Supplemental Table S-1a. A list of 1,740 ^{18}O/^{16}O labeled protein-specific peptides quantified by XPRESS, sorted by protein name.

Acc No	Peptide	MH+	z	XC	ΔCN	H/L ratio
130 kD Golgi-localized phosphoprotein						
O00461	R.EADPESEADR.A	1118.4596	2	2.3561	0.3911	0.26
24-dehydrocholesterol reductase precursor (EC 1.3.1.-) (3-beta-hydroxysterol delta-24-reductase)						
Q15392	K.LGC*QDAFPEVYDK.I	1541.6941	2	4.1631	0.5189	0.36
26S proteasome non-ATPase regulatory subunit 1 (26S proteasome regulatory subunit RPN2) (26S						
Q99460	R.QGALIASALIMIQQTEITCPK.V	2229.1981	2	3.0026	0.0846	0.01
Q99460	R.NNNTDLMILK.N	1175.6089	2	2.513	0.2882	0.80
Q99460	R.NNNTDLMILK[.N	1179.6169	2	2.6547	0.1091	0.80
Q99460	R.QGALIASALIMIQQTEITC*PK.V	2286.2196	2	2.7925	0.1863	0.50
Q99460	R.QGALIASALIMIQQTEITC*PK[.V	2290.2276	2	3.0259	0.2066	0.30
40S ribosomal protein S11						
P62280	R.DVQIGDIVTVGEC*RPLSK.T	1986.0325	2	3.6268	0.3622	0.90
40S ribosomal protein S14						
P62263	R.IEDVTPIPSDSTR.R	1429.7169	2	3.2863	0.614	0.34
40S ribosomal protein S18 (Ke-3) (Ke3)						
P62269	R.AGELTEDEVER.V	1247.575	1	1.9502	0.3589	0.38
P62269	R.AGELTEDEVER.V	1247.575	2	2.8509	0.4178	0.33
P62269	R.AGELTEDEVER.V	1247.575	2	3.5555	0.4745	0.33
40S ribosomal protein S3						
P23396	K.DEILPTTPISEQK.G	1470.7686	2	2.4952	0.3366	0.36
40S ribosomal protein S30						
P62861	R.FVNVVPTFGK.K	1107.6197	1	2.4055	0.3986	0.00
4F2 cell-surface antigen heavy chain (4F2hc) (Lymphocyte activation antigen 4F2 large subunit)						
P08195	K.GQSEDPGSLLSLFR.R	1505.7594	2	2.8546	0.5917	0.29
P08195	K.GQSEDPGSLLSLFR.R	1505.7594	2	4.1037	0.6528	0.41
P08195	K.ADLLLSTQPGR[.E	1174.6557	1	3.1942	0.395	0.78
P08195	K.ADLLLSTQPGR.E	1170.6477	2	2.7006	0.3314	0.48
P08195	R.IGDLQAFQGHGAGNLAGLK.G	1866.9821	2	4.7309	0.629	0.52
P08195	R.EEGSPLELER[.L	1162.5717	1	2.3073	0.2353	0.38
P08195	K.ADLLLSTQPGR.E	1170.6477	2	3.3911	0.4232	0.48

