357	2	1919.962621	1918.008746	1.953875316	K	S	N8:+0.984,N12:+0.984	1	17	2	0
Q9HAB3	Riboflavin transporter 3	1	4.49%	145	165	20	R	SFFLGQGLSALLPCVLALVQ	G	7.06%	11203	11203	712.0678711	3	2133.180138	2132.169918	1.010220585	R	G	C14:+57.021	1	20	1	0
Q9HBX8	Leucine-rich repeat-containing G-protein coupled receptor 6	1	3.31%	643	675	32	R	ATGFLAVLGSEASVLLLTLAAVQCSVSVSCVR	A	7.98%	7033	7033	1094.249268	3	3279.724328	3278.724492	0.999835406	R	A	Q23:+0.984,C24:+57.021,	1	32	1	0
Q9HCU4	Cadherin EGF LAG seven-pass G-type receptor 2	1	0.79%	653	676	23	R	NRFSITSQSGGGLVSLALPLDYK	L	5.91%	2929	2929	607.3168945	4	2425.236278	2423.269621	1.966656693	R	L	N1:+0.984	1	23	2	1
Q9HDB9	HERV-K_3q12.3 provirus ancestral Gag polyprotein	1	2.70%	556	574	18	R	SCPVLNKQNIINQAITAK	N	8.75%	4483	4483	1007.51062	2	2013.00559	2013.055979	-0.050388646	R	N	C2:+57.021,Q8:+0.984,N1	1	18	0	1
Q9HDC9	Adipocyte plasma membrane-associated protein	5	19.95%	1	10	9	M	SEADGLRQR	R	2.72%	6991	6991	516.7926025	2	1031.569555	1031.499566	0.06998855	M	R	Q8:+0.984	1	9	0	1
				93	120	27	R	LFENQLVGPESIAHIGDVMFTGTADGR	V	0.23%	7543	7543	1438.209961	2	2874.404272	2873.401791	1.002480363	R	V	-	5	27	1	0
				183	195	12	K	LLLSSETPIEGK	N	0.23%	2536	2536	644.3624268	2	1286.709203	1285.712929	0.996274292	K	N	-	5	12	1	0
				238	250	12	R	LLEYDTVTREVK	V	3.09%	16114	16114	489.9363098	3	1466.785454	1464.782406	2.003048515	R	V	-	1	12	2	1
				257	280	23	R	FPNGVQLSPAEDFVLVAETTMAR	I	0.23%	9281	9281	1247.638306	2	2493.260961	2492.225709	1.035252584	R	I	N3:+0.984	6	23	1	0
Q9NPB6	Partitioning defective 6 homolog alpha	1	9.25%	47	79	32	R	AVHQIPGLDVLLGYTDAHGDLLPLTNDDSLHR	A	8.93%	10940	10940	867.6787109	4	3466.683544	3466.73683	-0.053286034	R	A	Q4:+0.984,N26:+0.984	1	32	0	0
Q9NQC3	Reticulon-4	3	5.12%	57	91	34	R	KPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPR	G	1.00%	6012	6012	1091.894653	3	3272.660485	3271.669953	0.990532329	R	G	N26:+0.984	3	34	1	0
				91	104	13	R	GPLPAAPPVAPER	Q	1.04%	1779	1779	636.3603516	2	1270.705053	1270.703367	0.001685637	R	Q	-	2	13	0	0
				1157	1171	14	R	HQAQIDHYLGLANK	N	0.23%	1775	1775	402.96	4	1607.8087	1606.821585	0.987114544	R	N	-	2	14	1	0
Q9NRD9	Dual oxidase 1	1	1.61%	370	395	25	R	EHPSLQSAEDVDALLLGMASQIAER	E	9.25%	7002	7002	1340.665039	2	2679.314428	2679.317393	-0.002964971	R	E	-	1	25	0	0
Q9NS66	Probable G-protein coupled receptor 173	1	1.88%	206	213	7	K	LLLFEYR	H	2.59%	857	857	479.2475891	2	956.4795281	952.5381993	3.941328863	K	H	-	1	7	4	0
Q9NSA0	Solute carrier family 22 member 11	2	9.82%	227	253	26	R	AVTMTVVGCAFSAGQAALGGLAFALR	D	9.94%	10133	10133	847.4377441	3	2539.289757	2539.29222	-0.002462858	R	D	C9:+57.021,Q15:+0.984	1	26	0	0
				402	430	28	R	TIQAGSQAMAGLAILANMLVPQDLQTLR	V	5.13%	9648	9648	982.2225342	3	2943.644127	2942.508333	1.135794571	R	V	Q3:+0.984,Q7:+0.984,N17	2	28	1	0
Q9NSN8	Gamma-1-syntrophin	1	3.29%	11	28	17	K	TGICLLQDGNQEPFKVR	L	9.87%	1066	1066	658.6685791	3	1972.982262	1974.982829	-2.000567167	K	L	C4:+57.021,Q7:+0.984	1	17	-1	1
Q9NVN3	Synembryn-B	1	3.85%	355	375	20	K	GSSYREGLTPVLSLLTECSR	A	1.02%	4160	4160	1113.05957	2	2224.103491	2224.115316	-0.011825383	K	A	C18:+57.021	2	20	0	1
Q9NYQ8	Protocadherin Fat 2	2	1.26%	112	133	21	R	DSYTLIIQATEKTLELEALTR	V	0.95%	6183	6183	603.3022461	4	2409.177684	2408.268618	0.909065927	R	V	Q8:+0.984	3	21	1	1
				4262	4296	34	R	LVAPCLNEYTAISYYHSQFRQGGGGPCLADGGYK	G	3.04%	8458	8458	1251.241577	3	3750.701256	3749.723323	0.977933181	R	G	C5:+57.021,Q18:+0.984,C	2	34	1	1
Q9NZ53	Podocalyxin-like protein 2	1	1.98%	458	470	12	P	TQDVLSMLGDIR	R	9.00%	1890	1890	682.3584595	2	1362.701269	1362.681398	0.019870937	P	R	M7:+15.995	1	12	0	0
Q9NZV8	Potassium voltage-gated channel subfamily D member 2	1	4.13%	353	379	26	K	FTSIPAAFWYTIVTMTTLGYGDMVPK	T	0.76%	10761	10761	976.1811523	3	2925.519982	2925.433361	0.086620967	K	T	M15:+15.995	2	26	0	0
Q9P0L0	Vesicle-associated membrane protein-associated protein A	5	26.91%	10	24	14	K	HEQILVLDPPTDLK	F	0.23%	3594	3594	810.3938599	2	1618.77207	1616.877369	1.894700703	K	F	-	2	14	2	0
				24	38	14	K	FKGPFTDVVTTNLK	L	2.60%	3614	3614	522.5990601	3	1564.773705	1565.84534	-1.0716354	K	L	-	2	14	-1	1
				26	38	12	K	GPFTDVVTTNLK	L	0.23%	3475	3475	646.34	2	1290.66435	1290.681963	-0.017613392	K	L	-	6	12	0	0
				94	114	20	K	FMVQTIFAPPNTSDMEAVWK	E	0.23%	7330	7330	1157.557983	2	2313.100317	2311.101711	1.998606125	K	E	-	4	20	2	0
				154	173	19	K	QDGPMPKPHSVSLNDTETR	K	0.48%	1312	1312	703.666748	3	2107.976769	2107.995664	-0.018895395	K	K	-	4	19	0	0
Q9P1W8	Signal-regulatory protein gamma	1	6.20%	133	157	24	K	SGPGTEMALGAKPSAPVVLGPAAR	T	1.04%	3855	3855	745.75	3	2234.226525	2233.188885	1.037639816	K	T	-	3	24	1	0
Q9UHG3	Prenylcysteine oxidase 1	1	2.18%	211	222	11	K	FLNEMIAPVMR	V	0.23%	4686	4686	661.8388062	2	1321.661962	1319.672997	1.988964745	K	V	-	3	11	2	0
Q9UIA0	Cytohesin-4	1	4.06%	102	118	16	K	GEGLNKTAIGTYLGER	D	4.45%	2560	2560	560.9515381	3	1679.831139	1678.852595	0.97854393	K	D	N5:+0.984	2	16	1	1
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	6	16.59%	292	310	18	R	IAPLEEGTLPFNLAEAQR	Q	0.23%	5760	5760	986.0266724	2	1970.037695	1968.031638	2.006056623	R	Q	-	3	18	2	0
				331	353	22	R	FGLGSVAGAVGATAVYPIDLVK	T	0.23%	7362	7362	1053.085571	2	2104.155493	2104.156839	-0.001346166	R	T	-	7	22	0	0
				455	467	12	R	LQVAGEITTGPR	V	0.28%	1632	1632	621.3389282	2	1240.662206	1240.677547	-0.015340243	R	V	-	5	12	0	0
				455	475	20	R	LQVAGEITTGPRVSALSVVR	D	2.58%	8031	8031	685.7107544	3	2054.108788	2053.153135	0.955653368	R	D	Q2:+0.984	1	20	1	1
				508	545	37	K	ASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIK	T	0.50%	9217	9217	1181.290039	3	3540.846642	3537.838884	3.007757788	K	T	-	3	37	3	0
				626	641	15	R	INLPAPNPDHVGGYK	L	2.10%	1945	1945	531.6105957	3	1591.808312	1591.799437	0.008874709	R	L	N7:+0.984	1	15	0	0
Q9UN72	Protocadherin alpha-7	1	2.24%	766	787	21	K	TDLMAFSPSLPQGPSSTDNPR	Q	0.84%	3814	3814	745.5499268	3	2233.626305	2234.016195	-0.389889815	K	Q	M4:+15.995,Q12:+0.984	2	21	0	0
Q9UN73	Protocadherin alpha-6	1	3.26%	646	677	31	R	LLVLVKDHGEPALTATATVLVSLVESGQAPK	A	1.86%	9395	9395	1053.496094	3	3157.464806	3156.764563	0.700242722	R	A	Q28:+0.984	3	31	1	1
Q9UNK0	Syntaxin-8	1	4.24%	79	89	10	R	QNLLDDLVTR	E	1.31%	3954	3954	595.8040161	2	1189.592382	1187.603347	1.989034747	R	E	Q1:+0.984,N2:+0.984	2	10	2	0
Q9UPT5	Exocyst complex component 7	1	3.40%	393	418	25	K	TFDSLIQDALDGLMLEGENIVSAAR	K	2.37%	509	509	893.4147949	3	2677.22091	2678.310895	-1.089985434	K	K	N19:+0.984	1	25	-1	0
Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein 2	1	2.36%	108	121	13	K	VELDSRYLSAALK	K	4.56%	2165	2165	489.2750854	3	1464.801781	1463.79839	1.003391012	K	K	-	1	13	1	1
Q9Y289	Sodium-dependent multivitamin transporter	1	2.20%	139	153	14	K	TVRVCGTVTFIFQM	V	9.38%	8925	8925	838.9180298	2	1675.820409	1674.809554	1.010855666	K	V	C5:+57.021,Q13:+0.984,M	1	14	1	1
Q9Y2P5	Bile acyl-CoA synthetase	1	1.16%	404	412	8	R	LAMGNGLR	A	9.68%	9945	9945	416.86	2	831.7043499	831.4272541	0.277095864	R	A	N5:+0.984	3	8	0	0
Q9Y490	Talin-1	10	8.30%	613	624	11	K	GLAGAVSELLR	S	0.23%	5033	5033	543.817627	2	1085.619604	1084.624054	0.995549474	K	S	-	6	11	1	0
				765	786	21	R	GVGAAATAVTQALNELLQHVK	A	0.23%	9417	9417	697.7210693	3	2090.139733	2090.148399	-0.008666368	R	A	-	5	21	0	0
				1136	1161	25	R	GVAALTSDPAVQAIVLDTASDVLDK	A	1.50%	8339	8339	1235.62	2	2469.22435	2468.300997	0.923353224	R	A	-	3	25	1	0
				1510	1522	12	R	LASARTTNPTAK	R	6.84%	2298	2298	615.8262329	2	1229.636816	1229.672796	-0.035979836	R	R	-	3	12	0	1
				1690	1721	31	R	EGISQEALHTQMLTAVQEISHLIEPLANAAR	A	0.23%	10192	10192	1125.256348	3	3372.745568	3371.703088	1.042480113	R	A	Q5:+0.984,N28:+0.984	2	31	1	0
				1690	1730	40	R	EGISQEALHTQMLTAVQEISHLIEPLANAARAEASQLGHK	V	8.04%	11342	11342	1070.053345	4	4276.182079	4275.158918	1.023161066	R	V	E1:-18.011,Q5:+0.984,N2	1	40	1	1
				1895	1917	22	R	LASEAKPAAVAAENEEIGSHIK	H	0.23%	1734	1734	745.7252197	3	2234.152184	2234.154273	-0.002088556	R	H	-	3	22	0	0
				2241	2266	25	R	ECANGYLELLDHVLLTLQKPSPELK	Q	1.04%	8987	8987	721.385498	4	2881.510692	2880.493816	1.01687646	R	Q	C2:+57.021,Q18:+0.984	1	25	1	0
				2291	2321	30	K	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	K	0.29%	10433	10433	1018.516907	3	3052.527245	3050.508424	2.018821391	K	K	-	2	30	2	0
				2398	2423	25	R	MVAAATNNLCEAANAAVQGHASQEK	L	0.67%	2846	2846	853.3969727	3	2557.167443	2556.169205	0.998238345	R	L	C10:+57.021,Q23:+0.984	2	25	1	0
Q9Y493	Zonadhesin	1	0.53%	2266	2281	15	Q	CGCKDAHGGSIPLGK	S	4.79%	8018	8018	778.9459229	2	1555.876196	1555.722602	0.153593471	Q	S	C1:+57.021,C3:+57.021	4	15	0	1
Q9Y4D7	Plexin-D1	3	2.03%	251	266	15	K	LFTFDLNPSDDNILK	I	2.44%	7560	7560	877.4378052	2	1752.85996	1751.861763	0.998197328	K	I	N7:+0.984	1	15	1	0
				1441	1455	14	R	CSLASLLTIALHGK	L	7.05%	14876	14876	489.6046143	3	1465.790368	1465.795368	-0.005000523	R	L	C1:-17.027,C1:+57.021	1	14	0	0
				1538	1548	10	R	YTLSEEWLLR	E	4.34%	2137	2137	437.2290955	3	1308.663811	1308.671399	-0.007587335	R	E	-	1	10	0	0
Q9Y5E8	Protocadherin beta-15	1	3.43%	62	89	27	R	GARVVSEDNEQGLQLDLQTGQLILNEK	L	0.97%	6738	6738	990.5379028	3	2968.590233	2968.49889	0.09134292	R	L	Q14:+0.984,Q21:+0.984	2	27	0	1
Q9Y5P0	Olfactory receptor 51B4	1	9.35%	263	292	29	K	HAPHVVPITMSYVHFLFPPFVNPIIYSIK	T	7.06%	7026	7026	846.2050171	4	3380.788768	3379.783217	1.005551063	K	T	M10:+15.995,N22:+0.984	1	29	1	0
Q9Y5S2	Serine/threonine-protein kinase MRCK beta	1	1.11%	1222	1241	19	R	NQVVHVPLEAYDSSLPLIK	A	8.30%	8687	8687	709.71	3	2126.106525	2121.147002	4.959522608	R	A	-	1	19	5	0
Q9Y5Y9	Sodium channel protein type 10 subunit alpha	1	0.56%	416	427	11	K	KFQEALEMLRK	E	8.04%	1984	1984	696.8834229	2	1391.751196	1391.759503	-0.008307673	K	E	-	1	11	0	2
Q9Y5Z0	Beta-secretase 2	1	5.41%	226	254	28	N	VFSMQMCGAGLPVAGSGTNGGSLVLGGI	E	7.24%	5562	5562	880.4373169	3	2638.288476	2636.275601	2.012874964	N	E	C7:+57.021	1	28	2	0
Q9Y624	Junctional adhesion molecule A	1	7.69%	125	148	23	K	LIVLVPPSKPTVNIPSSATIGNR	A	0.83%	4353	4353	792.133728	3	2373.377709	2373.363128	0.01458121	K	A	N22:+0.984	1	23	0	0
Q9Y6C5	Protein patched homolog 2	1	1.41%	158	175	17	K	ICYKSGVPLIENGMIER	M	2.34%	1868	1868	661.0013428	3	1979.980553	1978.985139	0.995414544	K	M	C2:+57.021,N12:+0.984	2	17	1	1

Digestion method : On-filter
File conversion : PepArML batch uploader
Search engine : PepArML
Database : IPI Human
Specific cleavage : trypsin
Fixed modification : Carbamidomethyl (C)
Variable modification : Oxidation (M), Deamidation (NQ)
Data Processing : In-house tool - Coverage Table 1.7 with Parsimony
FDR < 10%

UniProt Accession number	Description	Number of peptides	Sequence Coverage	Start	End	Length	Left AA	peptide	Right AA	FDR	start_scan	end_scan	precursor_mz	assumed_charge	precursor_neutral_mass	calc_neutral_pep_mass	massdiff	leftaa	rightaa	modifications	number of agreed search engines	peptide_length	c13peak	misscleavages
A0FGR8	Extended synaptotagmin-2	1	0.98%	428	437	9	R	VIKENLSPK	W	8.35%	2758	2758	515.2982788	2	1028.580908	1026.607342	1.973565921	R	W	-	2	9	2	1
A4UGR9	Xin actin-binding repeat-containing protein 2	2	0.98%	1481	1496	15	K	GDVQQAIKNLFSEER	S	4.30%	769	769	579.3115234	3	1734.911095	1733.858409	1.052686297	K	S	Q4:+0.984	2	15	1	1
				3142	3160	18	R	TVQMAENFVNDPENEINR	W	6.49%	670	670	713.6591187	3	2137.953881	2134.95903	2.994850909	R	W	M4:+15.995	1	18	3	0
A6H8M9	Cadherin-related family member 4	1	1.90%	282	297	15	R	ADGVVRTTTPLELAR	T	1.37%	2197	2197	533.3096924	3	1596.905602	1597.878766	-0.9731639	R	T	-	1	15	-1	1
A8K7I4	Calcium-activated chloride channel regulator 1	1	1.20%	549	560	11	K	MAYLQIPGIAK	V	8.97%	5648	5648	610.3358154	2	1218.655981	1219.663563	-1.007582085	K	V	M1:+15.995	1	11	-1	0
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal	4	8.66%	204	220	16	R	IPDIVLWPTCHDDVVK	I	0.24%	5738	5738	636.328186	3	1905.961083	1905.965404	-0.004320895	R	I	C10:+57.021	4	16	0	0
				253	265	12	R	TIISLDTSQMNR	I	0.24%	2422	2422	464.9259338	3	1391.754326	1393.687212	-1.932885222	R	I	M10:+15.995	1	12	-1	0
				389	406	17	K	YGSVAFPNFEQGVACLR	E	0.24%	6202	6202	957.9580688	2	1913.900488	1913.908952	-0.008463961	K	E	C15:+57.021	4	17	0	0
				628	640	12	K	ESISDVGFGMLK	S	0.24%	5314	5314	641.8196411	2	1281.623632	1281.627486	-0.003853837	K	S	-	1	12	0	0
O00299	Chloride intracellular channel protein 1	2	14.52%	95	113	18	K	LAALNPESNTAGLDIFAK	F	0.24%	5784	5784	922.9891968	2	1843.962743	1843.967975	-0.005231573	K	F	-	5	18	0	0
				166	183	17	K	FLDGNELTLADCNLLPK	L	0.34%	6547	6547	966.9997559	2	1931.983862	1931.965798	0.018063759	K	L	C12:+57.021	2	17	0	0
O00559	Receptor-binding cancer antigen expressed on SiSo cells	1	3.76%	130	138	8	R	LAATQDLP	F	5.41%	10826	10826	415.57	2	829.1243499	828.4228791	0.701470808	R	F	Q5:+0.984	2	8	1	0
O14514	Brain-specific angiogenesis inhibitor 1	1	0.95%	1376	1391	15	R	LIHLSTAPEASLPAR	S	0.84%	936	936	526.2714233	3	1575.790795	1574.878038	0.9127573	R	S	-	3	15	1	0
O14520	Aquaporin-7	1	4.09%	92	106	14	H	MNAAVTFANCALGR	V	0.52%	6795	6795	748.8535767	2	1495.691503	1495.690688	0.000815728	H	V	N9:+0.984,C10:+57.021	2	14	0	0
O14672	Disintegrin and metalloproteinase domain-containing protein 10	2	3.61%	30	45	15	R	HYEGLSYNVDSLHQK	H	0.60%	2043	2043	597.6166382	3	1789.826439	1788.843109	0.983330695	R	H	-	4	15	1	0
				239	251	12	R	EAVIAQISSHVK	A	0.52%	2724	2724	642.3175049	2	1282.61936	1280.708847	1.910512918	R	A	-	5	12	2	0
O14775	Guanine nucleotide-binding protein subunit beta-5	1	2.53%	170	180	10	K	CSVYPLTFDK	N	3.89%	2987	2987	616.324646	2	1230.633642	1228.579344	2.054298264	K	N	C1:+57.021	2	10	2	0
O14917	Protocadherin-17	1	1.73%	1106	1126	20	R	ASRDSSEMGAVLEQLDHPNR	D	2.65%	4437	4437	1106.05481	2	2210.093969	2211.033841	-0.939871859	R	D	-	3	20	-1	1
O43739	Cytohesin-3	1	3.50%	303	317	14	K	EPRGIIPLENLSIR	E	0.35%	4055	4055	536.2836914	3	1605.827599	1605.920237	-0.092637709	K	E	-	5	14	0	1
O43815	Striatin	1	2.82%	22	44	22	K	GLGPLAEAAAAGDGAAAAGAAR	A	2.53%	4296	4296	603.6639404	3	1807.968346	1807.917671	0.050675409	K	A	-	3	22	0	0
O60437	Periplakin	1	0.57%	1004	1014	10	R	AQADEVLQLR	E	1.51%	6918	6918	572.3181152	2	1142.62058	1142.593133	0.027447789	R	E	Q2:+0.984	2	10	0	0
O60602	Toll-like receptor 5	1	0.82%	385	392	7	K	LQTLDLR	D	2.26%	1767	1767	429.755188	2	857.4947259	857.4970627	-0.002336831	K	D	-	1	7	0	0
O60721	Sodium/potassium/calcium exchanger 1	1	1.18%	217	230	13	R	TTVKDSDITATYK	I	8.30%	7784	7784	722.395874	2	1442.776098	1441.730036	1.046062087	R	I	-	2	13	1	1
O75106	Retina-specific copper amine oxidase	1	1.19%	523	532	9	K	LDLDVAGLK	N	6.35%	3083	3083	473.2756348	2	944.5356195	942.5385933	1.997026171	K	N	-	1	9	2	0
O75323	Protein NipSnap homolog 2	1	3.85%	275	286	11	R	IMIPLKTSPLQ	-	9.36%	4184	4184	622.3533325	2	1242.691015	1240.710078	1.980937135	R	-	Q11:+0.984	2	11	2	1
O75443	Alpha-tectorin	1	0.56%	767	779	12	R	GLRILVADQEVK	I	1.88%	4010	4010	447.9298401	3	1340.766045	1340.766346	-0.000300992	R	I	Q9:+0.984	1	12	0	1
O75712	Gap junction beta-3 protein	1	3.70%	32	42	10	R	VLVYVVAAER	V	5.71%	6177	6177	560.295105	2	1118.57456	1117.649541	0.925019057	R	V	-	2	10	1	0
O75912	Diacylglycerol kinase iota	1	1.31%	561	575	14	K	MFYAGAAFSDFLQR	S	1.18%	5597	5597	547.2612305	3	1638.760216	1639.734146	-0.973929978	K	S	M1:+15.995,Q13:+0.984	2	14	-1	0
O75923	Dysferlin	1	0.77%	361	377	16	K	EDIESNLLRPTGVALR	G	7.53%	11688	11688	594.33	3	1779.966525	1781.963558	-1.997033464	K	G	-	2	16	-1	0
O75955	Flotillin-1	3	10.30%	28	40	12	R	VFVLPCIQQIQR	I	0.24%	5480	5480	752.4143066	2	1502.812963	1499.827788	2.985175337	R	I	C6:+57.021	2	12	3	0
				78	91	13	K	EMLAAACQMFLGK	T	0.35%	5856	5856	736.3594971	2	1470.703344	1469.671199	1.032145341	K	T	C7:+57.021,Q8:+0.984	3	13	1	0
				133	152	19	K	VASSDLVNMGISVVSYTLK	D	0.24%	8345	8345	662.0154419	3	1983.022851	1982.039427	0.983423876	K	D	-	4	19	1	0
O76094	Signal recognition particle 72 kDa protein	2	4.17%	36	51	15	K	ILQINKDDVTALHCK	V	0.24%	1933	1933	589.9842529	3	1766.929284	1766.934438	-0.005154379	K	V	C14:+57.021	3	15	0	1
				241	254	13	R	TEEALQLYNQIIK	L	0.24%	5773	5773	781.9254761	2	1561.835302	1561.83517	0.000132332	R	L	-	3	13	0	0
O94779	Contactin-5	1	1.18%	422	435	13	R	WLKNGVPLSPQSR	V	4.54%	3487	3487	494.9362488	3	1481.785271	1481.799043	-0.013772062	R	V	N4:+0.984	1	13	0	1
O94905	Erlin-2	2	8.85%	149	169	20	K	LALQQDLTSMAPGLVIQAVR	V	0.24%	7523	7523	709.0664063	3	2124.175744	2124.161258	0.014485942	K	V	Q17:+0.984	2	20	0	0
				275	285	10	K	LTPEYLQLMK	Y	1.20%	4770	4770	618.3358154	2	1234.655981	1234.663143	-0.007162397	K	Y	-	2	10	0	0
O95279	Potassium channel subfamily K member 5	1	4.01%	436	456	20	K	SSLEDNLAGEESPQQGAEAK	A	2.01%	7830	7830	687.0338135	3	2058.077965	2059.918169	-1.840203202	K	A	Q14:+0.984	3	20	-1	0
O95297	Myelin protein zero-like protein 1	1	4.83%	138	151	13	K	NPPDIVVQPGHIR	L	2.66%	3353	3353	481.2559204	3	1440.744286	1441.767743	-1.02345701	K	L	N1:+0.984	1	13	-1	0
O95864	Fatty acid desaturase 2	1	2.48%	73	84	11	R	AFHPDLEFVGK	F	0.24%	3737	3737	421.5671692	3	1261.678032	1258.634619	3.043413376	R	F	-	2	11	3	0
O96005	Cleft lip and palate transmembrane protein 1	1	1.49%	304	314	10	R	VSFCPLSLWR	W	0.73%	7745	7745	633.3526611	2	1264.689672	1263.642947	1.046725234	R	W	C4:+57.021	3	10	1	0
O96019	Actin-like protein 6A	2	7.23%	112	130	18	K	SEASLHPVLMSEAPWNTR	A	0.24%	4501	4501	675.9979858	3	2024.970482	2023.978558	0.99192472	K	A	-	3	18	1	0
				194	207	13	K	SPLAGDFITMQCR	E	0.24%	4220	4220	748.3491211	2	1494.682592	1494.695454	-0.012862029	K	E	C12:+57.021	5	13	0	0
P00505	Aspartate aminotransferase, mitochondrial		6.05%	94	107	13	K	EYLPIGGLAEFCK	A	0.24%	6032	6032	748.8756714	2	1495.735693	1495.737635	-0.001942739	K	D	C12:+57.021	6	13	0	0
				325	338	13	R	IAAAILNTPDLRK	Q	0.73%	2912	2912	465.9465332	3	1394.816124	1394.824545	-0.008420855	R	Q	-	1	13	0	1
P00734	Prothrombin	1	2.41%	384	399	15	K	SPQELLCGASLISDR	W	0.24%	4895	4895	823.9118652	2	1645.80808	1644.813654	0.994426277	K	W	C7:+57.021	5	15	1	0
P01893	Putative HLA class I histocompatibility antigen, alpha chain H	5	22.65%	45	59	14	R	FISVGYVDDTQFVR	F	0.24%	5122	5122	823.411438	2	1644.807226	1644.814769	-0.007542727	R	F	-	4	14	0	0
				155	169	14	R	SWTAADMAAQITKR	K	0.91%	4818	4818	775.88	2	1549.74435	1548.771859	0.97249092	R	K	-	2	14	1	1
