ELECTROPHORESIS

Supporting Information
for Electrophoresis

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Proteomic analysis of detergent resistant membrane rafts

Supplementary table. A comprehensive list proteins identified from DRMR

	MH+	Charge	X_{corr}	ΔCn	Peptide	Peptide count	Acc. No.
14-3-3 protein beta/alpha							
	1189.6615	2	3.5664	0.3021	K.DSTLIMQLLR.D	1	P31946
26S proteasome non-ATPase regulatory subunit 2							
	2457.3645	2	2.4129	0.3859	R.AELATEEFLPVTPILEGFVILR.K	1	Q13200
3-hydroxyacyl-CoA dehydrogenase type II							
	2195.1672	2	2.3274	0.352	R.LVGQGASAVLLDLPNSGGEAQAK.K	1	Q99714
40S ribosomal protein S11							
	1266.6582	2	2.5133	0.2343	K.EAIEGTYIDKK.C	1	P04643
40S ribosomal protein S15 (RIG protein)							
	2053.0172	2	2.2108	0.3316	R.DMIILPEMVGSMVGVYNGK.T	1	P11174
	3168.6444	3	5.3801	0.5471	K.TFNQVEIKPEMIGHYLGEFSITYKPVK.H	1	P11174
40S ribosomal protein S15a							
	1700.8033	3	4.2831	0.4561	K.HGYIGEFEIIDDHR.A	1	P39027
40S ribosomal protein S16							
	1094.7189	2	2.5834	0.418	K.LLEPVLLLGK.E	1	P17008
40S ribosomal protein S17							
	2489.1935	2	4.7719	0.5976	R.DNYVPEVSALDQEIIEVDPDTK.E	1	P08708
40S ribosomal protein S18 (KE-3) (KE3)							
	1321.6752	2	2.6487	0.4483	K.YSQVLANGLDNK.L	1	P25232
	1060.558	2	2.2154	0.361	K.IPDWFLNR.Q	1	P25232
40S ribosomal protein S2 (S4) (LLREP3 protein)							
	1386.6945	2	2.9808	0.3981	K.TYSYLTPDLWK.E	1	P15880
	1551.8674	1	2.3705	0.3998	K.SLEEIYLFSLPIK.E	1	P15880
40S ribosomal protein S24 (S19)							
	1398.7422	2	2.4472	0.3579	K.TTPDVIFVFGFR.T	1	P16632

40S ribosomal protein S25							
	1318.7371	2	3.225	0.3684	R.DKLNNLVLFDK.A	1	P25111
40S ribosomal protein S3							
	1092.569	2	3.0709	0.452	K.AELNEFLTR.E	1	P23396
	1470.7692	2	3.0711	0.2517	K.DEILPTTPISEQK.G	1	P23396
	1029.6308	2	3.3255	0.2122	R.TEIIILATR.T	1	P23396
	1458.832	3	3.773	0.3897	K.KPLPDHVSIVEPK.D	2	P23396
40S ribosomal protein S30							
	1107.6203	2	2.2741	0.3114	R.FVNVVPTFGK.K	1	Q05472
40S ribosomal protein S4, X isoform (Single copy abundant mRNA protein) (SCR10)							
	1885.9257	2	2.7523	0.6076	R.TDITYPAGFMDVISIDK.T	1	P12750
40S ribosomal protein S5							
	2323.1458	2	3.1464	0.4346	K.WSTDDVQINDISLQDYIAVK.E	1	P46782
40S ribosomal protein S6 (Phosphoprotein NP33)							
	1620.758	2	4.3457	0.645	R.MATEVAADALGEEWK.G	1	P10660
40S ribosomal protein S7 (S8)							
	2367.2812	2	3.5746	0.3804	R.TLTAVHDAILEDLVFPSEIVGK.R	1	P23821
	1337.8561	2	3.141	0.3554	K.AIIIFVPVPQLK.S	1	P23821
40S ribosomal protein SA (P40) (34/67 kDa laminin receptor)							
	1698.8604	2	2.9934	0.5684	R.FTPGTFTNQIQAAFR.E	1	P08865
4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase)							
	1901.0649	2	2.2858	0.2352	K.QGKIVFVLSSALNPWNK.E	1	P32754
5'-nucleotidase (EC 3.1.3.5) (Ecto-5'-nucleotidase) (5'-NT) (CD73 antigen)							
	1934.021	2	3.2728	0.4836	K.VILPNFLANGGDGFQMIK.D	2	P21589
	1877.8881	2	3.9717	0.5116	R.HDSGDQDINVVSTYISK.M	1	P21589
	1606.8845	2	4.3431	0.6857	K.GPLASQISGLYLPYK.V	1	P21589
	1002.5988	2	2.7778	0.1113	K.FPILSANIK.A	1	P21589
	3003.4839	2	4.4913	0.571	K.ETPFLSNPGTNLVFEDEITALQPEVDK.L	3	P21589

60 kDa heat shock protein, mitochondrial							
	2482.402	2	6.4475	0.5858	R.TALLDAAGVASLLTTAEVVVTEIPK.E	2	P10809
	1344.7163	2	2.3746	0.3128	R.TVIIEQSWGSPK.V	1	P10809
	1504.7569	2	3.3812	0.4796	K.TLNDELEIIEGMK.F	1	P10809
	2560.2491	2	5.7248	0.5372	K.LVQDVANNTNEEAGDGTTTATVLAR.S	1	P10809
60S acidic ribosomal protein P0 (L10E)							
	1896.0006	2	3.9705	0.5456	R.VLALSVETDYTFPLAEK.V	1	P05388
60S acidic ribosomal protein P2							
	1868.9758	2	2.5775	0.3257	R.YVASYLLAALGGNSSPSAK.D	1	P05387
	1256.685	2	3.0978	0.5271	K.NIEDVIAQGIGK.L	1	P05387
60S ribosomal protein L17 (L23)							
	1778.9652	2	4.0082	0.5717	K.GLDVDSLVIEHIQVNK.A	1	P18621
	1623.8594	2	2.2625	0.3601	K.EQIVPKPEEEVAQK.K	1	P18621
60S ribosomal protein L18							
	1345.7327	2	3.3744	0.5287	K.TAVVVGTITDDVR.V	2	Q07020
60S ribosomal protein L19							
	1942.9259	2	3.8504	0.5248	K.VWLDPNETNEIANANSR.Q	1	P14118
60S ribosomal protein L27a							
	1111.6475	2	2.2368	0.426	K.TGAAPIIDVVR.S	1	P46776
	1232.6639	2	2.2115	0.267	K.LWTLVSEQTR.V	1	P46776
60S ribosomal protein L3 (HIV-1 TAR RNA binding protein B) (TARBP-B)							
	1696.8692	2	4.5241	0.6602	K.AHLMEIQVNGGTVAEK.L	1	P39023
78 kDa glucose-regulated protein (GRP 78) (Immunoglobulin heavy chain binding protein)							
	1397.7892	2	4.2019	0.463	K.ELEEIVQPIISK.L	1	P11021
	1836.9343	2	4.7886	0.5797	K.SQIFSTASDNQPTVTIK.V	2	P11021
	1659.8958	2	4.2746	0.5646	R.IINEPTAAAIAYGLDK.R	1	P11021
	1677.8084	2	4.5382	0.6529	K.NQLTSNPENTVFDAK.R	2	P11021
	1974.9085	2	3.273	0.5299	K.IEWLESHQDADIEDFK.A	1	P11021
Actin, aortic smooth muscle (Alpha-actin 2)							

	1198.5228	2	2.361	0.4326	K.DSYVGDEAQSK.R	1	P03996
	1171.5716	2	2.3614	0.2621	R.HQGVMVGMGQK.D	2	P03996
	1198.7061	2	2.3143	0.3696	R.AVFPSIVGRPR.H	1	P03996
	998.4869	1	2.4455	0.2668	R.DLTDYLMK.I	1	P03996
	1354.6239	2	2.4842	0.4896	K.DSYVGDEAQSKR.G	2	P03996
	1790.8925	1	2.5139	0.4239	K.SYELPDGQVITIGNER.F	3	P03996
	1960.9115	3	3.5405	0.2096	K.YPIEHGIITNWDDMEK.I	3	P03996
Actin, cytoplasmic 1 (Beta-actin)							
	1132.5275	2	2.9536	0.4971	R.GYSFTTTAER.E	11	P02570
	2215.0705	2	4.0675	0.5974	K.DLYANTVLSGGTTMYPGIADR.M	3	P02570
	1954.065	2	4.3759	0.616	R.VAPEEHPVLLTEAPLNPK.A	4	P02570
ADP,ATP carrier protein, fibroblast isoform							
	1219.6687	2	4.5955	0.558	K.DFLAGGVAAAISK.T	1	P05141
ADP-ribosyl cyclase 2 (EC 3.2.2.5) (Cyclic ADP-ribose hydrolase 2) (cADPr hydrolase 2) (Bone marrow stromal antigen 1)							
	1297.6615	2	2.6372	0.5422	R.FMPLSDVLYGR.V	1	Q10588
ADP-ribosylation factor 1							
	1630.7747	2	2.7911	0.4858	K.QDLPNAMNAAEITDK.L	1	P32889
	1087.6185	2	2.4165	0.4321	R.ILMVGLDAAGK.T	1	P32889
	2153.0416	2	2.5801	0.3502	R.HYFQNTQGLIFVVDSNDR.E	1	P32889
ADP-ribosylation factor 4							
	1103.6465	2	4.0053	0.4666	R.DAVLLLFANK.Q	1	P18085
ADP-ribosylation factor-like protein 1							
	1791.8839	2	2.612	0.4821	K.GTGLDEAMEWLVETLK.S	1	P40616
AHNAK-related protein (Fragment)							
	1156.6578	2	2.6785	0.3345	K.VKGDVDVSLPK.V	1	Q13727
	1695.8441	2	4.061	0.6036	K.VDIDVPDVNIEGPDAK.L	2	Q13727
Alpha enolase							
	1960.9252	2	4.5158	0.5426	K.DATNVGDEGGFAPNILENK.E	1	P06733

Annexin A2							
	1844.903	2	3.7941	0.5902	K.LSLEGDHSTPPSAYGSVK.A	1	P07355
	1908.8827	2	3.8369	0.5558	R.AEDGSVIDYELIDQDAR.D	1	P07355
	1244.6235	2	2.7429	0.2249	R.TNQELQEINR.V	1	P07355
	1650.9794	2	3.9558	0.599	K.SALSGHLETVILGLLK.T	2	P07355
Apoptosis regulator Bcl-X (BCL2-like 1 protein)							
	1703.7302	2	2.3611	0.4318	K.GYSWSQFSDVEENR.T	1	Q07817
Aquaporin-CHIP (Water channel protein for red blood cells and kidney proximal tubule)							
	1646.8138	2	3.3851	0.3887	K.YPVGNNQTAVQDNVK.V	4	P29972
	2312.0319	2	4.0661	0.6409	K.VWTSGQVEEYDLDADDINSR.V	7	P29972
	2501.406	2	2.9768	0.4433	R.AVVAEFLATTLFVFISIGSALGFK.Y	4	P29972
ASC-1 complex subunit P200 (DJ161I14.1) (RNA helicase) (Fragment)							
	1696.9651	2	2.2768	0.2672	K.VIDKRLWGWASPLR.Q	1	Q9H1I9
	2240.2688	2	2.5824	0.1692	R.RLEPLGIIVKELTGDMQLSK.S	1	Q9H1I9
ATP synthase alpha chain, mitochondrial (EC 3.6.3.14)							
	1624.891	2	3.5986	0.4426	R.TGAIVDVPVGEELLGR.V	1	P25705
ATP synthase beta chain, mitochondrial (EC 3.6.3.14)							
	3714.8867	3	3.3121	0.3377	K.GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR.A	1	P06576
ATP synthase gamma chain, mitochondrial (EC 3.6.3.14)							
	1096.6115	2	2.6524	0.3935	K.HLLIGVSSDR.G	1	P36542
ATP-binding cassette, sub-family D, member 3 (70 kDa peroxisomal membrane protein) (PMP70)							
	2542.486	2	3.1676	0.4614	K.GIEGVQVIPLIPGAGEIIIADNIIK.F	1	P28288
	1343.7476	2	3.2617	0.1021	R.VLGELWPLFGGR.L	1	P28288
	1074.6233	2	3.1305	0.3824	R.ITELMQVLK.D	1	P28288
	2094.9079	2	2.8316	0.5439	R.EGGWDSVQDWMDVLSGGEK.Q	1	P28288
BA382H24.3 (Multiple PDZ domain protein) (Fragment)							
	2321.1374	2	2.561	0.2952	K.LTIHAENPDSQAVPSAAGAASGEK.K	1	Q8WX31
Band 4.1-like protein 5							
	2298.1142	2	4.364	0.4947	R.DGNDYSLGLTPTGVLVFEGDTK.I	1	Q9HCM4

Basigin (Leukocyte activation antigen M6)							
	1784.8554	3	3.3865	0.361	R.KPEDVLDDDDAGSAPLK.S	1	P35613
B-cell receptor associated protein (D-prohibitin) (B-cell associated protein)							
	1723.9212	2	3.5559	0.5019	R.IPWFQYPIIYDIR.A	1	Q99623
	1177.6329	2	3.5482	0.4234	K.FNASQLITQR.A	1	Q99623
	1215.6221	2	2.2744	0.4165	K.IVQAEGEAEAAK.M	1	Q99623
	1853.9874	3	4.055	0.5013	R.IGGVQQDTILAEGLHFR.I	1	Q99623
B-cell receptor-associated protein 31 (BCR-associated protein Bap31)							
	2047.1439	3	3.313	0.372	R.LVTLISQQATLLASNEAFK.K	1	P51572
Beta-1,4-N-acetylgalactosaminyltransferase							
	1724.0144	2	2.2089	0.2958	K.LNMANTLINVIVPLAK.R	1	Q8IUF9
Bile salt export pump (ATP-binding cassette, sub-family B, member 11)							
	1847.949	2	4.7784	0.5379	K.ILLLDEATSALDTESEK.T	3	O95342
Biotinidase (EC 3.5.1.12)							
	2407.1795	2	2.213	0.1093	R.YQFNTNVVFSNNGTLVDRYR.K	1	P43251
Brain acid soluble protein 1							
	1966.9358	2	2.9624	0.315	K.AAEAAAAPAESAAPAAGEEPSK.E	1	P80723
	2636.2328	2	3.1647	0.2822	K.AAEAAAAPAESAAPAAGEEPSKEEGEPK.K	2	P80723
	2298.1366	3	3.3003	0.3835	K.AEPPKAPEQEQAAPGPAAGGEAPK.A	1	P80723
Bullous pemphigoid antigen 1, isoforms 6/9/10							
	1142.6534	2	2.2799	0.3015	K.TLEQALQLAR.R	1	O94833
C8ORF2 protein (Hypothetical protein)							
	2124.1851	2	5.1077	0.5633	K.LALQQDLTSMAPGLVIQAVR.V	1	O94905
	1142.504	2	2.6474	0.3898	R.NYELMESEK.T	2	O94905
	1649.8274	2	4.2053	0.4748	K.LSFGLEDEPLETATK.E	4	O94905
	1298.6051	2	2.5132	0.2976	R.RNYELMESEK.T	1	O94905
	1335.6697	2	2.5715	0.4079	K.IEEGHIGVYYR.G	1	O94905
	1306.7007	2	4.4342	0.5088	K.VAQVAEITYGQK.V	2	O94905