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P08195	R.LKLEPHEGLLLR.F	1417.8526	2	2.668	0.3659	0.75
P08195	K.EVELNELEPEK.Q	1328.658	2	3.6895	0.3369	0.26
P08195	K.EVELNELEPEK.Q	1328.658	1	3.3417	0.1638	0.13
P08195	K.EDFDSLLQSAK.K	1252.6056	2	3.308	0.5328	0.69
P08195	K.EDFDSLLQSAK.K	1252.6056	2	3.3159	0.5909	0.68
P08195	K.ADLLLSTQPGREEGSPLELER.L	2310.1936	2	2.952	0.5077	0.78
P08195	K.VAEDEAEAAAAAK.F	1245.5957	2	4.4078	0.577	0.83
P08195	K.VAEDEAEAAAAAK.F	1245.5957	1	2.6753	0.5419	0.69
P08195	R.LDYLSSLK.V	938.5193	1	2.2495	0.3191	0.13
P08195	K.ADLLLSTQPGR.E	1170.6477	1	2.6252	0.533	0.78
P08195	R.LDYLSSLK.V	938.5193	2	2.8924	0.3098	0.23
P08195	R.VILDLTPNYR.G	1203.6732	2	2.796	0.4189	0.28
P08195	R.IGDLQAFQGHGAGNLAGLK[.G	1870.9901	2	4.2409	0.4886	0.49
P08195	R.WC*SWSLSQAR.L	1280.5841	2	3.1134	0.3153	0.47
P08195	K.GQSEDPGSLLSLFR[.R	1509.7674	2	4.0502	0.3561	0.41
P08195	K.EVELNELEPEK.Q	1328.658	2	3.3901	0.2357	0.22
P08195	K.GLVLGPIHK.N	933.588	2	2.8694	0.4224	0.24
P08195	K.EDFDSLLQSAK.K	1252.6056	1	2.1534	0.4723	0.26
P08195	K.DLLLTSSYLSDSGSTGEHTK.S	2111.0139	3	3.3528	0.6266	0.63
P08195	K.EVELNELEPEK.Q	1328.658	2	2.8113	0.2608	1.23
P08195	K.GLVLGPIHK.N	933.588	1	2.0257	0.1698	0.34
P08195	K.SLVTQYLNATGNR.W	1436.7492	2	3.6913	0.5065	0.25
P08195	K.ADLLLSTQPGR.E	1170.6477	2	3.2401	0.4396	0.43
P08195	K.ADLLLSTQPGR.E	1170.6477	1	2.5305	0.4921	0.83
P08195	K.DLLLTSSYLSDSGSTGEHTK.S	2111.0139	2	5.4563	0.709	0.89
P08195	R.VILDLTPNYR.G	1203.6732	2	3.5257	0.294	0.28
P08195	R.IGDLQAFQGHGAGNLAGLK.G	1866.9821	2	5.9329	0.5703	0.49
P08195	R.LKLEPHEGLLLR.F	1417.8526	2	2.4311	0.3084	0.83
P08195	K.EVELNELEPEK.Q	1328.658	1	2.7061	0.1861	0.08
P08195	K.DLLLTSSYLSDSGSTGEHTK[.S	2115.0219	2	5.1395	0.6617	0.89
P08195	R.VILDLTPNYR.G	1203.6732	2	2.7295	0.2105	0.28
P08195	K.EDFDSLLQSAK.K	1252.6056	2	3.378	0.5002	0.75
P08195	K.GQSEDPGSLLSLFR.R	1505.7594	2	3.9349	0.656	0.52
P08195	R.GENSWFSTQVDTVATK.V	1769.8341	2	4.0791	0.5536	0.07
P08195	K.GQSEDPGSLLSLFR[.R	1509.7674	1	2.0698	0.2552	0.58
P08195	K.ADLLLSTQPGR[.E	1174.6557	1	3.0848	0.3806	0.83

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P08195	K.VAEDEAEAAAAAK[.F	1249.6037	1	2.7561	0.5152	0.69
P08195	K.ADLLLSTQPGR.E	1170.6477	2	3.3268	0.396	0.43
P08195	K.ADLLLSTQPGREEGSPLELER.L	2310.1936	2	3.2541	0.5601	1.08
P08195	K.ADLLLSTQPGR.E	1170.6477	2	2.37	0.3197	0.40
P08195	K.EDFDSLLQSAK[.K	1256.6136	1	2.0918	0.3818	0.26
P08195	K.EDFDSLLQSAK.K	1252.6056	2	3.5058	0.582	0.81
P08195	K.EDFDSLLQSAK.K	1252.6056	1	2.145	0.4649	0.30
P08195	K.GQSEDPGSLLSLFR[.R	1509.7674	2	3.4597	0.2675	0.45
P08195	R.VILDLTPNYR.G	1203.6732	2	3.0235	0.3155	0.18
P08195	R.LDYLSSLK.V	938.5193	2	2.8685	0.3376	0.17
P08195	K.DLLLTSSYLSDSGSTGEHTK.S	2111.0139	2	5.6482	0.7271	0.84
P08195	K.DLLLTSSYLSDSGSTGEHTK.S	2111.0139	2	2.8311	0.5666	3.17
P08195	K.GLVLGPIHK.N	933.588	2	2.845	0.416	0.17
P08195	K.DLLLTSSYLSDSGSTGEHTK[.S	2115.0219	2	5.0015	0.6361	0.84
P08195	R.VILDLTPNYR.G	1203.6732	2	3.0053	0.3354	0.18
P08195	K.VAEDEAEAAAAAK.F	1245.5957	2	4.5407	0.5817	1.01
P08195	K.ADLLLSTQPGR.E	1170.6477	2	2.7229	0.2916	0.43
P08195	R.LDYLSSLK.V	938.5193	2	2.6665	0.3018	0.27
P08195	K.VAEDEAEAAAAAK.F	1245.5957	1	2.6659	0.566	0.69
P08195	K.VAEDEAEAAAAAK[.F	1249.6037	1	2.8825	0.5394	0.69
P08195	R.GENSWFSTQVDTVATK.V	1769.8341	2	4.9976	0.6532	0.21
P08195	R.VILDLTPNYR.G	1203.6732	2	3.161	0.215	0.34
P08195	R.LDYLSSLK.V	938.5193	1	2.1654	0.3005	0.13
P08195	R.VILDLTPNYR.G	1203.6732	2	2.8242	0.3943	0.34
P08195	R.LLTSFLPAQLLR[.L	1375.8438	2	3.2762	0.2761	0.27
P08195	K.EDFDSLLQSAK.K	1252.6056	1	2.2368	0.4046	0.26
P08195	K.ADLLLSTQPGR.E	1170.6477	2	3.1322	0.4443	0.40
P08195	R.LLTSFLPAQLLR.L	1371.8358	2	3.1704	0.4813	0.27
P08195	R.IGDLQAFQGHGAGNLAGLK[.G	1870.9901	2	4.3607	0.4626	0.50
P08195	K.GLVLGPIHK.N	933.588	1	2.0628	0.3752	0.33
P08195	K.DLLLTSSYLSDSGSTGEHTK.S	2111.0139	2	5.3118	0.6972	0.89
P08195	R.VILDLTPNYR[.G	1207.6812	1	2.443	0.1769	0.38
P08195	K.DDVAQTDLLQIDPNFGSK.E	1975.9607	2	5.6426	0.5517	0.34
P08195	K.DDVAQTDLLQIDPNFGSK[.E	1979.9687	2	4.5744	0.4716	0.34
P08195	R.LLTSFLPAQLLR[.L	1375.8438	2	2.5959	0.0977	0.27
P08195	K.ADLLLSTQPGR.E	1170.6477	2	3.1946	0.3845	0.40