				243	267	24	R	DGEDQTQDTELVETRPAGDGTFQK	W	0.24%	2203	2203	880.0705566	3	2637.188195	2636.183795	1.004400074	R	W	-	3	24	1	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.24%	2754	2754	714.3647461	2	1426.713842	1426.720474	-0.006632036	K	Y	-	3	13	0	0
				280	297	17	R	YTCHVQHEGLPEPLTLR	W	0.24%	3221	3221	684.3406982	3	2049.99862	2049.009728	0.988891207	R	W	C3:+57.021	2	17	1	0
P02671	Fibrinogen alpha chain	1	2.54%	249	271	22	K	ALTDMPQMRMELERPGGNEITR	G	6.24%	5649	5649	861.1038818	3	2580.28817	2576.214697	4.073472964	K	G	M5:+15.995,M10:+15.995	1	22	4	1
P02786	Transferrin receptor protein 1	19	35.00%	6	22	16	R	SAFSNLFGGEPLSYTR	F	0.24%	6598	6598	873.4267578	2	1744.837866	1744.842046	-0.004180535	R	F	-	4	16	0	0
				130	145	15	K	LSEKLDSTDFTGTIK	L	0.24%	3039	3039	552.2857056	3	1653.833642	1653.846128	-0.012486877	K	L	-	2	15	0	1
				145	155	10	K	LLNENSYVPR	E	0.24%	2021	2021	602.8208008	2	1203.625951	1203.624783	0.001168803	K	E	-	4	10	0	0
				155	174	19	R	EAGSQKDENLALYVENQFR	E	0.24%	5748	5748	737.6916504	3	2210.051476	2211.044372	-0.992896084	R	E	Q5:+0.984	1	19	-1	1
				208	224	16	R	LVYLVENPGGYVAYSK	A	0.24%	4664	4664	886.4628296	2	1770.910009	1770.919234	-0.009224724	R	A	-	4	16	0	0
				267	287	20	K	VANAESLNAIGVLIYMDQTK	F	0.24%	7815	7815	717.7104492	3	2150.107873	2149.108903	0.998969184	K	F	-	3	20	1	0
				325	339	14	R	SSGLPNIPVQTISR	A	0.24%	3671	3671	734.9071045	2	1467.798559	1467.804538	-0.005979328	R	A	-	5	14	0	0
				344	358	14	K	LFGNMEGDCPSDWK	T	0.24%	4184	4184	828.3510132	2	1654.686376	1654.675113	0.011263591	K	T	C9:+57.021	5	14	0	0
				385	394	9	K	ILNIFGVIK	G	0.24%	6947	6947	509.3292847	2	1016.642919	1015.642999	0.999920448	K	G	-	3	9	1	0
				394	409	15	K	GFVEPDHYVVVGAQR	D	0.24%	3059	3059	558.2833862	3	1671.826684	1671.836901	-0.010217477	K	D	-	3	15	0	0
				418	428	10	K	SGVGTALLLK	L	0.60%	2703	2703	479.7991638	2	957.5826776	957.5858778	-0.003200291	K	L	-	2	10	0	0
				428	439	11	K	LAQMFSDMVLK	D	0.24%	5497	5497	641.8284912	2	1281.641332	1281.646114	-0.004781682	K	D	-	6	11	0	0
				495	508	13	K	VSASPLLYTLIEK	T	0.24%	6583	6583	717.4139404	2	1432.812231	1432.817729	-0.005497893	K	T	-	6	13	0	0
				514	531	17	K	HPVTGQFLYQDSNWASK	V	0.29%	3639	3639	989.9780884	2	1977.940527	1976.938072	1.002454806	K	V	-	2	17	1	0
				588	600	12	R	AAAEVAGQFVIK	L	0.24%	7055	7055	601.3422852	2	1200.66892	1202.665919	-1.996999	R	L	-	1	12	-1	0
				600	613	13	K	LTHDVELNLDYER	Y	0.29%	2759	2759	541.2893677	3	1620.844628	1616.768197	4.076431115	K	Y	N8:+0.984	1	13	4	0
				613	623	10	R	YNSQLLSFVR	D	0.24%	4901	4901	613.8279419	2	1225.640234	1225.645518	-0.005284411	R	D	-	5	10	0	0
				680	693	13	R	VEYHFLSPYVSPK	E	0.24%	3967	3967	783.4008789	2	1564.786108	1564.792577	-0.006468795	R	E	-	6	13	0	0
				698	717	19	R	HVFWGSGSHTLPALLENLK	L	0.34%	7098	7098	703.3743286	3	2107.099511	2105.105806	1.993704672	R	L	-	4	19	2	0
P04114	Apolipoprotein B-100	1	0.24%	262	273	11	K	EQHLFLPFSYK	N	8.26%	11362	11362	705.3821411	2	1408.748632	1407.718683	1.029948987	K	N	-	1	11	1	0
P04222	HLA class I histocompatibility antigen, Cw-3 alpha chain	7	29.78%	72	90	18	R	APWVEQEGPEYWDRETQK	Y	0.70%	3926	3926	750.3475342	3	2248.019127	2248.007258	0.011869131	R	Y	Q17:+0.984	2	18	0	1
				121	132	11	R	MYGCDVGPDGR	L	0.24%	825	825	613.7494507	2	1225.483251	1225.485127	-0.001875465	R	L	C4:+57.021	6	11	0	0
				155	169	14	R	SWTAADTAAQITQR	K	0.24%	3109	3109	760.8829346	2	1519.750219	1518.742666	1.007552821	R	K	-	4	14	1	0
				181	193	12	R	AYLEGLCVEWLR	R	0.24%	7028	7028	755.3827515	2	1508.749853	1507.748869	1.000984042	R	R	C7:+57.021	6	12	1	0
				243	267	24	W	DGEDQTQDTELVETRPAGDGTFQK	W	0.24%	2203	2203	880.0705566	3	2637.188195	2636.183795	1.004400074	R	W	-	3	24	1	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.24%	2754	2754	714.3647461	2	1426.713842	1426.720474	-0.006632036	K	Y	-	3	13	0	0
				280	297	17	R	YTCHVQHEGLPEPLTLR	W	0.24%	3221	3221	684.3406982	3	2049.99862	2049.009728	0.988891207	R	W	C3:+57.021	2	17	1	0
P04233	HLA class II histocompatibility antigen gamma chain	1	4.73%	80	94	14	K	LTVTSQNLQLENLR	M	0.24%	3938	3938	814.947876	2	1627.880102	1627.889331	-0.009228775	K	M	-	4	14	0	0
P04264	Keratin, type II cytoskeletal 1	1	1.24%	395	403	8	K	IEISELNR	V	2.41%	1229	1229	487.7582703	2	973.5008904	973.5080059	-0.007115409	K	V	N7:+0.984	1	8	0	0
P04275	von Willebrand factor	1	0.43%	2604	2616	12	R	CMVQVGVISGFK	L	4.40%	10783	10783	447.9344788	3	1340.779961	1339.662448	1.117512807	R	L	C1:+57.021,M2:+15.995	2	12	1	0
P04792	Heat shock protein beta-1	5	39.02%	5	12	7	R	VPFSLLR	G	2.26%	8140	8140	416.7	2	831.3843499	830.5014198	0.88293016	R	G	-	3	7	1	0
				27	37	10	R	LFDQAFGLPR	L	0.24%	5115	5115	583.3069458	2	1164.598242	1162.61349	1.98475189	R	L	-	5	10	2	0
				96	112	16	R	VSLDVNHFAPDELTVK	T	0.24%	4642	4642	595.310791	3	1782.908898	1782.915211	-0.006313193	R	T	-	2	16	0	0
				141	171	30	K	YTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	L	1.23%	6193	6193	1550.277832	2	3098.540014	3097.552932	0.987081767	K	L	-	2	30	1	0
				171	188	17	K	LATQSNEITIPVTFESR	A	0.24%	4835	4835	953.4960327	2	1904.976415	1904.984353	-0.007938106	K	A	-	5	17	0	0
P04839	Cytochrome b-245 heavy chain	2	4.74%	318	328	10	K	MEVGQYIFVK	C	1.38%	4744	4744	607.3161011	2	1212.616552	1212.621278	-0.004726228	K	C	-	2	10	0	0
				531	548	17	R	IGVFLCGPEALAETLSK	Q	0.24%	7795	7795	902.9767456	2	1803.937841	1803.943606	-0.005764653	R	Q	C6:+57.021	6	17	0	0
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	3	11.55%	54	67	13	K	IIHEDGYSEEECR	Q	6.04%	825	825	546.2388306	3	1635.693017	1635.683034	0.009982795	K	Q	C12:+57.021	2	13	0	0
				162	177	15	R	IAQSDYIPTQQDVLR	T	0.24%	3461	3461	874.4544067	2	1746.893163	1745.89481	0.998353389	R	T	-	5	15	1	0
				318	331	13	K	EIYTHFTCATDTK	N	0.24%	1639	1639	794.3635864	2	1586.711523	1585.707792	1.003730844	K	N	C8:+57.021	6	13	1	0
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	12	16.62%	162	173	11	K	NMVPQQALVIR	N	0.24%	3024	3024	634.8568726	2	1267.698095	1267.707074	-0.008978659	K	E	-	3	11	0	0
				430	444	14	R	AVFQANQENLPILK	R	0.24%	4563	4563	792.9403687	2	1583.865087	1583.867139	-0.002051327	R	R	-	5	14	0	0
				444	458	14	K	RAVAGDASESALLK	C	0.24%	1239	1239	694.8787231	2	1387.741796	1386.746689	0.995107265	K	C	-	5	14	1	1
				476	487	11	K	IVEIPFNSTNK	Y	0.24%	2740	2740	631.3374023	2	1260.659155	1260.671399	-0.012243984	K	Y	-	5	11	0	0
				494	508	14	K	NPNTSEPQHLLVMK	G	0.24%	1684	1684	804.4122925	2	1606.808935	1606.813724	-0.004788999	K	G	-	5	14	0	0
				535	551	16	K	DAFQNAYLELGGLGER	V	0.24%	6479	6479	584.9526978	3	1751.834618	1751.84786	-0.013241626	K	V	-	2	16	0	0
				612	625	13	K	VIMVTGDHPITAK	A	0.24%	1536	1536	691.3793945	2	1380.743139	1380.743519	-0.000379905	K	A	-	5	13	0	0
				629	647	18	K	GVGIISEGNETVEDIAAR	L	0.24%	4617	4617	915.4684448	2	1828.92124	1828.916668	0.004571792	K	L	-	6	18	0	0
				647	658	11	R	LNIPVSQVNPR	D	0.24%	2075	2075	618.8553467	2	1235.695043	1235.698616	-0.003573097	R	D	-	5	11	0	0
				671	683	12	K	DMTSEQLDDILK	Y	0.24%	4930	4930	704.3383789	2	1406.661108	1406.659908	0.001199261	K	Y	-	5	12	0	0
				707	726	19	R	QGAIVAVTGDGVNDSPALK	K	0.24%	2744	2744	906.977356	2	1811.939062	1810.942489	0.996573258	R	K	-	5	19	1	0
				726	743	17	K	KADIGVAMGIAGSDVSK	Q	0.24%	2545	2545	810.4265137	2	1618.837377	1617.839604	0.997772912	K	Q	-	6	17	1	1
P05067	Amyloid beta A4 protein	1	2.21%	469	486	17	R	RLALENYITALQAVPPR	P	1.22%	3965	3965	643.0239868	3	1926.048485	1926.057428	-0.008942311	R	P	N6:+0.984,Q12:+0.984	1	17	0	1
P05141	ADP/ATP translocase 2	10	38.26%	10	23	13	K	DFLAGGVAAAISK	T	0.24%	5128	5128	610.3446045	2	1218.673559	1218.660834	0.012725032	K	T	-	5	13	0	0
				63	72	9	K	EQGVLSFWR	G	0.24%	5534	5534	561.288269	2	1120.560888	1120.566539	-0.005651386	K	G	-	5	9	0	0
				80	92	12	R	YFPTQALNFAFK	D	0.24%	6746	6746	723.8726807	2	1445.729711	1445.734333	-0.004621992	R	D	-	5	12	0	0
				80	94	14	R	YFPTQALNFAFKDK	Y	0.24%	5805	5805	845.4338379	2	1688.852026	1688.85624	-0.004213803	R	Y	-	5	14	0	1
				96	105	9	K	QIFLGGVDK	R	0.24%	1962	1962	488.7755432	2	975.5354363	975.5389276	-0.003491262	K	H	-	1	9	0	0
				111	138	27	R	YFAGNLASGGAAGATSLCFVYPLDFAR	T	0.24%	8082	8082	932.7833862	3	2795.326684	2795.337271	-0.010587117	R	T	C18:+57.021	3	27	0	0
				155	163	8	R	GLGDCLVK	I	0.33%	1487	1487	431.2275391	2	860.439428	860.4421216	-0.002693587	R	I	C5:+57.021	4	8	0	0
				188	199	11	R	AAYFGIYDTAK	G	0.24%	3287	3287	610.3031616	2	1218.590673	1218.592086	-0.001412374	R	G	-	5	11	0	0
				244	259	15	R	KGTDIMYTGTLDCWR	K	0.24%	3861	3861	908.9219971	2	1815.828344	1815.827925	0.000418941	R	K	C13:+57.021	5	15	0	1
				272	280	8	K	GAWSNVLR	G	0.24%	2424	2424	451.7442627	2	901.4728753	901.4769959	-0.004120633	K	G	-	5	8	0	0
P05362	Intercellular adhesion molecule 1	5	16.35%	115	129	14	R	VELAPLPSWQPVGK	N	0.24%	5225	5225	760.9223633	2	1519.829076	1519.839861	-0.010784614	R	N	-	5	14	0	0
				273	287	14	K	ASVSVTAEDEGTQR	L	0.24%	668	668	725.3424683	2	1448.669286	1448.674312	-0.005025461	K	L	-	5	14	0	0
				339	353	14	K	VTLNGVPAQPLGPR	A	0.24%	2593	2593	710.4052124	2	1418.794775	1417.804144	0.990630493	K	A	-	3	14	1	0
				433	449	16	K	DGTFPLPIGESVTVTR	D	0.24%	5517	5517	844.9398193	2	1687.863989	1687.878097	-0.01410868	K	D	-	3	16	0	0
				478	507	29	R	YEIVIITVVAAAVIMGTAGLSTYLYNRQR	K	2.91%	12179	12179	1068.588135	3	3202.740929	3201.71084	1.030089081	R	K	M15:+15.995,Q28:+0.984	1	29	1	1
P06239	Tyrosine-protein kinase Lck	1	1.57%	379	387	8	K	IADFGLAR	L	0.76%	2411	2411	431.7414856	2	861.4673211	861.4708479	-0.003526817	K	D	-	4	8	0	0
P06576	ATP synthase subunit beta, mitochondrial	19	54.06%	94	109	15	R	LVLEVAQHLGESTVR	T	0.24%	4043	4043	825.9630127	2	1649.910375	1649.910066	0.000309223	R	T	-	5	15	0	0
				109	121	12	R	TIAMDGTEGLVR	G	0.24%	2759	2759	632.8656006	2	1263.715551	1261.633634	2.081917092	R	G	-	1	12	2	0
				133	143	10	K	IPVGPETLGR	I	0.24%	1941	1941	519.7989502	2	1037.58225	1037.586941	-0.004690193	K	I	-	5	10	0	0
				143	155	12	R	IMNVIGEPIDER	G	0.24%	3430	3430	694.36	2	1386.70435	1384.702048	2.002301912	R	G	-	2	12	2	0
				143	159	16	R	IMNVIGEPIDERGPIK	T	0.24%	3730	3730	891.4868774	2	1780.958105	1779.955303	1.002801875	R	T	-	5	16	1	1
				188	198	10	K	VVDLLAPYAK	G	0.24%	4260	4260	544.8185425	2	1087.621435	1087.627743	-0.006307847	K	G	-	5	10	0	0
				201	212	11	K	IGLFGGAGVGK	T	0.24%	3426	3426	488.2839355	2	974.552221	974.554912	-0.002691002	K	T	-	5	11	0	0
				212	225	13	K	TVLIMELINNVAK	A	0.24%	8650	8650	729.421875	2	1456.8281	1456.832334	-0.004234088	K	A	-	6	13	0	0

				225	239	14	K	AHGGYSVFAGVGER	T	0.24%	1938	1938	703.8405762	2	1405.665502	1405.673858	-0.008355968	K	T	-	6	14	0	0
				239	259	20	R	TREGNDLYHEMIESGVINLK	D	0.24%	5676	5676	773.7196045	3	2318.135338	2317.137243	0.998094893	R	D	-	4	20	1	1
				264	279	15	K	VALVYGQMNEPPGAR	A	0.24%	2738	2738	801.9122925	2	1601.808935	1600.803159	1.005775721	K	A	-	5	15	1	0
				281	294	13	R	VALTGLTVAEYFR	D	0.24%	6637	6637	720.3983154	2	1438.780981	1438.782012	-0.001031029	R	D	-	5	13	0	0
				310	324	14	R	FTQAGSEVSALLGR	I	0.24%	4657	4657	479.5891724	3	1435.744042	1434.746689	0.997353026	R	I	-	3	14	1	0
				324	345	21	R	IPSAVGYQPTLATDMGTMQER	I	0.24%	4534	4534	756.0318604	3	2265.072106	2265.076952	-0.004846513	R	I	-	5	21	0	0
				387	406	19	R	AIAELGIYPAVDPLDSTSR	I	0.24%	6067	6067	994.5182495	2	1987.020849	1987.026218	-0.005369393	R	I	-	6	19	0	0
				406	422	16	R	IMDPNIVGSEHYDVAR	G	0.24%	2976	2976	908.4396362	2	1814.863622	1814.862131	0.001491605	R	G	-	4	16	0	0
				432	451	19	K	SLQDIIAILGMDELSEEDK	L	0.35%	9147	9147	707.0211182	3	2118.039879	2118.040215	-0.000335316	K	L	-	3	19	0	0
				462	480	18	R	FLSQPFQVAEVFTGHMGK	L	0.24%	7293	7293	675.0060425	3	2021.994652	2022.003316	-0.008663503	R	L	-	1	18	0	0
				489	519	30	K	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	A	0.30%	9145	9145	1118.223755	3	3351.64779	3350.616914	1.0308756	K	A	Q3:+0.984	3	30	1	0
P06733	Alpha-enolase	21	66.59%	15	28	13	R	GNPTVEVDLFTSK	G	0.24%	4266	4266	703.8585815	2	1405.701513	1405.708906	-0.007393434	R	G	-	5	13	0	0
				32	50	18	R	AAVPSGASTGIYEALELR	D	0.24%	5666	5666	903.473877	2	1804.932104	1803.936675	0.995428938	R	D	-	6	18	1	0
				32	54	22	R	AAVPSGASTGIYEALELRDNDK	T	2.66%	4475	4475	759.713501	3	2276.117028	2276.128452	-0.011424006	R	T	-	1	22	0	1
				92	103	11	K	LMIEMDGTENK	S	0.24%	2356	2356	640.7944336	2	1279.573217	1279.578822	-0.005605236	K	S	-	5	11	0	0
				132	162	30	R	HIADLAGNSEVILPVPAFNVINGGSHAGNK	L	0.24%	6740	6740	753.8930664	4	3011.540965	3012.530465	-0.989499807	R	L	N8:+0.984,N19:+0.984	1	30	-1	0
				162	179	17	K	LAMQEFMILPVGAANFR	E	0.24%	8118	8118	954.4967651	2	1906.97788	1906.979745	-0.001864463	K	E	-	2	17	0	0
				183	193	10	R	IGAEVYHNLK	N	0.24%	1083	1083	572.3098145	2	1142.603979	1142.608404	-0.004425446	R	N	-	5	10	0	0
				202	221	19	K	DATNVGDEGGFAPNILENK	E	0.24%	4301	4301	980.9667969	2	1959.917944	1959.917396	0.000547566	K	E	-	4	19	0	0
				202	228	26	K	DATNVGDEGGFAPNILENKEGLELLK	T	0.24%	6538	6538	1373.195801	2	2744.375951	2743.355202	1.020749795	K	T	N18:+0.984	3	26	1	1
				239	253	14	K	VVIGMDVAASEFFR	S	0.24%	7280	7280	770.8970947	2	1539.778539	1539.775547	0.002991997	K	S	-	5	14	0	0
				253	262	9	R	SGKYDLDFK	S	0.24%	1719	1719	536.7679443	2	1071.520239	1071.523672	-0.003432936	R	S	-	5	9	0	1
				262	281	19	K	SPDDPSRYISPDQLADLYK	S	0.24%	5166	5166	727.352417	3	2179.033776	2179.043325	-0.009549215	K	S	-	2	19	0	1
				269	281	12	R	YISPDQLADLYK	S	0.24%	5403	5403	713.9034424	2	1425.791235	1424.718743	1.072491854	R	S	-	4	12	1	0
				281	306	25	K	SFIKDYPVVSIEDPFDQDDWGAWQK	F	0.52%	7800	7800	996.1367798	3	2985.386864	2986.354852	-0.967987533	K	F	Q17:+0.984,Q24:+0.984	3	25	-1	1
				285	306	21	K	DYPVVSIEDPFDQDDWGAWQK	F	0.24%	7725	7725	838.0408936	3	2511.099206	2510.091382	1.007823496	K	F	Q13:+0.984	3	21	1	0
				306	326	20	K	FTASAGIQVVGDDLTVTNPK	R	0.24%	15305	15305	678.46	3	2032.356525	2033.031682	-0.675157224	K	R	N18:+0.984	1	20	-1	0
				335	343	8	K	SCNCLLLK	V	0.60%	1717	1717	504.2540283	2	1006.492407	1006.493043	-0.000636159	K	V	C2:+57.021,C4:+57.021	4	8	0	0
				343	358	15	K	VNQIGSVTESLQACK	L	0.24%	2537	2537	817.4124756	2	1632.809301	1632.813654	-0.00435302	K	L	C14:+57.021	3	15	0	0
				358	372	14	K	LAQANGWGVMVSHR	S	0.24%	2965	2965	509.5878906	3	1525.740197	1525.745963	-0.005766181	K	S	N5:+0.984	3	14	0	0
				372	394	22	R	SGETEDTFIADLVVGLCTGQIK	T	0.24%	9234	9234	785.0544434	3	2352.139855	2352.151427	-0.011571834	R	T	C17:+57.021	6	22	0	0
				406	420	14	K	YNQLLRIEEELGSK	A	0.24%	5342	5342	564.6345215	3	1690.880089	1690.888996	-0.008906987	K	A	-	5	14	0	1
P06744	Glucose-6-phosphate isomerase	2	5.91%	57	73	16	K	NLVTEDVMRMLVDLAK	S	2.17%	4051	4051	924.4871216	2	1846.958593	1846.95324	0.005353476	K	S	N1:+0.984	1	16	0	1
				194	211	17	K	TLAQLNPESSLFIIASK	T	0.24%	6993	6993	916.5112305	2	1831.006811	1831.009112	-0.002300742	K	T	-	4	17	0	0
P07237	Protein disulfide-isomerase	6	21.06%	31	42	11	K	SNFAEALAAHK	Y	0.24%	1668	1668	580.298584	2	1158.581518	1157.582918	0.998600089	K	Y	-	5	11	1	0
				81	97	16	K	VDATEESDLAQQYGVR	G	0.24%	3161	3161	892.4854126	2	1782.955175	1779.827518	3.127656787	K	G	-	1	16	3	0
				132	162	30	R	TGPAATTLPDGAAAESLVESSEVAVIGFFK	D	0.24%	9906	9906	979.5056152	3	2935.493371	2934.486232	1.007138975	R	D	-	6	30	1	0
				170	195	25	K	QFLQAAEAIDDIPFGITSNSDVFSK	Y	1.81%	11463	11463	1358.15979	2	2714.30393	2713.312274	0.991655846	K	Y	N19:+0.984	1	25	1	0
				230	247	17	K	HNQLPLVIEFTEQTAPK	I	0.24%	6115	6115	983.5129395	2	1965.010229	1964.036723	0.973505442	K	I	-	4	17	1	0
				300	308	8	R	ILEFFGLK	K	0.24%	6298	6298	484.2861328	2	966.5566155	965.5586004	0.998015153	R	K	-	5	8	1	0
P07900	Heat shock protein HSP 90-alpha	7	12.30%	46	60	14	R	ELISNSSDALDKIR	Y	3.19%	1756	1756	515.9221802	3	1544.743065	1542.788497	1.954568455	R	Y	E1:-18.011,N5:+0.984	1	14	2	1
				58	69	11	K	IRYESLTDPSK	L	0.24%	1211	1211	655.3469849	2	1308.67832	1307.672127	1.006192727	K	L	-	1	11	1	1
				87	100	13	R	TLTIVDTGIGMTK	A	1.23%	4148	4148	675.3682861	2	1348.720922	1348.7272	-0.006277966	R	A	-	3	13	0	0
				100	112	12	K	ADLINNLGTIAK	S	0.24%	4087	4087	621.854248	2	1241.692846	1241.697948	-0.005101706	K	S	-	5	12	0	0
				314	327	13	K	SLTNDWEDHLAVK	H	0.24%	3714	3714	764.3757935	2	1526.735937	1526.736518	-0.00058139	K	H	-	5	13	0	0
				386	400	14	R	GVVDSEDLPLNISR	E	0.24%	4198	4198	757.3948364	2	1512.774023	1512.778383	-0.004360332	R	E	-	4	14	0	0
				632	647	15	K	HLEINPDHSIIETLR	Q	0.75%	3951	3951	596.3178101	3	1785.929955	1786.921344	-0.991388488	K	Q	N5:+0.984	2	15	-1	0
P07954	Fumarate hydratase, mitochondrial	10	36.08%	51	61	10	R	IEYDTFGELK	V	0.24%	3407	3407	607.7964478	2	1213.577245	1213.586666	-0.00942042	R	V	-	4	10	0	0
				100	115	15	K	RAAAEVNQDYGLDPK	I	0.24%	915	915	823.9106445	2	1645.805639	1645.805995	-0.000355906	K	I	-	4	15	0	1
				131	160	29	K	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	A	2.76%	9396	9396	1090.535645	3	3268.583458	3271.556758	-2.973299182	K	A	Q11:+0.984,N19:+0.984	1	29	-1	0
				160	172	12	R	AIEMLGGELGSK	I	0.24%	3402	3402	603.315918	2	1204.616186	1203.616921	0.999264594	R	I	-	5	12	1	0
				233	256	23	R	THTQDAVPLTLGQEFSGYVQQVK	Y	0.24%	6331	6331	1274.151245	2	2546.28684	2545.281264	1.005575914	R	Y	-	3	23	1	0
				268	286	18	R	IYELAAGGTAVGTGLNTR	I	0.24%	3450	3450	882.9682617	2	1763.920873	1762.921359	0.999514222	R	I	-	5	18	1	0
				296	311	15	K	VAALTGLPFVTAPNK	F	0.24%	5355	5355	749.9328003	2	1497.849951	1497.855511	-0.00556067	K	F	-	5	15	0	0
				350	371	21	R	SGLGELILPENEPGSSIMPGK	V	0.24%	5903	5903	1063.547974	2	2125.080297	2124.077269	1.003028322	R	V	-	5	21	1	0
				447	467	20	K	LMNESLMLVTALNPHIGYDK	A	1.85%	2564	2564	565.79	4	2259.1287	2259.12791	0.00079004	K	A	N13:+0.984	1	20	0	0
				483	504	21	K	ETAIELGYLTAEQFDEWVKPK	D	0.24%	10649	10649	823.4082031	3	2467.201134	2467.215854	-0.014720105	K	D	Q13:+0.984	1	21	0	0
P08195	4F2 cell-surface antigen heavy chain	13	29.68%	122	145	23	K	QPMNAASGAAMSLAGAEKNGLVK	I	6.87%	10741	10741	739.3696289	3	2215.085412	2217.076921	-1.991509665	K	I	Q1:+0.984,N4:+0.984	2	23	-1	1
				160	171	11	K	FTGLSKEELLK	V	0.30%	2268	2268	632.86	2	1263.70435	1263.70745	-0.003099864	K	V	-	1	11	0	1
				226	245	19	R	IGDLQAFQGHGAGNLAGLK	G	0.24%	3762	3762	934.4959106	2	1866.976171	1865.974792	1.001379489	R	G	-	5	19	1	0
				245	255	10	K	GRLDYLSSLK	V	0.24%	2483	2483	576.3224487	2	1150.629247	1150.634619	-0.005371691	K	V	-	2	10	0	1