	1932.0846	2	3.0335	0.38	R.IEVVNFLVPNAVYDIVK.N	1	O94905
Calcium/calmodulin-dependent protein kinase type II delta chain							
	2155.0559	2	2.4937	0.4095	K.VTEQLIEAINNGDFEAYTK.I	1	Q13557
Calnexin (Major histocompatibility complex class I antigen-binding protein p88) (p90) (IP90)							
	1770.8339	2	3.6526	0.4521	K.APVPTGEVYFADSFDR.G	1	P27824
	2107.9824	2	3.9746	0.641	K.IPDPEAVKPDDWDEDAPAK.I	1	P27824
	1061.5995	2	2.7583	0.3808	R.GTLSGWILSK.A	1	P27824
Calreticulin (CRP55) (Calregulin) (HACBP) (ERp60)							
	3268.4963	2	2.2382	0.4224	K.SGTIFDNFLITNDEAYAEEFGNETWGVTK.A	1	P27797
Carboxypeptidase M (EC 3.4.17.12)							
	1055.6366	2	3.1834	0.3409	R.NLWVLVVGR.F	1	P14384
Casein kinase I, gamma 1 isoform (EC 2.7.1.-) (CKI-gamma 1)							
	1126.6009	2	2.2683	0.1535	R.APQLHLEYR.F	1	Q9HCP0
Casein kinase I, gamma 3 isoform (EC 2.7.1.-) (CKI-gamma 3)							
	1978.0358	2	2.8245	0.4063	K.QLPTPVGAVQQDPALSSNR.E	1	Q9Y6M4
Caveolin-1							
	2405.1301	2	3.8433	0.3766	K.IDFEDVIAEPEGTHSFDGIWK.A	1	Q03135
	1648.8335	2	2.7717	0.5272	K.YVDSEGHLYTVPIR.E	1	Q03135
CD109							
	1799.791	2	3.0261	0.4476	R.AEQEGGMQFWVSSESK.L	1	Q8TDJ3
CD44 antigen							
	1386.7534	2	3.6001	0.4507	R.YGFIEGHVVIPR.I	1	P16070
	1184.6098	2	2.3649	0.4301	K.SQEMVHLVNK.E	10	P16070
CDEP							
	1730.8237	2	2.3353	0.2423	K.SSSPAPEFLASSPPDNK.S	1	Q9Y4F1
Cell division control protein 2 homolog							
	1801.9237	2	2.7903	0.2033	K.KPLFHGDSEIDQLFR.I	1	P06493
Centaurin alpha 2							
	1251.6293	2	2.2997	0.1417	R.LTASTESGRSSR.-	1	Q9NPF8

CGI-28 protein						
	1871.0002	2	2.6528	0.1703	R.LDILHQVAMWQKNFK.R	1	Q9Y317
Clathrin heavy chain 1 (CLH-17)						
	2355.1469	2	3.4548	0.4836	K.SVNESLNNLFITEEDYQALR.T	1	Q00610
	1630.7866	2	2.4334	0.5083	K.FNALFAQGNYSEAAK.V	1	Q00610
	2464.2221	2	2.2764	0.4352	R.LAELEEFINGPNNAHIQQVGDR.C	1	Q00610
Cleft lip and palate associated transmembrane protein 1						
	2615.1426	2	2.6725	0.3713	K.SPWNFLGDELYEQSDEEQDSVK.V	1	Q9BSS5
Collagen alpha 1(VII) chain (Long-chain collagen) (LC collagen)						
	1216.7418	2	2.2649	0.2029	K.GQGVKLFAVGIK.N	1	Q02388
Collagen alpha 2(VI) chain						
	2382.2894	2	2.588	0.1274	R.EEGIRLFAVAPNQNLKEQGLR.D	1	P12110
Cortactin-binding protein 2 (Hypothetical protein KIAA1758)						
	2350.238	2	3.0048	0.1537	R.QPGFGQTTAKRHPSQGQQAVVK.A	1	Q8WZ74
Crumbs protein homolog 1						
	2227.1359	2	3.1617	0.2116	K.IDWNHITLENISSGSSLNVK.A	2	P82279
Cyclin fold protein 1 variant b						
	1857.9711	2	3.2027	0.5013	R.SLAEANNLSFPLEPLSR.E	2	Q8TEX2
	2210.1861	2	2.4494	0.5219	R.QFLELLQFNINVPSSVYAK.Y	1	Q8TEX2
Cysteine-rich protein 2 (CRP2) (ESP1 protein)						
	3210.6799	2	2.891	0.5798	K.GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAAR.A	1	P52943
Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial						
	1622.8318	1	2.4016	0.2805	K.LFQEDDEIPLYLK.G	2	P14406
DEAD-box protein 3 (Helicase-like protein 2) (HLP2) (DEAD-box, X isoform)						
	2083.0249	3	3.4155	0.4522	K.HVINFDLPSDIEEYVHR.I	1	O00571
	1882.9187	2	3.8363	0.2383	R.LEQELFSGGNTGINFEK.Y	1	O00571
Desmin						
	1115.5697	2	2.3313	0.1868	K.VELQELNDR.F	5	P17661
Desmoglein 2 (HDGC)						

	1850.0104	2	3.2548	0.5244	R.IVSLEPAYPPVFYLNK.D	1	Q14126
	1876.9227	2	2.494	0.3707	R.DMAGAQAAAVALNEEFLR.N	1	Q14126
	1097.6471	2	2.3435	0.2591	R.AWITAPVALR.E	1	Q14126
	920.5093	2	2.3811	0.297	R.FLDDLGLK.F	1	Q14126
Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits							
	2097.0657	2	2.875	0.4723	R.VLLDAGFTNELVQNYWSK.Q	1	P54289
	2076.0402	2	2.8014	0.5283	R.EEDPSLLWQVFGSATGLAR.Y	1	P54289
	2335.9631	2	2.5085	0.4086	K.EAGENWQENPETYEDSFYK.R	1	P54289
Dipeptidyl peptidase IV (T-cell activation antigen CD26)							
	1689.776	2	2.4514	0.2667	R.HSYTASYDIYDLNK.R	1	P27487
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit							
	1372.7324	2	4.0095	0.4053	R.SIVEEIEDLVAR.L	1	P04844
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit (EC 2.4.1.119) (Ribophorin I) (RPN-I)							
	1311.6221	2	2.3399	0.28	R.SEDLLDYGPFR.D	1	P04843
Dynamin 2 (EC 3.6.1.50)							
	1137.5845	2	2.2426	0.247	K.FFLSHPAYR.H	1	P50570
Dynein heavy chain, cytosolic (DYHC) (Cytoplasmic dynein heavy chain 1) (DHC1) (Fragment)							
	2598.3568	2	3.7852	0.5522	R.FGNPLLVQDVESYDPVLNPVLNR.E	2	Q14204
	2445.2951	2	3.1048	0.5046	R.ALPDMEVVGLNFSSATTPELLLK.T	1	Q14204
EIF4GII							
	1664.8204	2	2.2169	0.2559	K.ASETDALRSSASSLNR.F	1	O43432
Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu)							
	1314.7422	2	2.6482	0.4658	R.EHALLAYTLGVK.Q	1	P04720
	975.5515	2	2.2206	0.2644	R.LPLQDVYK.I	1	P04720
	1025.6108	2	2.2384	0.1474	K.IGGIGTVPVGR.V	1	P04720
Emerin							
	1922.7721	2	2.2802	0.3257	K.GYNDDYYEESYFTTR.T	1	P50402
Endoplasmin (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog) (Tumor rejection antigen 1)							

	1275.6432	2	2.6877	0.4293	R.ELISNASDALDK.I	1	P14625
Enhancer of polycomb							
	1942.0043	2	2.3062	0.2249	R.YCLTTLTVPQRCIGFAR.R	1	Q9H2F5
Enigma protein							
	1741.8833	2	2.2309	0.3744	R.TSIVQAAAGGVPGGGSNNGK.T	1	Q14250
ER lumen protein retaining receptor 2 (KDEL receptor 2) (ELP-1)							
	2232.1341	2	2.677	0.4827	K.TGEAETITTHYLFFLGLYR.A	1	P33947
Erythrocyte band 7 integral membrane protein (Stomatin) (Protein 7.2b)							
	2127.1888	2	4.0478	0.5189	K.NSTIVFPLPIDMLQGIIGAK.H	2	P27105
	2345.072	2	4.7047	0.6776	R.EEIAHNMQSTLDDATDAWGIK.V	2	P27105
	1929.9994	2	5.1581	0.688	R.VQNATLAVANITNADSATR.L	3	P27105
	1601.8791	2	2.6543	0.4316	R.TISFDIPPQEILTK.D	2	P27105
	1351.7473	2	3.7029	0.3748	R.YLQTLTTIAAEK.N	4	P27105
	1045.5642	2	3.0397	0.2858	K.NLSQILSDR.E	2	P27105
	1715.9002	2	3.9111	0.5022	K.EASMVITESPAALQLR.Y	2	P27105
	1247.6054	2	3.1452	0.2351	K.VIAAEGEMNASR.A	1	P27105
Eukaryotic translation initiation factor 2 alpha kinase 1							
	1785.9459	2	2.2852	0.1075	K.QLNLLSQDKGVRDDGK.D	1	Q9BQI3
Eukaryotic translation initiation factor 5A (eIF-5A) (eIF-4D) (Rev-binding factor)							
	2580.2946	2	3.1545	0.4686	R.NDFQLIGIQDGYLSLLQDSGEVR.E	1	P10159
Exostosin-like 2							
	2042.9686	2	3.4902	0.5374	R.YSNIMISQFGFPYANYK.R	1	Q9UBQ6
Fibroblast growth factor receptor BFR-2 (EC 2.7.1.112)							
	862.4787	2	2.5483	0.3982	K.IADFGLAR.D	1	Q01742
Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (ABP-280) (Nonmuscle filamin)							
	1763.8564	2	3.6708	0.5297	R.VANPSGNLTETYVQDR.G	1	P21333
Filamin, muscle isoform							
	1601.8175	2	2.5554	0.2701	R.SPFEVQVSPEAGVQK.V	1	Q9Y503

	2516.1694	3	3.9249	0.4228	R.DNGDGTHTVHYTPATDGPYTVAVK.Y	1	Q9Y503
Flotillin-1							
	1215.6949	2	4.119	0.3645	K.VTGEVLDILTR.L	1	O75955
	1753.9336	2	4.0521	0.7255	K.LPQVAEEISGPLTSANK.I	3	O75955
	2018.0307	3	5.0816	0.619	K.TEAEIAHIALETLEGHQR.A	3	O75955
	2211.1008	2	5.6863	0.6228	K.AEAFQLYQEAAQLDMLLEK.L	1	O75955
	1983.0473	1	2.244	0.2705	K.VASSDLVNMGISVVSYTLK.D	1	O75955
	1151.5697	2	3.6993	0.3834	K.AAYDIEVNTR.R	2	O75955
	1091.5486	2	3.8478	0.4769	R.GEAEAFAIGAR.A	3	O75955
	1468.7358	2	3.2583	0.5331	K.VSAQYLSEIEMAK.A	1	O75955
	1655.7665	3	3.6432	0.3397	K.DIHDDQDYLHSLGK.A	2	O75955
	1405.8167	3	3.8498	0.368	R.HGVPISVTGIAQVK.I	1	O75955
Flotillin-2 (Epidermal surface antigen) (ESA)							
	1145.5439	2	2.9104	0.3761	R.DADIGVAEAER.D	1	Q14254
	1640.8972	3	3.3435	0.2777	K.IRQEEIEIEVVQR.K	2	Q14254
	1934.0963	2	3.6735	0.5522	R.LLAELPASVHALTGVDLSK.I	5	Q14254
	1601.8063	2	3.0847	0.4312	K.DVYDKVDYLSSLGK.T	1	Q14254
	1251.7023	2	3.8196	0.516	R.MGIEILSFTIK.D	1	Q14254
	1735.923	1	2.0597	0.2736	R.SILGTLTVEQIYQDR.D	1	Q14254
	1269.7167	2	2.4827	0.1487	K.QIAVEAQEILR.T	2	Q14254
	1467.8609	2	3.6901	0.3797	K.MALVLEALPQIAAK.I	1	Q14254
	981.5257	2	2.3425	0.32	K.VDYLSSLGK.T	1	Q14254
	1378.7807	2	4.1446	0.5563	K.NVVLQTLEGHLR.S	2	Q14254
	1374.7117	2	4.9397	0.5559	K.VDEIVVLSGDNSK.V	1	Q14254
	1123.5635	2	3.0029	0.4715	K.SAFSEEVNIK.T	2	Q14254
	1388.7095	2	3.1034	0.559	K.IGEAEAAVIEAMGK.A	2	Q14254
	1199.6636	2	2.8591	0.255	K.QVLLAQAEAEK.I	3	Q14254
FOAP-2							