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P08195	K.ADLLLSTQPGR[.E	1174.6557	1	2.7442	0.2839	0.71
P08195	K.ADLLLSTQPGR.E	1170.6477	1	2.8109	0.5393	0.71
P08195	R.IGDLQAFQGHGAGNLAGLK.G	1866.9821	2	5.4564	0.5266	0.50
P08195	R.LLTSFLPAQLLR.L	1371.8358	1	2.3019	0.437	0.20
P08195	K.GQSEDPGSLLSLFR.R	1505.7594	2	4.2693	0.6399	0.35
P08195	R.LLTSFLPAQLLR[.L	1375.8438	2	3.7368	0.5291	0.27
P08195	K.GQSEDPGSLLSLFR[.R	1509.7674	2	3.6804	0.2446	0.35
P08195	R.LLTSFLPAQLLR.L	1371.8358	2	3.1603	0.4851	0.27
P08195	K.GLVLGPIHK[.N	937.596	2	2.7477	0.2049	0.17
P08195	K.GLVLGPIHK.N	933.588	1	2.4828	0.372	0.33
P08195	R.LDYLSSLK.V	938.5193	1	2.1775	0.3099	0.20
P08195	R.IGDLQAFQGHGAGNLAGLK.G	1866.9821	3	4.0563	0.5262	0.45
60S ribosomal protein L18						
Q07020	K.ILTFDQLALDSPK.G	1460.7995	2	3.6579	0.5517	1.22
Q07020	K.ILTFDQLALDSPK.G	1460.7995	2	2.6792	0.3522	0.63
60S ribosomal protein L18a						
Q02543	R.DLTTAGAVTQC*YR.D	1455.6897	2	3.1017	0.4888	0.28
60S ribosomal protein L23 (Ribosomal protein L17)						
P62829	R.ISLGLPVGAVINC*ADNTGAK[.N	1974.0455	2	4.0143	0.4309	0.94
P62829	R.LPAAGVGDMVMATVK.K	1459.7647	2	3.2952	0.6551	0.17
P62829	R.ISLGLPVGAVINC*ADNTGAK.N	1970.0375	2	4.9863	0.6208	0.94
60S ribosomal protein L31						
P62899	K.LYTLVTYVPVTTFK.N	1644.9247	2	2.336	0.3148	0.37
60S ribosomal protein L36a (60S ribosomal protein L44) (Migration-inducing gene 6 protein)						
P83881	K.DSLYAQGK.R	881.4363	1	2.2964	0.3274	1.11
60S ribosomal protein L4 (L1)						
P36578	K.NVTLPAVFK.A	988.5826	1	2.1547	0.5096	3.01
P36578	R.IEEVPELPLVVEDK.V	1608.8731	2	3.0017	0.429	0.26
P36578	R.NIPGITLLNVSK.L	1268.7573	2	2.7097	0.5518	0.35
78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein)						
P11021	K.SQIFSTASDNQPTVTIK.V	1836.9338	2	4.6573	0.5038	0.37
P11021	K.LYGSAGPPPTGEEDTAEK.D	1818.8392	2	3.196	0.4042	2.41
P11021	K.VLEDSDLK.K	918.4779	1	2.0204	0.2116	0.32
P11021	K.SQIFSTASDNQPTVTIK.V	1836.9338	2	3.5309	0.458	0.36
P11021	K.NQLTSNPENTVFDAK.R	1677.8079	2	4.8444	0.672	2.85