				257	266	9	K	GLVLGPIHK	N	0.24%	1983	1983	467.2950745	2	932.5744988	932.5807328	-0.00623397	K	N	-	4	9	0	0
				303	313	10	R	VILDLTPNYR	G	0.24%	3903	3903	602.3404541	2	1202.665258	1202.665919	-0.000661109	R	G	-	5	10	0	0
				313	329	16	R	GENSWFSTQVDTVATK	V	0.24%	4460	4460	885.4188232	2	1768.821996	1768.82679	-0.004793596	R	V	-	5	16	0	0
				396	416	20	K	DLLLTSSYLSDSGSTGEHTK	S	0.24%	4118	4118	704.3407593	3	2109.998803	2110.006605	-0.007802512	K	S	-	2	20	0	0
				429	439	10	R	WCSWSLSQAR	L	0.24%	3649	3649	641.2991333	2	1280.582617	1279.576324	1.006292594	R	L	C2:+57.021	5	10	1	0
				439	451	12	R	LLTSFLPAQLLR	L	0.24%	7686	7686	686.4185791	2	1370.821508	1370.828568	-0.007059925	R	L	-	5	12	0	0
				510	524	14	K	GQSEDPGSLLSLFR	R	0.24%	7193	7193	754.8463135	2	1507.676977	1505.736168	1.940808569	K	R	Q2:+0.984	5	14	2	0
				592	613	21	K	ADLLLSTQPGREEGSPLELER	L	0.24%	4616	4616	770.7362061	3	2309.185143	2309.186301	-0.00115806	K	L	-	2	21	0	1
				613	625	12	R	LKLEPHEGLLLR	F	0.24%	3192	3192	473.2888489	3	1416.843072	1416.845281	-0.002209273	R	F	-	3	12	0	1
P08237	6-phosphofructokinase, muscle type	6	10.38%	184	201	17	R	IMEIVDAITTTAQSHQR	T	1.32%	5209	5209	639.3307495	3	1914.968773	1913.951659	1.017114783	R	T	Q13:+0.984	2	17	1	0
				201	210	9	R	TFVLEVMGR	H	7.28%	4508	4508	525.817627	2	1049.619604	1050.553199	-0.93359479	R	H	-	3	9	-1	0
				345	356	11	R	LPLMECVQVTK	D	0.24%	3382	3382	659.34	2	1316.66435	1316.682764	-0.018414184	R	D	C6:+57.021	3	11	0	0
				603	615	12	R	DLQANVEHLVQK	M	0.24%	3652	3652	697.3740845	2	1392.732519	1392.736124	-0.003605359	R	M	-	5	12	0	0
				656	673	17	K	NVLGHMQQGGSPTPFDR	N	6.80%	2749	2749	614.2943115	3	1839.859459	1839.868613	-0.00915367	K	N	-	1	17	0	0
				699	714	15	R	IFANTPDSGCVLGMR	K	0.24%	3598	3598	819.887146	2	1637.758642	1636.769682	0.98896008	R	K	C10:+57.021	2	15	1	0
P08574	Cytochrome c1, heme protein, mitochondrial	3	13.85%	99	112	13	R	GLLSSLDHTSIRR	G	0.24%	2445	2445	485.6040039	3	1453.788537	1453.800122	-0.011584929	R	G	-	3	13	0	1
				170	186	16	K	LFDYFPKPYPNSEAAR	A	0.24%	4495	4495	638.9813232	3	1913.920495	1914.915196	-0.994700921	K	A	N11:+0.984	4	16	-1	0
				186	202	16	R	AANNGALPPDLSYIVR	A	0.24%	5074	5074	835.9452515	2	1669.874853	1670.862766	-0.987913078	R	A	N3:+0.984	1	16	-1	0
P08684	Cytochrome P450 3A4	1	3.18%	476	492	16	K	LSLGGLLQPEKPVVLK	V	6.73%	10176	10176	565.6413574	3	1693.900597	1690.039289	3.861307714	K	V	-	1	16	4	0
P08865	40S ribosomal protein SA	3	19.32%	63	80	17	R	AIVAIENPADVSVISSR	N	0.24%	4529	4529	869.9766235	2	1737.937597	1739.94176	-2.004163258	R	N	-	2	17	-1	0
				89	102	13	K	FAAATGATPIAGR	F	0.24%	1158	1158	602.3269653	2	1202.638281	1202.640767	-0.002486504	K	F	-	5	13	0	0
				128	155	27	R	ADHQPLTEASYVNLPTIALCNTDSPLR	Y	0.24%	6409	6409	1499.21936	2	2996.423071	2995.47047	0.952600623	R	Y	C20:+57.021	5	27	1	0
P08962	CD63 antigen	1	10.08%	164	188	24	R	VPDSCCINVTVGCGINFNEKAIHK	E	6.08%	2851	2851	912.0879517	3	2733.24038	2733.254635	-0.014254908	R	E	C5:+57.021,C6:+57.021,N	1	24	0	1
P09382	Galectin-1	3	25.93%	37	49	12	K	DSNNLCLHFNPR	F	0.24%	2262	2262	496.2309875	3	1485.669488	1486.661829	-0.992341554	K	F	N4:+0.984,C6:+57.021	1	12	-1	0
				49	64	15	R	FNAHGDANTIVCNSK	D	0.24%	728	728	824.9115601	2	1647.80747	1646.746637	1.060832949	R	D	C12:+57.021	3	15	1	0
				100	108	8	K	LPDGYEFK	F	2.06%	1767	1767	485.2905579	2	968.5654656	967.4650939	1.100371731	K	F	-	3	8	1	0
P09601	Heme oxygenase 1	1	4.51%	100	113	13	R	WQEVIPYTPAMQR	Y	2.63%	4311	4311	809.9	2	1617.78435	1617.797345	-0.012995552	R	Y	-	1	13	0	0
P0CG47	Polyubiquitin-B	3	17.47%	11	27	16	K	TITLEVEPSDTIENVK	A	0.24%	4155	4155	894.465271	2	1786.914892	1786.920022	-0.005129912	K	A	-	5	16	0	0
				48	63	15	K	QLEDGRTLSDYNIQK	E	0.24%	2245	2245	594.3005981	3	1779.878319	1778.879888	0.998431058	K	E	-	1	15	1	1
				63	72	9	K	ESTLHLVLR	L	0.24%	2043	2043	534.3128052	2	1066.60996	1066.61349	-0.00352936	K	L	-	6	9	0	0
P11142	Heat shock cognate 71 kDa protein	21	43.50%	3	25	22	K	GPAVGIDLGTTYSCVGVFQHGK	V	0.24%	5123	5123	755.0410767	3	2262.099755	2262.109837	-0.010081708	K	V	C14:+57.021	3	22	0	0
				36	49	13	R	TTPSYVAFTDTER	L	0.24%	2869	2869	744.3529663	2	1486.690283	1486.693985	-0.003702151	R	L	-	6	13	0	0
				36	56	20	R	TTPSYVAFTDTERLIGDAAK	N	8.90%	6299	6299	719.3661499	3	2155.074975	2155.079711	-0.004736005	R	N	-	1	20	0	1
				56	71	15	K	NQVAMNPTNTVFDAK	R	0.24%	2963	2963	825.3998413	2	1648.784033	1648.787903	-0.003870543	K	R	-	4	15	0	0
				76	88	12	R	RFDDAVVQSDMK	H	0.24%	1538	1538	470.8927612	3	1409.654809	1409.660911	-0.006102885	R	H	-	4	12	0	1
				88	102	14	K	HWPFMVVNDAGRPK	V	0.24%	3884	3884	551.9439087	3	1652.808251	1653.808563	-1.000312302	K	V	N8:+0.984	6	14	-1	0
				112	126	14	K	SFYPEEVSSMVLTK	M	0.24%	5588	5588	808.895813	2	1615.775976	1615.780358	-0.004382183	K	M	-	6	14	0	0
				128	137	9	K	EIAEAYLGK	T	3.87%	1774	1774	497.75	2	993.4843499	992.5178578	0.96649208	K	T	-	3	9	1	0
				137	155	18	K	TVTNAVVTVPAYFNDSQR	Q	0.24%	4484	4484	661.3375854	3	1980.989281	1980.990501	-0.001220244	K	Q	-	1	18	0	0
				159	171	12	K	DAGTIAGLNVLR	I	0.24%	4531	4531	601.8459473	2	1201.676244	1198.666982	3.009262563	K	I	-	2	12	3	0
				171	187	16	R	IINEPTAAAIAYGLDK	K	0.24%	4861	4861	830.4494629	2	1658.883276	1658.887934	-0.004657963	R	K	-	5	16	0	0
				220	236	16	K	STAGDTHLGGEDFDNR	M	0.24%	996	996	564.579834	3	1690.716027	1690.718302	-0.002275263	K	M	-	5	16	0	0
				236	246	10	R	MVNHFIAEFK	R	0.24%	3455	3455	618.3128662	2	1234.610082	1234.616862	-0.00677925	R	R	-	5	10	0	0
				299	311	12	R	ARFEELNADLFR	G	0.24%	4408	4408	741.3814697	2	1480.747289	1479.747023	1.000266101	R	G	-	2	12	1	1
				301	311	10	R	FEELNADLFR	G	3.17%	4949	4949	628.8430786	2	1255.670507	1253.592798	2.077708875	R	G	N5:+0.984	1	10	2	0
				328	342	14	K	SQIHDIVLVGGSTR	I	0.24%	2442	2442	494.6054077	3	1480.792748	1480.799787	-0.007039175	K	I	-	1	14	0	0
				348	357	9	K	LLQDFFNGK	E	0.24%	4540	4540	541.2850952	2	1080.55454	1080.560391	-0.005851026	K	E	-	5	9	0	0
				361	384	23	K	SINPDEAVAYGAAVQAAILSGDK	S	0.24%	7717	7717	754.3870239	3	2260.137597	2260.122288	0.015308449	K	S	Q15:+0.984	3	23	0	0
				423	447	24	K	QTQTFTTYSDNQPGVLIQVYEGER	A	0.24%	5782	5782	1387.661987	2	2773.308325	2773.3195	-0.011175887	K	A	-	4	24	0	0
				539	550	11	K	NSLESYAFNMK	A	0.24%	3976	3976	652.3010864	2	1302.586523	1302.591435	-0.00491202	K	A	-	6	11	0	0
				573	583	10	K	CNEIINWLDK	N	0.24%	5574	5574	652.8172607	2	1303.618871	1303.622606	-0.003734108	K	N	C1:+57.021	5	10	0	0
P11166	Solute carrier family 2, facilitated glucose transporter member 1	1	3.05%	477	492	15	K	TPEELFHPLGADSQV	-	0.24%	4902	4902	820.9194336	2	1639.823217	1638.788948	1.034269284	K	-	-	5	15	1	0
P11277	Spectrin beta chain, erythrocyte	1	0.51%	1458	1469	11	K	RFLDLLEPLGR	R	1.04%	1232	1232	664.861145	2	1327.70664	1327.761217	-0.054576737	K	R	-	4	11	0	1
P11413	Glucose-6-phosphate 1-dehydrogenase	2	5.05%	136	152	16	R	LFYLALPPTVYEAVTK	N	0.62%	8071	8071	913.0065308	2	1823.997411	1824.007321	-0.009909173	R	N	-	3	16	0	0
				205	215	10	K	EMVQNLMVLR	F	0.30%	4473	4473	618.3384399	2	1234.66123	1231.641697	3.019532483	K	F	-	2	10	3	0
P12259	Coagulation factor V	1	0.45%	2189	2199	10	K	NFFNPPIISR	F	1.48%	4609	4609	603.8001709	2	1205.584692	1203.640039	1.944652957	K	F	-	3	10	2	0
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	2	7.69%	29	41	12	K	SEDFSLPAYMDR	R	0.42%	4469	4469	715.8178101	2	1429.61997	1429.618378	0.001592117	K	R	-	3	12	0	0
				29	42	13	K	SEDFSLPAYMDRR	D	0.24%	3907	3907	529.5789185	3	1585.71328	1585.719489	-0.006208821	K	D	-	4	13	0	1
P13473	Lysosome-associated membrane glycoprotein 2	1	1.95%	144	152	8	R	IPLNDLFR	C	0.33%	4893	4893	494.28	2	986.5443499	986.554912	-0.010562096	R	C	-	4	8	0	0
P13533	Myosin-6	2	1.50%	696	705	9	R	CNGVLEGIR	I	1.70%	1369	1369	509.2584229	2	1016.501196	1016.506847	-0.005651641	R	I	C1:+57.021	2	9	0	0
				1398	1418	20	R	LQDAEEAVEAVNAKCSSLEK	T	4.86%	6092	6092	732.0449829	3	2193.111474	2192.014962	1.096512018	R	T	Q2:+0.984,N12:+0.984,C1	2	20	1	1
P13591	Neural cell adhesion molecule 1	2	3.96%	592	604	12	K	GLGEISAASEFK	T	1.33%	3096	3096	605.3601685	2	1208.704687	1207.608464	1.09622289	K	T	-	2	12	1	0
				820	842	22	K	GPVEAKPECQETETKPAPAEVK	T	3.04%	572	572	599.5487671	4	2394.163768	2395.157225	-0.993456689	K	T	C9:+57.021,Q10:+0.984	3	22	-1	0
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	1	2.97%	379	391	12	K	RNISHYEEQLVK	M	2.20%	889	889	506.27	3	1515.786525	1515.768137	0.01838776	K	M	N2:+0.984	1	12	0	1
P13987	CD59 glycoprotein	1	9.38%	66	78	12	K	FEHCNFNDVTTR	L	0.24%	1266	1266	513.8903809	3	1538.647667	1539.640759	-0.993091854	K	L	C4:+57.021,N5:+0.984	4	12	-1	0
P14174	Macrophage migration inhibitory factor	2	17.39%	1	12	11	M	PMFIVNTNVPR	A	0.57%	3558	3558	644.3478394	2	1286.680029	1286.680525	-0.000495937	M	A	-	2	11	0	0
				78	87	9	K	LLCGLLAER	L	0.24%	4144	4144	523.8009644	2	1045.586279	1043.579284	2.006994655	K	L	C3:+57.021	2	9	2	0
P14410	Sucrase-isomaltase, intestinal	1	1.20%	554	576	22	K	QYDVHSLYGYSMAIATEQAVQK	V	1.98%	5970	5970	841.937561	3	2522.789208	2517.184673	5.604534921	K	V	M12:+15.995	1	22	6	0
P14550	Alcohol dehydrogenase [NADP+]	1	3.08%	13	23	10	K	MPLIGLGTWK	S	0.24%	5751	5751	558.3158569	2	1114.616064	1114.620884	-0.004820509	K	S	-	3	10	0	0
P14618	Pyruvate kinase isozymes M1/M2	30	60.45%	32	43	11	R	LDIDSPPITAR	N	0.24%	2708	2708	599.3253784	2	1196.635107	1196.640098	-0.004991676	R	N	-	6	11	0	0
				43	56	13	R	NTGIICTIGPASR	S	0.24%	2376	2376	680.3546143	2	1358.693578	1358.697168	-0.0035891	R	S	C6:+57.021	5	13	0	0
				63	73	10	E	MIKSGMNVAR	L	2.53%	1958	1958	554.2910767	2	1106.566503	1106.557618	0.0088856	E	L	N7:+0.984	1	10	0	1
				73	89	16	R	LNFSHGTHEYHAETIK	N	0.24%	1085	1085	471.7306519	4	1882.891307	1882.896207	-0.00489973	R	N	-	1	16	0	0
				92	115	23	R	TATESFASDPILYRPVAVALDTK	G	0.24%	6375	6375	1233.146973	2	2464.278295	2464.284953	-0.006657383	R	G	-	6	23	0	0
				141	151	10	K	ITLDNAYMEK	C	0.24%	2453	2453	599.2925415	2	1196.569433	1196.574722	-0.005289128	K	C	-	3	10	0	0
				151	162	11	K	CDENILWLDYK	N	0.24%	5646	5646	734.8394775	2	1467.663305	1467.66995	-0.006644754	K	N	C1:+57.021	6	11	0	0
				173	186	13	K	IYVDDGLISLQVK	Q	0.24%	5619	5619	731.9094238	2	1461.803198	1461.807892	-0.004694704	K	Q	-	5	13	0	0
				188	206	18	K	GADFLVTEVENGGSLGSK	K	0.24%	5421	5421	890.9335938	2	1779.851537	1779.852655	-0.00111746	K	K	N11:+0.984	6	18	0	0
				188	207	19	K	GADFLVTEVENGGSLGSKK	G	0.24%	4623	4623	636.661438	3	1906.960839	1906.963618	-0.002779171	K	G	-	4	19	0	1
				206	224	18	K	KGVNLPGAAVDLPAVSEK	D	0.24%	3865	3865	882.9946899	2	1763.97373	1763.978146	-0.004415965	K	D	-	6	18	0	1
				207	224	17	K	GVNLPGAAVDLPAVSEK	D	0.24%	4530	4530	818.9474487	2	1635.879247	1635.883183	-0.003935251	K	D	-	6	17	0	0

				230	246	16	K	FGVEQDVDMVFASFIR	K	0.24%	9582	9582	930.9529419	2	1859.890234	1858.892368	0.997865429	K	K	-	6	16	1	0
				230	247	17	K	FGVEQDVDMVFASFIRK	A	0.24%	8979	8979	663.3338623	3	1986.978112	1987.971331	-0.993219622	K	A	Q5:+0.984	3	17	-1	1
				278	294	16	R	RFDEILEASDGIMVAR	G	0.24%	11832	11832	607.9730225	3	1820.895592	1820.909081	-0.013488753	R	G	-	5	16	0	1
				294	305	11	R	GDLGIEIPAEK	V	0.24%	3239	3239	571.3063965	2	1140.597143	1140.60265	-0.005507367	R	V	-	5	11	0	0
				319	336	17	R	AGKPVICATQMLESMIK	K	0.24%	7133	7133	938.9855347	2	1875.955419	1875.961583	-0.006163824	R	K	C7:+57.021	4	17	0	0
				322	336	14	K	PVICATQMLESMIK	K	0.24%	7439	7439	810.9107056	2	1619.805761	1620.792042	-0.986281275	K	K	C4:+57.021,Q7:+0.984	1	14	-1	0
				342	367	25	R	AEGSDVANAVLDGADCIMLSGETAK	G	0.24%	7205	7205	832.0490723	3	2493.123742	2493.135854	-0.012112619	R	G	C16:+57.021	4	25	0	0
				342	376	34	R	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	M	0.24%	7812	7812	874.6643677	4	3494.626171	3494.61765	0.008520471	R	M	N8:+0.984,C16:+57.021	5	34	0	1
				367	376	9	K	GDYPLEAVR	M	0.24%	1584	1584	510.2597656	2	1018.503881	1018.508356	-0.004474606	K	M	-	5	9	0	0
				399	422	23	R	RLAPITSDPTEATAVGAVEASFK	C	0.24%	5628	5628	778.0747681	3	2331.200829	2330.211788	0.989041503	R	C	-	5	23	1	1
				400	422	22	R	LAPITSDPTEATAVGAVEASFK	C	0.24%	6146	6146	1088.062256	2	2174.108862	2174.110676	-0.001814785	R	C	-	6	22	0	0
				422	433	11	K	CCSGAIIVLTK	S	0.24%	2645	2645	611.3182983	2	1220.620947	1220.624785	-0.003838776	K	S	C1:+57.021,C2:+57.021	6	11	0	0
				443	455	12	R	YRPRAPIIAVTR	N	0.78%	1649	1649	471.6182556	3	1411.831292	1411.841198	-0.009906682	R	N	-	3	12	0	1
				447	455	8	R	APIIAVTR	N	2.49%	1344	1344	421.7562256	2	841.4968011	839.5228835	1.973917564	R	N	-	2	8	2	0
				447	461	14	R	APIIAVTRNPQTAR	Q	0.24%	1226	1226	503.2918396	3	1506.852044	1506.863056	-0.011012497	R	Q	-	3	14	0	1
				467	475	8	R	GIFPVLCK	D	0.24%	4444	4444	467.263855	2	932.5120599	932.5148927	-0.002832791	R	D	C7:+57.021	3	8	0	0
				475	489	14	K	DPVQEAWAEDVDLR	V	0.24%	5004	5004	821.8864746	2	1641.757299	1641.763461	-0.006162213	K	V	-	5	14	0	0
				489	498	9	R	VNFAMNVGK	A	0.24%	1729	1729	490.2527466	2	978.4898431	978.4956837	-0.005840572	R	A	-	6	9	0	0
P14625	Endoplasmin	9	15.32%	75	84	9	K	FAFQAEVNR	M	0.24%	2532	2532	540.7854004	2	1079.555151	1080.535239	-0.980088531	K	M	-	3	9	-1	0
				87	95	8	K	LIINSLYK	N	0.24%	3529	3529	482.2983093	2	962.5809686	962.5800642	0.000904412	K	N	-	2	8	0	0
				102	114	12	R	ELISNASDALDK	I	0.24%	2091	2091	638.3221436	2	1274.628637	1274.635407	-0.006770043	R	I	-	6	12	0	0
				142	161	19	K	NLLHVTDTGVGMTREELVK	N	0.24%	3443	3443	705.0446777	3	2112.110558	2111.104487	1.006071435	K	N	-	3	19	1	1
				384	395	11	K	SILFVPTSAPR	G	0.24%	4060	4060	594.3414307	2	1186.667211	1186.671005	-0.003793344	K	G	-	5	11	0	0
				434	448	14	K	GVVDSDDLPLNVSR	E	0.24%	3396	3396	743.38	2	1484.74435	1484.747083	-0.002733024	K	E	-	4	14	0	0
				511	530	19	R	FQSSHHPTDITSLDQYVER	M	0.24%	3467	3467	754.6942139	3	2261.059166	2260.039621	1.019545378	R	M	Q2:+0.984	3	19	1	0
				613	623	10	K	EFEPLLNWMK	D	0.24%	7324	7324	653.8275757	2	1305.639501	1305.642742	-0.003240777	K	D	-	6	10	0	0
				639	660	21	R	LTESPCALVASQYGWSGNMER	I	0.24%	5249	5249	1179.039429	2	2356.063207	2355.061901	1.001306086	R	I	C6:+57.021	4	21	1	0
P14868	Aspartyl-tRNA synthetase, cytoplasmic	9	22.16%	126	141	15	K	IGSCTQQDVELHVQK	I	0.24%	1140	1140	581.2848511	3	1740.831078	1740.846017	-0.014938825	K	I	C4:+57.021	4	15	0	0
				141	151	10	K	IYVISLAEPR	L	2.61%	4383	4383	581.3359375	2	1160.656225	1159.660106	0.996119376	K	L	-	1	10	1	0
				197	207	10	R	LQSGICHLFR	E	0.56%	2546	2546	410.8830872	3	1229.625786	1230.617445	-0.991658533	R	E	Q2:+0.984,C6:+57.021	1	10	-1	0
				241	254	13	K	NNAYLAQSPQLYK	Q	0.29%	2588	2588	755.39	2	1508.76435	1508.762339	0.002010896	K	Q	-	2	13	0	0
				264	273	9	K	VFSIGPVFR	A	1.18%	4883	4883	511.2960815	2	1020.576513	1020.575647	0.00086555	K	A	-	3	9	0	0
				345	356	11	R	LEYCEALAMLR	E	0.24%	5826	5826	684.8331909	2	1367.650732	1367.657278	-0.006545876	R	E	C4:+57.021	5	11	0	0
				356	374	18	R	EAGVEMGDEDDLSTPNEK	L	3.02%	3820	3820	645.3317871	3	1932.971886	1934.805129	-1.833242952	R	L	-	1	18	-1	0
				431	441	10	R	IHDPQLLTER	A	0.24%	1493	1493	611.328186	2	1220.640722	1220.651332	-0.010609818	R	A	-	4	10	0	0
				460	475	15	R	FGAPPHAGGGIGLER	V	0.24%	1942	1942	479.2514648	3	1434.730919	1434.736793	-0.005873469	R	V	-	5	15	0	0
P14923	Junction plakoglobin	1	2.28%	303	320	17	K	LIILANGGPQALVQIMR	N	2.71%	1549	1549	603.65	3	1807.926525	1809.006957	-1.080432544	K	N	N6:+0.984,Q10:+0.984,Q1	1	17	-1	0
P15153	Ras-related C3 botulinum toxin substrate 2	3	18.75%	132	147	15	K	KLAPITYPQGLALAK	E	0.24%	4022	4022	792.4768677	2	1582.938085	1582.944661	-0.006575352	K	E	-	4	15	0	1
				153	163	10	K	YLECSALTQR	G	0.24%	1580	1580	620.8037109	2	1239.591772	1239.591305	0.000466443	K	G	C4:+57.021	6	10	0	0
				163	174	11	R	GLKTVFDEAIR	A	2.28%	5754	5754	416.54	3	1246.596525	1247.687383	-1.09085812	R	A	-	1	11	-1	1
P15924	Desmoplakin	16	8.39%	64	84	20	R	HQNQNTIQELLQNCSDCLMR	A	0.35%	6079	6079	835.0414429	3	2502.100853	2502.104033	-0.003179523	R	A	Q8:+0.984,C14:+57.021,C	3	20	0	0
				140	150	10	K	RLLQLQEQMR	A	0.24%	1738	1738	658.3720703	2	1314.728491	1313.723786	1.004704113	K	A	-	5	10	1	1
				245	260	15	K	SAIYQLEEEYENLLK	A	0.24%	7981	7981	921.4665527	2	1840.917455	1840.909457	0.007998285	K	A	-	5	15	0	0
				270	281	11	R	QLQNIIQATSR	E	0.24%	2423	2423	636.3566895	2	1270.697729	1270.699345	-0.001615878	R	E	-	5	11	0	0
				689	705	16	K	NLPLADQGSSHHITVK	I	7.38%	1047	1047	429.980072	4	1715.888988	1715.895479	-0.006490738	K	I	-	1	16	0	0
				710	727	17	K	SVQNDSQAIAEVLNQLK	D	0.24%	7105	7105	929.4857178	2	1856.955785	1855.963952	0.991833123	K	D	-	5	17	1	0
				771	785	14	R	ALLQAILQTEDMLK	V	0.24%	8445	8445	794.44	2	1586.86435	1585.874927	0.989422704	R	V	-	6	14	1	0
				834	855	21	K	AQQIHSQTSQQYPLYDLDLGK	F	3.48%	4322	4322	812.0678101	3	2433.179955	2433.1812	-0.001245096	K	F	Q3:+0.984	1	21	0	0
				1002	1009	7	R	YIELLTR	S	0.52%	2749	2749	454.2626343	2	906.5096185	906.5174638	-0.007845365	R	S	-	1	7	0	0
				1611	1626	15	K	ITNLTQQLEQASIVK	K	0.24%	4829	4829	843.4768677	2	1684.938085	1684.935947	0.002138712	K	K	-	6	15	0	0
				1762	1775	13	R	TLELQGLINDLQR	E	0.24%	6974	6974	757.4209595	2	1512.826269	1511.830753	0.995515833	R	E	-	5	13	1	0
				1999	2013	14	K	SVEEVASEIQPFLR	G	0.24%	6277	6277	802.9212646	2	1603.826879	1602.825333	1.001545873	K	G	-	3	14	1	0
				2091	2103	12	K	AITGFDDPFSGK	T	0.29%	4436	4436	628.3049927	2	1254.594335	1253.592814	1.001521408	K	T	-	4	12	1	0
				2334	2356	22	R	AVTGYNDPETGNIISLFQAMNK	E	0.30%	7913	7913	795.3970337	3	2383.167626	2383.136559	0.031066738	R	E	N6:+0.984	3	22	0	0
				2366	2381	15	R	LLEAQIATGGIIDPK	E	0.24%	4358	4358	770.9312744	2	1539.846899	1537.871555	1.975343492	R	E	-	2	15	2	0
				2649	2668	19	R	LLEAQACTGGIIHPTTGQK	L	0.35%	1779	1779	665.678833	3	1994.013024	1994.025044	-0.012020249	R	L	C7:+57.021	1	19	0	0
P16188	HLA class I histocompatibility antigen, A-30 alpha chain	9	40.27%	30	45	15	R	YFSTSVSRPGSGEPR	F	0.24%	995	995	542.9332886	3	1625.776391	1625.77978	-0.003389485	R	F	-	5	15	0	0
				72	89	17	R	APWIEQERPEYWDQETR	N	0.35%	4191	4191	745.3417358	3	2233.001732	2233.007593	-0.005860216	R	N	Q6:+0.984	4	17	0	0
				92	106	14	K	AQSQTDRVDLGTLR	G	0.24%	1748	1748	520.6080933	3	1558.800805	1558.806329	-0.005524551	K	G	-	4	14	0	1
				155	169	14	R	SWTAADMAAQITQR	K	0.24%	4734	4734	775.3729858	2	1548.730322	1548.735473	-0.00515188	R	K	-	4	14	0	0
				181	193	12	R	AYLEGTCVEWLR	R	0.24%	5195	5195	749.3619385	2	1496.708227	1495.712483	0.995743585	R	R	C7:+57.021	5	12	1	0