	1711.8325	2	2.3138	0.1351	R.AGSLCSPLDEPVSPPSR.A	1	Q8WYR1
Galectin-1 (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galaptin) (14 kDa lectin) (HPL) (HBL)							
	1784.8529	2	3.8239	0.5875	R.LNLEAINYMAADGDFK.I	1	P09382
	877.5147	2	2.5915	0.2145	K.SFVLNLGK.D	1	P09382
Gamma-glutamyltranspeptidase 1 (EC 2.3.2.2) (Gamma-glutamyltransferase 1) (CD224 antigen)							
	1919.9463	2	4.9324	0.5289	K.DIQAAGGIVTAEDLNNYR.A	1	P19440
Glial fibrillary acidic protein, astrocyte (GFAP)							
	1277.7105	2	2.9584	0.3708	K.LALDIEIATYR.K	3	P14136
Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (GAPDH)							
	1763.8029	2	4.1068	0.5755	K.LISWYDNEFGYSNR.V	1	P04406
Glycogen [starch] synthase, liver (EC 2.4.1.11)							
	1955.9941	2	2.3618	0.2047	R.EANDMLIFGSLTAWFLK.E	1	P54840
Glypican-4 (K-glypican)							
	1462.7906	2	4.7869	0.5435	R.TFAQGLAVAGDVVSK.V	1	O75487
	863.4878	2	2.2181	0.2	K.DLFVELK.R	1	O75487
	2332.1072	2	5.1004	0.4636	R.YYVVGNVNLEEMLNDFWAR.L	1	O75487
	1902.9523	2	2.5167	0.3353	R.LEGPFNIESVMDPIDVK.I	8	O75487
	3456.8127	3	5.9708	0.58	R.YLFAVTGNGLANQGNNPEVQVDTSKPDILILR.Q	1	O75487
	1730.8212	2	2.9924	0.4145	K.TYGHLYMQNSELFK.D	2	O75487
	1572.777	2	2.6258	0.4836	K.NDAPLHEINGDHLK.I	1	O75487
	960.4831	2	2.2342	0.1262	K.KFDEFFK.E	2	O75487
	2007.948	2	5.8408	0.5396	K.ISDAIMNMQDNSVQVSQK.V	3	O75487
Glypican-6							
	2292.0396	2	3.2519	0.4993	R.YYTGGNVNLEEMLNDFWAR.L	1	Q9Y625
Golgi apparatus protein 1 (Golgi sialoglycoprotein MG-160) (E-selectin ligand 1)							
	1363.6415	2	3.6789	0.4689	R.VEELEMTEDIR.L	1	Q92896
GTP-binding nuclear protein RAN (TC4) (Ran GTPase) (Androgen receptor-associated protein 24)							
	1294.6068	2	3.0902	0.3221	K.FNVWDTAGQEK.F	1	P17080

Guanine nucleotide-binding protein beta subunit-like protein 12.3 (P205) (Receptor of activated protein kinase C 1) (RACK1) (Receptor for activated C kinase)						
1309.6388	2	4.1416	0.5695	K.DVLSVAFSSDNR.Q	1	P25388
1059.5951	2	2.9277	0.4096	R.VWQVTIGTR.-	1	P25388
Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate cyclase-inhibiting G alpha protein)						
2365.2478	2	3.0932	0.4834	R.QLFVLAGAAEEGFMTAELAGVIK.R	1	P04898
2062.9358	2	5.5165	0.6325	R.EYQLNDSAAYYLNDLDR.I	2	P04898
Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate cyclase-inhibiting G alpha protein)						
1736.9621	2	5.1799	0.5739	R.AVVYSNTIQSIMAIVK.A	1	P04899
2076.9514	2	4.0608	0.6169	R.EYQLNDSAAYYLNDLER.I	1	P04899
1746.9026	1	2.4499	0.4892	R.IAQSDYIPTQQDVLR.T	2	P04899
1274.5905	2	3.2122	0.5538	K.YDEAASYIQSK.F	3	P04899
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-10 subunit						
1512.8175	2	3.3621	0.5511	K.DALLVGVPAGSNPFR.E	1	P50151
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-12 subunit						
1727.922	2	3.4751	0.5444	R.SDPLLIGIPTSENPFK.D	3	Q9UBI6
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-7 subunit						
1696.891	2	3.1057	0.511	R.NDPLLVGVPASENPFK.D	1	O60262
Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1 (Transducin beta chain 1)						
1353.7054	2	3.575	0.4072	K.LIIWDSYTTNK.V	1	P04901
1336.6108	2	2.7155	0.4926	K.IYAMHWGTDSR.L	2	P04901
Guanine nucleotide-binding protein G(k), alpha subunit (G(i) alpha-3)						
1707.9322	2	2.6367	0.3506	K.NVQFVFDAVTDVIIK.N	1	P08754
1761.9135	2	3.17	0.3015	R.ISQSNYIPTQQDVLR.T	2	P08754
2078.9307	2	4.7564	0.6008	R.EYQLNDSASYYLNDLDR.I	1	P08754
2359.2583	2	4.3715	0.5462	R.QLFVLAGSAEEGVMTPELAGVIK.R	1	P08754
Guanine nucleotide-binding protein G(O), alpha subunit 1						
1057.6257	2	2.462	0.2499	K.LLLLGAGESGK.S	1	P09471
2092.9827	2	2.3082	0.1663	R.EYQLNDSAKYYLDSLDR.I	1	P09471
1380.7163	2	3.1776	0.3921	K.TTGIVETHFTFK.N	1	P09471

Guanine nucleotide-binding protein G(O), alpha subunit 2							
	1597.863	2	5.0053	0.5463	K.WFTDTSIILFLNK.K	2	P29777
Guanine nucleotide-binding protein G(Y), alpha subunit (Alpha-11)							
	2237.1858	2	4.7237	0.4764	R.VPTTGIIEYPFDLENIIFR.M	1	P29992
	1087.6363	2	2.3959	0.2524	K.LLLLGTGESGK.S	1	P29992
Guanine nucleotide-binding protein, alpha-12 subunit (G alpha 12)							
	1057.6257	2	2.7594	0.2775	K.ILLLGAGESGK.S	4	Q03113
Heat shock 27 kDa protein (HSP 27) (Stress-responsive protein 27) (SRP27) (Estrogen-regulated 24 kDa protein)							
	3098.5608	2	4.3296	0.636	K.YTLPPGVDPTQVSSSLSPEGTLTVEAPMPK.L	1	P04792
	1163.6213	2	3.5863	0.463	R.LFDQAFGLPR.L	1	P04792
Heat shock 70 kDa protein 6 (Heat shock 70 kDa protein B')							
	1228.6286	2	2.4414	0.2986	R.VEILANDQGNR.T	2	P17066
Heat shock cognate 71 kDa protein							
	1303.5993	2	3.9319	0.4444	K.NSLESYAFNMK.A	1	P11142
	2260.1461	2	2.3815	0.463	K.SINPDEAVAYGAAVQAAILSGDK.S	2	P11142
	1481.8076	3	3.4006	0.4105	K.SQIHDIVLVGGSTR.I	1	P11142
	1199.6748	2	2.7171	0.2425	K.DAGTIAGLNVLR.I	1	P11142
	1649.7957	2	3.8102	0.5495	K.NQVAMNPTNTVFDAK.R	1	P11142
Heat shock protein HSP 90-alpha (HSP 86)							
	1242.7058	2	2.8182	0.3117	K.ADLINNLGTIAK.S	1	P07900
	1311.5705	2	2.2486	0.3765	K.EDQTEYLEER.R	1	P07900
	1348.665	2	2.2124	0.4322	K.HFSVEGQLEFR.A	1	P07900
Heat shock protein HSP 90-beta (HSP 84) (HSP 90)							
	2988.5319	3	4.4744	0.5972	K.DLVVLLFETALLSSGFSLEDPQTHSNR.I	1	P08238
Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2)							
	1081.5682	2	2.2851	0.2947	K.LLQDFFNGK.E	1	P54652
	1691.7261	2	2.6459	0.2264	K.STAGDTHLGGEDFDNR.M	2	P54652
Hepatitis B virus X interacting protein (HBX-interacting protein) (HBV X interacting protein)							
	2046.0112	2	2.8273	0.1923	K.NPSIVGVLCTDSQGLNLGCR.G	1	O43504

1995.0511	3	3.87	0.4056	R.GTLSDEHAGVISVLAQQAAK.L	4	O43504
Hepatocellular carcinoma-associated antigen 90 (BA243J16.2.2) (Targeting protein for XKLP2 involved in spindle formation (TPX2,						
2079.0293	2	2.3419	0.2457	K.KDDIKTGSCSVTQAGVQWR.D	1	Q96RR5
Heterogeneous nuclear ribonucleoprotein F (hnRNP F)						
1996.9769	2	2.9459	0.4664	K.ATENDIYNFFSPLNPVR.V	2	P52597
1867.9442	2	2.8839	0.5021	K.ITGEAFVQFASQELAEK.A	1	P52597
Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (DC-stretch binding protein) (CSBP)						
2589.3888	2	3.4744	0.6064	R.IITITGTQDQIQNAQYLLQNSVK.Q	1	Q07244
Heterogeneous nuclear ribonucleoprotein L (hnRNP L)						
2890.2628	3	4.4103	0.5593	K.NDQDTWDYTNPNLSGQGDPGSNPNKR.Q	1	P14866
Heterogeneous nuclear ribonucleoprotein M (hnRNP M)						
2178.051	2	2.8433	0.2348	K.GIGMGNIGPAGMGMEGIGFGINK.M	1	P52272
Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)						
2495.0401	2	3.3368	0.5863	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGR.G	1	P22626
2189.9059	2	2.9597	0.6301	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S	1	P22626
High-affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A (EC 3.1.4.17)						
1604.6968	2	2.6179	0.4461	R.ISEEYFSQTDEEK.Q	1	O60658
Histone H1.1						
1107.5686	2	2.6564	0.3463	K.ALAAAGYDVEK.N	2	Q02539
Histone H1.2 (Histone H1d)						
845.5096	2	2.5192	0.1625	R.SGVSLAALK.K	1	P16403
Histone H2A.a (H2A/a) (H2A.2)						
2915.5882	3	4.6085	0.6287	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	1	P28001
1931.1694	2	3.684	0.599	R.VTIAQGGVLPNIQAVLLPK.K	3	P28001
Histone H2A.x (H2a/x)						
2271.3804	2	2.2791	0.3459	K.LLGGVTIAQGGVLPNIQAVLLPK.K	1	P16104
Histone H2A.z (H2A/z)						
1315.7235	2	2.3697	0.2119	R.SQRAGLQFPVGR.I	1	P17317

Histone H4							
	1310.703	2	2.9448	0.4322	K.TVTAMDVVYALK.R	1	P02304
	989.5784	2	2.8106	0.2174	K.VFLENVIR.D	1	P02304
HLA class I histocompatibility antigen, alpha chain F (HLA F antigen) (Leukocyte antigen F) (CDA12)							
	2651.2073	3	4.2073	0.4689	R.DGEEQTQDTELVETRPAGDGTFQK.W	1	P30511
HLA class I histocompatibility antigen, CW-1 CW*0101 alpha chain (CW1.1)							
	1761.7873	2	2.4944	0.5155	R.APWVEQEGPEYWDR.E	1	P30499
HSPC121							
	1346.7221	2	2.3224	0.3818	K.RPLFLAPDFDR.W	1	Q9P035
Hypothetical protein							
	1460.7419	2	2.3	0.1539	K.GSVEEIMSQPKQK.E	1	Q8N3L0
Hypothetical protein							
	1800.9384	1	2.2266	0.1573	R.FLLPGLEEELEEAVGR.I	1	Q96C12
Hypothetical protein							
	2351.2683	2	2.3695	0.147	R.TGSQPLRVIAHDTGTSLDQVKK.A	1	Q9BT08
Hypothetical protein							
	1660.887	2	2.6388	0.1997	K.EETKEAGSLRSVLNK.E	1	Q9BVH6
Hypothetical protein							
	1832.8779	2	4.073	0.4648	R.DDGVFVQEVTQNSPAAR.T	1	Q9BVU3
Hypothetical protein							
	1086.5544	2	2.2506	0.278	R.NLALDEAGQR.S	3	Q9H0Q8
	1304.6083	2	3.5718	0.5037	K.SDSELNNEVAAR.K	10	Q9H0Q8
Hypothetical protein							
	2668.1619	2	3.2538	0.5905	K.TASNIIDVSAADSQGMEQHEYMDR.A	1	Q9NWT0
	1388.7637	2	3.3937	0.4035	R.TDEQALLSSILAK.T	7	Q9NWT0
	1696.8407	1	2.0581	0.3157	K.ALNGAEPNYHSLPSAR.T	1	Q9NWT0
	1167.6625	2	3.015	0.2076	K.LLLDPSSPPTK.A	1	Q9NWT0
	1295.7575	2	3.1647	0.3121	R.KLLLDPSSPPTK.A	1	Q9NWT0

	1341.7531	2	3.1034	0.3485	R.LAVLSSSLTHWK.K	2	Q9NWT0
Hypothetical protein (Fragment)							
	1037.5672	2	2.2404	0.4128	K.ILFEQQIF.-	1	O60648
Hypothetical protein (Fragment)							
	1305.6691	2	2.7771	0.5113	K.EQADFALEALAK.A	1	Q8WV23
Hypothetical protein (GPRC5B protein) (Orphan G-protein coupled receptor) (G protein-coupled receptor, family C, group 1, member B)							
	2894.4471	3	4.6041	0.6081	R.SNVYQPTEMAVVLNGGTIPTAPPSHTGR.H	1	O75205
	1361.6272	2	2.8264	0.3029	K.AFSMDEHNAALR.T	1	O75205
Hypothetical protein (Putative alpha mannosyltransferase)							
	1829.0471	2	2.2021	0.2317	R.GLGCSLLFIPLGLVDRR.T	1	Q9BV10
Hypothetical protein FLJ10579							
	2405.2816	2	2.3315	0.4561	K.TATALLESPLSATVEDALQSFLK.A	1	Q9NVQ6
Hypothetical protein FLJ10737							
	2349.0411	2	3.7309	0.4437	R.YDEEYEDVSGSSFPQIEINK.M	1	Q9NVH1
	2091.0551	2	4.6112	0.452	K.GWGELEFGAGDLQGPLFGLK.L	1	Q9NVH1
Hypothetical protein FLJ13222 (Testis expressed sequence 27)							
	1563.7615	1	2.2131	0.2348	R.LLENTERSEETSR.S	1	Q9H8U3
Hypothetical protein FLJ13885							
	2499.2554	2	2.4949	0.2161	R.QENPSPFNSPTLSACLIISDLPR.K	1	Q9H881
Hypothetical protein FLJ13940							
	1410.7745	2	2.8237	0.4146	R.QIFHPEQLITGK.E	1	Q9H853
Hypothetical protein FLJ14827 (Hypothetical protein NT2RP1001002)							
	1294.7272	2	2.3443	0.3073	R.GGATQKPKPPWK.-	1	Q96K30
Hypothetical protein FLJ14971 (Hypothetical protein FLJ14851)							
	1340.5911	2	2.828	0.4779	R.GDFFYHSENPK.Y	3	Q9BTV4
Hypothetical protein FLJ20084							
	2184.228	2	2.3977	0.3307	K.KQAAPVTLQLLFLDGEEALK.E	1	Q9NXS2
Hypothetical protein FLJ20673							
	1344.6647	2	2.3432	0.1591	K.LLDENENLQEK.E	1	Q9NWQ8