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
7-dehydrocholesterol reductase (EC 1.3.1.21) (7-DHC reductase) (Sterol delta-7-reductase) (Putative						
Q9UBM7	K.VIEC*SYTSADGQR.H	1485.6638	2	3.3168	0.5371	0.29
Q9UBM7	K.FLPGYVGGIQEGAVTPAGVVNK.Y	2173.1652	2	6.2106	0.7391	1.98
Q9UBM7	K.FLPGYVGGIQEGAVTPAGVVNK[.Y	2177.1732	2	4.9744	0.5372	0.68
Q9UBM7	K.FLPGYVGGIQEGAVTPAGVVNK[.Y	2177.1732	2	4.9687	0.5679	1.98
Q9UBM7	K.VIEC*SYTSADGQR[.H	1489.6718	2	2.9336	0.3505	0.29
Q9UBM7	K.FLPGYVGGIQEGAVTPAGVVNK.Y	2173.1652	2	6.1304	0.7303	0.68
Acetyl-coenzyme A transporter 1 (AT-1) (Acetyl-CoA transporter) (Solute carrier family 33 member 1)						
O00400	R.EALLGDTGTGDFLK.A	1436.7268	2	3.6994	0.6013	0.27
O00400	K.EETQGITDTYK.L	1284.5954	2	2.23	0.483	0.10
ADAM metallopeptidase with thrombospondin type 1 motif, 7, preproprotein						
Q6P7J9	R.SC*GGGSSVRDVQC*VDTRDLR[.P	2228.0273	2	2.6319	0.1887	1.87
Adenosine 3'-phospho 5'-phosphosulfate transporter 1 (PAPS transporter 1) (Solute carrier family 35						
Q8TB61	K.ASDEVPLAPR.T	1054.5527	2	2.5056	0.3631	0.84
Q8TB61	K.ASDEVPLAPR.T	1054.5527	1	2.3418	0.4769	1.41
Q8TB61	K.FVSFPTQVLAK.A	1236.6987	2	2.6723	0.5354	0.48
ADP/ATP translocase 1 (Adenine nucleotide translocator 1) (ANT 1) (ADP,ATP carrier protein 1)						
P12235	K.DFLAGGVAAAVSK.T	1205.6525	2	4.0261	0.5817	0.24
ADP/ATP translocase 2 (Adenine nucleotide translocator 2) (ANT 2) (ADP,ATP carrier protein 2)						
P05141	R.AAYFGIYDTAK.G	1219.5994	2	2.9743	0.413	0.25
P05141	R.AAYFGIYDTAK.G	1219.5994	2	3.2597	0.5131	0.15
P05141	K.DFLAGGVAAAISK.T	1219.6681	2	4.7771	0.4931	0.28
P05141	K.DFLAGGVAAAISK.T	1219.6681	2	4.2866	0.5367	0.25
P05141	K.DFLAGGVAAAISK.T	1219.6681	2	4.4021	0.5945	0.28
P05141	R.AAYFGIYDTAK.G	1219.5994	2	2.5474	0.4942	0.27
P05141	K.DFLAGGVAAAISK.T	1219.6681	2	4.6233	0.4712	0.25
P05141	K.DFLAGGVAAAISK.T	1219.6681	1	2.6867	0.5442	0.58
P05141	K.GTDIMYTGTLDC*WR.K	1688.7407	2	2.6801	0.4136	0.16
P05141	K.DFLAGGVAAAISK.T	1219.6681	2	3.8827	0.4361	0.25
Alkyldihydroxyacetonephosphate synthase, peroxisomal precursor (EC 2.5.1.26) (Alkyl-DHAP						
O00116	R.GISDPLTVFEQTEAAAR.E	1804.9076	2	5.0421	0.6511	1.08
Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase						
Q11128	R.PGLMAVEPVTGAPNGSR.C	1652.8425	2	2.3874	0.1033	1.59
Alpha-1,2-mannosyltransferase ALG9 (EC 2.4.1.-) (Asparagine-linked glycosylation protein 9						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9H6U8	R.IVPTDMNDQNLEEPSR.Y	1857.8647	2	3.5877	0.4193	0.36
Alpha-actinin 2 (Alpha actinin skeletal muscle isoform 2) (F-actin cross linking protein)						
P35609	R.RELPPDQAQYCIK[.R	1564.7919	2	2.7597	0.1242	11.07
Alpha-fetoprotein enhancer binding protein (AT motif-binding factor) (AT-binding transcription						
Q15911	R.PHEEPGAAAGSSSK[.K	1328.6208	2	2.3634	0.2826	1.42
Amphoterin-induced protein 1 precursor (Alivin-2)						
Q86WK6	K.QQGMTKVWVTPSNER.V	1760.8748	2	2.2178	0.1162	0.42
Ankyrin repeat, SAM and basic leucine zipper domain-containing protein 1 (Germ cell-specific						
Q8WWH4	R.QGHKNIVLKLLELGANK[.M	1879.1254	2	2.2218	0.1496	0.05
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindin-9) (p35) (Phospholipase A2						
P04083	R.SEDFGVNEDLADSDAR[.A	1743.7435	2	2.6003	0.3123	2.53
Apoptotic chromatin condensation inducer in the nucleus (Acinus)						
Q9UKV3	R.TSTSSSSVQARRLSQPESAEK[.H	2240.1244	2	2.9231	0.2222	3.23
Q9UKV3	K.LSEGSQPAEEEEDQETPSR.N	2117.9105	2	4.0193	0.5932	1.59
Apoptotic protease-activating factor 1 (Apaf-1)						
O14727	K.CIFLRGHQETVK[.D	1434.7653	2	2.3164	0.1678	0.14
ARP5 actin-related protein 5 homolog						
Q8IUY5	K.LSIAVEQAKQK.I	1214.7103	1	1.9497	0.0908	0.26
Aspartyl(Asparaginyl)beta-hydroxylase						
Q9Y4J0	K.EGIESGDPGTDDGR.F	1404.5874	2	3.7684	0.5693	0.36
Q9Y4J0	K.EGIESGDPGTDDGR.F	1404.5874	2	2.5142	0.3463	0.36
ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14)						
P25705	K.TGTAEMSSILEER.I	1423.6733	2	3.8487	0.5386	0.77
P25705	R.ELIIGDR.Q	815.4621	1	2.0026	0.1656	0.22
P25705	R.VLSIGDGIAR[.V	1004.5866	2	2.8526	0.4199	0.38
P25705	R.ELIIGDR[.Q	819.4701	1	1.9729	0.1096	0.22
P25705	R.VLSIGDGIAR.V	1000.5786	2	2.5929	0.3203	0.38
P25705	K.AVDSLVPIGR.G	1026.5942	2	3.0766	0.578	0.32
P25705	R.LTDADAMK[.Y	868.4211	1	2.073	0.2054	0.12
P25705	K.AVDSLVPIGR[.G	1030.6022	1	2.1591	0.2203	0.62
P25705	K.AVDSLVPIGR.G	1026.5942	1	1.9243	0.375	0.61
P25705	R.FNDGSDEK.K	911.3741	2	2.7129	0.2535	0.23
P25705	K.AVDSLVPIGR.G	1026.5942	2	2.4601	0.3902	0.32
P25705	R.TGAIVDVPVGEELLGR[.V	1628.8985	2	3.5287	0.3383	1.20