				205	226	21	R	TDPPKTHMTHHPISDHEATLR	C	6.43%	739	739	808.0684204	3	2421.181786	2420.165524	1.016262206	R	C	-	2	21	1	1
				243	267	24	R	DGEDQTQDTELVETRPAGDGTFQK	W	0.24%	2203	2203	880.0705566	3	2637.188195	2636.183795	1.004400074	R	W	-	3	24	1	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.24%	2754	2754	714.3647461	2	1426.713842	1426.720474	-0.006632036	K	Y	-	3	13	0	0
				280	297	17	R	YTCHVQHEGLPKPLTLR	W	0.24%	1572	1572	684.0253906	3	2049.052697	2049.046098	0.006598427	R	W	C3:+57.021,Q6:+0.984	3	17	0	0
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	12	19.48%	7	30	23	K	TVEEVLGHFGVNESTGLSLEQVK	K	0.42%	6291	6291	824.4009399	3	2470.179345	2471.254381	-1.07503608	K	K	-	3	23	-1	0
				143	158	15	K	DIVPGDIVEIAVGDK	V	0.24%	6793	6793	770.4142456	2	1538.812841	1538.819185	-0.006344197	K	V	-	6	15	0	0
				174	189	15	R	VDQSILTGESVSVIK	H	0.24%	3880	3880	788.4414673	2	1574.867284	1573.856299	1.010985314	R	H	-	5	15	1	0
				205	218	13	K	NMLFSGTNIAAGK	A	0.24%	3520	3520	663.34	2	1324.66435	1322.665268	1.999081432	K	A	-	2	13	2	0
				334	352	18	R	SLPSVETLGCTSVICSDK	T	0.24%	4337	4337	977.4768677	2	1952.938085	1951.92215	1.01593544	R	T	C10:+57.021,C15:+57.021	6	18	1	0
				436	451	15	K	VGEATETALTCLVEK	M	0.24%	4347	4347	810.9071655	2	1619.798681	1619.807172	-0.008490793	K	M	C11:+57.021	5	15	0	0
				559	572	13	R	CLALATHDNPLRR	E	0.24%	1321	1321	513.2730103	3	1536.795556	1535.798613	0.996942626	R	E	C1:+57.021	1	13	1	1
				637	650	13	R	IGIFGQDEDVTSK	A	0.24%	3159	3159	704.848999	2	1407.682348	1407.688171	-0.005823033	R	A	-	5	13	0	0
				685	711	26	K	IVEFLQSFDEITAMTGDGVNDAPALK	K	2.56%	10188	10188	928.8126831	3	2783.414574	2780.357861	3.056713284	K	K	-	1	26	3	0
				711	727	16	K	KAEIGIAMGSGTAVAK	T	0.24%	1840	1840	752.4087524	2	1502.801855	1502.812661	-0.010806421	K	T	-	6	16	0	1
				727	750	23	K	TASEMVLADDNFSTIVAAVEEGR	A	0.42%	8506	8506	809.0546875	3	2424.140587	2425.131868	-0.991280476	K	A	N11:+0.984	4	23	-1	0
				971	984	13	K	ISLPVILMDETLK	F	0.52%	7975	7975	736.4223633	2	1470.829076	1470.836751	-0.007674229	K	F	-	4	13	0	0
P17600	Synapsin-1	1	3.12%	565	587	22	R	QTSVSGPAPPKASGAPPGGQQR	Q	2.76%	3621	3621	687.0154419	3	2058.022851	2058.012561	0.010289132	R	Q	Q1:-17.027,Q21:+0.984	1	22	0	1
P17987	T-complex protein 1 subunit alpha	19	44.42%	18	33	15	R	SQNVMAAASIANIVK	S	0.24%	4824	4824	758.9069824	2	1515.798315	1515.80791	-0.009595428	R	S	-	5	15	0	0
				43	63	20	K	MLVDDIGDVTITNDGATILK	L	0.24%	6357	6357	1053.047607	2	2104.079565	2103.076935	1.002630228	K	L	-	5	20	1	0
				73	84	11	K	VLCELADLQDK	E	0.24%	3301	3301	652.33	2	1302.64435	1302.648486	-0.004136064	K	E	C3:+57.021	5	11	0	0
				84	102	18	K	EVGDGTTSVVIIAAELLK	N	0.24%	8846	8846	908.5141602	2	1815.01267	1814.003692	1.008978321	K	N	-	6	18	1	0
				109	122	13	K	QKIHPTSVISGYR	L	6.70%	1264	1264	495.943573	3	1484.807244	1484.809958	-0.002714046	K	L	-	1	13	0	1
				111	122	11	K	IHPTSVISGYR	L	0.24%	1151	1151	410.5583191	3	1228.651482	1228.656417	-0.004935013	K	L	-	2	11	0	0
				130	145	15	R	YINENLIVNTDELGR	D	0.24%	4446	4446	882.4558105	2	1762.895971	1761.889725	1.006246366	R	D	-	4	15	1	0
				130	153	23	R	YINENLIVNTDELGRDCLINAAK	T	0.24%	5792	5792	883.7836304	3	2648.327416	2648.3111	0.016316025	R	T	C17:+57.021,N20:+0.984	2	23	0	1
				189	199	10	R	YPVNSVNILK	A	0.24%	3146	3146	574.33	2	1146.64435	1145.644455	0.999894456	R	A	-	5	10	1	0
				189	203	14	R	YPVNSVNILKAHGR	S	2.56%	547	547	522.6835327	3	1565.027123	1566.863056	-1.835933151	R	S	-	1	14	-1	1
				233	243	10	K	IACLDFSLQK	T	0.24%	4120	4120	598.3112793	2	1194.606909	1193.610978	0.995930378	K	T	C3:+57.021	5	10	1	0
				247	264	17	K	LGVQVVITDPEKLDQIR	Q	1.19%	4959	4959	642.036438	3	1923.085839	1922.083674	1.002165221	K	Q	-	1	17	1	1
				355	365	10	R	ICDDELILIK	N	0.24%	4585	4585	616.3329468	2	1230.650243	1230.652509	-0.002265213	R	N	C2:+57.021	5	10	0	0
				390	400	10	R	SLHDALCVVK	R	0.24%	1393	1393	571.3061523	2	1140.596655	1140.595662	0.000992224	R	R	C7:+57.021	5	10	0	0
				406	433	27	K	SVVPGGGAVEAALSIYLENYATSMGSR	E	0.24%	9290	9290	900.7874756	3	2699.338952	2699.311229	0.02772223	K	E	N19:+0.984	6	27	0	0
				433	443	10	R	EQLAIAEFAR	S	0.24%	4031	4031	574.3056641	2	1146.595678	1146.603319	-0.007640867	R	S	-	4	10	0	0
				443	466	23	R	SLLVIPNTLAVNAAQDSTDLVAK	L	0.24%	7063	7063	785.1032104	3	2352.286156	2353.274038	-0.987881748	R	L	N7:+0.984	3	23	-1	0
				481	496	15	K	NLKWIGLDLSNGKPR	D	2.60%	5074	5074	572.3131714	3	1713.916039	1711.925685	1.990354056	K	D	N1:+0.984,N11:+0.984	1	15	2	1
				515	526	11	K	FATEAAITILR	I	1.07%	4662	4662	603.3438721	2	1204.672094	1204.681569	-0.009475251	K	I	-	1	11	0	0
P18084	Integrin beta-5	1	1.13%	176	185	9	R	LGFGSFVDK	D	0.30%	3540	3540	485.2540283	2	968.4924066	968.4967284	-0.004321839	R	D	-	4	9	0	0
P20273	B-cell receptor CD22	1	1.06%	288	297	9	K	QNTFTLNLR	E	2.14%	1790	1790	554.2909546	2	1106.566259	1106.572003	-0.00574406	K	E	Q1:+0.984	1	9	0	0
P20701	Integrin alpha-L	1	1.03%	857	869	12	R	ALSCNVSSPIFK	A	1.95%	7785	7785	662.364563	2	1322.713476	1322.653556	0.059920145	R	A	C4:+57.021,N5:+0.984	2	12	0	0
P21283	V-type proton ATPase subunit C 1	1	4.71%	86	104	18	K	VQENLLANGVDLVTYITR	F	0.24%	8688	8688	673.3658447	3	2017.074059	2017.084402	-0.010342892	K	F	-	4	18	0	0
P21757	Macrophage scavenger receptor types I and II	1	2.66%	245	257	12	K	VLNNITNDLRLK	D	2.02%	4608	4608	471.93927	3	1412.794335	1412.798709	-0.004374013	K	D	N3:+0.984	1	12	0	1
P21796	Voltage-dependent anion-selective channel protein 1	14	66.78%	20	28	8	K	GYGFGLIK	L	0.24%	3944	3944	427.7413635	2	853.467077	853.4697853	-0.002708301	K	L	-	4	8	0	0
				63	74	11	R	WTEYGLTFTEK	W	0.24%	4574	4574	687.8303223	2	1373.644994	1373.650329	-0.005334373	R	W	-	5	11	0	0
				74	93	19	K	WNTDNTLGTEITVEDQLAR	G	0.24%	5673	5673	1088.527832	2	2175.040014	2175.044388	-0.004373746	K	G	-	4	19	0	0
				96	109	13	K	LTFDSSFSPNTGK	K	0.24%	3193	3193	700.8358154	2	1399.655981	1399.661956	-0.005975421	K	K	-	6	13	0	0
				96	110	14	K	LTFDSSFSPNTGKK	N	0.24%	2507	2507	764.8839722	2	1527.752294	1527.756919	-0.00462508	K	N	-	3	14	0	1
				120	139	19	R	EHINLGCDMDFDIAGPSIR	G	0.24%	8686	8686	721.3301392	3	2160.966942	2159.961109	1.00583352	R	G	N4:+0.984,C7:+57.021	1	19	1	0
				139	163	24	R	GALVLGYEGWLAGYQMNFETAKSR	V	2.42%	6383	6383	893.4135132	3	2677.217064	2677.283706	-0.066641537	R	V	Q15:+0.984,M16:+15.994	1	24	0	1
				161	174	13	K	SRVTQSNFAVGYK	T	0.24%	1286	1286	487.2701111	3	1458.786858	1455.747023	3.03983486	K	T	-	2	13	3	1
				163	174	11	R	VTQSNFAVGYK	T	0.29%	1325	1325	607.31	2	1212.60435	1212.613884	-0.009533712	R	T	-	4	11	0	0
				174	197	23	K	TDEFQLHTNVNDGTEFGGSIYQK	V	0.24%	4227	4227	867.4005737	3	2599.178246	2599.182672	-0.004426329	K	V	-	2	23	0	0
				200	218	18	K	KLETAVNLAWTAGNSNTR	F	0.24%	3626	3626	974.0103149	2	1946.00498	1945.001735	1.003244955	K	F	-	3	18	1	1
				224	236	12	K	YQIDPDACFSAK	V	0.24%	2922	2922	707.817688	2	1413.619726	1413.623	-0.003273615	K	V	C8:+57.021	5	12	0	0
				236	256	20	K	VNNSSLIGLGYTQTLKPGIK	L	0.24%	4394	4394	1052.089722	2	2102.163793	2102.173551	-0.009758121	K	L	-	3	20	0	0
				256	266	10	K	LTLSALLDGK	N	0.24%	5680	5680	515.8098145	2	1029.603979	1029.607007	-0.003028462	K	N	-	3	10	0	0
P21817	Ryanodine receptor 1	1	0.32%	2770	2786	16	K	IQNNWSYGENIDEELK	T	4.90%	7594	7594	977.0827637	2	1952.149877	1951.879932	0.269944928	K	T	N10:+0.984	2	16	0	0
P21926	CD9 antigen	3	15.35%	144	169	25	K	AIHYALNCCGLAGGVEQFISDICPK	K	0.24%	8496	8496	932.1115723	3	2793.311242	2793.291036	0.020205797	K	K	N7:+0.984,C8:+57.021,C9	4	25	0	0
				169	179	10	K	KDVLETFTVK	S	0.24%	2702	2702	590.3317261	2	1178.647802	1178.654686	-0.006883788	K	S	-	4	10	0	1
				170	179	9	K	DVLETFTVK	S	0.24%	3774	3774	526.286438	2	1050.557226	1050.559723	-0.002496823	K	S	-	5	9	0	0
P22223	Cadherin-3	1	0.97%	562	570	8	R	QVLNITDK	D	4.03%	2873	2873	466.2804565	2	930.545263	930.5021922	0.043070838	R	D	N4:+0.984	3	8	0	0
P22897	Macrophage mannose receptor 1	3	2.61%	299	314	15	R	YLNWLPGSPSAEPGK	S	0.24%	4718	4718	808.4060059	2	1614.796362	1614.804204	-0.007842265	R	S	-	3	15	0	0
				604	616	12	R	TGIAGGLWDVLK	C	0.24%	6795	6795	615.8480225	2	1229.680395	1228.681569	0.99882553	R	C	-	5	12	1	0
				1254	1265	11	R	NWGQASLECLR	M	0.24%	3434	3434	667.8178711	2	1333.620092	1332.624003	0.996089612	R	M	C9:+57.021	5	11	1	0
P23634	Plasma membrane calcium-transporting ATPase 4	2	2.50%	534	547	13	K	TECALLGFVTDLK	Q	1.23%	10527	10527	733.8839722	2	1465.752294	1465.7482	0.004094104	K	Q	C3:+57.021	2	13	0	0
				686	704	18	K	QAGITVRMVTGDNINTAR	A	2.44%	3159	3159	645.329834	3	1932.966027	1932.968791	-0.002764223	K	A	Q1:+0.984,M8:+15.995	1	18	0	1
P25098	Beta-adrenergic receptor kinase 1	1	1.31%	422	431	9	R	SLLEGLLQR	D	0.35%	5279	5279	515.8105469	2	1029.605444	1027.602591	2.002853086	R	D	-	2	9	2	0
P25445	Tumor necrosis factor receptor superfamily member 6	1	3.88%	274	287	13	K	VQLLRNWHQLHGK	K	6.80%	1997	1997	543.6345825	3	1627.880272	1627.905924	-0.025651601	K	K	-	2	13	0	1
P25705	ATP synthase subunit alpha, mitochondrial	25	53.71%	45	58	13	K	TGTAEMSSILEER	I	0.24%	3504	3504	712.338562	2	1422.661474	1422.666056	-0.004582545	K	I	-	6	13	0	0
				58	73	15	R	ILGADTSVDLEETGR	V	0.24%	3261	3261	788.3948364	2	1574.774023	1574.778777	-0.004754332	R	V	-	6	15	0	0
				73	83	10	R	VLSIGDGIAR	V	0.24%	2589	2589	500.7913818	2	999.5671136	999.5712904	-0.004176832	R	V	-	5	10	0	0
				83	103	20	R	VHGLRNVQAEEMVEFSSGLK	G	2.77%	1270	1270	749.6990967	3	2246.073815	2246.099199	-0.025384465	R	G	Q8:+0.984,M12:+15.994	1	20	0	1
				88	103	15	R	NVQAEEMVEFSSGLK	G	0.24%	5327	5327	836.4432983	2	1670.870947	1667.771234	3.099712176	R	G	Q3:+0.984	1	15	3	0
				103	123	20	K	GMSLNLEPDNVGVVVFGNDK	L	0.24%	6662	6662	1052.520874	2	2103.026098	2103.030653	-0.004554985	K	L	-	3	20	0	0
				132	149	17	K	RTGAIVDVPVGEELLGR	V	0.24%	5020	5020	890.9990845	2	1779.982519	1779.984294	-0.001774919	K	V	-	6	17	0	1
				133	149	16	R	TGAIVDVPVGEELLGR	V	0.24%	5672	5672	813.4487915	2	1624.881933	1623.883183	0.998750296	R	V	-	5	16	1	0
				149	161	12	R	VVDALGNAIDGK	G	0.24%	2341	2341	586.3170776	2	1170.618505	1170.624448	-0.005943159	R	G	-	5	12	0	0
				149	167	18	R	VVDALGNAIDGKGPIGSK	T	0.24%	3072	3072	570.9813843	3	1709.920678	1710.915196	-0.994517816	R	T	N7:+0.984	2	18	-1	1
				182	194	12	R	ISVREPMQTGIK	A	0.24%	1586	1586	679.8761597	2	1357.736669	1357.738768	-0.0020986	R	A	-	5	12	0	1
				194	204	10	K	AVDSLVPIGR	G	0.24%	2841	2841	514.8018799	2	1027.58811	1025.586941	2.001169182	K	G	-	1	10	2	0
				218	230	12	K	TSIAIDTIINQK	R	0.24%	4053	4053	658.8726196	2	1315.729589	1315.734727	-0.005138062	K	R	-	6	12	0	0
				305	316	11	K	HALIIYDDLSK	Q	0.24%	3348	3348	644.3482666	2	1286.680883	1286.687049	-0.006165549	K	Q	-	5	11	0	0

				322	329	7	R	QMSLLLR	R	0.76%	2821	2821	430.7538147	2	859.4919793	860.4789553	-0.986976013	R	R	Q1:+0.984	1	7	-1	0
				329	347	18	R	RPPGREAYPGDVFYLHSR	L	0.42%	2260	2260	530.0181885	4	2116.041454	2116.060253	-0.018799046	R	L	-	3	18	0	1
				334	347	13	R	EAYPGDVFYLHSR	L	0.24%	3758	3758	518.5825195	3	1552.724083	1552.731039	-0.00695539	R	L	-	1	13	0	0
				402	416	14	K	GIRPAINVGLSVSR	V	0.29%	2753	2753	480.2855835	3	1437.833275	1437.841592	-0.00831704	K	V	-	2	14	0	0
				427	441	14	K	QVAGTMKLELAQYR	E	1.65%	3337	3337	536.6217651	3	1606.84182	1606.850109	-0.00828911	K	E	-	1	14	0	1
				434	441	7	K	LELAQYR	E	0.24%	1621	1621	446.7470093	2	891.4783685	891.4814126	-0.003044173	K	E	-	5	7	0	0
				441	463	22	R	EVAAFAQFGSDLDAATQQLLSR	G	0.24%	9173	9173	780.3896484	3	2338.14547	2338.144086	0.001383888	R	G	Q7:+0.984	4	22	0	0
				472	493	21	K	QGQYSPMAIEEQVAVIYAGVR	G	0.24%	7828	7828	1155.579956	2	2309.144262	2308.152165	0.992096813	K	G	-	1	21	1	0
				493	503	10	R	GYLDKLEPSK	I	0.24%	2040	2040	575.3104248	2	1148.6052	1148.607736	-0.002536087	R	I	-	5	10	0	1
				506	527	21	K	FENAFLSHVVSQHQALLGTIR	A	0.37%	6501	6501	791.4139404	3	2371.218346	2367.23351	3.984835761	K	A	Q12:+0.984	1	21	4	0
				541	553	12	K	EIVTNFLAGFEA	-	0.24%	8155	8155	655.8278809	2	1309.640112	1309.655414	-0.015302545	K	-	-	4	12	0	0
P26010	Integrin beta-7	9	20.55%	35	53	18	R	NPHLSMLGSCQPAPSCQK	C	0.24%	1318	1318	671.3076172	3	2010.899376	2010.906458	-0.00708155	R	C	C10:+57.021,C16:+57.021	3	18	0	0
				53	65	12	K	CILSHPSCAWCK	Q	0.24%	2060	2060	760.3395996	2	1518.663549	1517.656368	1.007181131	K	Q	C1:+57.021,C8:+57.021,C	5	12	1	0
				89	116	27	R	GCPLEELEEPRGQQEVLQDQPLSQGAR	G	0.24%	4449	4449	1022.164551	3	3063.470177	3063.456261	0.01391624	R	G	C2:+57.021,Q20:+0.984	2	27	0	1
				127	143	16	R	VRVTLRPGEPQQLQVR	F	3.08%	3549	3549	627.317688	3	1878.929589	1877.04826	1.881328941	R	F	Q11:+0.984,Q14:+0.984	1	16	2	1
				129	143	14	R	VTLRPGEPQQLQVR	F	0.24%	1968	1968	540.9760742	3	1619.904748	1619.910735	-0.005987208	R	F	-	4	14	0	0
				190	199	9	R	IGFGSFVDK	T	0.41%	3546	3546	485.2539673	2	968.4922845	968.4967284	-0.00444391	R	T	-	3	9	0	0
				199	211	12	K	TVLPFVSTVPSK	L	0.24%	4045	4045	637.8669434	2	1273.718237	1273.728185	-0.009948585	K	L	-	4	12	0	0
				248	278	30	R	QSVSGNLDSPEGGFDAILQAALCQEQIGWR	N	0.50%	9264	9264	1083.517456	3	3247.528893	3245.540675	1.988218052	R	N	C23:+57.021	3	30	2	0
				321	361	40	R	STEFDYPSVGQVAQALSAANIQPIFAVTSAALPVYQELSK	L	4.30%	11155	11155	1054.29	4	4213.1287	4211.131405	1.997295312	R	L	Q22:+0.984	1	40	2	0
P27105	Erythrocyte band 7 integral membrane protein	6	28.82%	55	62	7	K	IIKEYER	A	3.24%	1577	1577	476.2935181	2	950.5713861	949.5232775	1.048108525	K	A	-	1	7	1	1
				77	93	16	K	GPGLFFILPCTDSFIK	V	0.24%	8709	8709	906.9770508	2	1811.938451	1810.932313	1.006138747	K	V	C10:+57.021	5	16	1	0
				220	232	12	K	VIAAEGEMNASR	A	0.24%	803	803	624.3045044	2	1246.593359	1246.597583	-0.004224099	K	A	-	6	12	0	0
				235	251	16	K	EASMVITESPAALQLR	Y	0.24%	4660	4660	858.9576416	2	1715.899633	1714.892368	1.007264843	K	Y	-	5	16	1	0
				251	263	12	R	YLQTLTTIAAEK	N	0.24%	3445	3445	676.3670654	2	1350.718481	1350.739478	-0.020997493	R	N	-	6	12	0	0
				263	283	20	K	NSTIVFPLPIDMLQGIIGAK	H	0.24%	10179	10179	710.0683594	3	2127.181603	2127.164946	0.016656941	K	H	Q14:+0.984	4	20	0	0
P28907	ADP-ribosyl cyclase 1	7	28.00%	47	58	11	R	QQWSGPGTTKR	F	2.39%	14189	14189	416.39	3	1246.146525	1246.59418	-0.447654784	R	F	Q1:+0.984,Q2:+0.984	1	11	0	1
				57	66	9	K	RFPETVLAR	C	0.24%	1453	1453	544.8103638	2	1087.605077	1087.613824	-0.008746501	K	C	-	5	9	0	1
				78	90	12	R	HVDCQSVWDAFK	G	0.24%	4333	4333	746.8353271	2	1491.655004	1490.660782	0.994222201	R	G	C4:+57.021	4	12	1	0
				129	140	11	K	DLAHQFTQVQR	D	0.24%	1985	1985	671.838501	2	1341.661352	1341.678944	-0.017591719	K	D	-	5	11	0	0
				178	190	12	K	DCSNNPVSVFWK	T	0.24%	5385	5385	726.8318481	2	1451.648046	1451.649883	-0.001836759	K	T	C2:+57.021	5	12	0	0
				234	247	13	K	VQTLEAWVIHGGR	E	3.12%	4781	4781	489.2655945	3	1464.773308	1464.783743	-0.010434793	K	E	-	1	13	0	0
				251	268	17	R	DLCQDPTIKELESIISK	R	3.65%	6143	6143	498.3261108	4	1989.273143	1988.997142	0.276001079	R	R	C3:+57.021,Q4:+0.984	1	17	0	1
P29033	Gap junction beta-2 protein	1	6.64%	0	15	15	-	MDWGTLQTILGGVNK	H	9.14%	7153	7153	550.6144409	3	1648.819848	1647.829125	0.990722642	-	H	M1:+15.995	1	15	1	0
P30460	HLA class I histocompatibility antigen, B-8 alpha chain	10	37.57%	45	59	14	R	FISVGYVDDTQFVR	F	0.24%	5122	5122	823.411438	2	1644.807226	1644.814769	-0.007542727	R	F	-	4	14	0	0
				72	86	14	R	APWIEQEGPEYWDR	N	0.24%	5107	5107	888.4012451	2	1774.78684	1774.795096	-0.008255686	R	N	-	4	14	0	0
				121	132	11	S	MYGCDVGPDGR	L	0.24%	825	825	613.7494507	2	1225.483251	1225.485127	-0.001875465	R	L	C4:+57.021	6	11	0	0
				155	169	14	R	SWTAADTAAQITQR	K	0.24%	3109	3109	760.8829346	2	1519.750219	1518.742666	1.007552821	R	K	-	4	14	1	0
				181	193	12	R	AYLEGTCVEWLR	R	0.24%	5195	5195	749.3619385	2	1496.708227	1495.712483	0.995743585	R	R	C7:+57.021	5	12	1	0
				205	226	21	R	ADPPKTHVTHHPISDHEATLR	C	3.01%	699	699	590.8023071	4	2359.177928	2358.182887	0.995040972	R	C	-	2	21	1	1
				210	226	16	K	THVTHHPISDHEATLR	C	0.34%	687	687	463.4855957	4	1849.911083	1849.918339	-0.007256763	K	C	-	3	16	0	0
				243	263	20	R	DGEDQTQDTELVETRPAGDR	T	0.24%	882	882	745.0070801	3	2231.997765	2230.993809	1.00395633	R	T	-	2	20	1	0
				267	280	13	K	WAAVVVPSGEEQR	Y	0.24%	2754	2754	714.3647461	2	1426.713842	1426.720474	-0.006632036	K	Y	-	3	13	0	0
				280	297	17	R	YTCHVQHEGLPKPLTLR	W	0.24%	1572	1572	684.0253906	3	2049.052697	2049.046098	0.006598427	R	W	C3:+57.021,Q6:+0.984	3	17	0	0
P30519	Heme oxygenase 2	1	2.85%	29	38	9	R	MADLSELLK	E	0.24%	5135	5135	510.2750244	2	1018.534399	1018.53688	-0.002481132	R	E	-	5	9	0	0
P30825	High affinity cationic amino acid transporter 1	1	1.75%	4	15	11	K	VLLNIGQQMLR	R	0.24%	5007	5007	642.8643799	2	1283.71311	1283.738374	-0.02526417	K	R	-	6	11	0	0
P31146	Coronin-1A	5	16.49%	29	45	16	R	VSQTTWDSGFCAVNPK	F	0.24%	3588	3588	898.9136963	2	1795.811743	1795.819468	-0.007725302	R	F	C11:+57.021	4	16	0	0
				343	354	11	R	RCEPIAMTVPR	K	0.24%	1816	1816	665.3422852	2	1328.66892	1328.668845	7.48965E-05	R	K	C2:+57.021	6	11	0	1
				354	383	29	R	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	D	0.24%	7818	7818	1059.184692	3	3174.530602	3172.535307	1.995294868	R	D	-	3	29	2	1
				383	393	10	R	DAGPLLISLK	D	0.92%	4579	4579	513.8112793	2	1025.606909	1025.612093	-0.005184134	R	D	-	3	10	0	0
				439	449	10	K	LQATVQELQK	R	0.24%	1121	1121	579.329834	2	1156.644018	1156.645184	-0.001165903	K	R	-	4	10	0	0
P32942	Intercellular adhesion molecule 3	1	1.83%	214	224	10	R	TFVLPVTPPR	L	0.24%	3988	3988	563.8320313	2	1125.648412	1125.654626	-0.006213764	R	L	-	5	10	0	0
P33151	Cadherin-5	1	2.04%	386	402	16	K	KPLIGTVLAMDPDAAR	H	1.00%	1252	1252	556.2817993	3	1665.821923	1666.907624	-1.085701531	K	H	-	4	16	-1	0
P33527	Multidrug resistance-associated protein 1	1	1.76%	867	894	27	R	TYASTEQEQDAEENGVTGVSGPGKEAK	Q	1.32%	7783	7783	696.8579102	4	2783.40034	2783.225688	0.174652369	R	Q	Q7:+0.984,Q9:+0.984	2	27	0	1
P35221	Catenin alpha-1	1	1.32%	204	216	12	R	DQMAAARGILQK	N	2.17%	1064	1064	440.2298279	3	1317.666009	1317.671152	-0.005143421	R	N	M3:+15.995,Q11:+0.984	1	12	0	1
P35232	Prohibitin	13	60.29%	11	35	24	K	FGLALAVAGGVVNSALYNVDAGHR	A	0.24%	12557	12557	791.4234009	3	2371.246728	2370.244425	1.002302469	K	A	-	4	24	1	0
				83	93	10	K	DLQNVNITLR	I	0.24%	3208	3208	593.3311157	2	1184.646581	1184.651332	-0.004750443	K	I	-	5	10	0	0