Hypothetical protein FLJ22125							
	2331.0186	2	2.4884	0.2309	-.MEEYEESGLLETDEATLDTR.K	1	Q9H6L9
Hypothetical protein FLJ23660							
	1749.9023	2	3.6248	0.5506	R.AQQLIQTYELNETAK.Q	1	Q8TEC1
Hypothetical protein FLJ25012							
	1905.8902	2	2.2151	0.1828	K.APSEGESSGNSNAGSSALKR.K	1	Q96LW0
Hypothetical protein FLJ25091							
	1552.7794	1	1.9612	0.1216	K.EAFAAALKANNSMSK.K	1	Q96LT0
Hypothetical protein FLJ25359							
	2334.2103	2	2.3865	0.1703	R.WRLPKQPFSGDLLSLSQMCK.A	1	Q96LN0
Hypothetical protein FLJ31413							
	1767.8423	2	2.2687	0.1275	K.HPAAPPGGRPFTCATCGK.S	1	Q96N48
Hypothetical protein FLJ31641							
	1687.8941	2	2.263	0.3232	R.LSLDLLSQMSPGDLAK.V	1	Q96MZ7
Hypothetical protein FLJ31890 (Zinc finger protein 25)							
	2355.075	2	2.3763	0.1578	R.KHTGEKPYECQECGETFIQK.S	2	Q96MU2
Hypothetical protein FLJ32603							
	1901.8841	2	2.6718	0.3558	R.ESQENLGNPSKNEDNVK.S	6	Q96MC7
Hypothetical protein FLJ32752							
	1317.7605	2	2.6094	0.1249	R.LLTMLLFQNPK.R	1	Q96M86
Hypothetical protein FLJ33834							
	1917.9194	3	3.601	0.3145	K.GPHVDVSGPDIDIEGPEGK.L	1	Q8N274
	1667.8128	2	3.7418	0.5487	K.VDIEGPDVNIEGPEGK.L	1	Q8N274
Hypothetical protein FLJ38043							
	1598.7922	1	1.9357	0.1115	K.DYIKMMLQNDSLK.F	1	Q8N1P4
Hypothetical protein FLJ38708 (Vacuolar H+ ATPase d2 subunit)							
	1640.89	1	3.0511	0.4457	R.AFIITLNSFGTELSK.E	1	Q8N8Y2
Hypothetical protein KIAA0143 (Fragment)							
	1579.9787	2	6.1681	0.7053	R.AGIIQVLLEAVAIAAK.G	1	Q14156

	1289.7292	2	2.5289	0.4368	K.IVPSLLFNMQK.I	1	Q14156
	1225.6469	2	2.697	0.3442	K.LTFYAVSAPEK.L	1	Q14156
	1355.6418	2	2.8561	0.2346	R.ATIWEPQHMDK.I	1	Q14156
Hypothetical protein KIAA0321 (Fragment)							
	2329.1564	2	2.3427	0.1558	K.ADEVEWILDLKEEENELVR.S	1	O15035
Hypothetical protein KIAA0666 (Fragment)							
	2429.2029	2	3.022	0.5342	K.IQPDEFFGIFDQFLQAVSEAK.Q	1	Q9Y4D1
Hypothetical protein KIAA0912 (Fragment)							
	1960.8823	2	3.0201	0.1354	R.QMVQDFDHDKQEAVDR.C	1	O94986
Hypothetical protein KIAA1079							
	2645.1976	2	2.4869	0.4045	K.ELGPCGGEACGPDLSGPAPASGSPYLSR.C	1	Q9UPS3
	1339.6858	2	3.0895	0.4833	K.EHINDLQTELK.N	1	Q9UPS3
	2950.4872	3	4.1537	0.525	K.IFDLMELNGVQADFKPATLSSSLDNPK.E	1	Q9UPS3
Hypothetical protein KIAA1250 (Fragment)							
	3096.4133	3	3.8258	0.5325	K.RGDVIDYSSSGVSTNDASPLDPITEEDEK.S	1	Q9ULH0
Hypothetical protein KIAA1265 (Fragment)							
	2027.9773	2	2.5867	0.4645	R.LNETELTDLEGQQESPPK.N	1	Q9ULF5
Hypothetical protein KIAA1568 (Fragment)							
	2359.1993	2	2.2105	0.1502	R.NEVVITENNNSITEQITDVVK.Q	1	Q9HCK4
Hypothetical protein KIAA1591 (Fragment)							
	1978.0497	2	2.4114	0.1376	K.LFTESTGVLALEDKELGR.V	1	Q9HCI1
Hypothetical protein KIAA1983 (Fragment)							
	2243.24	2	3.0638	0.3097	K.QKIALLPNNAADLGKYITGDK.V	1	Q8TF19
Integral membrane protein 2B (Transmembrane protein BRI) [Contains: ABri/ADan amyloid peptide]							
	1182.7462	2	2.9601	0.2434	R.NLLELLINIK.A	1	Q9Y287
Integrin beta-2 (Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 beta-subunit) (CD18)							
	2202.9072	2	2.5728	0.2225	R.DSEGCWVAYTLEQQDGMDR.Y	1	P05107
Intestinal membrane A4 protein (Differentiation-dependent protein A4) (Proteolipid protein 2)							
	1248.5861	2	3.033	0.4651	R.HTAAPTDPADGPV.-	1	Q04941

INVERSIN protein						
1898.9738	2	2.2532	0.1927	R.RAGASLPPHDSHWKPSR.R	1	Q9Y283
Junction plakoglobin (Desmoplakin III)						
2347.3026	3	4.1779	0.6342	R.LNTIPLFVQLLYSSVENIQR.V	1	P14923
KE04p (Similar to Caenorhabditis elegans protein C42C1.9)						
1348.696	2	2.5737	0.3648	R.SVQTTLQTDEVK.N	3	O75477
1611.8892	1	2.2704	0.3497	K.DLNLMAPGLTIQAVR.V	1	O75477
1334.6956	2	2.2951	0.2647	R.ISEIEDAAFLAR.E	3	O75477
Keratin, type I cuticular HA6 (Hair keratin, type I HA6)						
1278.6806	2	2.5951	0.2749	K.ARLEGEIATYR.H	2	O76013
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)						
1165.5853	2	2.4746	0.224	R.LENEIQTYR.S	5	P13645
1707.7727	2	5.3663	0.6973	K.GSLGGGFSSGGFSGGSFSR.G	4	P13645
1390.6814	2	3.6974	0.5856	K.QSLEASLAETEGR.Y	2	P13645
2096.0473	2	2.7673	0.5365	K.ADLEMQIESLTEELAYLK.K	1	P13645
1381.6487	2	4.0784	0.5638	R.ALEESNYELEGK.I	9	P13645
1031.5989	2	2.953	0.46	R.VLDELTLTK.A	1	P13645
1109.4904	2	2.904	0.4445	K.DAEAWFNEK.S	2	P13645
1234.6796	2	2.8646	0.1239	R.LKYENEVALR.Q	1	P13645
2367.2632	2	5.3529	0.6601	K.NQILNLTTDNANILLQIDNAR.L	1	P13645
1996.9715	2	4.5145	0.5647	K.ELTTEIDNNIEQISSYK.S	8	P13645
1262.5977	2	2.7271	0.4537	R.SLLEGEGSSGGGGR.G	2	P13645
2224.1423	2	3.0752	0.4938	K.ADLEMQIESLTEELAYLKK.N	1	P13645
1365.6399	2	3.0311	0.225	R.SQYEQLAEQNR.K	1	P13645
1797.0122	2	2.555	0.3753	R.NVQALEIELQSQLALK.Q	4	P13645
1237.5853	2	2.5702	0.2782	R.KDAEAWFNEK.S	1	P13645
Keratin, type I cytoskeletal 13 (Cytokeratin 13) (K13) (CK 13)						
1122.5795	2	2.6457	0.3095	R.LEQEIATYR.S	3	P13646

1301.6589	2	3.9009	0.4875	R.ALEEANADLEVK.I	4	P13646
Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)						
1892.9462	2	2.5153	0.3098	R.TMQNLEIELQSQLSMK.A	1	P02533
1242.5537	2	2.6543	0.4812	K.NHEEEMNALR.G	1	P02533
1361.6913	2	2.5022	0.4611	R.EVATNSELVQSGK.S	1	P02533
2085.9875	2	5.2495	0.6505	R.GQVGGDVNVEMDAAPGVDLSR.I	1	P02533
1029.5944	2	3.6917	0.4311	R.VLDELTLAR.A	1	P02533
1220.601	2	2.6867	0.456	K.ASLENSLEETK.G	3	P02533
Keratin, type I cytoskeletal 16 (Cytokeratin 16) (K16) (CK 16)						
1096.5315	2	2.9974	0.4192	R.DAETWFLSK.T	1	P08779
2064.1453	2	5.3815	0.6869	K.IIAATIENAQPILQIDNAR.L	1	P08779
2087.9668	2	4.5567	0.6061	R.GQTGGDVNVEMDAAPGVDLSR.I	2	P08779
Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)						
1345.6851	2	2.2261	0.3407	R.ALEEANTELEVK.I	1	Q04695
Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18)						
1041.6057	2	2.2355	0.3993	R.IVLQIDNAR.L	1	P05783
2670.3925	3	3.9576	0.4133	R.YALQMEQLNGILLHLESELAQTR.A	3	P05783
1319.6708	2	3.4373	0.4864	R.AQIFANTVDNAR.I	1	P05783
Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)						
1060.5639	2	2.4295	0.3137	K.TLLDIDNTR.M	1	P35527
1837.966	2	6.3086	0.6	R.HGVQELEIELQSQLSK.K	9	P35527
1157.5915	2	2.8059	0.3841	R.QGVDADINGLR.Q	2	P35527
1190.6091	2	2.7982	0.1038	R.QVLDNLTMEK.S	1	P35527
1307.6782	2	2.4757	0.356	R.IKFEMEQNLR.Q	1	P35527
1586.7662	2	5.3977	0.4654	K.VQALEEANNDLENK.I	1	P35527
2510.1323	3	5.4882	0.4959	K.EIETYHNLLEGGQEDFESSGAGK.I	4	P35527
2895.3907	3	4.0103	0.2963	K.NHKEEMSQLTGQNSGDVNVEINVAPGK.D	2	P35527
1066.4992	2	2.345	0.2964	K.FEMEQNLR.Q	1	P35527

	2705.1617	2	2.3712	0.4234	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	4	P35527
	3223.2821	3	5.003	0.6618	R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	3	P35527
	2299.1202	3	3.9061	0.5053	K.SDLEMQYETLQEELMALKK.N	2	P35527
	3392.6094	3	3.5184	0.4125	R.KDIENQYETQITQIEHEVSSSGQEVQSSAK.E	1	P35527
	1605.7437	2	3.0568	0.4728	K.NYSPYYNTIDDLK.D	1	P35527
	2902.4111	3	3.7949	0.5661	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2	P35527
	897.414	2	2.2312	0.4544	R.MTLDDFR.I	1	P35527
	1315.6858	2	3.8776	0.3796	K.DQIVDLTVGNNK.T	1	P35527
	2171.0252	2	4.2528	0.5366	K.SDLEMQYETLQEELMALK.K	1	P35527
	3264.5144	3	6.0711	0.5403	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	2	P35527
Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protein)							
	1308.6548	2	2.6174	0.37	R.NKYEDEINKR.T	2	P04264
	1125.5428	2	2.3548	0.3897	K.AEAESLYQSK.Y	2	P04264
	1657.7934	1	2.0386	0.1857	R.SGGGFSSGSAGIINYQR.R	2	P04264
	1340.6698	2	4.0149	0.5668	K.SKAEAESLYQSK.Y	3	P04264
	1302.7157	2	4.5716	0.4063	R.SLDLDSIIAEVK.A	3	P04264
	1300.5302	2	3.8207	0.4449	K.NMQDMVEDYR.N	2	P04264
	2508.1459	2	2.7137	0.48	R.MSGECAPNVSVSVSTSHTTISGGGSR.G	1	P04264
	1357.6963	2	4.4349	0.3644	K.LNDLEDALQQAK.E	3	P04264
	1277.7105	2	2.4797	0.3849	K.LALDLEIATYR.T	2	P04264
	1383.6909	2	4.262	0.4211	K.SLNNQFASFIDK.V	4	P04264
	1716.8517	2	4.5917	0.6487	K.QISNLQQSISDAEQR.G	1	P04264
	1599.8342	3	4.2024	0.3882	K.NKLNDLEDALQQAK.E	2	P04264
	1393.7327	2	3.2164	0.3085	R.TNAENEFVTIKK.D	5	P04264
	1033.5166	2	2.2487	0.2969	R.TLLEGEESR.M	1	P04264
	1993.9772	3	4.4515	0.2533	R.THNLEPYFESFINNLR.R	8	P04264
	1475.7494	2	4.0427	0.5623	K.WELLQQVDTSTR.T	2	P04264
	1141.52	2	3.0494	0.3398	R.DYQELMNTK.L	2	P04264