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P25705	R.EPMQTGIK.A	903.4604	1	1.9365	0.2242	2.60
P25705	K.AVDSLVPIGR.G	1026.5942	2	3.0327	0.5883	0.35
P25705	R.TGAIVDVPVGEELLGR.V	1624.8905	2	2.8547	0.5265	1.64
P25705	R.FNDGSDEK.K	911.3741	1	2.0677	0.2809	0.42
P25705	R.ELIIGDR.Q	815.4621	1	1.9248	0.1114	0.23
P25705	K.AVDSLVPIGR.G	1026.5942	1	2.1381	0.425	0.34
P25705	K.AVDSLVPIGR.G	1026.5942	1	2.1506	0.4655	0.81
P25705	R.ILGADTSVDLEETGR.V	1575.7861	2	4.8393	0.5628	1.08
P25705	K.LELAQYR.E	892.4887	1	1.9911	0.2211	1.01
P25705	R.TGAIVDVPVGEELLGR.V	1624.8905	2	3.8239	0.5479	0.80
P25705	K.TSIAIDTIINQK.R	1316.742	2	3.7828	0.2722	0.44
P25705	K.TSIAIDTIINQK.R	1316.742	2	3.6439	0.435	0.44
P25705	R.VLSIGDGIAR.V	1000.5786	2	2.226	0.3094	0.27
P25705	R.TGAIVDVPVGEELLGR.V	1624.8905	2	4.311	0.5605	0.78
ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)						
P06576	K.VLDSGAPIKIPVGPETLGR.I	1919.096	2	3.6348	0.5321	0.36
P06576	K.IPVGPETLGR.I	1038.5942	1	2.7726	0.4105	0.31
P06576	K.VVDLLAPYAK.G	1088.635	1	2.6209	0.3918	0.41
P06576	K.VVDLLAPYAK.G	1088.635	1	2.1423	0.3224	0.50
P06576	R.AIAELGIYPAVDPLDSTSR.I	1988.0335	2	4.6401	0.5969	0.41
P06576	K.VALVYGQMNEPPGAR.A	1601.8104	2	3.4399	0.4323	0.58
P06576	R.IPSAVGYQPTLATDMGTMQER.I	2266.0842	2	5.0319	0.6729	0.53
P06576	R.TIAMDGTEGLVR.G	1262.6409	2	2.9888	0.3167	0.21
P06576	K.VLDSGAPIK.I	899.5197	1	2.1032	0.3619	0.74
P06576	K.IPVGPETLGR.I	1038.5942	1	2.4551	0.2697	0.26
P06576	R.IMNVIGEPIDER[.G	1389.7173	2	3.9778	0.3267	0.59
P06576	R.IMNVIGEPIDER.G	1385.7093	2	3.6385	0.4971	0.59
P06576	R.TIAMDGTEGLVR.G	1262.6409	2	3.4373	0.5083	0.13
P06576	K.IPVGPETLGR.I	1038.5942	1	2.8809	0.3844	0.30
P06576	R.AIAELGIYPAVDPLDSTSR.I	1988.0335	2	2.6007	0.4884	0.49
ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14) (ATPase subunit F6)						
P18859	R.QTSGGPVDASSEYQQELER.E	2080.9418	2	5.2328	0.6064	0.93
ATP synthase D chain, mitochondrial (EC 3.6.3.14)						
O75947	R.LAALPENPPAIDWAYYK.A	1931.9902	2	4.0681	0.4824	2.23
O75947	K.AGLVDDFEK.K	993.4888	2	2.6613	0.1975	0.13