				93	105	12	R	ILFRPVASQLPR	I	0.24%	3568	3568	466.2844849	3	1395.829979	1395.83505	-0.005070922	R	I	-	4	12	0	0
				105	117	12	R	IFTSIGEDYDER	V	0.24%	3041	3041	722.8317871	2	1443.647924	1443.651785	-0.003861341	R	V	-	6	12	0	0
				105	128	23	R	IFTSIGEDYDERVLPSITTEILK	S	0.24%	7363	7363	880.7937622	3	2639.357812	2638.374162	0.983649765	R	S	-	6	23	1	1
				117	128	11	R	VLPSITTEILK	S	0.24%	5037	5037	607.3721313	2	1212.728613	1212.732936	-0.004323641	R	S	-	5	11	0	0
				133	143	10	R	FDAGELITQR	E	0.24%	3346	3346	575.2973633	2	1148.579076	1148.582583	-0.003506989	R	E	-	5	10	0	0
				157	177	20	R	AATFGLILDDVSLTHLTFGK	E	3.17%	8545	8545	707.3884277	3	2119.141808	2118.136103	1.005704859	R	E	-	2	20	1	0
				207	219	12	K	KAAIISAEGDSK	A	2.38%	9347	9347	595.3334961	2	1188.651342	1188.635013	0.016329036	K	A	-	1	12	0	1
				219	239	20	K	AAELIANSLATAGDGLIELR	K	0.24%	7223	7223	999.5426025	2	1997.069555	1997.079317	-0.009761594	K	K	-	5	20	0	0
				239	253	14	R	KLEAAEDIAYQLSR	S	0.24%	4349	4349	803.9232178	2	1605.830785	1605.836232	-0.005446925	R	S	-	5	14	0	1
				253	272	19	R	SRNITYLPAGQSVLLQLPQ	-	0.24%	6253	6253	1050.084839	2	2098.154028	2098.142236	0.011792006	R	-	Q16:+0.984	2	19	0	1
				255	272	17	R	NITYLPAGQSVLLQLPQ	-	0.24%	6970	6970	928.0211792	2	1854.026708	1854.025096	0.00161231	R	-	-	5	17	0	0
P35579	Myosin-9	45	29.95%	14	29	15	K	NFINNPLAQADWAAK	K	0.24%	5615	5615	836.9237671	2	1671.831884	1671.836901	-0.005016948	K	K	-	4	15	0	0
				29	38	9	K	KLVWVPSDK	S	0.24%	2119	2119	536.3109741	2	1070.606298	1070.612427	-0.006128814	K	S	-	4	9	0	1
				38	63	25	K	SGFEPASLKEEVGEEAIVELVENGK	K	0.56%	7260	7260	887.7774658	3	2660.308922	2659.322854	0.986067877	K	K	-	4	25	1	1
				82	102	20	K	VEDMAELTCLNEASVLHNLK	E	1.19%	6165	6165	763.0404053	3	2286.097741	2286.086703	0.01103722	K	D	C9:+57.021,N11:+0.984	2	20	0	0
				125	139	14	K	NLPIYSEEIVEMYK	G	0.24%	6209	6209	864.932251	2	1727.848852	1726.848772	1.000079785	K	G	-	6	14	1	0
				209	225	16	R	QLLQANPILEAFGNAK	T	0.24%	7216	7216	863.9764404	2	1725.937231	1725.941366	-0.004135469	R	T	-	5	16	0	0
				301	316	15	R	FLSNGHVTIPGQQDK	D	0.24%	3468	3468	548.9416504	3	1643.801476	1641.799816	2.001660364	R	D	Q12:+0.984,Q13:+0.984	1	15	2	0
				316	327	11	K	DMFQETMEAMR	I	0.24%	5692	5692	694.8726807	2	1387.729711	1387.557042	0.172669088	K	I	-	5	11	0	0
				327	341	14	R	IMGIPEEEQMGLLR	V	0.24%	5463	5463	808.4121704	2	1614.808691	1614.810948	-0.002257084	R	V	-	5	14	0	0
				373	387	14	K	VSHLLGINVTDFTR	G	0.24%	5256	5256	787.8930054	2	1573.770361	1570.846737	2.923623222	K	G	-	2	14	3	0
				576	587	11	K	VDYKADEWLMK	N	4.18%	3425	3425	699.3413696	2	1396.667089	1396.669685	-0.002596014	K	N	-	1	11	0	1
				587	606	19	K	NMDPLNDNIATLLHQSSDK	F	0.24%	7583	7583	1064.500977	2	2126.986303	2125.99498	0.991322877	K	F	N6:+0.984	1	19	1	0
				606	613	7	K	FVSELWK	D	0.24%	3579	3579	454.7460938	2	907.4765374	907.48035	-0.003812572	K	D	-	2	7	0	0
				617	637	20	R	IIGLDQVAGMSETALPGAFK	T	0.24%	7054	7054	1010.04	2	2018.06435	2017.055411	1.008938824	R	T	-	6	20	1	0
				656	670	14	K	LMATLRNTNPNFVR	C	2.67%	3874	3874	555.9414673	3	1664.800927	1664.819242	-0.018315089	K	C	M2:+15.995,N7:+0.984,N9	1	14	0	1
				679	693	14	K	AGKLDPHLVLDQLR	C	2.82%	3691	3691	525.6365356	3	1573.886132	1574.878022	-0.991890194	R	C	Q12:+0.984	1	14	-1	1
				682	693	11	K	LDPHLVLDQLR	C	0.78%	4875	4875	659.3762207	2	1316.736791	1317.740481	-1.00368993	K	C	-	4	11	-1	0
				693	702	9	R	CNGVLEGIR	I	1.70%	1369	1369	509.2584229	2	1016.501196	1016.506847	-0.005651641	R	I	C1:+57.021	2	9	0	0
				705	718	13	R	QGFPNRVVFQEFR	Q	2.81%	4263	4263	542.2851563	3	1623.831994	1623.815756	0.016237614	R	Q	N5:+0.984	2	13	0	1
				711	718	7	R	VVFQEFR	Q	1.18%	2474	2474	462.7480164	2	923.4803826	923.486498	-0.006115373	R	Q	-	3	7	0	0
				718	731	13	R	QRYEILTPNSIPK	G	0.24%	3166	3166	779.9360352	2	1557.85642	1557.851488	0.004931761	R	G	-	4	13	0	1
				745	755	10	K	ALELDSNLYR	I	0.24%	3356	3356	597.31	2	1192.60435	1192.608798	-0.004448352	K	I	-	5	10	0	0
				764	778	14	R	AGVLAHLEEERDLK	I	0.78%	2244	2244	527.28479	3	1578.830895	1578.836567	-0.005671723	R	I	-	1	14	0	1
				867	882	15	R	LTEMETLQSQLMAEK	L	0.24%	5263	5263	876.4281616	2	1750.840673	1750.848121	-0.007448182	R	L	-	4	15	0	0
				909	923	14	K	KQELEEICHDLEAR	V	0.24%	2623	2623	590.6195068	3	1768.835045	1768.840932	-0.00588618	K	V	C8:+57.021	2	14	0	1
				974	989	15	K	KLEEEQIILEDQNCK	L	0.24%	2424	2424	630.6479492	3	1888.920373	1887.924327	0.996045536	K	L	C14:+57.021	4	15	1	1
				1000	1014	14	R	IAEFTTNLTEEEEK	S	0.24%	3081	3081	827.3946533	2	1652.773657	1652.778108	-0.004451887	R	S	-	3	14	0	0
				1022	1035	13	K	NKHEAMITDLEER	L	2.43%	1321	1321	529.2525024	3	1584.734032	1584.756603	-0.022570716	K	L	-	2	13	0	1
				1024	1035	11	K	HEAMITDLEER	L	0.24%	1482	1482	672.824585	2	1343.63352	1342.618712	1.014807594	K	L	-	5	11	1	0
				1080	1091	11	K	KEEELQAALAR	V	1.00%	1233	1233	629.3341675	2	1256.652685	1256.672461	-0.019776367	R	A	-	4	11	0	1
				1174	1191	17	K	TLEEEAKTHEAQIQEMR	Q	0.24%	2487	2487	681.9931641	3	2042.956017	2041.973866	0.982150748	K	Q	-	3	17	1	1
				1193	1209	16	K	HSQAVEELAEQLEQTK	R	0.24%	4450	4450	920.4524536	2	1838.889257	1838.901018	-0.011760549	K	R	-	4	16	0	0
				1219	1234	15	K	QTLENERGELANEVK	V	0.29%	1721	1721	865.9355469	2	1729.855444	1729.848238	0.007205494	K	V	N5:+0.984	3	15	0	1
				1248	1260	12	K	KVEAQLQELQVK	F	0.24%	2059	2059	706.9084473	2	1411.801244	1411.803476	-0.002231125	K	F	-	5	12	0	1
				1277	1295	18	K	LQVELDNVTGLLSQSDSK	S	0.24%	6020	6020	973.5063477	2	1944.997045	1945.000398	-0.003352303	K	S	-	3	18	0	0
				1301	1322	21	K	DFSALESQLQDTQELLQEENR	Q	0.45%	7315	7315	831.7271118	3	2492.15786	2493.150688	-0.992827663	K	Q	Q10:+0.984	5	21	-1	0
				1301	1324	23	K	DFSALESQLQDTQELLQEENRQK	L	0.73%	6876	6876	917.4458618	3	2749.31411	2749.304229	0.009881585	K	L	N20:+0.984	2	23	0	1
				1357	1370	13	K	QIATLHAQVADMK	K	0.24%	1787	1787	475.9212036	3	1424.740136	1425.728582	-0.988445824	K	K	Q8:+0.984	1	13	-1	0
				1417	1433	16	R	LQQELDDLLVDLDHQR	Q	0.24%	6905	6905	650.6645508	3	1948.970177	1948.985416	-0.015238888	R	Q	-	4	16	0	0
				1444	1454	10	K	KFDQLLAEEK	T	0.24%	1975	1975	610.8289795	2	1219.642309	1219.644849	-0.00254056	R	N	-	2	10	0	1
				1527	1538	11	K	RALEQQVEEMK	T	0.42%	1244	1244	454.2351074	3	1359.681847	1359.681647	0.00020025	K	T	-	2	11	0	1
				1676	1694	18	K	SMEAEMIQLQEELAAAER	A	0.24%	7672	7672	683.9907837	3	2048.948876	2048.93944	0.00943577	K	A	Q10:+0.984	3	18	0	0
				1754	1770	16	K	ANLQIDQINTDLNLER	S	0.24%	4955	4955	935.4852905	2	1868.954931	1868.959201	-0.004270337	K	S	-	5	16	0	0
				1815	1828	13	K	IAQLEEQLDNETK	E	0.24%	2470	2470	765.8850708	2	1529.754492	1529.757313	-0.002821814	K	E	-	6	13	0	0
				1922	1932	10	R	RGDLPFVVPR	R	0.24%	3386	3386	578.3294067	2	1154.643163	1154.656023	-0.012859771	R	R	-	4	10	0	1
P35613	Basigin	2	7.79%	227	243	16	K	SSEHINEGETAMLVCK	S	0.24%	6088	6088	911.4006958	2	1820.785742	1820.790669	-0.004927518	K	S	N6:+0.984,M12:+15.994,C	1	16	0	0
				243	257	14	K	SESVPPVTDWAWYK	I	0.24%	5786	5786	832.899231	2	1663.782812	1663.78822	-0.005407662	K	I	-	6	14	0	0
P37802	Transgelin-2	5	38.19%	57	78	21	K	DGTVLCELINALYPEGQAPVK	K	0.24%	9267	9267	763.06073	3	2286.158715	2286.156118	0.002596669	K	K	C6:+57.021	1	21	0	0
				88	102	14	K	QMEQISQFLQAAER	Y	0.24%	6099	6099	560.2756348	3	1677.803429	1677.814452	-0.011023031	K	Y	-	3	14	0	0
				102	120	18	R	YGINTTDIFQTVDLWEGK	N	0.24%	8292	8292	1050.514404	2	2099.013159	2099.021133	-0.007974462	R	N	-	3	18	0	0
				127	139	12	R	TLMNLGGLAVAR	D	0.24%	4615	4615	608.3392334	2	1214.662817	1214.680525	-0.017707851	R	D	-	5	12	0	0
				171	182	11	K	NVIGLQMGTNR	G	2.82%	2028	2028	602.8340454	2	1203.652441	1201.623738	2.028702804	K	G	-	2	11	2	0
P38398	Breast cancer type 1 susceptibility protein	1	0.59%	1726	1737	11	R	KMLNEHDFEVR	G	1.27%	2321	2321	478.8923035	3	1433.653435	1433.660981	-0.007545944	R	G	M2:+15.995,N4:+0.984	1	11	0	1
P38570	Integrin alpha-E	1	0.93%	1155	1166	11	K	YQQLNLESIRK	A	5.23%	2071	2071	464.9255371	3	1391.753136	1391.74086	0.012276544	K	A	N5:+0.984	1	11	0	1
P38606	V-type proton ATPase catalytic subunit A	3	6.48%	44	56	12	R	VGHSELVGEIIR	L	0.24%	2400	2400	437.2320557	3	1308.672692	1307.719746	0.952946056	R	L	-	2	12	1	0
				220	232	12	K	LPANHPLLTGQR	V	5.95%	1099	1099	439.5857239	3	1315.733697	1315.736065	-0.002368041	K	V	-	1	12	0	0
				307	323	16	K	RTALVANTSNMPVAAR	E	1.08%	1587	1587	558.6347656	3	1672.880822	1671.87262	1.008201523	K	E	N7:+0.984	3	16	1	1
P38646	Stress-70 protein, mitochondrial	15	31.22%	85	99	14	R	TTPSVVAFTADGER	L	0.24%	2890	2890	726.357666	2	1450.699682	1449.709969	0.989712855	R	L	-	5	14	1	0
				106	121	15	K	RQAVTNPNNTFYATK	R	0.24%	971	971	575.6273193	3	1723.858483	1723.864179	-0.005695616	K	R	-	5	15	0	1
				159	173	14	K	LYSPSQIGAFVLMK	M	0.24%	7015	7015	777.4194336	2	1552.823217	1552.832334	-0.0091169	K	M	-	5	14	0	0
				187	202	15	K	NAVITVPAYFNDSQR	Q	0.24%	4478	4478	847.9232178	2	1693.830785	1693.84238	-0.011594941	T	Q	-	3	15	0	0
				206	218	12	K	DAGQISGLNVLR	V	0.24%	3675	3675	621.8414917	2	1241.667333	1241.672796	-0.005462258	K	V	-	5	12	0	0
				218	234	16	R	VINEPTAAALAYGLDK	S	0.24%	4693	4693	823.4407959	2	1644.865942	1644.872284	-0.006341867	R	S	-	5	16	0	0
				265	284	19	K	STNGDTFLGGEDFDQALLR	H	0.24%	6270	6270	1028.984009	2	2055.952368	2054.95451	0.997857546	K	H	-	5	19	1	0
				348	360	12	R	AQFEGIVTDLIR	R	0.24%	6466	6466	681.3728638	2	1360.730077	1360.735062	-0.004984109	R	R	-	5	12	0	0
				348	361	13	R	AQFEGIVTDLIRR	T	2.61%	6027	6027	506.6176147	3	1516.829369	1516.836173	-0.006803602	R	T	-	1	13	0	1
				368	391	23	K	AMQDAEVSKSDIGEVILVGGMTR	M	4.43%	10412	10412	803.7329712	3	2408.175438	2406.177045	1.99839343	K	M	Q3:+0.984	1	23	2	1
				394	405	11	K	VQQTVQDLFGR	A	0.24%	3595	3595	645.8419189	2	1289.668188	1289.672796	-0.004607765	K	A	-	5	11	0	0
				394	409	15	K	VQQTVQDLFGRAPSK	A	3.23%	2723	2723	558.635376	3	1672.882653	1672.889665	-0.007012166	K	A	-	1	15	0	1
				498	513	15	K	LLGQFTLIGIPPAPR	G	0.24%	6864	6864	797.4769287	2	1592.938207	1591.944995	0.99321239	K	G	-	5	15	1	0
				541	563	22	R	EQQIVIQSSGGLSKDDIENMVK	N	0.24%	4422	4422	807.0741577	3	2418.198998	2419.178803	-0.979804479	R	N	Q2:+0.984,Q3:+0.984	1	22	-1	1
				576	595	19	K	ERVEAVNMAEGIIHDTETK	M	0.24%	4812	4812	715.0177002	3	2142.029625	2141.04228	0.987345138	K	M	-	4	19	1	1
P40763	Signal transducer and activator of transcription 3	1	1.17%	354	363	9	K	FPELNYQLK	I	3.44%	3854	3854	576.8169556	2	1151.618261	1150.602256	1.016004797	K	I	-	2	9	1	0
P40818	Ubiquitin carboxyl-terminal hydrolase 8	1	1.07%	30	42	12	K	ISTKSYVHSALK	I	9.71%	5944	5944	666.8428345	2	1331.670019	1332.740147	-1.070128063	K	I	-	3	12	-1	1

P40926	Malate dehydrogenase, mitochondrial	5	20.12%	26	45	19	K	VAVLGASGGIGQPLSLLLK	N	0.24%	7807	7807	897.5531006	2	1793.090551	1792.082217	1.008334124	K	N	-	6	19	1	0
				91	104	13	K	GCDVVVIPAGVPR	K	0.29%	3290	3290	669.8620605	2	1337.708471	1337.712089	-0.003618274	K	K	C2:+57.021	3	13	0	0
				203	215	12	K	TIIPLISQCTPK	V	0.24%	3959	3959	687.3469849	2	1372.67832	1370.747456	1.930863415	K	V	Q8:+0.984,C9:+57.021	4	12	2	0
				215	229	14	K	VDFPQDQLTALTGR	I	4.00%	5447	5447	780.8937988	2	1559.771948	1559.794368	-0.022419936	K	I	-	2	14	0	0
				314	324	10	K	MISDAIPELK	A	0.24%	3463	3463	559.7999268	2	1117.584203	1115.589644	1.994559628	K	A	-	3	10	2	0
P41240	Tyrosine-protein kinase CSK	1	2.89%	94	107	13	R	LLYPPETGLFLVR	E	0.24%	7182	7182	759.9390259	2	1517.862402	1516.865348	0.99705411	R	E	-	3	13	1	0
P42785	Lysosomal Pro-X carboxypeptidase	1	4.64%	114	137	23	K	AMLVFAEHRYYGESLPFGDNSFK	D	3.76%	10143	10143	674.3250732	4	2693.268993	2693.258507	0.010486049	K	D	M2:+15.995	1	23	0	1
P43121	Cell surface glycoprotein MUC18	2	4.95%	251	263	12	K	VWLEVEPVGMLK	E	0.24%	6292	6292	700.3897705	2	1398.763891	1398.758106	0.005784624	K	E	-	6	12	0	0
				292	312	20	R	EAEEETTNDNGVLVLEPARK	E	9.29%	5839	5839	739.3555908	3	2215.043297	2215.049167	-0.005869907	R	E	N8:+0.984,N10:+0.984	1	20	0	1
P46940	Ras GTPase-activating-like protein IQGAP1	16	13.88%	36	51	15	R	QNVAYEYLCHLEEAK	R	0.24%	5281	5281	622.9570923	3	1865.847802	1865.861333	-0.013530945	R	R	C9:+57.021	2	15	0	0
				80	88	8	K	LGNFFSPK	V	5.32%	2321	2321	454.2642517	2	906.5128533	908.475599	-1.962745622	K	V	-	2	8	-1	0
				191	201	10	K	YGIQMPAFSK	I	0.24%	4010	4010	571.2858887	2	1140.556127	1140.563763	-0.007636072	K	I	-	3	10	0	0
				241	266	25	K	NPNAMLVNLEEPLASTYQDILYQAK	Q	0.24%	8753	8753	953.4664307	3	2857.375817	2852.379045	4.996772344	K	Q	N1:+0.984,N3:+0.984,M5:	1	25	5	0
				326	336	10	R	ALQSPALGLR	G	3.12%	659	659	514.7104492	2	1027.405248	1024.602925	2.802323446	R	G	-	1	10	3	0
				388	401	13	R	LAAVALINAAIQK	G	2.90%	1457	1457	433.5655518	3	1297.67318	1295.781268	1.891912265	R	G	N8:+0.984	1	13	2	0
				406	431	25	K	TVLELMNPEAQLPQVYPFAADLYQK	E	0.24%	8390	8390	960.4935303	3	2878.457116	2877.462266	0.99484926	K	E	-	4	25	1	0
				465	477	12	R	ALESGDVNTVWK	Q	2.66%	2427	2427	659.3427124	2	1316.669775	1317.656477	-0.986702115	R	Q	-	2	12	-1	0
				538	556	18	R	ILAIGLINEALDEGDAQK	T	0.24%	7625	7625	942.0040894	2	1881.992529	1882.004755	-0.012225937	G	T	-	4	18	0	0
				567	585	18	K	LEGVLAEVAQHYQDTLIR	A	0.24%	7249	7249	686.7024536	3	2057.083886	2056.047651	1.0362348	K	A	Q10:+0.984,Q13:+0.984	3	18	1	0
				738	751	13	R	EQLWLANEGLITR	L	3.75%	5461	5461	771.4421387	2	1540.868627	1541.820188	-0.951561048	R	L	-	3	13	-1	0
				901	916	15	R	SNQQLENDLNLMDIK	I	0.24%	5482	5482	887.9367065	2	1773.857763	1773.856711	0.001051918	R	I	-	6	15	0	0
				924	935	11	K	ITLQDVVSHSK	K	1.27%	2925	2925	409.5626831	3	1225.664574	1225.666648	-0.002073364	K	K	-	1	11	0	0
				988	997	9	K	LIFQMPQNK	S	0.55%	3220	3220	559.8033447	2	1117.591039	1117.595398	-0.004358451	K	S	-	1	9	0	0
				1035	1053	18	K	SKVDQIQEIVTGNPTVIK	M	0.24%	3929	3929	985.5540771	2	1969.092504	1968.089153	1.003351233	K	M	-	3	18	1	1
				1477	1487	10	K	YQELINDIAR	D	0.24%	2955	2955	617.8239136	2	1233.632177	1233.635347	-0.003170332	K	D	-	2	10	0	0
P48023	Tumor necrosis factor ligand superfamily member 6	1	6.76%	156	175	19	R	SMPLEWEDTYGIVLLSGVK	Y	1.94%	11138	11138	712.7080688	3	2135.100731	2136.081292	-0.980560145	R	Y	-	1	19	-1	0
P48047	ATP synthase subunit O, mitochondrial	9	52.11%	26	40	14	K	LVRPPVQVYGIEGR	Y	0.24%	3236	3236	791.9587402	2	1581.90183	1581.899107	0.002723021	K	Y	-	5	14	0	0
				73	84	11	K	VAASVLNPYVK	R	0.24%	2791	2791	581.328064	2	1160.640478	1159.660106	0.980372306	K	R	-	4	11	1	0
				98	117	19	K	ERFSPLTTNLINLLAENGR	L	0.60%	7853	7853	720.3910522	3	2158.149682	2157.154213	0.995468674	K	L	-	2	19	1	1
				100	117	17	R	FSPLTTNLINLLAENGR	L	0.24%	8378	8378	937.510376	2	1873.005102	1872.010509	0.994593289	R	L	-	6	17	1	0
				117	136	19	R	LSNTQGVVSAFSTMMSVHR	G	0.24%	6276	6276	684.6679688	3	2050.980431	2050.992829	-0.012397558	R	G	-	2	19	0	0
				136	158	22	R	GEVPCTVTSASPLEEATLSELK	T	0.24%	5695	5695	1160.077515	2	2318.139379	2317.135442	1.003936833	R	T	C5:+57.021	6	22	1	0
				162	172	10	K	SFLSQGQVLK	L	0.24%	2968	2968	552.821106	2	1103.626562	1105.613155	-1.98659347	K	L	-	5	10	-1	0
				162	176	14	K	SFLSQGQVLKLEAK	T	0.24%	3364	3364	774.4348145	2	1546.853979	1546.87189	-0.017910758	K	T	-	6	14	0	1
				176	188	12	K	TDPSILGGMIVR	I	0.24%	4907	4907	629.8434448	2	1257.67124	1257.675105	-0.003865312	K	I	-	5	12	0	0
P48357	Leptin receptor	1	1.12%	793	806	13	K	KYYIHDHFIPIEK	Y	1.22%	4452	4452	851.4081421	2	1700.800634	1701.887874	-1.087239892	K	Y	-	1	13	-1	1
P49327	Fatty acid synthase	24	16.13%	257	274	17	K	EQGVTFPSGDIQEQLIR	S	0.24%	5317	5317	958.9780884	2	1915.940527	1915.963952	-0.023425666	K	S	-	6	17	0	0
				274	298	24	R	SLYQSAGVAPESFEYIEAHGTGTK	V	0.24%	4789	4789	848.4064331	3	2542.195824	2541.202345	0.993479012	R	V	-	2	24	1	0
				326	343	17	K	SNMGHPEPASGLAALAK	V	0.24%	2108	2108	550.95	3	1649.826525	1649.819538	0.006987312	K	V	-	2	17	0	0
				373	384	11	R	LQVVDQPLPVR	G	0.24%	3018	3018	632.3722534	2	1262.728857	1262.734668	-0.005810812	R	G	-	5	11	0	0
				646	667	21	K	DTVTISGPQAPVFEFVEQLRK	E	0.24%	8105	8105	788.0886841	3	2361.242577	2361.221608	0.02096875	K	E	Q18:+0.984	2	21	0	1
				711	728	17	R	WLSTSIPEAQWHSSLAR	T	0.24%	4779	4779	657.0018921	3	1967.982201	1967.985356	-0.00315529	R	T	-	1	17	0	0
				802	825	23	R	LHLSGIDANPNALFPPVEFPAPR	G	0.24%	7068	7068	825.78	3	2474.316525	2473.264126	1.05239856	R	G	N9:+0.984,N11:+0.984	3	23	1	0
				825	835	10	R	GTPLISPLIK	W	0.56%	3643	3643	519.8303833	2	1037.645117	1037.648478	-0.003361646	R	W	-	3	10	0	0
				901	927	26	R	ALGLGVEQLPVVFEDVVLHQATILPK	T	0.24%	10040	10040	929.5274048	3	2785.558739	2785.56295	-0.004210853	R	T	Q20:+0.984	6	26	0	0
				1116	1131	15	K	FCFTPHTEEGCLSER	A	0.24%	2823	2823	624.6040039	3	1870.788537	1868.781239	2.007297159	K	A	C2:+57.021,C11:+57.021	2	15	2	0
				1131	1142	11	R	AALQEELQLCK	G	0.24%	3056	3056	652.34	2	1302.66435	1301.66447	0.999879528	R	G	C10:+57.021	5	11	1	0
				1158	1180	22	K	MVVPGLDGAQIPRDPSQQELPR	L	0.24%	4497	4497	802.0886841	3	2403.242577	2402.237626	1.004950838	K	L	-	4	22	1	1
				1208	1225	17	K	LPEDPLLSGLLDSPALK	A	0.24%	11950	11950	889.4980469	2	1776.980444	1776.987314	-0.006869834	K	A	-	6	17	0	0
				1225	1239	14	K	ACLDTAVENMPSLK	M	0.24%	3967	3967	775.3739624	2	1548.732275	1547.731899	1.000375397	K	M	C2:+57.021	3	14	1	0
				1241	1255	14	K	VVEVLAGHGHLYSR	I	2.77%	1379	1379	513.2783813	3	1536.811669	1535.820857	0.990811955	K	I	-	1	14	1	0
				1349	1383	34	R	GHPLGDIVAFLTSTEPQYGQGILSQDAWESLFSR	V	3.17%	8590	8590	1240.584229	3	3718.72921	3719.810739	-1.081528157	R	V	Q17:+0.984	1	34	-1	0
				1404	1423	19	R	RPTPQDSPIFLPVDDTSFR	W	0.24%	5289	5289	730.37	3	2188.086525	2187.096029	0.990495552	R	W	-	3	19	1	0
				1444	1461	17	K	AINCATSGVVGLVNCLR	R	0.24%	5806	5806	902.9701538	2	1803.924658	1802.912194	1.012463441	K	R	C4:+57.021,C15:+57.021	5	17	1	0
				1470	1495	25	R	CVLLSNLSSTSHVPEVDPGSAELQK	V	1.64%	4666	4666	890.1083984	3	2667.30172	2667.30568	-0.003960088	R	V	C1:+57.021,N6:+0.984	4	25	0	0
				1694	1705	11	R	VFTTVGSAEKR	A	2.85%	1151	1151	598.0645142	2	1194.113378	1193.640433	0.47294548	R	A	-	1	11	0	1
				1739	1752	13	K	GVDLVLNSLAEEK	L	0.24%	5091	5091	694.3781738	2	1386.740698	1385.740207	1.000490976	K	L	-	4	13	1	0
				2220	2233	13	R	SLLVNPEGPTLMR	L	0.24%	4362	4362	713.8887329	2	1425.761816	1425.764983	-0.003166916	R	L	-	5	13	0	0
				2382	2391	9	R	VLEALLPLK	G	0.24%	4863	4863	499.7457275	2	997.475805	994.6426645	2.833140518	R	G	-	2	9	3	0