	1265.6378	2	3.3797	0.5102	R.TNAENEFVTIK.K	3	P04264
	1179.601	2	3.4259	0.4617	K.YEELQITAGR.H	4	P04264
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)							
	3048.4948	2	4.6081	0.624	K.VLYDAEISQIHQSVTDTNVILSMDNSR.N	2	P35908
	1391.6807	2	2.8066	0.2479	R.SKEEAEALYHSK.Y	1	P35908
	4092.0732	3	5.0771	0.6635	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	1	P35908
	973.5318	2	2.7373	0.1944	K.IEISELNR.V	2	P35908
	1320.5834	2	3.317	0.6013	R.HGGGGGGFGGGGFGSR.S	1	P35908
	1193.6166	2	3.9504	0.4548	K.YEELQVTVGR.H	1	P35908
	1329.7266	1	2.6251	0.3642	R.NLDLDSIIAEVK.A	4	P35908
	1838.9149	2	4.7726	0.6814	K.SISISVAGGGGGFGAAGGFGGR.G	2	P35908
	1371.712	2	3.7196	0.35	K.LNDLEEALQQAK.E	2	P35908
	1613.8499	2	4.406	0.3623	R.NKLNDLEEALQQAK.E	1	P35908
	1329.6399	2	4.138	0.3472	K.NVQDAIADAEQR.G	2	P35908
Keratin, type II cytoskeletal 2 oral (Cytokeratin 2P) (K2P) (CK 2P)							
	1476.8062	2	4.4737	0.4369	R.FLEQQNKVLETK.W	1	Q01546
Keratin, type II cytoskeletal 5 (Cytokeratin 5) (K5) (CK 5) (58 kDa cytokeratin)							
	1203.6374	2	2.5383	0.2718	K.WTLLQEQGTK.T	1	P13647
	1890.9714	2	3.096	0.5409	R.QNLEPLFEQYINNLR.R	3	P13647
	1143.6261	2	3.4116	0.2643	K.LAELEEALQK.A	1	P13647
Keratin, type II cytoskeletal 6A (Cytokeratin 6A) (CK 6A) (K6A keratin)							
	1212.5537	2	3.1242	0.3026	R.AEAESWYQTK.Y	2	P02538
Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)							
	2109.0134	2	4.7203	0.6239	R.ELQSQISDTSVVLSMDNSR.S	1	P05787
	1344.6759	2	3.9315	0.3787	R.ASLEAAIADAEQR.G	1	P05787
	1419.7484	2	3.9263	0.5596	R.LEGLTDEINFLR.Q	1	P05787
	1129.6217	2	3.908	0.3115	K.LSELEAALQR.A	1	P05787
	1320.6721	2	3.9099	0.4941	R.SLDMDSIIAEVK.A	1	P05787

	1352.6772	2	3.2262	0.3739	R.TEMENEFVLIK.K	1	P05787
KIAA0378 protein (Fragment)							
	1327.7698	2	2.2153	0.1708	K.KKNAQLLEEVR.R	1	O15083
KIAA0947 protein (Fragment)							
	1866.8946	2	2.5198	0.2549	R.RASPPDPSPSPSAASASER.V	1	Q9Y2F5
KIAA1004 protein (Fragment)							
	1341.7266	2	2.5048	0.1604	K.ILLEELANSDPK.L	1	Q9Y2K7
Kinesin-like protein 2							
	1841.0496	2	2.7995	0.1432	K.LKAQLLQIQTELNNSK.Q	1	Q9NS87
Kinesin-like protein KIF1A (Axonal transporter of synaptic vesicles)							
	1334.6956	2	2.2781	0.1668	R.EDGGTLGVFSPKK.T	1	Q12756
Lamin B1							
	2107.997	2	4.1142	0.5832	R.DQMQQQLNDYEQLLDVK.L	1	P20700
	1817.9245	2	4.381	0.5757	R.SLETENSALQLQVTER.E	1	P20700
	2528.3096	2	2.2173	0.454	K.SLEGDLEDLKDQIAQLEASLAAAK.K	1	P20700
	1173.6479	2	3.311	0.3815	K.DAALATALGDKK.S	1	P20700
	1446.7804	2	4.446	0.421	R.IESLSSQLSNLQK.E	1	P20700
Late endosomal/lysosomal Mp1 interacting protein (p14) (HSPC003)							
	1931.0126	1	2.9194	0.5155	K.AQALVQYLEEPLTQVAAS.-	3	Q9Y2Q5
	1363.6242	2	2.4204	0.2912	R.NGNQAFNEDNLK.F	2	Q9Y2Q5
	1621.8338	2	4.6953	0.656	R.VTAAIASNIWAAYDR.N	1	Q9Y2Q5
	3897.947	3	5.4818	0.6857	K.ALTQVLSQANTGGVQSTLLLNNEGSLLAYSGYGDTDAR.V	1	Q9Y2Q5
LIM and SH3 domain protein 1 (LASP-1) (MLN 50)							
	1551.7365	1	2.115	0.342	R.TGDTGMLPANYVEAI.-	1	Q14847
Lysosomal acid phosphatase (EC 3.1.3.2) (LAP)							
	1180.5598	2	2.4275	0.1358	R.YEQLQNETR.Q	1	P11117
LYST-interacting protein LIP7 (Fragment)							
	1684.9234	1	2.141	0.1556	R.EEIQTLKQQIADLR.E	1	Q9C061
Melanotransferrin (Melanoma-associated antigen p97) (CD228 antigen)							

1200.5861	2	2.2491	0.4237	K.HSTVLENTDGK.T	1	P08582
Membrane associated progesterone receptor component 1 (mPR)						
3623.6553	3	5.1636	0.5134	K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK.Y	1	O00264
Membrane associated protein SLP-2 (Stomatin-like protein 2) (Stomatin-like 2) (Hypothetical protein FLJ14499)						
1662.7459	2	2.9111	0.359	R.DVQGTDASLDEELDR.V	1	Q9UJZ1
1675.0158	2	2.9132	0.4994	R.ILEPGLNILIPVLDR.I	1	Q9UJZ1
1337.583	2	2.5698	0.1169	K.ESMQMQVEAER.R	1	Q9UJZ1
1670.8713	1	2.0306	0.3676	K.AEQINQAAGEASAVLAK.A	1	Q9UJZ1
Microrchidia						
2410.2591	2	2.5003	0.2324	K.EDNLLFQNNLNKVTIDARHR.L	1	Q9Y6D4
Microsomal glutathione S-transferase 3 (EC 2.5.1.18) (Microsomal GST-3) (Microsomal GST-III)						
1312.7741	2	2.9987	0.4035	R.IASGLGLAWIVGR.V	3	O14880
2872.4939	3	3.4057	0.5189	R.AHQNTLEVYPPFLFFLAVGGVYHPR.I	1	O14880
1610.7743	1	2.9594	0.5047	R.VLYAYGYYTGEPSK.R	1	O14880
Mitochondrial import receptor subunit TOM20 homolog (Mitochondrial 20 kDa outer membrane protein)						
2385.1866	2	5.3672	0.7346	K.FFLEEIQLGEELLAQGEYEK.G	1	Q15388
Mitochondrial import receptor subunit TOM22 homolog (Translocase of outer membrane 22 kDa subunit homolog) (hTom22) (1C9-2)						
1378.6829	2	2.5264	0.1499	R.LWGLTEMFPER.V	1	Q9NS69
2921.2184	3	5.3094	0.4573	K.GDAEKPEEELEEDDDEELDETLSER.L	1	Q9NS69
2275.2484	2	4.4752	0.6226	R.QILLGPNTGLSGGMPGALPSLPGK.I	2	Q9NS69
Mitochondrial inner membrane protein (Mitofilin) (p87/89)						
1115.5948	2	3.1274	0.2535	K.AVDEAADALLK.A	1	Q16891
1871.9966	2	3.4415	0.4896	K.TSSAETPTIPLGSAVEAIK.A	3	Q16891
2198.073	2	4.8535	0.6255	R.LSQEQVDNFTLDINTAYAR.L	1	Q16891
1509.8099	3	3.5451	0.4238	K.LHNMIVDLDNVVK.K	1	Q16891
1823.8888	2	4.751	0.6359	R.GIEQAVQSHAVAEEEAR.K	2	Q16891
Mitogen-activated protein kinase kinase 1 interacting protein 1 (MEK binding partner 1) (Mp1) (PRO2783)						
1591.8808	3	4.4722	0.5528	K.LPSVEGLHAIVVSDR.D	2	Q9UHA4

	1216.6578	2	3.0002	0.4449	K.ELAPLFEELR.Q	1	Q9UHA4
	2345.3332	2	3.6367	0.6152	R.LPLVVSFIASSSANTGLIVSLEK.E	1	Q9UHA4
	1719.9757	3	3.6912	0.4245	K.KLPSVEGLHAIVVSDR.D	1	Q9UHA4
	2927.4652	3	4.3741	0.4761	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2	Q9UHA4
Monocarboxylate transporter 5 (MCT 5) (MCT 4)							
	1761.9283	2	2.2438	0.1027	R.FCAGPLVAIICDILGEK.T	1	O15374
Mucolipidin							
	1999.0805	2	2.2727	0.268	R.YLTFFHNYNILIATLR.V	1	Q9H4B5
Multi PDZ domain protein MUPP1							
	2567.0923	2	2.2404	0.3473	R.EEGEGEESELQNTAYSNWNQPR.R	1	O75970
Multidrug resistance protein 1 (P-glycoprotein 1) (CD243 antigen)							
	2399.3186	3	4.4789	0.5031	R.EIIGVVSQEPVLFATTIAENIR.Y	1	P08183
	1201.5563	2	2.3996	0.2481	K.EANAYDFIMK.L	1	P08183
Multidrug resistance-associated protein 4 (MRP/cMOAT-related ABC transporter) (Multi-specific organic anion tranporter-B) (MOAT-B)							
	2638.2888	2	2.2561	0.3596	R.AVYQDADIYLLDDPLSAVDAEVSR.H	1	O15439
Muscle-specific DNase I-like (EC 3.1.21.-) (DNase X) (XIB)							
	2306.1457	2	3.0485	0.5152	K.ELNALYDVFLEVSQHWQSK.D	1	P49184
	2029.962	2	4.0058	0.6277	R.TEPGFHWVIADGEDTTVR.A	1	P49184
Myeloid-associated differentiation marker (SB135)							
	3714.8493	3	3.4735	0.3838	R.NFPITFACYAALFCLSASIIYPTTYVQFLSHGR.S	1	Q96S97
	1646.8828	1	1.8042	0.2227	R.PGEITGYMATVPGLLK.V	2	Q96S97
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A)							
	1348.6232	1	2.034	0.3901	R.DELADEIANSSGK.G	2	P35579
	1653.7859	2	4.4823	0.5037	R.IAEFTTNLTEEEEK.S	1	P35579
	1672.8447	2	4.5889	0.4192	K.NFINNPLAQADWAAK.K	1	P35579
	2333.0567	2	6.0102	0.6285	K.MQQNIQELEEQLEEEESAR.Q	1	P35579
	2472.1742	2	3.7145	0.513	R.IAQLEEELEEEQGNTELINDR.L	2	P35579
	1839.9089	2	2.3854	0.4075	K.HSQAVEELAEQLEQTK.R	1	P35579

	1996.01	3	4.47	0.4547	K.HSQAVEELAEQLEQTKR.V	2	P35579
	1220.6527	2	2.7776	0.3694	K.KFDQLLAEEK.T	1	P35579
	1726.9492	2	4.3313	0.5618	R.QLLQANPILEAFGNAK.T	1	P35579
	1530.7651	2	4.7554	0.5462	K.IAQLEEQLDNETK.E	2	P35579
	2493.1745	2	5.639	0.5165	K.DFSALESQLQDTQELLQEENR.Q	2	P35579
	1378.616	2	2.3676	0.202	R.EMEAELEDERK.Q	1	P35579
	2033.9515	2	5.7488	0.5126	R.ELESQISELQEDLESER.A	2	P35579
	1869.967	2	4.9154	0.5957	K.ANLQIDQINTDLNLER.S	2	P35579
	1871.9602	2	2.6567	0.3997	K.EEVGEEAIVELVENGKK.V	1	P35579
	2487.2466	2	4.6	0.6279	K.LEGDSTDLSDQIAELQAQIAELK.M	1	P35579
	1946.0082	2	5.3836	0.6604	K.LQVELDNVTGLLSQSDSK.S	2	P35579
	1242.5901	2	3.1511	0.5443	K.THEAQIQEMR.Q	2	P35579
	1751.856	2	4.2034	0.5814	R.LTEMETLQSQLMAEK.L	1	P35579
	2048.9633	2	3.9996	0.5405	K.SMEAEMIQLQEELAAAER.A	1	P35579
	1949.9933	3	4.2101	0.4473	R.LQQELDDLLVDLDHQR.Q	1	P35579
	1961.9191	2	6.1705	0.6721	K.TQLEELEDELQATEDAK.L	1	P35579
	1204.5884	2	3.2267	0.4751	R.ALEQQVEEMK.T	1	P35579
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B)							
	1933.9355	2	3.8369	0.5398	K.TELEDTLDTTAAQQELR.T	2	P35580
Myosin Ib (Myosin I alpha) (MMI-alpha) (MMIa) (MYH-1c) (Fragment)							
	2182.1185	2	2.3247	0.3568	K.ALYPSSVGQPFQGAYLEINK.N	1	O43795
	1143.6625	2	2.5303	0.2948	R.LEDLATLIQK.I	1	O43795
Myosin Ic (Myosin I beta) (MMI-beta) (MMIb)							
	1911.0955	2	3.1646	0.3218	R.VLQALGSEPIQYAVPVVK.Y	1	O00159
Myosin light chain alkali, non-muscle isoform (MLC3nm) (LC17A) (LC17-NM) (Smooth muscle myosin alkali light chain)							
	995.589	2	2.5513	0.4543	R.HVLVTLGEK.M	1	P16475
	1233.5898	2	2.2462	0.2126	K.EGNGTVMGAEIR.H	2	P16475
	1354.7331	2	2.6137	0.2031	R.ALGQNPTNAEVLK.V	1	P16475