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
O75947	K.AGLVDDFEK.K	993.4888	1	1.9111	0.219	0.10
O75947	K.AGLVDDFEK.K	993.4888	1	1.9376	0.1638	0.14
O75947	R.LAALPENPPAIDWAYYK[.A	1935.9982	2	3.0622	0.3789	2.23
O75947	K.AGLVDDFEK.K	993.4888	1	2.0714	0.2039	0.29

ATP synthase delta chain, mitochondrial precursor (EC 3.6.3.14)

P30049	K.AQAELVGTADEATR[.A	1435.7154	2	3.7319	0.4232	1.55

ATP synthase e chain, mitochondrial (EC 3.6.3.14)

P56385	R.ELAEDDSILK.-	1132.5732	1	2.6403	0.1065	0.15
P56385	R.ELAEDDSILK.-	1132.5732	1	2.7343	0.091	0.10
P56385	R.ELAEDDSILK.-	1132.5732	1	2.1288	0.2411	0.10
P56385	R.ELAEDDSILK.-	1132.5732	1	2.2688	0.3171	0.10
P56385	R.ELAEDDSILK.-	1132.5732	1	2.63	0.1087	0.10
P56385	R.ELAEDDSILK.-	1132.5732	1	2.227	0.2934	0.15
P56385	-.VPPVQVSPLIK.L	1176.7351	2	2.4016	0.3292	0.67

ATP synthase g chain, mitochondrial (EC 3.6.3.14) (ATPase subunit G)

O75964	K.IVNSAQTGSFK.Q	1151.6055	1	2.2891	0.3657	0.37
O75964	K.IVNSAQTGSFK.Q	1151.6055	2	3.1396	0.5648	0.44
O75964	K.IVNSAQTGSFK[.Q	1155.6135	1	2.1805	0.3865	0.37
O75964	K.IVNSAQTGSFK.Q	1151.6055	1	2.2135	0.486	0.37

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14)

P36542	R.THSDQFLVAFK[.E	1296.6714	2	2.4223	0.3128	0.52
P36542	R.THSDQFLVAFK.E	1292.6634	2	2.9288	0.5005	0.25
P36542	K.EVMLVGIGDK.I	1060.5707	1	2.8721	0.4574	0.54
P36542	K.EVMLVGIGDK.I	1060.5707	1	2.5732	0.3065	0.26

ATP synthase O subunit, mitochondrial precursor (EC 3.6.3.14) (Oligomycin sensitivity conferral

P48047	K.SFLSQGQVLK[.L	1110.6284	2	2.3338	0.3292	0.83
P48047	K.VAASVLNPYVK.R	1160.6674	1	2.3375	0.4208	0.04
P48047	K.VAASVLNPYVK.R	1160.6674	2	3.4735	0.5028	0.14
P48047	R.GEVPC*TVTSASPLEEATLSELK.T	2318.1432	2	4.1369	0.702	1.07
P48047	K.SFLSQGQVLK.L	1106.6204	1	1.9651	0.2884	0.55
P48047	K.SFLSQGQVLK.L	1106.6204	2	2.7249	0.5528	0.83
P48047	R.GEVPC*TVTSASPLEEATLSELK.T	2318.1432	2	4.3242	0.659	1.32
P48047	K.SFLSQGQVLK.L	1106.6204	2	2.6159	0.502	1.20