				2382	2396	14	R	VLEALLPLKGLEER	V	0.24%	5793	5793	527.6474609	3	1579.918908	1578.93449	0.984417789	R	V	-	5	14	1	1
P49368	T-complex protein 1 subunit gamma	15	37.61%	45	68	23	S	MMKMLLDPMGGIVMTNDGNAILR	E	2.49%	10798	10798	635.3508301	4	2537.37202	2536.234487	1.137533401	S	E	M4:+15.995	1	23	1	1
				48	68	20	K	MLLDPMGGIVMTNDGNAILR	E	0.24%	7321	7321	1066.033813	2	2130.051977	2130.063552	-0.011575127	K	E	-	4	20	0	0
				128	138	10	K	ALDDMISTLK	K	0.24%	4314	4314	553.7895508	2	1105.563451	1105.568908	-0.005456885	K	K	-	6	10	0	0
				138	163	25	K	KISIPVDISDSDMMLNIINSSITTK	A	0.62%	8373	8373	912.4760742	3	2734.404748	2734.413268	-0.008520936	K	A	-	2	25	0	1
				167	181	14	R	WSSLACNIALDAVK	M	0.24%	5427	5427	774.3967285	2	1546.777807	1546.780897	-0.003090345	R	M	C6:+57.021	6	14	0	0
				203	216	13	K	IPGGIIEDSCVLR	G	0.24%	4040	4040	714.8777466	2	1427.739843	1427.743783	-0.003940364	K	G	C10:+57.021	5	13	0	0
				237	248	11	R	IVLLDSSLEYK	K	0.24%	4581	4581	640.3584595	2	1278.701269	1278.707115	-0.005846591	R	K	-	5	11	0	0
				294	306	12	K	GISDLAQHYLMR	A	0.24%	4876	4876	702.8590088	2	1403.702368	1402.702717	0.999650834	K	A	-	5	12	1	0
				389	399	10	R	NLQDAMQVCR	N	0.24%	1547	1547	617.7838745	2	1233.552099	1233.55896	-0.006861505	R	N	C9:+57.021	4	10	0	0
				399	425	26	R	NVLLDPQLVPGGGASEMAVAHALTEK	S	0.24%	6801	6801	873.1252441	3	2616.352257	2616.358136	-0.005878266	R	S	-	3	26	0	0
				438	449	11	R	AVAQALEVIPR	T	0.24%	3599	3599	583.8460693	2	1165.676489	1165.681904	-0.005415048	R	T	-	6	11	0	0
				449	461	12	R	TLIQNCGASTIR	L	0.24%	1050	1050	667.3482056	2	1332.680761	1332.681517	-0.000756403	R	L	C6:+57.021	5	12	0	0
				491	502	11	K	ELGIWEPLAVK	L	0.24%	6051	6051	627.8554077	2	1253.695165	1253.70197	-0.006805074	K	L	-	6	11	0	0
				507	518	11	K	TAVETAVLLLR	I	0.24%	5542	5542	594.8231812	2	1187.630712	1184.712869	2.917842753	K	I	-	2	11	3	0
				529	545	16	K	GDDQSRQGGAPDAGQE	-	2.99%	2947	2947	530.2976685	3	1587.86953	1587.639702	0.229828475	K	-	Q15:+0.984	1	16	0	1
P49755	Transmembrane emp24 domain-containing protein 10	7	40.64%	0	10	10	-	MSGLSGPPAR	R	2.86%	8815	8815	495.2923584	2	988.5690667	987.4808473	1.088219453	-	R	M1:+15.995	1	10	1	0
				50	71	21	K	DLLVTGAYEISDQSGGAGGLR	S	0.24%	8509	8509	1040.515381	2	2079.015112	2078.028009	0.987102319	K	S	-	4	21	1	0
				75	92	17	K	ITDSAGHILYSKEDATK	G	0.24%	1069	1069	617.3146362	3	1848.920434	1847.926504	0.993929403	K	G	-	4	17	1	1
				112	127	15	K	GTGRIPDQLVILDMK	H	0.67%	4728	4728	552.6419678	3	1654.902428	1654.907624	-0.00519616	K	H	-	1	15	0	1
				116	127	11	R	IPDQLVILDMK	H	0.24%	5776	5776	642.8618164	2	1283.707983	1283.715907	-0.007924371	R	K	-	5	11	0	0
				143	152	9	K	LKPLEVELR	R	0.42%	2114	2114	548.8392334	2	1095.662817	1095.665191	-0.002374187	K	R	-	1	9	0	0
				153	170	17	R	LEDLSESIVNDFAYMKK	R	2.65%	6171	6171	675.362915	3	2023.06527	2017.955492	5.109777957	R	R	N10:+0.984,M15:+15.995	1	17	5	1
P50395	Rab GDP dissociation inhibitor beta	2	8.54%	118	137	19	K	VPSTEAEALASSLMGLFEK	R	0.24%	9584	9584	660.6705322	3	1978.988122	1978.992142	-0.00402056	K	R	-	6	19	0	0
				221	240	19	K	SPYLYPLYGLGELPQGFAR	L	1.88%	7866	7866	714.7112427	3	2141.110253	2140.099324	1.010929203	K	L	-	1	19	1	0
P50570	Dynamin-2	2	1.84%	369	376	7	R	FPFELVK	M	1.25%	4624	4624	440.2514343	2	878.4872186	878.4901864	-0.002967812	R	M	-	1	7	0	0
				562	571	9	K	YMLPLDNLK	I	1.15%	4344	4344	555.2877808	2	1108.559911	1105.584164	2.975746995	K	I	-	2	9	3	0
P51148	Ras-related protein Rab-5C	3	18.06%	23	34	11	K	LVLLGESAVGK	S	2.69%	2945	2945	543.3310547	2	1084.646459	1084.649207	-0.002747201	K	S	-	1	11	0	0
				121	135	14	R	QASPNIVIALAGNK	A	0.24%	4197	4197	698.3970337	2	1394.778417	1394.78816	-0.009742521	R	A	-	5	14	0	0
				166	180	14	K	TAMNVNEIFMAIAK	K	0.24%	7522	7522	776.894165	2	1551.77268	1551.778919	-0.006239338	K	K	-	5	14	0	0
P51153	Ras-related protein Rab-13	2	12.32%	10	21	11	K	LLLIGDSGVGK	T	0.24%	3662	3662	536.3224487	2	1070.629247	1070.633556	-0.004309035	K	T	-	5	11	0	0
				153	167	14	K	SSMNVDEAFSSLAR	D	2.07%	7499	7499	765.835022	2	1529.654394	1529.665855	-0.011460719	K	D	M3:+15.994,N4:+0.984	1	14	0	0
P51159	Ras-related protein Rab-27A	2	9.05%	69	80	11	H	LQLWDTAGQER	F	0.91%	3368	3368	658.8347168	2	1315.653784	1315.65206	0.001723378	S	F	-	2	11	0	0
				191	200	9	K	SWIPEGVVR	S	6.70%	4163	4163	521.2685547	2	1040.521459	1041.560726	-1.039266409	K	S	-	2	9	-1	0
P51572	B-cell receptor-associated protein 31	3	17.07%	79	95	16	K	VNLQNNPGAMEHFHMK	L	1.08%	1914	1914	622.9608154	3	1865.858971	1865.866506	-0.007534551	K	L	-	1	16	0	0
				167	182	15	K	LDVGNAEVKLEEENR	S	0.34%	2396	2396	572.62	3	1714.836525	1714.837339	-0.000814248	K	S	N5:+0.984	1	15	0	1
				221	232	11	K	EYDRLLEEHAK	L	3.01%	1117	1117	468.2376099	3	1401.689354	1401.68884	0.000514814	K	L	-	1	11	0	1
P52272	Heterogeneous nuclear ribonucleoprotein M	20	38.08%	17	37	20	K	MEEESGAPGVPSGNGAPGPK	G	2.86%	1950	1950	623.3235474	3	1866.947167	1866.841789	0.105377634	K	G	-	1	20	0	0
				72	83	11	R	AFITNIPFDVK	W	0.24%	5734	5734	632.8482666	2	1263.680883	1263.68632	-0.005437221	R	W	-	5	11	0	0
				94	110	16	K	VGEVTYVELLMDAEGK	S	0.24%	7261	7261	585.2940063	3	1752.858544	1751.865151	0.993393427	K	S	-	1	16	1	0
				201	214	13	R	LGSTVFVANLDYK	V	0.24%	4482	4482	713.8793335	2	1425.743017	1425.750377	-0.007360408	R	V	-	5	13	0	0
				221	232	11	K	EVFSMAGVVVR	A	0.24%	4545	4545	597.3174438	2	1192.619238	1192.627426	-0.008188697	K	A	-	5	11	0	0
				322	345	23	K	GIGMGNIGPAGMGMEGIGFGINK	M	0.24%	6757	6757	1089.526978	2	2177.038305	2177.043151	-0.00484589	K	M	-	4	23	0	0
				345	362	17	K	MGGMEGPFGGGMENMGR	F	0.24%	4363	4363	857.8424072	2	1713.669164	1713.673153	-0.003988275	K	F	-	4	17	0	0
				345	371	26	K	MGGMEGPFGGGMENMGRFGSGMNMGR	I	3.51%	8129	8129	911.4099731	3	2731.206444	2732.016997	-0.810552438	K	I	M1:+15.994,M4:+15.994,N	1	26	-1	1
				371	381	10	R	INEILSNALK	R	0.24%	3416	3416	557.8250732	2	1113.634496	1113.63937	-0.0048737	R	R	-	5	10	0	0
				456	471	15	R	MGPLGLDHMASSIER	M	0.24%	4212	4212	538.59552	3	1612.763085	1612.770146	-0.007060661	R	M	-	1	15	0	0
				485	496	11	R	MGAGMGFGLER	M	0.24%	3389	3389	563.2606201	2	1124.50559	1124.510683	-0.005092838	R	M	-	6	11	0	0
				496	510	14	R	MAAPIDRVGQTIER	M	0.29%	2437	2437	519.6106567	3	1555.808495	1555.814058	-0.005563113	R	M	-	1	14	0	1
				531	543	12	R	MVPAGMGAGLER	M	0.24%	2085	2085	594.7947388	2	1187.573827	1187.579097	-0.005269541	R	M	-	5	12	0	0
				591	606	15	R	MGPAMGPALGAGIER	M	0.24%	3325	3325	714.3599854	2	1426.704321	1426.706089	-0.001768001	R	M	-	5	15	0	0
				606	621	15	R	MGLAMGGGGGASFDR	A	0.24%	3206	3206	693.3109131	2	1384.606176	1382.607103	1.999073308	R	A	-	2	15	2	0
				621	650	29	R	AIEMERGNFGGSFAGSFGGAGGHAPGVAR	K	2.89%	7879	7879	691.57	4	2762.2487	2763.293578	-1.044878344	R	K	-	1	29	-1	1
				627	650	23	R	GNFGGSFAGSFGGAGGHAPGVAR	K	0.24%	3531	3531	678.9866943	3	2033.936608	2033.945617	-0.009008984	R	K	-	5	23	0	0
				658	667	9	R	NLPFDFTWK	M	0.35%	6821	6821	584.293335	2	1166.57102	1166.576041	-0.005021614	R	M	-	2	9	0	0
				672	685	13	K	FNECGHVLYADIK	M	0.24%	2709	2709	522.5825806	3	1564.724267	1564.733947	-0.009680477	K	M	C4:+57.021	1	13	0	0
				692	707	15	K	GCGVVKFESPEVAER	A	0.24%	2124	2124	555.274292	3	1662.799401	1662.803089	-0.003688535	K	A	C2:+57.021	5	15	0	1
P52798	Ephrin-A4	1	6.47%	8	21	13	R	TVLWAAFLGSPLR	G	0.24%	906	906	477.59	3	1429.746525	1429.808167	-0.061642056	R	G	-	4	13	0	0
P53618	Coatomer subunit beta	10	17.52%	128	141	13	K	EAELLEPLMPAIR	A	0.24%	6344	6344	741.9104004	2	1481.805151	1480.795948	1.009202213	K	A	-	5	13	1	0
				279	291	12	K	AAAQCYIDLIIK	E	0.24%	6074	6074	689.8753052	2	1377.73496	1377.732156	0.0028042	K	E	C5:+57.021	5	12	0	0
				316	327	11	R	VLQDLVMDILR	V	0.24%	8091	8091	657.89	2	1313.76435	1313.737705	0.02664472	R	V	-	5	11	0	0
				513	534	21	K	LVTEMGTYATQSALSSSRPTK	K	2.37%	2881	2881	743.7088623	3	2228.103112	2227.115445	0.987666426	K	K	-	2	21	1	0
				618	633	15	K	VLSECSPLMNDIFNK	E	0.24%	5945	5945	884.4240723	2	1766.832494	1765.837427	0.995067267	K	E	C5:+57.021	4	15	1	0
				660	679	19	K	RNVTVQPDDPISFMQLTAK	N	0.24%	5557	5557	720.7081299	3	2159.100915	2159.104487	-0.00357212	K	N	-	3	19	0	1
				679	702	23	K	NEMNCKEDQFQLSLLAAMGNTQR	K	1.88%	3670	3670	900.7476807	3	2699.219567	2699.198441	0.021125528	K	K	N1:+0.984,C5:+57.021,N2	2	23	0	1
				767	786	19	K	LVEKPSPLTLAPHDFANIK	A	0.24%	4395	4395	523.2931519	4	2089.141307	2089.157173	-0.01586573	K	A	-	1	19	0	1
				852	871	19	K	VTVNTNMVDLNDYLQHILK	S	0.24%	7942	7942	744.3883667	3	2230.141625	2230.130352	0.01127345	K	S	N11:+0.984	1	19	0	0
				898	913	15	R	SIFGEDALANVSIEK	P	1.21%	5386	5386	796.9135132	2	1591.811376	1591.809349	0.002027351	R	P	-	1	15	0	0
P53985	Monocarboxylate transporter 1	1	3.00%	224	239	15	K	DLHDANTDLIGRHPK	Q	0.24%	1025	1025	567.958313	3	1700.851464	1700.859427	-0.007963627	K	Q	-	4	15	0	1
P54709	Sodium/potassium-transporting ATPase subunit beta-3	4	18.28%	97	112	15	R	SDPTSYAGYIEDLKK	F	0.24%	3996	3996	843.9110107	2	1685.806371	1685.814828	-0.008456892	R	F	-	6	15	0	1
				177	188	11	R	IIGLKPEGVPR	I	0.24%	2018	2018	591.2930298	2	1180.570409	1177.718289	2.85212033	R	I	-	2	11	3	0
				188	213	25	R	IDCVSKNEDIPNVAVYPHNGMIDLK	Y	0.91%	4560	4560	711.6011353	4	2842.373241	2841.367236	1.006005	R	Y	C3:+57.021,N12:+0.984	1	25	1	1
				194	213	19	K	NEDIPNVAVYPHNGMIDLK	Y	0.24%	4573	4573	714.0167847	3	2139.026879	2138.046637	0.980241524	K	Y	-	2	19	1	0
P55061	Bax inhibitor 1	1	3.38%	7	15	8	K	INFDALLK	F	2.06%	5508	5508	467.2742004	2	932.5327508	932.5331139	-0.000363121	K	F	-	1	8	0	0
P56975	Pro-neuregulin-3, membrane-bound isoform	1	2.22%	501	517	16	R	LGGIVGPAYQQLEESR	I	3.15%	1373	1373	572.9685059	3	1715.882042	1715.884245	-0.00220283	R	I	-	1	16	0	0
P57729	Ras-related protein Rab-38	1	5.21%	49	60	11	K	VLHWDPETVVR	L	3.46%	1328	1328	450.9068298	3	1349.697014	1349.709181	-0.012166714	K	L	-	1	11	0	0
P57735	Ras-related protein Rab-25	1	8.45%	108	126	18	K	ELYDHAEATIVVMLVGNK	S	7.21%	9718	9718	1007.991516	2	2013.967382	2017.019111	-3.051728789	K	S	M13:+15.995	1	18	-1	0
P58173	Olfactory receptor 2B6	1	3.51%	223	234	11	R	AVLRIQSAEGR	Q	8.47%	2579	2579	400.2379761	3	1197.690453	1198.678215	-0.987762161	R	Q	-	2	11	-1	1
P58743	Prestin	1	2.28%	577	594	17	K	YAKEVGNANMANATVVK	A	2.91%	1680	1680	599.9595947	3	1796.855309	1796.861516	-0.006207236	K	A	N7:+0.984,M10:+15.995,N	1	17	0	1
P60953	Cell division control protein 42 homolog	1	5.76%	16	27	11	K	TCLLISYTTNK	F	0.89%	3040	3040	657.3412476	2	1312.666845	1312.669221	-0.002376387	K	F	C2:+57.021	3	11	0	0
P61006	Ras-related protein Rab-8A	6	28.02%	10	21	11	K	LLLIGDSGVGK	T	0.24%	3662	3662	536.3224487	2	1070.629247	1070.633556	-0.004309035	K	T	-	5	11	0	0
				58	69	11	K	LQIWDTAGQER	F	9.71%	2789	2789	658.8314209	2	1315.647192	1315.65206	-0.004868419	K	F	-	2	11	0	0
				58	71	13	K	LQIWDTAGQERFR	T	2.26%	7572	7572	810.9127808	2	1619.809911	1619.805585	0.004326147	K	S	Q9:+0.984	2	13	0	1

				104	116	12	R	NIEEHASADVEK	M	1.19%	743	743	447.8795166	3	1340.615075	1340.62082	-0.005744963	R	M	-	1	12	0	0
				138	146	8	K	LALDYGIK	F	2.26%	2689	2689	446.7400818	2	891.4645135	891.5065648	-0.042051298	K	F	-	2	8	0	0
				153	167	14	K	ANINVENAFFTLAR	D	0.24%	6964	6964	790.9126587	2	1579.809667	1578.815437	0.994230023	K	D	-	4	14	1	0
P61026	Ras-related protein Rab-10	4	17.00%	11	22	11	K	LLLIGDSGVGK	T	0.24%	3662	3662	536.3224487	2	1070.629247	1070.633556	-0.004309035	K	T	-	5	11	0	0
				59	70	11	K	LQIWDTAGQER	F	9.71%	2789	2789	658.8314209	2	1315.647192	1315.65206	-0.004868419	K	F	-	2	11	0	0
				161	172	11	K	AFLTLAEDILR	K	0.24%	8096	8096	631.8624878	2	1261.709326	1260.707784	1.001541394	K	K	-	3	11	1	0
				161	173	12	K	AFLTLAEDILRK	T	0.24%	7317	7317	695.9093018	2	1389.802953	1388.802747	1.000206188	K	T	-	5	12	1	1
P61077	Ubiquitin-conjugating enzyme E2 D3	1	7.48%	90	101	11	R	SQWSPALTISK	V	0.41%	3288	3288	609.3295898	2	1216.64353	1216.645184	-0.001654184	R	V	-	1	11	0	0
P61106	Ras-related protein Rab-14	4	26.98%	61	72	11	K	LQIWDTAGQER	F	9.71%	2789	2789	658.8314209	2	1315.647192	1315.65206	-0.004868419	K	F	-	2	11	0	0
				61	74	13	K	LQIWDTAGQERFR	A	2.26%	7572	7572	810.9127808	2	1619.809911	1619.805585	0.004326147	K	S	Q9:+0.984	2	13	0	1
				156	170	14	K	TGENVEDAFLEAAK	K	0.24%	4757	4757	747.3543701	2	1492.69309	1492.704549	-0.011459254	K	K	-	5	14	0	0
				170	201	31	K	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	L	0.24%	2626	2626	820.66	4	3278.6087	3278.627963	-0.019263472	K	L	Q21:+0.984	2	31	0	1
P61158	Actin-related protein 3	4	16.75%	18	38	20	K	LGYAGNTEPQFIIPSCIAIK	E	0.24%	6539	6539	1097.077148	2	2192.138647	2191.13426	1.004386411	K	E	C16:+57.021	2	20	1	0
				91	99	8	R	FMEQVIFK	Y	0.24%	4071	4071	521.2709961	2	1040.526342	1040.536486	-0.010143772	R	Y	-	4	8	0	0
				161	191	30	R	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	H	0.24%	6818	6818	1020.526733	3	3058.556725	3057.568787	0.987937891	R	H	C28:+57.021	6	30	1	0
				317	329	12	K	NIVLSGGSTMFR	D	0.24%	3676	3676	641.3411865	2	1280.666723	1280.654704	0.012019199	K	D	-	4	12	0	0
P61224	Ras-related protein Rap-1b	3	20.65%	5	16	11	K	LVVLGSGGVGK	S	0.24%	1846	1846	493.3009949	2	984.5863397	984.5967769	-0.01043723	K	S	-	5	11	0	0
				102	117	15	R	VKDTDDVPMILVGNK	C	3.34%	3218	3218	822.9050293	2	1643.794409	1642.860005	0.93440305	R	C	-	2	15	1	1
				151	163	12	K	INVNEIFYDLVR	Q	0.24%	8474	8474	747.9047241	2	1493.793798	1493.787826	0.005972666	K	Q	-	6	12	0	0
P61421	V-type proton ATPase subunit d 1	1	3.13%	246	257	11	R	LYPEGLAQLAR	A	1.08%	4233	4233	615.97	2	1229.92435	1229.676818	0.24753164	R	A	-	4	11	0	0
P61586	Transforming protein RhoA	1	6.22%	150	162	12	R	IGAFGYMECSAK	T	0.24%	3073	3073	667.29	2	1332.56435	1332.583778	-0.019428344	R	T	C9:+57.021	5	12	0	0
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	6	15.88%	23	42	19	K	ACADATLSQITNNIDPVGR	I	0.24%	5165	5165	1008.494141	2	2014.972631	2014.973737	-0.00110571	K	I	C2:+57.021	6	19	0	0
				197	209	12	R	LFVSGACDASAK	L	0.24%	1147	1147	613.2996216	2	1224.583593	1224.580406	0.00318678	R	L	C7:+57.021	4	12	0	0
				314	337	23	R	VSCLGVTDDGMAVATGSWDSFLK	I	0.24%	7411	7411	1208.5625	2	2415.10935	2415.108183	0.00116708	R	I	C3:+57.021	6	23	0	0
				23	42	19	K	ACGDSTLTQITAGLDPVGR	I	0.24%	5562	5562	967.482605	2	1932.94956	1931.925374	1.024185817	K	I	C2:+57.021,Q9:+0.984	4	19	1	0
				197	209	12	R	TFVSGACDASIK	L	2.65%	1110	1110	627.8598022	2	1253.703954	1254.590971	-0.887016612	R	L	C7:+57.021	2	12	-1	0
				314	337	23	R	VSCLGVTDDGMAVATGSWDSFLK	I	0.24%	7411	7411	1208.5625	2	2415.10935	2415.108183	0.00116708	R	I	C3:+57.021	6	23	0	0
P63000	Ras-related C3 botulinum toxin substrate 1	3	18.75%	132	147	15	K	KLTPITYPQGLAMAK	E	0.24%	3363	3363	544.6405029	3	1630.898034	1630.911647	-0.013613395	K	E	-	2	15	0	1
				153	163	10	K	YLECSALTQR	G	0.24%	1580	1580	620.8037109	2	1239.591772	1239.591305	0.000466443	K	G	C4:+57.021	6	10	0	0
				163	174	11	R	GLKTVFDEAIR	A	2.28%	5754	5754	416.54	3	1246.596525	1247.687383	-1.09085812	R	A	-	1	11	-1	1
P63010	AP-2 complex subunit beta	4	5.76%	78	93	15	K	SQPDMAIMAVNSFVK	D	0.24%	6636	6636	819.4031982	2	1636.790746	1636.795298	-0.00455134	K	D	-	4	15	0	0
				344	359	15	R	LASQANIAQVLAELK	E	0.24%	6973	6973	784.9539185	2	1567.892187	1567.893353	-0.001166518	R	E	-	5	15	0	0
				390	402	12	R	CVSTLLDLIQTK	V	0.24%	6630	6630	695.8861694	2	1389.756689	1389.753286	0.003403275	R	V	C1:+57.021	5	12	0	0
				796	808	12	K	MEPLNNLQVAVK	N	2.27%	3354	3354	678.37	2	1354.72435	1354.727869	-0.003518888	K	N	-	1	12	0	0
P63167	Dynein light chain 1, cytoplasmic	1	13.48%	48	60	12	K	KYNPTWHCIVGR	N	0.53%	2096	2096	510.9239807	3	1529.748467	1530.739685	-0.991218461	K	N	N3:+0.984,C8:+57.021	2	12	-1	1
P63215	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-3	1	17.33%	18	31	13	K	MVEQLKIEASLCR	I	0.91%	10189	10189	789.4182129	2	1576.820776	1575.810818	1.009957317	K	I	C12:+57.021	2	13	1	1
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	15	70.03%	12	36	24	K	GHNGWVTQIATTPQFPDMILSASR	D	0.24%	7067	7067	876.4366455	3	2626.286461	2626.296204	-0.009742501	K	D	-	2	24	0	0
				44	57	13	K	LTRDETNYGIPQR	A	0.24%	1057	1057	782.3953857	2	1562.775121	1561.784865	0.990255956	K	A	-	4	13	1	1
				88	99	11	R	LWDLTTGTTTR	R	0.24%	3498	3498	632.8278809	2	1263.640112	1263.645912	-0.005800481	R	R	-	5	11	0	0
				106	118	12	K	DVLSVAFSSDNR	Q	0.24%	4341	4341	655.3210449	2	1308.62644	1308.63099	-0.004550604	K	Q	-	3	12	0	0
				130	139	9	K	LWNTLGVCK	Y	0.24%	3128	3128	545.7869263	2	1089.558202	1089.563634	-0.005431437	K	Y	C8:+57.021	5	9	0	0
				139	155	16	K	YTVQDESHSEWVSCVR	F	0.24%	2575	2575	991.4304199	2	1980.84519	1980.863124	-0.0179339	K	F	C14:+57.021	5	16	0	0
				155	172	17	R	FSPNSSNPIIVSCGWDK	L	0.24%	4399	4399	954.4498291	2	1906.884008	1906.887882	-0.003873685	R	L	C13:+57.021	4	17	0	0
				175	183	8	K	VWNLANCK	L	0.24%	1911	1911	502.750824	2	1003.485998	1003.490469	-0.004470987	K	L	C7:+57.021	5	8	0	0
				185	212	27	K	TNHIGHTGYLNTVTVSPDGSLCASGGK	D	0.24%	2978	2978	686.5811157	4	2742.293163	2742.302676	-0.009513421	K	D	C22:+57.021	2	27	0	0
				212	225	13	K	DGQAMLWDLNEGK	H	0.24%	4766	4766	738.8404541	2	1475.665258	1475.671476	-0.006218053	K	H	-	5	13	0	0
				245	257	12	R	YWLCAATGPSIK	I	0.24%	4017	4017	683.8427734	2	1365.669897	1365.674641	-0.004744317	R	I	C4:+57.021	6	12	0	0
				257	264	7	K	IWDLEGK	I	2.28%	2731	2731	430.7287292	2	859.4418084	859.4439645	-0.002156056	K	I	-	2	7	0	0
				264	280	16	K	IIVDELKQEVISTSSK	A	0.24%	4275	4275	895.9485474	2	1789.881445	1787.988042	1.893402815	K	A	-	5	16	2	1
				280	308	28	K	AEPPQCTSLAWSADGQTLFAGYTDNLVR	V	0.24%	7282	7282	1535.723022	2	3069.430395	3067.434084	1.996310362	K	V	C6:+57.021	4	28	2	0
				308	317	9	R	VWQVTIGTR	-	0.24%	2778	2778	529.3134766	2	1056.611303	1058.587275	-1.975971787	R	-	-	5	9	-1	0
P68400	Casein kinase II subunit alpha	1	3.84%	107	122	15	R	TPALVFEHVNNTDFK	Q	0.35%	3535	3535	578.2928467	3	1731.855065	1731.846782	0.008283399	R	Q	N10:+0.984	2	15	0	0
P78504	Protein jagged-1	1	0.90%	119	130	11	R	IVLPFSFAWPR	S	1.98%	4090	4090	666.8582764	2	1331.700903	1331.739025	-0.038121946	R	S	-	3	11	0	0
P78562	Phosphate-regulating neutral endopeptidase	1	1.87%	702	716	14	R	EQVQIGAHSPPQFR	V	7.36%	2256	2256	533.30896	3	1596.903405	1595.757935	1.145469547	R	V	Q2:+0.984,Q4:+0.984,Q12	1	14	1	0