	1025.5056	2	2.7438	0.4343	K.EAFQLFDR.T	1	P16475
	1786.8248	3	3.5739	0.5211	K.NKDQGTYEDYVEGLR.V	2	P16475
Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)							
	1415.6331	2	3.348	0.3795	R.FTDEEVDELYR.E	1	P19105
	1260.6013	2	3.538	0.2294	K.GNFNYIEFTR.I	1	P19105
	1228.6174	2	2.8924	0.4551	K.LNGTDPEDVIR.N	1	P19105
	2090.9857	2	4.7839	0.6588	R.ATSNVFAMFDQSQIQEFK.E	2	P19105
Myosin VIIa							
	1820.9441	2	2.3756	0.1916	K.QIFQADVAMGAETRKR.S	1	Q13402
Myosin-binding protein H (MyBP-H) (H-protein)							
	1364.7327	2	2.2374	0.2857	K.KTGQWFTVLER.Y	1	Q13203
Myotonic dystrophy kinase-related CDC42-binding protein kinase alpha (Fragment)							
	916.5104	2	2.934	0.1447	K.EEIEKLR.K	1	Q9NYF6
NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R)							
	1371.7371	2	2.9796	0.1886	R.STPAITLESPDIK.Y	1	P00387
NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial (EC 1.6.5.3) (EC 1.6.99.3)							
	2240.9624	2	2.7094	0.5434	R.DTPENNPDTPFDFTPENYK.R	1	P19404
Neuroblast differentiation associated protein AHNAK (Desmoyokin) (Fragments)							
	2789.5049	2	3.4782	0.5981	K.GGKPGLTIQAPQLEVSVPSANIEGLEGK.L	1	Q09666
	1641.7972	2	2.2335	0.1094	K.VDTNAPDLSLEGPEGK.L	1	Q09666
	1668.8332	2	3.7816	0.5455	K.VDVEVPDVSLEGPEGK.L	1	Q09666
	2512.1731	2	3.7004	0.4311	R.EFSGPSTPTGTLEFEGGEVSLEGGK.V	1	Q09666
	1239.6221	2	2.9252	0.418	K.GEGPDVDVNLPK.A	2	Q09666
	2581.3249	2	2.2075	0.3716	K.SPSLDVTVPEAELNLETPEISVGGK.G	1	Q09666
	1253.6378	2	3.0714	0.2834	K.GEGPEVDVNLPK.A	2	Q09666
	1267.6534	2	3.3126	0.303	K.AEGPEVDVNLPK.A	3	Q09666
	1709.8598	2	2.8071	0.4377	K.VDIDVPDVNLEAPEGK.L	1	Q09666
	1732.8241	2	3.3261	0.4994	K.ASLGSLEGEAEAEASSPK.G	1	Q09666

	1654.8176	2	3.5477	0.5394	K.VDIEAPDVSLEGPEGK.L	2	Q09666
	2027.9827	2	2.4194	0.4179	K.VDIDAPDVDVHGPDWHLK.M	3	Q09666
Neuroligin 1							
	1740.8881	2	2.401	0.3288	K.KRDEATLNPPDTDIR.D	1	Q8N2Q7
Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal NOS) (N-NOS) (nNOS) (Constitutive NOS) (NC-NOS) (bNOS)							
	1367.7058	2	2.3355	0.1504	R.SESIAFIEESKK.D	1	P29475
N-methyl-D-aspartate receptor 2C subunit							
	1305.6287	2	2.3803	0.1063	R.DSGGLDEISSVAR.G	2	O15398
NUB1 (NEDD8 ultimate buster-1)							
	1674.8815	2	2.3785	0.306	K.VDNLLQLGFTAQEAR.L	1	Q9BXR2
Nucleolin (Protein C23)							
	1648.7383	2	2.4735	0.473	K.FGYVDFESAEDLEK.A	1	P19338
	1322.6327	2	2.3616	0.1752	K.GLSEDTTEETLK.E	1	P19338
	2312.1563	2	4.4722	0.6385	K.VEGTEPTTAFNLFVGNLNFNK.S	2	P19338
Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar protein NO38)							
	2227.2161	2	4.8617	0.6825	K.MSVQPTVSLGGFEITPPVVLR.L	1	P06748
	2145.0174	2	4.8264	0.4618	K.DELHIVEAEAMNYEGSPIK.V	1	P06748
P532							
	1924.1456	2	2.2836	0.4044	R.RLASELLLGLAAQRGSLR.Y	1	Q15751
P63 protein							
	1473.7801	2	2.5618	0.2422	R.SVGELPSTVESLQK.V	1	Q07065
PalBH (EC 3.4.22.17)							
	1639.8543	2	2.2324	0.2543	R.YTAEEIEVLRTTSK.I	1	Q9Y6W3
Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase 1) (hPanK1) (hPanK)							
	2039.027	2	2.4567	0.1938	K.PQGGSGEIKTPENDLQRGR.L	1	Q8TE04
Paralemmin							
	2324.2601	2	4.8735	0.5442	K.VLGLQDTITAELVVIEDAAEPK.E	1	O75781
	1835.8623	2	3.2008	0.4483	K.ADEVTLSEAGSTAGAAETR.G	1	O75781
Peripherin							

	1309.6065	2	2.9787	0.4539	K.NLQEAEEWYK.S	1	P41219
	1295.667	2	3.8812	0.5483	K.MALDIEIATYR.K	1	P41219
Phosphate carrier protein, mitochondrial (PTP)							
	1361.7177	2	2.2196	0.3618	R.IQTQPGYANTLR.D	1	Q00325
Phosphotyrosine independent ligand for the LCK SH2 domain P62 (Sequestosome 1)							
	3526.6383	2	3.8921	0.6555	K.EVDPSTGELQSLQMPESEGPSSLDPSQEGPTGLK.E	1	Q13501
Plectin 1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1)							
	2072.026	2	4.9749	0.6088	K.EQELQQTLQQEQSVLDR.L	1	Q15149
	2168.9545	2	3.3628	0.5175	R.GLFDEEMNEILTDPSDDTK.G	2	Q15149
	1653.8488	1	2.1126	0.3396	R.DPYTGQSVSLFQALK.K	1	Q15149
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1)							
	1360.6596	2	2.2863	0.2751	R.KGDEVDGVDEVAK.K	1	P09874
Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (Nucleic acid binding protein SUB2.3)							
	2089.9824	2	2.7061	0.4299	R.ESTGAQVQVAGDMLPNSTER.A	1	Q15365
Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1)							
	1928.9143	2	3.2184	0.6195	R.SLGYAYVNFQQPADAER.A	1	P11940
POU domain, class 6, transcription factor 1 (mPOU homeobox protein) (Brain-specific homeobox/POU domain protein 5) (Brain-5)							
	2410.1891	2	2.5315	0.1278	K.PHTPSLDEDGINLEEIREFAK.N	1	Q14863
Presenilin 1 (PS-1) (S182 protein)							
	1932.8926	2	3.2329	0.436	R.QVVEQDEEEDEELTLK.Y	1	P49768
PRO1433							
	1832.8392	2	2.3088	0.3223	R.FFSLYCDIVFSNCFK.V	1	Q9H372
PRO1855							
	1724.8608	2	3.5701	0.574	R.HEILQWVLQTDSQQ.-	1	Q9P189
Prohibitin							
	2119.1439	2	3.9048	0.5307	R.AATFGLILDDVSLTHLTFGK.E	1	P35232
	2371.2523	2	3.0872	0.5352	K.FGLALAVAGGVVNSALYNVDAGHR.A	1	P35232
	1149.5904	2	2.429	0.3996	R.FDAGELITQR.E	1	P35232

	1855.0329	1	2.5835	0.269	R.NITYLPAGQSVLLQLPQ.-	1	P35232
	1998.0872	2	2.5293	0.3788	K.AAELIANSLATAGDGLIELR.K	1	P35232
Protein c20orf178							
	2676.2926	2	3.1347	0.5579	K.VDELMQDIADQQELAEEISTAISK.P	1	Q9H444
	2485.3918	2	3.1346	0.5343	K.NLLEISGPETVPLPNVPSIALPSK.P	1	Q9H444
Protein disulfide isomerase (PDI) (EC 5.3.4.1) (Prolyl 4-hydroxylase beta subunit) (Cellular thyroid hormone binding protein)							
	1780.8354	2	3.4948	0.4619	K.VDATEESDLAQQYGVR.G	1	P07237
Protein kinase C substrate, 80 kDa protein, heavy chain (PKCSH) (80K-H protein)							
	2180.9923	2	2.6601	0.3974	K.MPPYDEQTQAFIDAAQEAR.N	1	P14314
Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A)							
	2550.1142	2	2.4507	0.125	K.RCHEFVTFSCPGADKGPDTDDPR.S	1	P17252
Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1)							
	2322.173	2	2.9868	0.5303	R.FSGNLLVSLLGTWSDTSSGGPAR.A	1	P38378
Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48) (Protein-tyrosine phosphatase 1E) (PTP-E1) (hPTPE1) (PTP-BAS)							
	1679.8645	2	2.3703	0.3712	R.VPLGDEGGYINASFIK.I	1	Q12923
Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (p61-YES) (C-YES)							
	1878.8775	2	3.2035	0.4287	R.FQIINNTEGDWWEAR.S	1	P07947
	2527.341	2	4.5744	0.5154	K.LVPLYAVVSEEPIYIVTEFMSK.G	1	P07947
PTD015							
	1892.9614	2	2.2218	0.1705	-.MTSPEIASLSWGQMKVK.G	1	Q9Y6B1
Putative G protein-coupled receptor (Hypothetical protein FLJ10899) (Retinoic acid induced 3)							
	1433.7389	2	4.0286	0.5126	R.TNVNVFSELSAPR.R	1	O95357
Putative vascular inducible G protein-coupled receptor							
	2243.1249	2	3.2952	0.2977	K.GNVVDWQNDFWNIPNLALK.A	1	Q8IXA4
Rab3 interacting protein variant 6 (Fragment)							
	2228.2264	2	2.2888	0.2011	R.SRLPNVPLQRSLDEIHPTR.R	1	Q9HBA1
RAD50							
	1718.9077	2	2.3776	0.1384	K.SYENELDPLKNRLK.E	2	Q92878

Ras-related C3 botulinum toxin substrate 1 (p21-Rac1) (Ras-like protein TC25)							
	1948.9041	2	2.607	0.493	K.PVNLGLWDTAGQEDYDR.L	2	P15154
Ras-related protein Rab-10							
	1932.8939	2	3.1884	0.6138	K.EPNSENVDISSGGGVTGWK.S	1	O88386
	1261.7156	2	2.6937	0.3511	K.AFLTLAEDILR.K	2	O88386
Ras-related protein Rab-11B (GTP-binding protein YPT3)							
	2329.12	2	5.0624	0.7242	K.NNLSFIETSALDSTNVEEAFK.N	1	Q15907
Ras-related protein Rab-18							
	2101.997	2	3.1175	0.4742	R.FTDDTFDPELAATIGVDFK.V	1	Q9NP72
Ras-related protein Rab-1A (YPT1-related protein)							
	2172.0025	2	4.1301	0.6364	R.FADDTYTESYISTIGVDFK.I	1	P11476
Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY)							
	1071.6414	2	2.4816	0.2708	K.LLIIGDSGVGK.S	2	Q15286
Ras-related protein Rab-39B							
	1316.6599	2	3.3172	0.1961	K.LQIWDTAGQER.F	1	Q96DA2
Ras-related protein Rab-5C (RAB5L) (L1880)							
	1299.6293	2	3.3902	0.418	R.GVDLQENNPASR.S	1	P51148
Ras-related protein Rab-7							
	1964.9493	2	2.3409	0.2364	K.QETEVELYNEFPEPIK.L	1	P51149
Ras-related protein Rab-8 (Rab-8A) (Oncogene c-mel)							
	1071.6414	2	2.6581	0.2682	K.LLLIGDSGVGK.T	1	P24407
Ras-related protein Ral-A							
	2426.1114	2	5.2427	0.6642	K.SALTLQFMYDEFVEDYEPTK.A	1	P11233
	2732.3631	2	2.6396	0.542	K.VVLDGEEVQIDILDTAGQEDYAAIR.D	1	P11233
	1700.9223	2	2.291	0.4328	R.VKEDENVPFLLVGNK.S	1	P11233
Ras-related protein RAP-1A (C21KG) (KREV-1 protein) (GTP-binding protein SMG-P21A) (G-22K)							
	1665.9216	2	3.4279	0.5105	K.SALTVQFVQGIFVEK.Y	1	P10113
Ras-related protein R-Ras2 (Ras-like protein TC21) (Teratocarcinoma oncogene)							
	3045.4621	2	3.5699	0.5934	K.SALTIQFIQSYFVTDYDPTIEDSYTK.Q	1	P17082