ATPase family AAA domain containing protein 1

Q8NBU5	K.DTVILPIK.K	898.5608	1	2.3637	0.4174	0.13

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q8NBU5	K.DTVILPIK.K	898.5608	1	2.3799	0.2664	0.13
Q8NBU5	R.FINLQPSTLTDK.W	1376.742	2	2.9193	0.4107	0.03
Q8NBU5	K.DTVILPIK.K	898.5608	1	1.9319	0.3795	2.15
ATP-binding cassette sub-family A member 12 (ATP-binding cassette transporter 12) (ATP-binding						
Q86UK0	K.MLTGDIIPSSGNILIR.N	1699.9411	2	2.2357	0.2752	2.19
ATP-binding cassette sub-family D member 1 (Adrenoleukodystrophy protein) (ALDP)						
P33897	R.GLQAPAGEPTQEASGVAAAK.A	1852.9399	2	5.2088	0.6485	1.95
P33897	R.GLQAPAGEPTQEASGVAAAK.A	1852.9399	2	5.0644	0.6384	1.01
P33897	R.ELEDAQAGSGTIGR.S	1403.6761	2	3.7786	0.5674	0.62
P33897	K.DAGIALLSITHR.P	1266.7165	2	3.7231	0.444	0.31
P33897	R.TAVLLALAAYGAHK.V	1398.8104	2	3.4657	0.557	0.47
P33897	R.NLLTAAADAIER.I	1257.6797	2	3.2762	0.5198	0.09
ATP-binding cassette sub-family D member 3 (70 kDa peroxisomal membrane protein) (PMP70)						
P28288	R.DLNFEVR[.S	896.4603	1	2.3262	0.1808	1.04
P28288	R.ITELMQVLK.D	1074.6227	2	2.7454	0.4653	0.67
P28288	R.DLNFEVR.S	892.4523	2	2.2795	0.3568	0.27
P28288	R.DLNFEVR.S	892.4523	1	2.2997	0.2036	1.04
P28288	K.FDHVPLATPNGDVLIR[.D	1767.9519	2	3.6449	0.3449	0.45
P28288	R.DQVIYPDGR.E	1062.5214	2	2.2105	0.3351	0.45
P28288	K.FDHVPLATPNGDVLIR.D	1763.9439	2	3.2123	0.5129	0.45
P28288	R.PFLDLSHPR.H	1081.5789	2	3.2434	0.3988	0.07
P28288	R.DQVIYPDGR.E	1062.5214	1	2.1845	0.2868	0.33
P28288	R.DQVIYPDGR.E	1062.5214	1	2.3109	0.1551	0.33
ATP-binding cassette sub-family G member 2 (Placenta-specific ATP-binding cassette transporter)						
Q9UNQ0	R.VIQELGLDK.V	1014.583	2	3.0177	0.3041	0.15
Q9UNQ0	K.ATEIIEPSK.Q	987.5357	1	2.0232	0.2845	0.15
Q9UNQ0	K.VGTQFIR.G	820.4676	1	2.0238	0.2071	1.22
Q9UNQ0	K.SSLLDVLAAR.K	1044.6048	1	2.0431	0.3501	0.54
Q9UNQ0	K.VGTQFIR.G	820.4676	1	1.9684	0.1283	1.45
Q9UNQ0	R.VIQELGLDK.V	1014.583	1	2.3869	0.416	0.16
Q9UNQ0	K.PGLNAILGPTGGGK.S	1251.7056	2	4.1023	0.4446	2.82
Q9UNQ0	K.ATEIIEPSK.Q	987.5357	1	2.2986	0.1822	0.15
Q9UNQ0	R.TIIFSIHQPR.Y	1211.6895	2	2.8926	0.4252	0.75
Q9UNQ0	K.ATEIIEPSK.Q	987.5357	1	2.0328	0.2716	0.05
Q9UNQ0	K.SSLLDVLAAR.K	1044.6048	2	2.658	0.3183	0.53

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9UNQ0	R.VIQELGLDK.V	1014.583	1	2.2646	0.3424	0.09
Q9UNQ0	R.VIQELGLDK.V	1014.583	1	2.181	0.2753	0.16
Q9UNQ0	R.KDPSGLSGDVLINGAPR.P	1695.9024	2	3.3053	0.5589	0.16
Q9UNQ0	K.ATEIIEPSK.Q	987.5357	1	2.3074	0.2402	0.05
Q9UNQ0	K.SSLLDVLAAR[.K	1048.6128	1	2.2245	0.3245	0.54
ATP-dependent RNA helicase DDX1 (EC 3.6.1.-) (DEAD box protein 1) (DEAD box protein						
Q92499	K.NQALFPAC*VLKNAELKFNFGEEEFK[.F	2947.4789	3	3.3837	0.2259	2.08
Autophagy protein 3-like (APG3-like) (hApg3) (PC3-96 protein)						
Q9NT62	R.TYDLYITYDKYYQTPR[.L	2107.0149	2	2.516	0.1074	1.82
Autophagy protein 9-like 1 (APG9-like 1)						
Q7Z3C6	R.ESDESGESAPDEGGEGAR[.A	1782.7027	2	3.4797	0.3897	1.46
B aggressive lymphoma protein						
Q8IXQ6	K.FGC*ISTLVSPVQEGNSK.S	1822.9004	2	2.434	0.2143	0.87
BAG family molecular chaperone regulator 2 (BCL2-associated athanogene 2) (BAG-2)						
O95816	R.LLESLDQLELR[.V	1332.75	2	3.3921	0.3237	0.41
O95816	R.LLESLDQLELR.V	1328.742	2	4.0268	0.3869	0.41
O95816	K.TLQQNAESR.F	1046.5225	1	2.0149	0.1727	1.14
Bardet-Biedl syndrome 2 protein						
Q9BXC9	R.NYEENAK.A	867.3843	1	2.0976	0.1334	0.08
Q9BXC9	R.NYEENAK.A	867.3843	1	2.04	0.1384	0.97
Q9BXC9	R.NYEENAK.A	867.3843	1	2.1729	0.1418	0.19
Basigin precursor (CD147 antigen) (Leukocyte activation antigen M6) (Collagenase stimulatory						
P35613	K.EDALPGQK.T	857.4363	1	2.1153	0.3096	0.82
P35613	R.FFVSSSQGR.S	1014.5003	1	2.6565	0.409	0.42
P35613	K.GSDQAIITLR.V	1073.5949	1	2.1307	0.2812	0.24
P35613	K.EDALPGQK.T	857.4363	1	2.1645	0.171	0.38
B-cell lymphoma/leukemia 11B (B-cell CLL/lymphoma 11B) (Radiation-induced tumor suppressor						
Q9C0K0	R.GGGFAPGTEPFPGLFPR.K	1703.854	2	2.5239	0.1244	0.27
B-cell receptor-associated protein 29 (BCR-associated protein Bap29)						
Q9UHQ4	K.EYDQLLK.E	908.4724	1	2.1049	0.1511	0.28
Q9UHQ4	K.EYDQLLK.E	908.4724	1	2.083	0.1769	0.34
B-cell receptor-associated protein 31 (BCR-associated protein Bap31) (p28 Bap31) (CDM protein)						
P51572	K.LKDELASTK.Q	1004.5623	2	3.0098	0.3154	0.33
P51572	K.LKDELASTK[.Q	1008.5703	2	2.7348	0.1531	0.33