Q00325	Phosphate carrier protein, mitochondrial	7	20.44%	101	112	11	K	GIFNGFSVTLK	E	0.24%	6024	6024	591.8284302	2	1181.64121	1181.644455	-0.003245192	K	E	-	4	11	0	0
				121	137	16	K	GWAPTFLGYSMQGLCK	F	0.24%	7080	7080	908.925354	2	1815.835058	1814.847932	0.987125696	K	F	C15:+57.021	5	16	1	0
				137	145	8	K	FGFYEVFK	V	0.24%	5871	5871	518.7584839	2	1035.501318	1035.506565	-0.005247099	K	V	-	4	8	0	0
				189	201	12	R	IQTQPGYANTLR	D	0.24%	1167	1167	681.3605347	2	1360.705419	1360.709909	-0.004490168	R	D	-	6	12	0	0
				189	206	17	R	IQTQPGYANTLRDAAPK	M	0.29%	1955	1955	615.3260498	3	1842.954674	1842.958807	-0.004133018	R	M	-	2	17	0	1
				218	226	8	K	GVAPLWMR	Q	0.24%	3828	3828	465.2537231	2	928.4917962	928.4952897	-0.003493447	K	Q	-	4	8	0	0
				341	355	14	R	LPRPPPPEMPESLK	K	0.24%	2771	2771	530.6290283	3	1588.86361	1586.849047	2.014563097	R	K	-	2	14	2	0
Q00341	Vigilin	1	1.97%	788	813	25	K	ELEALIQNLDNVVEDSMLVDPKHHR	H	6.46%	6612	6612	733.3724365	4	2929.458446	2929.460454	-0.002008474	K	H	M17:+15.995	1	25	0	1
Q00610	Clathrin heavy chain 1	26	21.55%	86	96	10	K	TLQIFNIEMK	S	1.58%	5897	5897	620.3209229	2	1238.626196	1235.658392	2.967803479	K	S	-	2	10	3	0
				86	98	12	K	TLQIFNIEMKSK	M	2.85%	4050	4050	490.6054688	3	1468.792931	1466.780384	2.012547362	K	M	M9:+15.995	1	12	2	1
				144	157	13	R	HSSLAGCQIINYR	T	0.24%	1652	1652	506.9172058	3	1517.728142	1517.740429	-0.012287088	R	T	C7:+57.021	3	13	0	0
				189	205	16	K	VSQPIEGHAASFAQFK	M	0.24%	2900	2900	859.940918	2	1717.866186	1716.847116	1.01907001	K	M	Q3:+0.984	4	16	1	0
				227	245	18	K	LHIIEVGTPPTGNQPFPK	K	0.24%	3417	3417	649.3560181	3	1945.044579	1944.046894	0.997684975	K	K	-	5	18	1	0
				354	366	12	R	NNLAGAEELFAR	K	0.24%	4336	4336	652.83	2	1303.64435	1303.65206	-0.007710216	R	K	-	5	12	0	0
				354	367	13	R	NNLAGAEELFARK	F	0.24%	3160	3160	717.3795166	2	1432.743383	1431.747023	0.996359851	R	F	-	6	13	1	1
				367	382	15	K	FNALFAQGNYSEAAK	V	0.24%	3640	3640	816.3929443	2	1630.770239	1629.778717	0.99152116	K	V	-	2	15	1	0
				468	481	13	K	SVDPTLALSVYLR	A	0.24%	10252	10252	717.41	2	1432.80435	1432.792577	0.011773392	K	A	-	3	13	0	0
				487	500	13	K	VIQCFAETGQVQK	I	0.24%	1478	1478	754.3806763	2	1506.745702	1506.749597	-0.003894677	K	I	C4:+57.021	4	13	0	0
				625	637	12	R	ALEHFTDLYDIK	R	0.24%	4396	4396	733.8657227	2	1465.715795	1463.729642	1.986153353	R	R	-	2	12	2	0
				837	851	14	R	GQFSTDELVAEVEK	R	0.24%	4738	4738	776.8827515	2	1551.749853	1550.746414	1.003438562	R	R	-	5	14	1	0
				856	865	9	K	LLLPWLEAR	I	0.24%	7373	7373	555.835022	2	1109.654394	1109.659712	-0.005317679	K	I	-	2	9	0	0
				892	903	11	R	FLRENPYYDSR	V	1.72%	1486	1486	487.2345581	3	1458.680199	1458.689174	-0.008974788	R	V	-	1	11	0	1
				911	923	12	K	RDPHLACVAYER	G	0.24%	909	909	496.2428894	3	1485.705193	1485.714215	-0.009021507	K	G	C7:+57.021	6	12	0	1
				923	941	18	R	GQCDLELINVCNENSLFK	S	0.24%	6054	6054	1077	2	2151.98435	2151.991961	-0.007610904	R	S	C3:+57.021,C11:+57.021	5	18	0	0
				951	967	16	K	DPELWGSVLLESNPYR	R	7.07%	7357	7357	939.4328003	2	1876.849951	1874.905025	1.944925698	K	R	N13:+0.984	1	16	2	0
				967	993	26	R	RPLIDQVVQTALSETQDPEEVSVTVK	A	0.24%	7752	7752	961.8452759	3	2882.512353	2881.49203	1.020322813	R	A	Q9:+0.984	2	26	1	0
				993	1010	17	K	AFMTADLPNELIELLEK	I	0.24%	10954	10954	974.0097656	2	1946.003881	1946.007064	-0.003182702	K	I	-	5	17	0	0
				1010	1022	12	K	IVLDNSVFSEHR	N	0.29%	3157	3157	708.3627319	2	1414.709814	1414.720474	-0.010660357	K	N	-	2	12	0	0
				1101	1113	12	R	CNEPAVWSQLAK	A	0.24%	3539	3539	701.8413086	2	1401.666967	1401.670618	-0.0036513	R	A	C1:+57.021	5	12	0	0
				1182	1204	22	R	LAELEEFINGPNNAHIQQVGDR	C	0.24%	4925	4925	822.0758057	3	2463.203942	2464.198247	-0.994305344	R	C	N13:+0.984	1	22	-1	0
				1215	1226	11	K	LLYNNVSNFGR	L	0.24%	2802	2802	648.8355713	2	1295.655493	1295.662231	-0.006738358	K	L	-	4	11	0	0
				1226	1245	19	R	LASTLVHLGEYQAAVDGAR	K	0.24%	4252	4252	657.6776733	3	1970.009545	1970.022136	-0.01259106	R	K	-	4	19	0	0
				1461	1481	20	K	SVNESLNNLFITEEDYQALR	T	0.24%	6714	6714	1178.078369	2	2354.141088	2354.139017	0.002071665	K	T	-	4	20	0	0
				1481	1498	17	R	TSIDAYDNFDNISLAQR	L	0.24%	4825	4825	972.4584351	2	1942.90122	1941.906831	0.994388653	R	L	-	5	17	1	0
Q00839	Heterogeneous nuclear ribonucleoprotein U	12	17.94%	186	204	18	K	SSGPTSLFAVTVAPPGAR	Q	0.24%	5196	5196	857.9569092	2	1713.898168	1713.904981	-0.006812449	K	Q	-	6	18	0	0
				255	265	10	R	GYFEYIEENK	Y	0.24%	3591	3591	646.29	2	1290.56435	1290.576829	-0.012479536	R	Y	-	5	10	0	0
				462	484	22	K	EKPYFPIPEEYTFIQNVPLEDR	V	0.24%	7166	7166	908.7894287	3	2723.344811	2723.348281	-0.003470251	K	V	-	4	22	0	0
				495	510	15	K	DCEVVMMIGLPGAGK	T	0.24%	5872	5872	789.3760986	2	1576.736547	1575.745442	0.991105178	K	T	C2:+57.021	6	15	1	0
				524	536	12	K	YNILGTNTIMDK	M	0.24%	4232	4232	691.8500977	2	1381.684545	1381.691149	-0.006603727	K	M	-	5	12	0	0
				565	572	7	K	FIEIAAR	K	0.37%	1893	1893	410.2364807	2	818.4573113	818.4650342	-0.007722894	K	K	-	1	7	0	0
				574	590	16	K	RNFILDQTNVSAAAQR	R	0.24%	2815	2815	902.4724731	2	1802.929296	1802.938741	-0.009444319	K	R	-	3	16	0	1
				575	590	15	R	NFILDQTNVSAAAQR	R	0.24%	3534	3534	824.4259033	2	1646.836157	1646.837629	-0.001472815	R	R	-	3	15	0	0
				592	601	9	K	MCLFAGFQR	K	0.24%	4766	4766	565.2661743	2	1128.516699	1128.52039	-0.003691391	K	K	C2:+57.021	5	9	0	0
				732	739	7	R	RGNMPQR	G	2.85%	3310	3310	430.7538757	2	859.4921014	859.397001	0.095100425	R	G	N3:+0.984,Q6:+0.984	1	7	0	1
				773	787	14	R	GGMPNRGNYNQNFR	G	3.41%	4998	4998	549.6334839	3	1645.876977	1641.695454	4.18152278	R	G	M3:+15.995,N8:+0.984,N1	1	14	4	1
				796	814	18	K	NQSGGYNQWQQGQFWGQK	P	2.10%	4090	4090	1107.000122	2	2211.984594	2210.98821	0.996383981	K	P	-	1	18	1	0
Q01082	Spectrin beta chain, brain 1	1	0.68%	1394	1410	16	K	WLHGLESQIQSDDYGK	D	8.47%	2324	2324	625.321228	3	1872.940209	1875.863888	-2.923679294	K	D	Q10:+0.984	1	16	-1	0
Q01518	Adenylyl cyclase-associated protein 1	1	4.84%	37	60	23	K	AGAAPYVQAFDSLLAGPVAEYLK	I	0.24%	9589	9589	784.4104614	3	2350.207909	2350.220896	-0.012986483	K	I	-	4	23	0	0
Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein	2	8.60%	62	73	11	K	TSFHALTSILK	A	2.49%	3646	3646	406.9016724	3	1217.681542	1216.681569	0.999972658	K	A	-	1	11	1	0
				190	206	16	R	AVVVNAAQLASYSQSK	Q	0.24%	3008	3008	818.9381714	2	1635.860693	1634.862782	0.997911173	R	Q	-	6	16	1	0
Q03518	Antigen peptide transporter 1	2	6.81%	653	678	25	R	SLQENIAYGLTQKPTMEEITAAAVK	S	0.24%	6075	6075	903.4701538	3	2707.386986	2705.394581	1.992405546	R	S	-	2	25	2	0
				678	708	30	K	SGAHSFISGLPQGYDTEVDEAGSQLSGGQR	Q	0.24%	5025	5025	1018.476807	3	3052.406945	3050.385333	2.021612018	K	Q	Q12:+0.984	2	30	2	0
Q04912	Macrophage-stimulating protein receptor	1	0.79%	1183	1194	11	K	DLISFGLQVAR	S	1.42%	6645	6645	610.3345947	2	1218.653539	1218.660818	-0.007278907	K	S	Q8:+0.984	1	11	0	0
Q04941	Proteolipid protein 2	1	9.87%	6	21	15	R	LSAPGCWAACTNFSR	T	0.24%	3879	3879	849.3759766	2	1696.736303	1696.744066	-0.007762875	R	T	C6:+57.021,C10:+57.021	4	15	0	0
Q06481	Amyloid-like protein 2	1	2.36%	521	539	18	K	AAQMKSQVMTHLHVIEER	R	3.76%	1220	1220	709.3594971	3	2125.055016	2125.029662	0.025353707	K	R	Q3:+0.984,Q7:+0.984,M9:	1	18	0	1
Q08722	Leukocyte surface antigen CD47	1	2.48%	85	93	8	K	IEVSQLLK	G	0.34%	3685	3685	465.2854614	2	928.5552728	928.5593287	-0.004055948	K	G	-	3	8	0	0
Q10589	Bone marrow stromal antigen 2	1	8.33%	111	126	15	K	KVEELEGEITTLNHK	L	0.24%	2481	2481	580.6432495	3	1738.906273	1738.910126	-0.003852345	K	L	-	3	15	0	1
Q12974	Protein tyrosine phosphatase type IVA 2	1	8.38%	15	29	14	R	FLITHNPTNATLNK	F	1.27%	1493	1493	528.6216431	3	1582.841454	1582.846737	-0.005283361	R	F	-	2	14	0	0
Q13177	Serine/threonine-protein kinase PAK 2	1	2.48%	504	517	13	K	PLSSLTPLIMAAK	E	1.22%	5766	5766	671.3891602	2	1340.76267	1340.773756	-0.011086159	K	E	-	1	13	0	0
Q13283	Ras GTPase-activating protein-binding protein 1	1	4.94%	276	299	23	K	VPASQPRPESKPESQIPPQRPQR	D	2.56%	605	605	653.3530273	4	2609.380809	2610.351378	-0.970569161	K	D	Q15:+0.984,Q22:+0.984	1	23	-1	0
Q13291	Signaling lymphocytic activation molecule	1	3.58%	124	136	12	K	NVSVQRFCLQLR	L	0.91%	3613	3613	507.2774048	3	1518.808739	1518.808449	0.000289827	K	L	C8:+57.021	1	12	0	1
Q13308	Tyrosine-protein kinase-like 7	1	1.87%	427	447	20	K	PGYLDCLTQATPKPTVVWYR	N	8.14%	5262	5262	789.4	3	2365.176525	2365.177172	-0.000647448	K	N	C6:+57.021,Q9:+0.984	1	20	0	0
Q14254	Flotillin-2	4	14.25%	233	247	14	K	TAEAQLAYELQGAR	E	0.24%	3726	3726	760.8891602	2	1519.76267	1519.763067	-0.000397119	K	E	-	4	14	0	0
				321	335	14	K	IGEAEAAVIEAMGK	A	0.24%	5052	5052	694.8563232	2	1387.696996	1387.701714	-0.004717276	K	A	-	5	14	0	0
				356	370	14	K	MALVLEALPQIAAK	I	0.24%	6730	6730	734.8623657	2	1467.709081	1466.853069	0.856011917	K	I	-	2	14	1	0
				397	416	19	R	LLAELPASVHALTGVDLSK	I	0.24%	6161	6161	645.3695679	3	1933.085228	1933.088425	-0.003196163	R	I	-	3	19	0	0
Q14258	E3 ubiquitin/ISG15 ligase TRIM25	4	9.68%	65	83	18	K	NTVLCNVVEQFLQADLAR	E	0.24%	9687	9687	697.3599854	3	2089.056481	2089.062158	-0.005677065	K	E	C5:+57.021	5	18	0	0
				184	203	19	K	TCSPASLSQASADLEATLR	H	0.24%	5967	5967	989.4787598	2	1976.941869	1976.946853	-0.004983973	K	H	C2:+57.021	5	19	0	0
				273	283	10	K	FDTIYQILLK	K	0.24%	7370	7370	627.8638306	2	1253.712011	1252.706721	1.005289597	K	K	-	4	10	1	0
				402	416	14	K	LPTFGAPEQLVDLK	Q	0.24%	5921	5921	764.930603	2	1527.845556	1526.834441	1.011114567	K	Q	-	4	14	1	0
Q14289	Protein-tyrosine kinase 2-beta	1	1.59%	287	303	16	R	QLTSQDAKPTCLAEFK	Q	8.97%	2498	2498	613.6247559	3	1837.850792	1835.908283	1.942509538	R	Q	C11:+57.021	1	16	2	0
Q14676	Mediator of DNA damage checkpoint protein 1	5	3.16%	132	142	10	R	LDVSLPFVSR	G	0.78%	5671	5671	567.828064	2	1133.640478	1131.628805	2.011672466	R	G	-	2	10	2	0
				1894	1904	10	K	VLFTGVVDAR	G	2.82%	3424	3424	540.7799072	2	1079.544164	1075.602591	3.941573789	K	G	-	1	10	4	0
				1977	1989	12	K	NFGFSLQDALSR	A	0.24%	6360	6360	678.3425293	2	1354.669409	1353.66771	1.001698298	K	A	-	5	12	1	0
				2037	2054	17	R	VVITCPQDFPHCSIPLR	V	0.24%	4216	4216	680.3418579	3	2038.002099	2038.995908	-0.993809654	R	V	C5:+57.021,Q7:+0.984,C1	3	17	-1	0
				2054	2071	17	R	VGLPLLSPEFLLTGVLK	Q	0.24%	9977	9977	899.5479126	2	1797.080175	1795.085905	1.994269771	R	Q	-	6	17	2	0
Q14BN4	Sarcolemmal membrane-associated protein	1	1.33%	543	554	11	K	QIQVLQAQLQR	L	7.85%	6382	6382	664.8529663	2	1327.690283	1327.698279	-0.007996815	K	L	Q3:+0.984,Q6:+0.984,Q8:	1	11	0	0
Q15046	Lysyl-tRNA synthetase	2	4.19%	111	127	16	K	YSHLQPGDHLTDITLK	V	0.29%	2545	2545	460.2408447	4	1836.932079	1836.937009	-0.00493047	K	V	-	1	16	0	0
				305	314	9	K	MLVVGGIDR	V	9.63%	2248	2248	481.2632446	2	960.5108392	958.5269838	1.983855362	K	V	-	2	9	2	0
Q15084	Protein disulfide-isomerase A6	4	13.41%	85	102	17	K	HHSLGGQYGVQGFPTIK	I	0.24%	3155	3155	610.3162842	3	1827.925377	1825.911113	2.014264267	K	I	Q7:+0.984	2	17	2	0
				118	132	14	R	TGEAIVDAALSALR	Q	0.24%	7306	7306	695.4075317	2	1388.799413	1385.75144	3.047973421	R	Q	-	2	14	3	0
				241	256	15	K	IFQKGESPVDYDGGR	T	1.25%	1483	1483	556.6016846	3	1666.781579	1666.795096	-0.013517249	K	T	-	2	15	0	1
				373	386	13	K	GSFSEQGINEFLR	E	0.24%	5163	5163	742.36	2	1482.70435	1482.710303	-0.005953504	K	E	-	6	13	0	0
Q15149	Plectin	20	6.17%	477	493	16	K	GIYQSLEGAVQAGQLK	V	0.24%	5444	5444	831.4478149	2	1660.87998	1660.878432	0.001548203	K	V	-	5	16	0	0
				750	764	14	R	SLESLHSFVAAATK	E	0.24%	4602	4602	731.3885498	2	1460.76145	1459.76709	0.994359473	R	E	-	4	14	1	0
				1186	1201	15	K	VLALPEPSPAAPTLR	S	0.24%	3990	3990	766.9467163	2	1531.877783	1530.876975	1.000807593	K	S	-	4	15	1	0
				1350	1364	14	R	ESADPLGAWLQDAR	R	6.14%	6383	6383	766.4430542	2	1530.870458	1528.715767	2.154691126	R	R	Q11:+0.984	1	14	2	0
				2318	2329	11	K	AQVEQELTTLR	L	0.24%	2558	2558	645.2879028	2	1288.560156	1286.683026	1.877129616	K	L	-	5	11	2	0

				2650	2663	13	K	AKLEQLFQDEVAK	A	0.24%	3599	3599	760.4137573	2	1518.811865	1517.808955	1.002909632	K	A	-	5	13	1	1
				2743	2761	18	R	AALAHSEEVTASQVAATK	T	0.24%	1235	1235	595.6464233	3	1783.915795	1782.911188	1.004606484	R	T	-	1	18	1	0
				2794	2808	14	R	LQEAGILSAEELQR	L	0.24%	3505	3505	779.4179688	2	1556.820287	1555.820582	0.999705108	R	L	-	5	14	1	0
				2808	2822	14	R	LAQGHTTVDELARR	E	7.92%	955	955	523.61	3	1567.806525	1565.827399	1.979125896	R	E	-	2	14	2	1
				2832	2841	9	R	SSIAGLLLK	A	0.24%	4618	4618	451.2891541	2	900.562658	900.5644141	-0.001756055	R	A	-	3	9	0	0
				3115	3127	12	R	SLVPAAELLESR	V	0.24%	5021	5021	642.8582764	2	1283.700903	1283.708512	-0.007609786	R	V	-	3	12	0	0
				3183	3212	29	K	DLLPSDMAVALLEAQAGTGHIIDPATSAR	L	0.24%	8535	8535	979.5088501	3	2935.503075	2933.48042	2.022654933	K	L	Q15:+0.984	2	29	2	0
				3269	3285	16	R	LLDAQLSTGGIVDPSK	S	0.42%	3707	3707	808.3960571	2	1614.776464	1612.867198	1.909265954	R	S	-	3	16	2	0
				3355	3368	13	R	ARQEELYSELQAR	E	0.24%	1912	1912	797.40979	2	1592.80393	1591.79543	1.00849983	R	E	-	4	13	1	1
				3518	3540	22	R	ATTAALLLEAQAATGFLVDPVR	N	0.52%	8934	8934	743.4141846	3	2227.219079	2227.22123	-0.002151377	R	N	-	1	22	0	0
				3551	3568	17	K	AGVVGPELHEQLLSAEK	A	0.24%	2933	2933	592.9853516	3	1775.93258	1775.94176	-0.00918068	K	A	-	1	17	0	0
				3783	3793	10	R	LTAEDLFEAR	I	0.52%	4432	4432	583.2919922	2	1164.568334	1163.582249	0.986085151	R	I	-	4	10	1	0
				3935	3950	15	R	LLDAQLATGGIVDPR	L	0.24%	4200	4200	769.9281616	2	1537.840673	1537.846403	-0.00572995	R	L	-	5	15	0	0
				3991	3999	8	R	LSYTQLLR	R	0.24%	3568	3568	497.2885742	2	992.5614984	992.5654767	-0.003978379	R	R	-	5	8	0	0
				4158	4167	9	K	LISLFQAMK	K	0.24%	5650	5650	525.8015747	2	1049.587499	1049.594335	-0.006835834	K	K	-	4	9	0	0
Q15382	GTP-binding protein Rheb	1	8.70%	135	151	16	K	ALAESWNAAFLESSAK	E	0.24%	5600	5600	847.9242554	2	1693.832861	1693.831147	0.00171363	K	E	-	5	16	0	0
Q15700	Disks large homolog 2	1	1.26%	171	182	11	K	EAGSIVRLYVR	R	1.25%	2057	2057	422.2416687	3	1263.701531	1261.714266	1.987264528	K	R	-	2	11	2	1
Q15758	Neutral amino acid transporter B(0)	3	8.13%	178	189	11	K	EVLDSFLDLAR	N	0.24%	6784	6784	639.8400879	2	1277.664526	1276.666313	0.998212469	K	N	-	5	11	1	0
				189	202	13	R	NIFPSNLVSAAFR	S	0.24%	6963	6963	718.3869629	2	1434.758276	1434.761945	-0.003669323	R	S	-	5	13	0	0
				502	522	20	K	SELPLDPLPVPTEEGNPLLK	H	0.24%	6928	6928	1080.086914	2	2158.158178	2157.156898	1.001279709	K	H	-	4	20	1	0
Q15833	Syntaxin-binding protein 2	1	2.53%	424	439	15	K	LIQHANVQAHSSLIR	N	3.46%	867	867	422.4890137	4	1685.924755	1685.932533	-0.007778313	K	N	-	1	15	0	0
Q15907	Ras-related protein Rab-11B	6	33.94%	30	41	11	R	FTRNEFNLESK	S	0.24%	1339	1339	692.8433838	2	1383.671118	1383.678275	-0.007157438	R	S	-	4	11	0	1
				41	51	10	K	STIGVEFATR	S	0.88%	1935	1935	541.2904663	2	1080.565283	1079.56112	1.004162833	K	S	-	5	10	1	0
				61	72	11	K	AQIWDTAGQER	Y	0.24%	1576	1576	637.802063	2	1273.588476	1273.60511	-0.016633999	K	Y	-	5	11	0	0
				82	95	13	R	GAVGALLVYDIAK	H	0.24%	11076	11076	645.36	2	1288.70435	1288.739084	-0.034734352	R	H	-	6	13	0	0
				145	166	21	K	NNLSFIETSALDSTNVEEAFK	N	0.24%	7037	7037	1165.554199	2	2329.092748	2328.112133	0.980615278	K	N	-	4	21	1	0
				166	174	8	K	NILTEIYR	I	0.24%	4632	4632	511.2875977	2	1020.559545	1020.560391	-0.000846143	K	I	-	4	8	0	0
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	1	6.57%	133	155	22	K	VAGHPNIVINNAAGNFISPTER	L	1.79%	3623	3623	764.399231	3	2290.174218	2290.181825	-0.007606977	K	L	-	3	22	0	0
Q16720	Plasma membrane calcium-transporting ATPase 3	1	0.98%	81	93	12	R	RQIYGQNFIPPK	Q	1.70%	6062	6062	488.9360657	3	1463.784722	1461.76158	2.023142389	R	Q	Q6:+0.984,N7:+0.984	2	12	2	1
Q4VCS5	Angiomotin	1	0.74%	535	543	8	K	TISQLFAK	N	1.14%	2333	2333	454.2645264	2	906.5134027	906.5174638	-0.004061186	K	N	-	1	8	0	0
Q5D1E8	Ribonuclease ZC3H12A	1	2.67%	71	87	16	K	LGVQADTNTVLGELVK	H	7.17%	760	760	553.6269531	3	1657.857384	1657.877397	-0.020013177	K	H	Q4:+0.984,N8:+0.984	1	16	0	0
Q5R3F8	Leucine-rich repeat and fibronectin type-III domain-containing protein 6	1	1.83%	480	495	15	K	LPTAKGLEAGLDTPK	V	0.87%	1991	1991	505.2582092	3	1512.751153	1509.840255	2.91089747	K	V	-	2	15	3	1
Q63HR2	Tensin-like C1 domain-containing phosphatase	1	1.92%	1244	1271	27	R	IPSKDPLEETPEAPVPTNMSTAADLLR	Q	1.81%	10407	10407	964.8602905	3	2891.557396	2892.442638	-0.885241274	R	Q	N18:+0.984	1	27	-1	1
Q6PHW0	Iodotyrosine dehalogenase 1	1	2.77%	270	278	8	K	EATVPDLK	R	9.20%	1259	1259	435.7729797	2	869.5303094	871.4650939	-1.934784519	K	R	-	2	8	-1	0
Q6UVK1	Chondroitin sulfate proteoglycan 4	1	0.52%	655	667	12	K	VVAIRPAIQIHR	S	9.08%	1371	1371	460.226593	3	1377.656304	1372.830284	4.826020165	K	S	Q9:+0.984	1	12	5	0
Q6ZRP7	Sulfhydryl oxidase 2	1	2.29%	190	206	16	R	LDPIQPSDVLSLLDNR	G	9.63%	7864	7864	599.3239136	3	1794.948266	1793.952325	0.995940635	R	G	-	1	16	1	0
Q7L576	Cytoplasmic FMR1-interacting protein 1	2	2.15%	300	317	17	K	QLQVVPLFGDMQIELAR	Y	0.87%	11681	11681	979.5368652	2	1957.05808	1956.050266	1.007814325	K	Y	-	4	17	1	0
				563	573	10	R	TMLESLIADK	S	0.35%	4678	4678	561.2989502	2	1120.58225	1119.584558	0.997691863	R	S	-	5	10	1	0
Q7RTW8	Otoancorin	1	0.78%	439	448	9	K	SQVIILSAK	Y	6.87%	5612	5612	479.8020325	2	957.5884149	957.5858778	0.002537013	K	Y	-	1	9	0	0
Q86UE4	Protein LYRIC	1	2.58%	246	261	15	K	NKGDSHLNVQVSNFK	S	1.27%	1520	1520	562.9558105	3	1685.843957	1686.832528	-0.988571903	K	S	N8:+0.984	2	15	-1	1
Q86UP2	Kinectin	1	0.66%	861	870	9	K	VQELQNLLK	G	7.38%	9726	9726	543.3111572	2	1084.606664	1084.612805	-0.006141011	K	G	Q2:+0.984	1	9	0	0
Q86WJ1	Chromodomain-helicase-DNA-binding protein 1-like	1	1.78%	3	19	16	R	AGATSRGGQAPGFLLR	L	2.07%	1337	1337	520.6123047	3	1558.813439	1558.82157	-0.008130761	R	L	Q9:+0.984	1	16	0	1
Q86YW5	Trem-like transcript 1 protein	1	5.47%	53	70	17	R	FLPEGCQPLVSSAVDRR	A	4.38%	2819	2819	645.3322754	3	1932.973351	1929.972615	3.0007365	R	A	C6:+57.021	1	17	3	1
Q8IXI1	Mitochondrial Rho GTPase 2	2	4.53%	179	191	12	K	QLRPACAQALTR	I	2.66%	930	930	462.2521057	3	1383.732842	1383.740035	-0.007193381	K	I	C6:+57.021	1	12	0	0
				214	230	16	K	SCFGHPLAPQALEDVK	T	0.24%	3456	3456	590.6287842	3	1768.862877	1767.860939	1.001938739	K	T	C2:+57.021	2	16	1	0
Q8IY63	Angiomotin-like protein 1	1	1.57%	576	591	15	R	HIEILDQALSNAQAR	V	2.53%	999	999	560.3008423	3	1677.879052	1677.879829	-0.000776849	R	V	-	1	15	0	0