	1765.8431	2	4.9612	0.5876	R.LDILDTAGQEEFGAMR.E	2	P17082
	972.4678	2	2.3253	0.1494	R.GSFEEIYK.F	1	P17082
Receptor protein-tyrosine kinase erbB-2 (EC 2.7.1.112) (p185erbB2) (NEU proto-oncogene) (C-erbB-2)							
	2368.1825	2	3.4361	0.1435	R.FVVIQNEDLGPASPLDSTFYR.S	1	P04626
Renin receptor							
	2228.1199	3	3.5239	0.4744	K.DHSPDLYSLELAGLDEIGKR.Y	1	Q8NG15
RER1 protein							
	1902.8643	2	4.6505	0.5919	K.VDPSLMEDSDDGPSLPTK.Q	1	O15258
Reticulocalbin 1							
	1652.7655	2	2.4253	0.2644	R.IDNDGDGFVTTEELK.T	1	Q15293
Reticulocalbin 2 (Calcium-binding protein ERC-55) (E6-binding protein) (E6BP)							
	2214.9679	2	4.4003	0.4944	R.VIDFDENTALDDAEEESFR.K	1	Q14257
Rho-related GTP-binding protein RhoG (Sid10750)							
	2131.9936	2	2.4508	0.2042	K.EYIPTVFDNYSAQSAVDGR.T	1	P35238
Ribosome binding protein 1 (Ribosome receptor protein) (180 kDa ribosome receptor homolog) (ES/130 related protein)							
	1776.8503	2	3.2574	0.603	R.TAGPLESSETEEASQLK.E	1	Q9P2E9
RLIP76 protein (Similar to ralA binding protein 1)							
	1850.0024	2	2.4796	0.2195	R.TTETEKVQEFQRLLK.E	1	Q15311
RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein)							
	2480.0537	3	3.3316	0.4362	R.QDHPSSMGVYGQESGGFSGPGENR.S	1	Q01844
S100 calcium-binding protein A14 (S114)							
	1667.7149	2	2.2147	0.4299	R.SANAEDAQEFSDVER.A	1	Q9HCY8
Semaphorin 7A (Semaphorin L) (Sema L) (Semaphorin K1) (Sema K1) (John-Milton-Hargen human blood group Ag)							
	2187.028	2	5.5244	0.6528	R.GESELYTSDTVMQNPQFIK.A	1	O75326
	2825.3647	3	3.5299	0.3688	R.VDFGQTEPHTVLFHEPGSSSVWVGGR.G	3	O75326
	1770.9179	2	3.2219	0.2911	R.LQDVFLLPDPSGQWR.D	1	O75326
	2805.3259	2	4.4983	0.6385	R.GYAPFSPDENSLVLFEGDEVYSTIR.K	2	O75326
Serine/threonine protein kinase 3 (EC 2.7.1.37) (STE20-like kinase MST2) (MST-2) (Mammalian STE20-like protein kinase 2)							

	1361.735	2	2.3131	0.1307	R.DLITEAMEIKAK.R	1	Q13188
Serum paraoxonase/arylesterase 2 (EC 3.1.1.2) (EC 3.1.8.1) (PON 2) (Serum aryldialkylphosphatase 2) (A-esterase 2)							
	1947.93	2	2.2021	0.3293	K.VVAEGFDSANGINISPDDK.Y	1	Q15165
Seven transmembrane helix receptor							
	2604.2833	2	2.2558	0.3267	K.SQETLNSDDLDATDKLIFIFYR.V	1	Q8NGS8
Seven transmembrane helix receptor							
	1804.0094	1	1.8081	0.122	R.FRGAPPGLHALTSRPAR.R	1	Q8NGZ7
Similar to endocrine regulator							
	2107.046	2	2.4193	0.2879	K.SSDFQKEGLQQTFLPPER.Q	1	Q8NEM6
Similar to expressed sequence AI415388 (Fragment)							
	2530.3339	2	2.3274	0.1649	K.GSFIQHSVSGLCLETKPAQLVTSK.C	1	Q8N428
Similar to hypothetical protein FLJ10856							
	1760.8303	2	3.8661	0.5014	R.DDSQLNGDSSALLNPSK.E	1	Q96H09
Similar to nuclear VCP-like							
	1985.9602	2	2.3433	0.1143	K.KNPEMEDLPSKGVQEER.L	1	Q96EM7
Similar to RIKEN cDNA 2610024G14 gene							
	1962.0013	2	2.2081	0.1519	R.FLFPEYILDPEPQPTR.E	1	Q9BSQ9
Similar to RIKEN cDNA 5830480G12 gene							
	2288.2727	2	2.3565	0.1817	R.GLDVDGIYRVSGNLATIQKLR.F	1	Q8IXX1
Similar to tubulin, beta, 4							
	1857.9421	2	2.3098	0.4512	K.MASTFIGNSTAIQELFK.R	2	Q9BUF5
Sodium bicarbonate cotransporter							
	1923.9526	2	3.4191	0.493	R.AIATLMSDEVFHDIAYK.A	1	O15153
	1747.8714	2	2.7493	0.3868	R.NLTSSSLNDISDKPEK.D	1	O15153
Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) (Sodium pump 1) (Na+/K+ ATPase 1)							
	1829.9245	2	3.5253	0.6517	K.GVGIISEGNETVEDIAAR.L	1	P05023
	1519.7029	2	3.3363	0.4539	R.SPDFTNENPLETR.N	1	P05023
Solute carrier family 12 member 4 (Electroneutral potassium-chloride cotransporter 1) (Erythroid K-Cl cotransporter 1) (hKCC1)							
	1956.8562	2	4.3705	0.667	R.LESLYSDEEDESAVGADK.I	1	Q9UP95

Solute carrier family 2, facilitated glucose transporter, member 1 (Glucose transporter type 1, erythrocyte/brain)							
	1639.7968	2	4.4272	0.6032	K.TPEELFHPLGADSQV.-	2	P11166
	1444.6742	2	4.2424	0.4286	R.GTADVTHDLQEMK.E	1	P11166
	990.5988	2	3.5635	0.4315	K.VTILELFR.S	1	P11166
	2498.1799	2	2.2905	0.4215	R.QGGASQSDKTPEELFHPLGADSQV.-	1	P11166
	1142.5482	2	3.8007	0.4137	R.TFDEIASGFR.Q	1	P11166
Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II spectrin) (Fodrin beta chain)							
	1887.93	2	3.0799	0.4384	K.EIEELQSQAQALSQEGK.S	1	Q01082
Stathmin 2 (SCG10 protein) (Superior cervical ganglion-10 protein)							
	1332.764	2	2.2191	0.1431	K.RASGQAFELILK.P	1	Q93045
Steroid receptor coactivator							
	2495.1572	2	2.3256	0.1051	K.DNKEIASILNEMIQSDNSSSDGK.P	1	O43792
SWI/SNF-related, matrix associated, actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 (Helicase 1)							
	974.5787	2	2.3713	0.1387	R.KKNVFNPK.R	1	Q9H4L7
Synaptosomal-associated protein 23 (SNAP-23) (Vesicle-membrane fusion protein SNAP-23)							
	1983.981	2	4.0984	0.6076	K.DMALNIGNEIDAQNPQIK.R	4	O00161
	2119.0229	2	5.3366	0.5441	R.EDEMEENLTQVGSILGNLK.D	2	O00161
	1158.6006	2	3.2435	0.3254	R.IEEGLDQINK.D	2	O00161
TAR DNA-binding protein-43 (TDP-43)							
	1726.7686	2	2.2225	0.177	R.FGGNPGGFGNQGGFGNSR.G	1	Q13148
T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta)							
	1912.9544	2	3.1834	0.4628	K.LGGSLADSYLDEGFLLDK.K	1	P78371
	1330.6603	2	2.8622	0.2171	R.GATQQILDEAER.S	1	P78371
Tousled-like kinase 2							
	1949.0027	2	2.6553	0.1823	K.PPAMGQAPPATNEQKQRK.S	1	Q9UKI7
Transcription intermediary factor 1-beta (TIF1-beta) (Tripartite motif protein 28) (Nuclear corepressor KAP-1)							
	1849.8667	2	3.7043	0.5396	K.EEDGSLSLDGADSTGVVAK.L	1	Q13263
Transcriptional coactivator ALY (Fragment)							
	2034.9732	2	3.373	0.4623	K.QQLSAEELDAQLDAYNAR.M	1	O43672

Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin containing protein) (VCP) [Contains: Valosin]						
1329.6915	2	2.5441	0.3001	R.WALSQSNPSALR.E	1	P55072
Transmembrane protein Tmp21 (21 kDa Transmembrane trafficking protein) (p24delta) (S31III125) (S31I125) (Tmp-21-I)						
1873.8894	2	2.693	0.3471	R.LEDLSESIVNDFAYMK.K	2	P49755
Trifunctional enzyme alpha subunit, mitochondrial (TP-alpha) (78 kDa gastrin-binding protein) [Includes: Long-chain enoyl-						
1630.84	2	3.8793	0.4567	K.TLQEVTQLSQEAQR.I	1	P40939
1679.8566	1	2.029	0.4491	K.ADMVIEAVFEDLSLK.H	1	P40939
2274.2168	3	4.616	0.4584	K.MGLVDQLVEPLGPGLKPPEER.T	1	P40939
1318.7292	2	3.7202	0.4082	K.MQLLEIITTEK.T	1	P40939
2061.9769	2	3.1413	0.5636	R.DSIFSNLTGQLDYQGFEK.A	1	P40939
TRIP protein						
2021.0337	2	2.2675	0.1829	K.MTKEELNALKSTGDGTLGR.A	1	O75766
Tubulin alpha-1 chain (Alpha-tubulin 1)						
2348.9054	2	3.7662	0.6492	K.DYEEVGVDSVEGEGEEEGEEY.-	1	P05209
1487.8797	2	4.1482	0.5933	R.LISQIVSSITASLR.F	2	P05209
1015.5788	2	2.8707	0.2808	K.DVNAAIATIK.T	2	P05209
1085.6207	2	3.2369	0.3669	K.EIIDLVLDR.I	2	P05209
2330.0188	3	5.194	0.5504	R.AFVHWYVGEGMEEGEFSEAR.E	2	P05209
1824.986	1	2.9202	0.4391	K.VGINYQPPTVVPGGDLAK.V	3	P05209
1701.9063	1	2.271	0.3284	R.AVFVDLEPTVIDEVR.T	4	P05209
1756.9638	3	3.4008	0.2411	R.IHFPLATYAPVISAEK.A	2	P05209
2007.8936	2	5.4319	0.5863	K.TIGGGDDSFNTFFSETGAGK.H	2	P05209
Tubulin alpha-4 chain (Alpha-tubulin 4)						
1715.922	2	3.2929	0.2605	R.AVFVDLEPTVIDEIR.N	1	P05215
Tubulin beta-1 chain						
1319.7033	2	2.9302	0.3811	R.IMNTFSVVPSPK.V	2	P07437
2798.3439	2	3.2457	0.5143	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	4	P07437
1620.8361	3	4.0657	0.3865	R.LHFFMPGFAPLTSR.G	2	P07437

	3102.4081	3	5.3179	0.5463	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	2	P07437
	1229.5989	2	3.734	0.4243	R.ISEQFTAMFR.R	3	P07437
	1958.9824	2	7.0219	0.5554	K.GHYTEGAELVDSVLDVVR.K	3	P07437
	1446.6899	2	4.4188	0.3187	K.EVDEQMLNVQNK.N	1	P07437
	1615.8365	2	4.1403	0.5596	R.AILVDLEPGTMDSVR.S	2	P07437
	1869.9785	2	3.4405	0.5469	K.MAVTFIGNSTAIQELFK.R	3	P07437
	1696.8335	1	3.0428	0.5211	K.NSSYFVEWIPNNVK.T	4	P07437
	1039.594	2	3.0993	0.3501	R.YLTVAAVFR.G	1	P07437
	1143.6349	2	3.1694	0.386	K.LAVNMVPFPR.L	2	P07437
Tubulin beta-2 chain							
	1601.8209	2	3.8849	0.363	R.AVLVDLEPGTMDSVR.S	1	P05217
	1691.8678	2	2.4048	0.513	R.ALTVPELTQQMFDAK.N	1	P05217
	1328.6487	2	2.5235	0.3655	R.INVYYNEATGGK.Y	1	P05217
	1857.9421	2	4.6222	0.6329	K.MSATFIGNSTAIQELFK.R	1	P05217
Tubulin beta-4 chain (Tubulin beta-III)							
	1069.6046	2	2.7953	0.4879	R.YLTVATVFR.G	1	Q13509
	1873.937	2	2.7601	0.2358	K.MSSTFIGNSTAIQELFK.R	4	Q13509
Tubulin beta-5 chain							
	1659.8958	1	2.0203	0.2241	R.ALTVPELTQQVFDAK.N	2	P05218
Tubulin, beta polypeptide							
	1053.6097	2	2.3205	0.4407	R.YLTVAAIFR.G	1	Q9BVA1
Tyrosine-protein kinase LYN (EC 2.7.1.112)							
	2121.9704	2	3.2819	0.4712	R.LGAGQFGEVWMGYYNNSTK.V	1	P07948
	1599.798	2	2.4526	0.4144	R.EEPIYIITEYMAK.G	1	P07948
Tyrosine-protein kinase receptor UFO (EC 2.7.1.112) (AXL oncogene)							
	2100.9878	2	2.3886	0.3697	R.GQTPYPGVENSEIYDYLR.Q	1	P30530
Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial (EC 1.10.2.2) (Complex III subunit II)							
	1909.966	2	2.5608	0.5159	K.ATAAPAGAPPQPQDLEFTK.L	1	P22695

Ubiquitin						
1787.9279	1	2.3268	0.3638	K.TITLEVEPSDTIENVK.A	2	P02248
1067.6213	2	2.6706	0.3547	K.ESTLHLVLR.L	1	P02248
Urokinase plasminogen activator surface receptor (uPAR) (U-PAR) (Monocyte activation antigen Mo3) (CD87 antigen)						
2179.0487	2	2.4602	0.3522	K.ITSLTEVVCGLDLCNQGNSGR.A	1	Q03405
Vacuolar ATP synthase 16 kDa proteolipid subunit (EC 3.6.3.14)						
3030.4382	2	5.6089	0.7261	K.SGPEYASFFAVMGASAAMVFSALGAAYGTAK.S	2	P27449
2873.5889	3	4.0027	0.5508	K.SFLQLGAGLSVGLSGLAAGFAIGIVGDAGVR.G	7	P27449
1906.9553	2	3.2941	0.4318	K.SGTGIAAMSVMRPEQIMK.S	3	P27449
Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (EC 3.6.3.14) (V-ATPase A subunit 1)						
1145.6108	2	2.6917	0.2399	K.HFTEFVPLR.T	2	P38606
1515.7953	2	3.9952	0.4925	R.TALVANTSNMPVAAR.E	1	P38606
1308.7276	2	3.2465	0.3951	R.VGHSELVGEIIR.L	2	P38606
2055.0861	3	4.1223	0.4285	K.EILQEEEDLAEIVQLVGK.A	1	P38606
1800.8227	2	5.1145	0.6445	K.SDYAQLLEDMQNAFR.S	4	P38606
1577.8116	2	3.4802	0.5078	K.HFPSVNWLISYSK.Y	1	P38606
1781.8533	2	2.8382	0.4525	R.LAEMPADSGYPAYLGAR.L	1	P38606
4142.196	3	3.442	0.6286	R.TGKPLSVELGPGIMGAIFDGIQRPLSDISSQTQSIYIPR.G	2	P38606
3688.875	3	4.8475	0.6521	R.EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDK.K	2	P38606
1380.6357	2	3.1566	0.5584	R.DFPELTMEVDGK.V	1	P38606
1731.7615	2	3.6934	0.5878	K.DDFLQQNGYTPYDR.F	1	P38606
2070.1058	3	4.3358	0.4439	K.PLSVELGPGIMGAIFDGIQR.P	1	P38606
3856.0319	3	4.0403	0.5522	K.PLSVELGPGIMGAIFDGIQRPLSDISSQTQSIYIPR.G	1	P38606
2086.0246	3	3.3083	0.2899	K.LIKDDFLQQNGYTPYDR.F	1	P38606
1804.9445	2	3.4788	0.5298	R.PLSDISSQTQSIYIPR.G	1	P38606
3816.97	3	3.7663	0.4451	R.EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDKK.L	2	P38606
2665.3031	2	3.9492	0.6485	R.LEGDMATIQVYEETSGVSVGDPVLR.T	1	P38606
1316.7439	2	2.3428	0.2141	K.LPANHPLLTGQR.V	1	P38606