Q8IZF6	Probable G-protein coupled receptor 112	1	0.23%	132	139	7	K	LELFLNK	E	1.74%	3774	3774	438.7606201	2	875.5055902	875.5116502	-0.006059998	K	E	-	1	7	0	0
Q8NGV7	Olfactory receptor 5H2	1	3.50%	300	311	11	K	QVIDSFTKMVK	R	0.24%	2522	2522	648.3342896	2	1294.652929	1294.695506	-0.04257697	K	R	-	5	11	0	1
Q8TCT9	Minor histocompatibility antigen H13	2	4.51%	234	251	17	K	SFEAPIKLVFPQDLLEK	G	8.59%	7618	7618	659.0496216	3	1974.12539	1974.071362	0.054027626	K	G	Q12:+0.984	2	17	0	1
				241	251	10	K	LVFPQDLLEK	G	0.24%	5823	5823	601.3423462	2	1200.669042	1200.675421	-0.006378993	K	G	-	5	10	0	0
Q8TDJ6	DmX-like protein 2	1	0.53%	3020	3036	16	R	VLPNAFNIPNRILDIL	-	8.97%	6281	6281	911.3997192	2	1820.783788	1822.035251	-1.251462739	R	-	N4:+0.984	2	16	-1	1
Q8TEW8	Partitioning defective 3 homolog B	1	0.58%	227	234	7	R	ILGLFIR	G	1.59%	7257	7257	416.63	2	831.2443499	830.5378053	0.70654464	R	G	-	1	7	1	0
Q8TF72	Protein Shroom3	1	0.50%	1882	1892	10	K	ILAGQHEDAR	E	4.98%	4478	4478	555.2876587	2	1108.559667	1108.562517	-0.002849385	K	E	-	2	10	0	0
Q8WTV0	Scavenger receptor class B member 1	2	4.35%	45	57	12	R	IDPSSLSFNMWK	E	0.24%	6172	6172	713.3475342	2	1424.679418	1423.680584	0.998834039	R	E	-	4	12	1	0
				288	300	12	K	ESGVFEGIPTYR	F	0.24%	3971	3971	677.8312378	2	1353.646826	1353.656477	-0.009651334	K	F	-	4	12	0	0
Q8WVM8	Sec1 family domain-containing protein 1	1	2.18%	381	395	14	K	LTSAVSSLPELLEK	K	0.24%	5469	5469	743.9165039	2	1485.817358	1485.829022	-0.011663987	K	K	-	5	14	0	0
Q8WWV6	High affinity immunoglobulin alpha and immunoglobulin mu Fc receptor	1	3.38%	510	528	18	K	MLQDDSLPAGASLTAPER	N	8.55%	4879	4879	936.4494629	2	1870.883276	1870.909475	-0.026199315	K	N	-	1	18	0	0
Q8WXG6	MAP kinase-activating death domain protein	1	0.55%	236	245	9	K	SSALLHDLR	E	1.71%	3957	3957	506.2809448	2	1010.54624	1010.550889	-0.004649744	K	E	-	2	9	0	0
Q8WXH0	Nesprin-2	2	0.41%	1758	1769	11	K	TQIGMTESLLK	A	2.19%	1426	1426	407.5547791	3	1219.640862	1219.648221	-0.007359386	K	A	-	1	11	0	0
				1838	1855	17	K	LLNDQCKNFNDWFSNIK	V	7.24%	9171	9171	720.010498	3	2157.008019	2157.967208	-0.959188739	K	V	N3:+0.984,C6:+57.021,N8	1	17	-1	1
Q92542	Nicastrin	2	3.24%	391	403	12	R	NQVEDLLATLEK	S	0.24%	7108	7108	686.8671875	2	1371.718725	1371.724557	-0.0058316	R	S	-	5	12	0	0
				485	496	11	K	ALADVATVLGR	A	0.77%	4157	4157	544.8190918	2	1087.622534	1084.624054	2.998479162	K	A	-	1	11	3	0
Q92888	Rho guanine nucleotide exchange factor 1	1	0.88%	684	692	8	R	LLLKSHSR	T	1.74%	18012	18012	477.302124	2	952.588598	952.5817955	0.006802495	R	T	-	5	8	0	1
Q92930	Ras-related protein Rab-8B	4	16.43%	10	21	11	K	LLLIGDSGVGK	T	0.24%	3662	3662	536.3224487	2	1070.629247	1070.633556	-0.004309035	K	T	-	5	11	0	0
				58	69	11	K	LQIWDTAGQER	F	9.71%	2789	2789	658.8314209	2	1315.647192	1315.65206	-0.004868419	K	F	-	2	11	0	0
				58	71	13	K	LQIWDTAGQERFR	T	2.26%	7572	7572	810.9127808	2	1619.809911	1619.805585	0.004326147	K	S	Q9:+0.984	2	13	0	1
				94	104	10	K	SFDNIKNWIR	N	8.32%	3658	3658	431.5582275	3	1291.651208	1291.667316	-0.016108719	K	N	-	1	10	0	1
Q92974	Rho guanine nucleotide exchange factor 2	1	1.52%	666	681	15	K	DLLVGPGVELLLTPR	E	0.24%	7963	7963	796.4732666	2	1590.930883	1590.93449	-0.003606781	K	E	-	5	15	0	0
Q969Z4	Tumor necrosis factor receptor superfamily member 19L	1	3.72%	129	145	16	R	RGVEVAAGASSGGETR	Q	9.71%	816	816	501.946228	3	1502.815209	1502.743729	0.071480066	R	Q	-	2	16	0	1
Q96CX2	BTB/POZ domain-containing protein KCTD12	2	6.77%	62	74	12	R	MFTQQQPQELAR	D	0.29%	1625	1625	738.8236084	2	1475.631567	1475.719095	-0.087528355	R	D	-	2	12	0	0
				273	283	10	K	FNFLEQAFDK	L	0.24%	6305	6305	629.8187866	2	1257.621923	1257.602985	0.018938578	K	L	-	3	10	0	0
Q96JY6	PDZ and LIM domain protein 2	1	2.56%	68	77	9	K	IRQSPSPLR	L	6.96%	7417	7417	528.8129883	2	1055.610326	1053.593073	2.017253555	K	L	Q3:+0.984	2	9	2	1
Q96PV0	Ras GTPase-activating protein SynGAP	1	1.86%	736	761	25	R	QSERPRPQPVVLRGPSAEMQGYMMR	D	2.29%	11950	11950	983.1708374	3	2946.489037	2948.405756	-1.916719033	R	D	Q8:+0.984,M19:+15.995,M	2	25	-1	1
Q96QU1	Protocadherin-15	1	0.51%	1572	1582	10	R	LWSQSVSLPR	R	1.19%	6132	6132	587.3361206	2	1172.656591	1171.634953	1.021637731	R	R	-	4	10	1	0
Q96RT1	Protein LAP2	1	1.13%	1358	1374	16	R	VQPEGPASKLLQPGDK	I	4.98%	1351	1351	555.6303101	3	1663.867455	1663.878082	-0.010626624	R	I	Q2:+0.984	1	16	0	1
Q96RW7	Hemicentin-1	1	0.25%	926	940	14	K	NSAMLLQNPYITVR	S	3.12%	5055	5055	819.4104004	2	1636.805151	1636.813109	-0.007958699	K	S	N1:+0.984,M4:+15.995,Q7	1	14	0	0
Q96SB3	Neurabin-2	1	1.23%	489	499	10	R	LELFPVELEK	D	7.52%	6063	6063	610.3341064	2	1218.652563	1215.675087	2.977475843	K	D	-	1	10	3	0
Q96T49	Protein phosphatase 1 regulatory inhibitor subunit 16B	1	2.65%	414	429	15	K	IPRGELDMPVENGLR	A	1.98%	4295	4295	571.6241455	3	1711.848961	1711.855387	-0.006425453	K	A	M8:+15.994,N12:+0.984	1	15	0	1
Q99541	Perilipin-2	1	3.66%	55	71	16	K	TITSVAMTSALPIIQK	L	0.52%	8491	8491	559.3434448	3	1675.006859	1673.927341	1.079518129	K	L	Q15:+0.984	3	16	1	0
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	13	84.67%	9	29	20	K	GLVAVITGGASGLGLATAER	L	0.24%	6664	6664	907.0103149	2	1812.00498	1812.010509	-0.005528781	K	L	-	6	20	0	0
				29	52	23	R	LVGQGASAVLLDLPNSGGEAQAK	K	0.24%	4975	4975	1098.087036	2	2194.158422	2194.159358	-0.00093579	R	K	-	4	23	0	0
				52	69	17	K	KLGNNCVFAPADVTSEK	D	0.24%	2420	2420	617.3066406	3	1848.896447	1848.903532	-0.007085133	K	D	C6:+57.021	4	17	0	1
				69	79	10	K	DVQTALALAK	G	0.30%	2631	2631	515.2984009	2	1028.581152	1028.586606	-0.005454498	K	G	-	3	10	0	0
				84	99	15	R	VDVAVNCAGIAVASK	T	0.24%	2704	2704	737.8885498	2	1473.76145	1472.765247	0.996202313	R	T	C7:+57.021	6	15	1	0
				116	130	14	R	VLDVNLMGTFNVIR	L	0.24%	11600	11600	797.4759521	2	1592.936254	1589.859946	3.076308425	R	L	-	2	14	3	0
				130	147	17	R	LVAGEMGQNEPDQGGQR	G	0.24%	773	773	893.9193726	2	1785.823095	1784.811158	1.011937205	R	G	-	4	17	1	0
				147	172	25	R	GVIINTASVAAFEGQVGQAAYSASK	G	0.24%	6671	6671	1220.130005	2	2438.24436	2438.24415	0.000209294	R	G	-	4	25	0	0
				172	184	12	K	GGIVGMTLPIAR	D	0.24%	4923	4923	592.8432617	2	1183.670873	1183.674711	-0.003837522	K	D	-	6	12	0	0
				184	192	8	R	DLAPIGIR	V	0.24%	2260	2260	427.7573547	2	853.4990594	853.5021481	-0.003088695	R	V	-	2	8	0	0
				192	212	20	R	VMTIAPGLFGTPLLTSLPEK	V	0.24%	8068	8068	695.7263184	3	2084.15548	2084.159148	-0.00366801	R	V	-	5	20	0	0
				212	226	14	K	VCNFLASQVPFPSR	L	0.24%	5102	5102	811.41	2	1620.80435	1620.807781	-0.003430832	K	L	C2:+57.021	5	14	0	0
				226	252	26	R	LGDPAEYAHLVQAIIENPFLNGEVIR	L	0.24%	9862	9862	720.883728	4	2879.503612	2878.486491	1.017121277	R	L	N17:+0.984	3	26	1	0
Q99805	Transmembrane 9 superfamily member 2	3	7.24%	90	104	14	K	RPSENLGQVLFGER	I	0.24%	4234	4234	534.6130981	3	1600.815819	1600.83215	-0.016330702	K	I	-	5	14	0	0
				172	187	15	R	FCNPGFPIGCYITDK	G	0.24%	5682	5682	894.9100952	2	1787.80454	1787.800184	0.004356454	R	G	C2:+57.021,C10:+57.021	5	15	0	0
				241	260	19	K	HTHIDKPDCSGPPMDISNK	A	0.29%	921	921	537.9989624	4	2147.964549	2147.972358	-0.007808359	K	A	C9:+57.021	1	19	0	0
Q99884	Sodium-dependent proline transporter	1	4.72%	530	560	30	R	FPPWAELLGILMGLLSCLMIPAGMLVAVLR	E	3.15%	12063	12063	1093.576172	3	3277.705041	3280.797157	-3.092116007	R	E	C17:+57.021	2	30	-1	0
Q9BQL6	Fermitin family homolog 1	1	2.81%	475	494	19	K	TMADSSYQPEVLNILSFLR	M	0.24%	12513	12513	1092.540283	2	2183.064916	2183.093253	-0.028336946	K	M	-	5	19	0	0
Q9BV40	Vesicle-associated membrane protein 8	2	24.00%	14	24	10	R	NLQSEVEGVK	N	7.85%	1306	1306	551.7884521	2	1101.561254	1101.566599	-0.005344847	R	N	-	1	10	0	0
				45	59	14	R	NKTEDLEATSEHFK	T	0.24%	1077	1077	550.2609863	3	1647.759484	1647.774026	-0.014542208	R	T	-	5	14	0	1
Q9BVG8	Kinesin-like protein KIFC3	1	1.44%	5	17	12	R	RTWNLGATPSLR	G	5.59%	4668	4668	687.3652344	2	1372.714819	1370.741878	1.97294043	R	G	-	2	12	2	1
Q9BX59	Tapasin-related protein	2	5.34%	31	43	12	R	AVDVVLDCFLAK	D	0.24%	6310	6310	675.3598022	2	1348.703954	1348.705607	-0.001652532	R	D	C8:+57.021	5	12	0	0
				251	264	13	K	GATLEPAQLGMAR	D	1.63%	2497	2497	658.34	2	1314.66435	1313.676168	0.988182384	K	D	-	3	13	1	0
Q9BXM0	Periaxin	1	1.16%	1229	1246	17	R	EAQAGEAATGEGGLRLK	L	0.33%	844	844	553.6266479	3	1657.856469	1657.827109	0.029359992	R	L	Q3:+0.984	3	17	0	1
Q9BYB0	SH3 and multiple ankyrin repeat domains protein 3	1	1.09%	1510	1529	19	R	SLGEEPVGGLGSLLDPAKK	S	0.45%	6493	6493	622.9711304	3	1865.889916	1866.00984	-0.119923935	R	S	-	3	19	0	1
Q9H2X9	Solute carrier family 12 member 5	1	1.40%	880	896	16	R	IFTVAQMDDNSIQMKK	D	8.95%	6819	6819	634.3502808	3	1900.027367	1899.907204	0.120163157	R	D	M7:+15.995,M14:+15.995	1	16	0	1
Q9H4D0	Calsyntenin-2	1	1.68%	542	558	16	K	EGLDINSLESLGQGIK	Y	3.73%	1932	1932	558.6239014	3	1672.848229	1672.851927	-0.00369757	K	Y	N6:+0.984	1	16	0	0
Q9H4M9	EH domain-containing protein 1	2	4.49%	13	26	13	K	EPELFQTVAEGLR	Q	1.23%	6196	6196	744.8916626	2	1487.767675	1487.762005	0.005670419	K	Q	-	2	13	0	0
				124	135	11	K	LNAFGNAFLNR	F	0.24%	4289	4289	618.8249512	2	1235.634252	1235.641101	-0.006849152	K	F	-	5	11	0	0
Q9HC29	Nucleotide-binding oligomerization domain-containing protein 2	1	1.35%	494	508	14	K	CHQELLLQEGGSPK	T	1.25%	2155	2155	530.9417725	3	1589.801842	1595.760875	-5.959032329	K	T	C1:+57.021,Q3:+0.984	2	14	-1	0
Q9HCL0	Protocadherin-18	1	0.97%	856	867	11	R	SYRYALQDMDK	F	8.18%	1151	1151	463.8875427	3	1388.639153	1388.639448	-0.000294634	R	F	-	1	11	0	1
Q9HDB9	HERV-K_3q12.3 provirus ancestral Gag polyprotein	1	2.70%	556	574	18	R	SCPVLNKQNIINQAITAK	N	0.94%	4929	4929	1007.507629	2	2012.999609	2013.055979	-0.056370091	R	N	C2:+57.021,Q8:+0.984,Q1	1	18	0	1
Q9HDC9	Adipocyte plasma membrane-associated protein	5	14.90%	8	29	21	R	QRRPLRPQVVTDDDGQAPEAK	D	8.47%	758	758	595.07	4	2376.2487	2376.214566	0.034133888	R	D	Q8:+0.984	2	21	0	1
				10	29	19	R	RPLRPQVVTDDDGQAPEAK	D	0.24%	739	739	698.3657837	3	2092.073876	2092.054877	0.01899877	R	D	Q6:+0.984	1	19	0	0
				120	134	14	R	VVKLENGEIETIAR	F	0.73%	2597	2597	524.302063	3	1569.882714	1570.856618	-0.973904067	R	F	N6:+0.984	3	14	-1	1
				141	156	15	K	TRDDEPVCGRPLGIR	A	0.24%	1238	1238	581.2963257	3	1740.865502	1739.873235	0.992267219	K	A	C8:+57.021	4	15	1	1
				183	195	12	K	LLLSSETPIEGK	N	0.24%	2585	2585	643.8677979	2	1285.719946	1285.712929	0.007016479	K	N	-	5	12	0	0
Q9NPB6	Partitioning defective 6 homolog alpha	1	2.31%	180	188	8	R	VAPQGLER	V	4.18%	5113	5113	435.2395935	2	868.4635369	869.4606616	-0.997124684	R	V	Q4:+0.984	3	8	-1	0
Q9NQC3	Reticulon-4	2	1.93%	201	210	9	R	SSAENMDLK	E	8.90%	1580	1580	505.83	2	1009.64435	1009.438708	0.205642192	R	E	M6:+15.995	2	9	0	0
				1157	1171	14	R	HQAQIDHYLGLANK	N	0.35%	2338	2338	536.6092529	3	1606.804284	1606.821585	-0.017301627	R	N	-	4	14	0	0
Q9NR16	Scavenger receptor cysteine-rich type 1 protein M160	1	0.83%	1170	1182	12	R	NITTAIAGIVCR	Q	9.91%	15475	15475	645.9609375	2	1289.906225	1287.696439	2.209785712	R	Q	C11:+57.021	1	12	2	0
Q9NR48	Probable histone-lysine N-methyltransferase ASH1L	1	0.44%	389	402	13	K	KIVASSAMGLVNK	D	2.66%	2400	2400	445.2527161	3	1332.734673	1332.742604	-0.007931175	K	D	M8:+15.994	1	13	0	1
Q9NRJ7	Protocadherin beta-16	1	1.68%	50	63	13	K	DLGLGLTEMSTRK	A	7.99%	7646	7646	711.3699951	2	1420.72434	1419.739162	0.985178298	K	A	-	2	13	1	1
Q9NRK6	ATP-binding cassette sub-family B member 10, mitochondrial	1	2.98%	617	639	22	R	NFPQGFNTVVGEKGVLLSGGQK	Q	8.42%	10403	10403	760.3865967	3	2278.136315	2278.148078	-0.011762905	R	Q	N1:+0.984,Q4:+0.984,Q21	1	22	0	1
Q9NS66	Probable G-protein coupled receptor 173	1	1.88%	206	213	7	K	LLLFEYR	H	2.20%	12035	12035	477.3031006	2	952.5905511	952.5381993	0.052351812	K	H	-	3	7	0	0
Q9NS67	Probable G-protein coupled receptor 27	1	5.60%	0	21	21	-	MANASEPGGSGGGEAAALGLK	L	8.68%	6489	6489	922.3894653	2	1842.763281	1843.873424	-1.11014324	-	L	-	3	21	-1	0
Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1	3	6.76%	424	433	9	K	GQHIKQLSR	F	3.06%	3726	3726	534.7935181	2	1067.571386	1065.604322	1.967064157	Q	F	-	1	9	2	1
				452	465	13	R	MVIITGPPEAQFK	A	0.24%	4221	4221	716.3862305	2	1430.756811	1429.76392	0.992890858	R	A	-	5	13	1	0
				508	525	17	K	TVNELQNLTAAEVVVPR	D	0.92%	4628	4628	928.4949341	2	1854.974218	1853.973423	1.00079486	K	D	Q6:+0.984,N7:+0.984	2	17	1	0
Q9P0L0	Vesicle-associated membrane protein-associated protein A	5	30.92%	10	24	14	K	HEQILVLDPPTDLK	F	0.24%	3949	3949	809.446228	2	1616.876806	1616.877369	-0.000562969	K	F	-	5	14	0	0
				26	38	12	K	GPFTDVVTTNLK	L	0.24%	3979	3979	646.3473511	2	1290.679052	1290.681963	-0.002911244	K	L	-	5	12	0	0
				94	114	20	K	FMVQTIFAPPNTSDMEAVWK	E	0.93%	11858	11858	1157.140991	2	2312.266332	2311.101711	1.16462175	K	E	-	1	20	1	0
				127	138	11	R	CVFEMPNENDK	L	2.89%	4242	4242	699.8720703	2	1397.728491	1397.558771	0.169719393	R	L	C1:+57.021,M5:+15.995	1	11	0	0
				154	174	20	K	QDGPMPKPHSVSLNDTETRK	L	0.89%	781	781	746.3709106	3	2236.089257	2236.090628	-0.001370738	K	L	-	3	20	0	1
Q9UBC2	Epidermal growth factor receptor substrate 15-like 1	1	1.85%	330	346	16	K	DQFALAMYFIQQKVSK	G	8.70%	7144	7144	645.659729	3	1933.955712	1933.949603	0.006108804	K	G	M7:+15.995,Q11:+0.984,C	1	16	0	1
Q9UBJ2	ATP-binding cassette sub-family D member 2	1	1.49%	0	11	11	-	MTHMLNAAADR	V	6.80%	4660	4660	416.52	3	1246.536525	1246.54251	-0.005984696	-	V	M4:+15.994,N6:+0.984	1	11	0	0
Q9UGI8	Testin	1	4.51%	355	374	19	K	NHAVVCQGCHNAIDPEVQR	V	0.24%	837	837	735.666687	3	2203.976586	2203.984174	-0.007588565	K	V	C6:+57.021,Q7:+0.984,C9	4	19	0	0
Q9UHG3	Prenylcysteine oxidase 1	1	2.18%	211	222	11	K	FLNEMIAPVMR	V	0.24%	5131	5131	661.3457642	2	1320.675878	1319.672997	1.00288076	K	V	-	4	11	1	0
Q9UI47	Catenin alpha-3	1	1.23%	831	842	11	K	IIRIQSPAGPR	H	4.98%	1135	1135	604.347168	2	1206.678686	1206.719686	-0.041000286	K	H	-	3	11	0	1
Q9UIW2	Plexin-A1	1	1.48%	156	184	28	K	EHYLSSVQEAGSMAGVLIAGPPGQGQAK	L	1.92%	7647	7647	928.8105469	3	2783.408166	2784.327577	-0.919411127	K	L	Q8:+0.984,Q24:+0.984,Q2	1	28	-1	0
Q9UJF2	Ras GTPase-activating protein nGAP	2	2.99%	241	260	19	K	DKNNYVGLVNIPTASVTGR	Q	0.62%	7211	7211	673.3604126	3	2017.057763	2017.05925	-0.001487135	K	Q	-	3	19	0	1
				822	837	15	K	LSGPSNSSMEDFTKR	S	9.44%	6248	6248	551.6459351	3	1651.91433	1654.762082	-2.847752224	K	S	-	2	15	-1	1
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	10	24.30%	43	56	13	R	YLNIFGESQPNPK	T	0.24%	4048	4048	754.380127	2	1506.744604	1505.75144	0.99316385	R	T	-	4	13	1	0

				164	174	10	K	QAFVQRDNAR	T	2.77%	1828	1828	402.2377319	3	1203.689721	1204.594864	-0.905143231	K	T	Q1:+0.984	1	10	-1	1
				292	310	18	R	IAPLEEGTLFFNLAEAQR	Q	0.24%	6237	6237	985.0239258	2	1968.032201	1968.031638	0.000563458	R	Q	-	4	18	0	0
				312	331	19	K	ASGDSARPVLLQVAESAYR	F	0.24%	5291	5291	664.0136719	3	1989.017541	1989.02795	-0.010409143	K	F	-	4	19	0	0
				331	353	22	R	FGLGSVAGAVGATAVYPIDLVK	T	0.24%	7857	7857	1053.083862	2	2104.152075	2104.156839	-0.004764135	R	T	-	6	22	0	0
				392	405	13	R	GLLPQLLGVAPEK	A	0.24%	6121	6121	668.406311	2	1334.796972	1333.796934	1.00003843	R	A	-	4	13	1	0
				408	416	8	K	LTVNIDFVR	D	0.24%	3144	3144	482.2950745	2	962.5744988	962.5185265	0.05597235	K	D	-	3	8	0	0
				455	467	12	R	LQVAGEITTGPR	V	0.24%	1785	1785	621.3439941	2	1240.672338	1240.677547	-0.005208407	R	V	-	5	12	0	0
				508	545	37	K	ASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIK	T	0.35%	9227	9227	1180.952759	3	3539.834801	3537.838884	1.995916967	K	T	-	4	37	2	0
				641	653	12	K	LAVATFAGIENK	F	0.24%	3738	3738	617.8477173	2	1233.679784	1232.676484	1.003300538	K	F	-	5	12	1	0
Q9UKF5	Disintegrin and metalloproteinase domain-containing protein 29	1	1.95%	804	820	16	R	QPQLMPSQSQPPVTPS	-	8.54%	2526	2526	581.3091431	3	1740.903954	1737.824418	3.079536039	R	-	M5:+15.995,Q8:+0.984	1	16	3	0
Q9UKU0	Long-chain-fatty-acid--CoA ligase 6	1	2.30%	340	356	16	R	VGFFQGDIRLLSDDMK	A	6.48%	4105	4105	929.4542847	2	1856.892919	1856.897917	-0.004998152	R	A	Q5:+0.984,M15:+15.995	1	16	0	1
Q9UKX5	Integrin alpha-11	1	1.18%	100	114	14	K	DNMRLGLSLATNPK	D	5.59%	991	991	515.9224854	3	1544.743981	1544.798159	-0.054178225	K	D	M3:+15.995	2	14	0	1
Q9ULD2	Microtubule-associated tumor suppressor 1	1	0.87%	866	877	11	K	NLFTALNAVEK	S	2.75%	6254	6254	610.336853	2	1218.658056	1218.660834	-0.002777897	K	S	-	1	11	0	0
Q9ULH4	Leucine-rich repeat and fibronectin type-III domain-containing protein 2	1	1.39%	58	69	11	R	LGGNFIIHISR	Q	8.95%	6877	6877	613.8405151	2	1225.66538	1225.693137	-0.027756823	R	Q	-	2	11	0	0
Q9UP52	Transferrin receptor protein 2	1	1.12%	171	180	9	G	MAALTQDIR	A	1.08%	1653	1653	510.2609253	2	1018.506201	1018.511712	-0.005511638	G	A	Q6:+0.984	1	9	0	0
Q9Y2M5	Kelch-like protein 20	1	1.48%	591	600	9	R	LGGIGVGVIK	M	9.53%	2112	2112	401.2426758	2	800.4697015	798.4963344	1.973367083	R	M	-	1	9	2	0
Q9Y490	Talin-1	10	6.93%	765	786	21	R	GVGAAATAVTQALNELLQHVK	A	0.83%	12643	12643	697.7255859	3	2090.153283	2090.148399	0.004883436	R	A	-	3	21	0	0
				957	971	14	K	AVAEQIPLLVQGVR	G	0.24%	5104	5104	747.44	2	1492.86435	1491.877309	0.987040648	K	G	-	5	14	1	0
				1025	1035	10	K	NLGTALAELR	T	1.51%	3770	3770	529.8031006	2	1057.590551	1056.592754	0.9977969	K	T	-	3	10	1	0
				1096	1122	26	K	AVSSAAKQLLGEVAQGNENYAGIAAR	D	0.57%	8408	8408	858.781189	3	2573.320092	2573.308526	0.011565671	K	D	N17:+0.984	3	26	0	0
				1136	1161	25	R	GVAALTSDPAVQAIVLDTASDVLDK	A	0.97%	11899	11899	1236.617554	2	2471.219457	2469.284997	1.934460646	R	A	Q12:+0.984	3	25	2	0
				1604	1618	14	K	TMLESAGGLIQTAR	A	0.24%	3808	3808	724.8867798	2	1447.757909	1446.750061	1.007848586	K	A	-	4	14	1	0
				1766	1780	14	K	TLAESALQLLYTAK	E	0.24%	7463	7463	761.9302368	2	1521.844824	1520.845006	0.999817425	K	E	-	6	14	1	0
				1917	1933	16	K	HRVDELGHGCAALVTK	A	0.24%	928	928	444.9900513	4	1775.928905	1774.925605	1.003300278	K	A	C10:+57.021	3	16	1	1
				2119	2130	11	K	VMVTNVTSLLK	T	0.24%	4720	4720	604.3019409	2	1206.588232	1203.689692	2.898539452	K	T	-	2	11	3	0
				2398	2423	25	R	MVAAATNNLCEAANAAVQGHASQEK	L	0.33%	3046	3046	852.7337036	3	2555.177636	2555.185205	-0.007568784	R	L	C10:+57.021	2	25	0	0
Q9Y5G0	Protocadherin gamma-B5	1	1.30%	171	183	12	K	LSLNFSFSLIIK	E	3.44%	7985	7985	667.3449097	2	1332.674169	1331.770035	0.904134744	K	E	N4:+0.984	1	12	1	0
Q9Y5S2	Serine/threonine-protein kinase MRCK beta	1	0.82%	775	789	14	K	LTAENEKLCSFVDK	L	9.36%	7900	7900	827.4078369	2	1652.800024	1652.807506	-0.007482348	K	L	C9:+57.021	1	14	0	1