2913.441	3	3.7252	0.3395	R.GTVTYIAPPGNYDTSDVVLELEFEGVK.E	1	P38606
1034.4941	2	2.3005	0.343	R.GNEMSEVLR.D	2	P38606
Vacuolar ATP synthase membrane sector associated protein M8-9 (V-ATPase M8.9 subunit)						
1237.6217	2	2.3596	0.3687	K.NPASPYNLAYK.Y	2	O75787
Vacuolar ATP synthase subunit B, brain isoform (EC 3.6.3.14) (V-ATPase B2 subunit) (Vacuolar proton pump B isoform 2)						
2000.0929	2	3.0487	0.4933	R.GIVNGAAPELPVPTGGPAVGAR.E	3	P21281
2353.2179	2	5.6881	0.6466	K.AVVGEEALTSDDLLYLEFLQK.F	1	P21281
1308.6337	2	3.3565	0.2938	R.NFIAQGPYENR.T	2	P21281
1520.7961	2	5.0042	0.59	K.AVVQVFEGTSGIDAK.K	2	P21281
1712.9335	3	3.8977	0.4585	R.YAEIVHLTLPDGTKR.S	1	P21281
1690.9168	2	3.4698	0.5509	R.TVFETLDIGWQLLR.I	1	P21281
1647.9434	2	3.3568	0.5704	K.TVSGVNGPLVILDHVK.F	2	P21281
Vacuolar ATP synthase subunit B, kidney isoform (EC 3.6.3.14) (V-ATPase B1 subunit) (Vacuolar proton pump B isoform 1)						
1896.8842	2	2.4545	0.6126	R.GFPGYMYTDLATIYER.A	4	P15313
1918.0108	3	4.04	0.4936	K.HVLVILTDMSSYAEALR.E	1	P15313
1104.5359	2	2.9645	0.4601	R.TPVSEDMLGR.V	2	P15313
Vacuolar ATP synthase subunit C (EC 3.6.3.14) (V-ATPase C subunit) (Vacuolar proton pump C subunit)						
2018.0922	3	4.906	0.5401	K.VQENLLANGVDLVTYITR.F	2	P21283
1468.6994	2	4.1224	0.4746	K.VAQYMADVLEDSK.D	1	P21283
1076.5992	2	3.6032	0.3477	K.LDAFVEGVVK.K	1	P21283
1102.5744	2	2.7197	0.2629	K.GVTQIDNDLK.S	2	P21283
948.5518	2	2.3191	0.2591	R.VFVESVLR.Y	1	P21283
1332.5418	2	3.0114	0.4018	R.DFQYNEEEMK.A	1	P21283
1628.9111	3	3.7265	0.3863	K.VGTLDVLVGLSDELAK.L	2	P21283
1832.9733	1	2.0813	0.1856	R.YGLPVNFQAMLLQPNK.K	1	P21283
Vacuolar ATP synthase subunit D (EC 3.6.3.14) (V-ATPase D subunit) (Vacuolar proton pump D subunit) (V-ATPase 28 kDa accessory						
1741.8761	1	2.861	0.4932	K.FTAGDFSTTVIQNVNK.A	1	Q9Y5K8
1653.8699	1	3.3125	0.5858	R.AAGEVLEPANLLAEEK.D	1	Q9Y5K8

1436.7637	2	4.9798	0.6114	R.TLAYIITELDER.E	1	Q9Y5K8
2489.3755	2	3.7764	0.5857	K.AVELLVELASLQTSFVTLDEAIK.I	1	Q9Y5K8
3090.4809	2	2.523	0.4796	K.DNVAGVTLPVFEHYHEGTDSYELTGLAR.G	1	Q9Y5K8
1260.7428	2	3.3885	0.4627	R.VNAIEHVIIPR.I	1	Q9Y5K8
Vacuolar ATP synthase subunit d (EC 3.6.3.14) (V-ATPase d subunit) (Vacuolar proton pump d subunit) (V-ATPase AC39 subunit) (V-						
1261.5741	2	3.1294	0.5163	K.NVADYYPEYK.L	2	P12953
1020.5042	2	3.4	0.2522	K.AYLESFYK.F	1	P12953
1230.6847	2	2.3886	0.2373	R.LYPEGLAQLAR.A	1	P12953
935.4627	2	2.2074	0.2261	R.FFEHEVK.L	2	P12953
1304.6487	2	2.7565	0.3233	K.LLFEGAGSNPGDK.T	4	P12953
2975.4751	3	4.9306	0.5946	K.LHLQSTDYGNFLANEASPLTVSVIDDR.L	1	P12953
1640.89	2	4.5987	0.6052	R.AFIITINSFGTELSK.E	1	P12953
Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subunit) (Vacuolar proton pump E subunit) (V-ATPase 31 kDa subunit)						
3123.4395	2	4.9354	0.7063	K.NDVDVQIDQESYLPEDIAGGVEIYNGDR.K	1	P36543
1586.839	3	4.216	0.3253	R.ARDDLITDLLNEAK.Q	4	P36543
2330.3124	2	4.378	0.6873	R.YQVLLDGLVLQGLYQLLEPR.M	2	P36543
1359.7008	2	2.674	0.3653	R.DDLITDLLNEAK.Q	2	P36543
3251.5344	3	4.0286	0.5731	K.NDVDVQIDQESYLPEDIAGGVEIYNGDRK.I	1	P36543
974.5675	2	2.2522	0.11	R.KQDFPLVK.A	1	P36543
1108.5162	2	2.9482	0.2982	K.AEEEFNIEK.G	10	P36543
1305.6408	2	3.6985	0.3731	K.IQMSNLMNQAR.L	2	P36543
1577.7092	2	5.0091	0.4562	K.HMMAFIEQEANEK.A	1	P36543
Vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit)						
1453.6811	2	3.6142	0.5374	K.DTTINEIEDTFR.Q	1	Q16864
1082.5999	2	2.7411	0.358	R.HPNFLVVEK.D	1	Q16864
Vacuolar ATP synthase subunit G 1 (EC 3.6.3.14) (V-ATPase G subunit 1) (Vacuolar proton pump G subunit 1) (V-ATPase 13 kDa						
1172.6138	2	2.8798	0.3201	K.MTILQTYFR.Q	1	O75348
1365.6287	2	2.2737	0.2174	K.EEAQAEIEQYR.L	8	O75348

Vacuolar ATP synthase subunit S1 (EC 3.6.3.14) (V-ATPase S1 subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45

1915.0388	2	3.1763	0.4995	R.EVLTGNDEVIGQVLSTLK.S	2	Q15904

Vacuolar protein sorting 33B (hVPS33B)

2193.1636	2	2.3962	0.2004	K.QEHRLLSLHIGACESIMKK.K	1	Q9H267

Vacuolar proton translocating ATPase 116 kDa subunit A isoform 1 (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa

1826.8707	2	3.4002	0.3317	R.IDDLQMVLNQTEDHR.Q	2	Q93050
2154.0355	2	4.5015	0.6551	R.QAEIENPLEDPVTGDYVHK.S	2	Q93050
1315.697	2	2.3045	0.2995	K.EINTNQEALKR.N	2	Q93050
1045.6158	2	3.5193	0.2793	R.LGFVAGVINR.E	1	Q93050
3049.4208	2	3.3929	0.4987	R.SEEMTLAQLFLQSEAAYCCVSELGELGK.V	1	Q93050
1184.654	2	2.5593	0.4867	K.HLGTLNFGGIR.V	2	Q93050
1292.6792	2	2.2283	0.2275	K.FLPFSFEHIR.E	1	Q93050
2085.0082	2	3.0048	0.6109	K.FTYGFQNIVDAYGIGTYR.E	1	Q93050
1106.6098	2	3.2665	0.346	R.NFLELTELK.F	2	Q93050
969.5409	2	2.6056	0.3654	K.LTFLNSFK.M	1	Q93050
1324.6095	1	2.8264	0.4572	R.DMIDLEANFEK.I	2	Q93050
3476.8371	2	3.9352	0.6241	R.GNPVLQLNPALPGVFGGPYPFGIDPIWNIATNK.L	1	Q93050
1316.6599	2	3.2269	0.4738	R.DLNPDVNVFQR.K	1	Q93050
1541.8368	2	3.6695	0.426	K.SVFIIFFQGDQLK.N	2	Q93050

Vacuolar proton translocating ATPase 116 kDa subunit A isoform 2 (V-ATPase 116-kDa isoform a2) (TJ6)

1896.9972	2	2.2607	0.369	R.GPYPLGIDPIWNLATNR.L	2	Q9Y487
1358.736	2	2.3065	0.4368	K.FVPFSFSLLSSK.F	1	Q9Y487

Vacuolar proton translocating ATPase 116 kDa subunit A isoform 3 (V-ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116

2102.9882	2	3.9778	0.4019	K.AGLLDLPDASVNGWSSDEEK.A	2	Q13488
1125.6268	2	2.3937	0.1666	R.DLPALQEALR.D	1	Q13488
919.5365	2	2.9036	0.3307	R.FLSQVLGR.V	1	Q13488
910.5151	2	2.2826	0.4354	R.GFLIASFR.E	1	Q13488
1132.6366	2	3.9063	0.5366	R.LGELGLVEFR.D	1	Q13488

	1687.8444	2	3.4589	0.5666	R.FTASFQGIVDAYGVGR.Y	1	Q13488
Vam6/Vps39-like protein (hVam6p)							
	1829.0285	2	2.4261	0.1204	R.TFEPRLLVQSIELQR.P	1	Q96JC1
Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2)							
	1665.8084	2	3.4933	0.5241	R.ADALQAGASQFETSAAK.L	1	P19065
Vesicle-associated membrane protein-associated protein A (VAMP-associated protein A) (VAMP-A) (VAP-A) (33 kDa Vamp-associated							
	1617.8852	2	2.3521	0.2635	K.HEQILVLDPPTDLK.F	1	Q9P0L0
	1291.6898	2	2.9686	0.3407	K.GPFTDVVTTNLK.L	1	Q9P0L0
Vesicular integral-membrane protein VIP36 (GP36b glycoprotein)							
	1249.5449	2	2.8202	0.3258	K.DNVDDPTGNFR.S	1	Q12907
Vimentin							
	1836.8	2	2.4352	0.3075	R.DGQVINETSQHHDDLE.-	1	P08670
	3923.0151	3	6.1504	0.6606	K.LHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALR.D	1	P08670
	1093.5278	2	2.8007	0.4851	K.FADLSEAANR.N	2	P08670
	1570.8957	2	2.7479	0.4681	R.ISLPLPNFSSLNLR.E	1	P08670
	1323.6181	2	2.6183	0.3555	R.EEAENTLQSFR.Q	1	P08670
Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1)							
	1959.8783	2	2.6735	0.573	K.SENGLEFTSSGSANTETTK.V	11	P21796
	1374.6582	2	3.1519	0.5309	R.WTEYGLTFTEK.W	1	P21796
	2418.1804	2	5.7635	0.7148	R.GALVLGYEGWLAGYQMNFETAK.S	1	P21796
	2176.0522	2	4.288	0.5876	K.WNTDNTLGTEITVEDQLAR.G	1	P21796
	2103.1814	2	4.64	0.4708	K.VNNSSLIGLGYTQTLKPGIK.L	1	P21796
	2600.1905	3	4.7466	0.4428	K.TDEFQLHTNVNDGTEFGGSIYQK.V	2	P21796
	1030.6148	2	2.9597	0.4453	K.LTLSALLDGK.N	1	P21796
	1946.0096	2	4.6729	0.6118	K.KLETAVNLAWTAGNSNTR.F	1	P21796
Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)							
	2103.1562	3	3.5693	0.3588	K.VNNSSLIGVGYTQTLRPGVK.L	2	P45880
	2528.1694	3	4.132	0.4599	R.TGDFQLHTNVNDGTEFGGSIYQK.V	1	P45880

	1016.5992	2	3.1577	0.5029	K.LTLSALVDGK.S	1	P45880
Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3) (Outer mitochondrial membrane protein porin 3)							
	1030.6148	2	3.2986	0.4853	K.LTLSALIDGK.N	2	Q9Y277
	1907.8776	2	2.9167	0.3396	K.WNTDNTLGTEISWENK.L	1	Q9Y277
Wolframin							
	2263.0618	2	2.2454	0.3421	K.GVIPSSLFLQDDEDDDELAGK.S	1	O76024
XRP2 protein							
	1127.6465	2	2.4498	0.3195	K.APDFLPLLNK.G	1	O75695
	5372.6167	3	3.7283	0.5105	K.DAGLSIFDNTWSNIHDFTPVSGELNWSLLPEDAVVQDYVPIPTTEELK.A	1	O75695
Zinc finger DHHC domain containing protein 5 (Zinc finger protein 375)							
	2618.295	3	5.0735	0.5796	K.GSLEITESQSADAEPPPPPKPDLSR.Y	1	Q9C0B5
Zinc finger protein 305							
	2495.0666	2	3.3221	0.3528	R.CGETREPEEITEEPSACSREDK.Q	1	O43309
Zyxin (Zyxin 2)							
	2597.2748	3	3.7627	0.3524	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	1	Q15942