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P51572	K.LQAAVDGPMDK.K	1144.5667	1	1.9635	0.4228	0.08
P51572	R.LVTLISQQATLLASNEAFK.K	2047.1434	2	2.7579	0.3968	0.44
P51572	K.YMEENDQLK.K	1169.5143	1	1.9326	0.1312	0.19
P51572	K.LQAAVDGPMDK.K	1144.5667	1	2.1836	0.3546	0.08
P51572	K.LDVGNAEVK.L	944.5047	2	3.087	0.3621	0.31
P51572	K.LKDELASTK.Q	1004.5623	1	2.182	0.3932	0.21
P51572	K.LQAAVDGPMDK.K	1144.5667	1	2.516	0.4703	0.08
P51572	K.AENQVLAMR.K	1031.5302	1	2.0222	0.222	0.19
P51572	K.LDVGNAEVK.L	944.5047	2	3.08	0.3915	0.28
P51572	K.LDVGNAEVK.L	944.5047	2	2.9108	0.2819	0.71
P51572	K.AENQVLAMR.K	1031.5302	1	2.1338	0.1173	0.23
P51572	K.LQAAVDGPMDK.K	1144.5667	2	3.0964	0.4683	0.10
P51572	K.DELASTK[.Q	767.3912	1	2.0142	0.3284	0.43
P51572	K.YDDVTEK.V	869.3887	1	2.4214	0.1691	0.32
P51572	K.LDVGNAEVK[.L	948.5127	2	2.563	0.2699	0.28
Beta crystallin B1						
P53674	R.AEFSGEC*SNLADRGFDR.V	1930.8348	2	2.5747	0.0872	0.19
Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3]						
P61769	R.VNHVTLSQPK.I	1122.6266	2	2.8432	0.5642	0.50
P61769	R.VNHVTLSQPK[.I	1126.6346	2	2.406	0.3905	0.50
Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase (UDP-GlcNAc-2-						
Q9Y223	K.DYIVALQHPVTTDIK[.H	1716.9298	2	2.3158	0.163	1.00
Brain acid soluble protein 1 (BASP1 protein) (Neuronal axonal membrane protein NAP-22) (22 kDa						
P80723	K.KTEAPAAPAAQETK.S	1412.738	2	4.7604	0.6182	0.62
P80723	K.ESEPQAAAEPAEAK.E	1427.6649	2	3.2145	0.4687	0.24
P80723	K.APEQEQAAPGPAAGGEAPK.A	1775.8559	2	5.1826	0.6473	0.71
P80723	K.AEGAATEEEGTPK.E	1289.5856	2	4.4561	0.547	0.21
P80723	K.AEGAATEEEGTPK.E	1289.5856	1	2.0237	0.3947	0.12
P80723	K.ETPAATEAPSSTPK.A	1386.6747	2	2.6031	0.5839	0.32
P80723	K.SDGAPASDSKPGSSEAAPSSK.E	1932.8781	2	3.7348	0.4294	0.16
P80723	K.KTEAPAAPAAQETK[.S	1416.746	2	2.2564	0.1347	0.62
Brefeldin A-inhibited guanine nucleotide-exchange protein 1 (Brefeldin A-inhibited GEP 1) (p200						
Q9Y6D6	K.FPEQKLFAALLIK[.C	1521.917	2	2.335	0.2207	1.66
BTB/POZ domain-containing protein 5						
Q9NXS3	K.ECCAFLESQLDPGNC*IGISR[.F	2215.9911	2	2.9027	0.0916	0.61

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
C-4 methylsterol oxidase (EC 1.14.13.72) (Methylsterol monooxygenase)						
Q15800	R.IFGTDSQYNAYNEK.R	1649.7442	2	4.4459	0.601	1.79
CAAX prenyl protease 1 homolog (EC 3.4.24.84) (Prenyl protein-specific endoprotease 1)						
O75844	K.VYVVEGSK.R	880.4775	1	1.9031	0.2592	0.20
O75844	R.NEEEGNSEEIK.A	1277.5492	1	2.4285	0.2163	0.05
O75844	K.VYVVEGSK.R	880.4775	1	2.1941	0.3554	0.22
O75844	R.NEEEGNSEEIK.A	1277.5492	2	2.7341	0.2253	0.14
O75844	R.NEEEGNSEEIK.A	1277.5492	2	3.587	0.2997	0.08
O75844	R.NEEEGNSEEIK.A	1277.5492	1	2.6227	0.3134	0.06
O75844	R.NEEEGNSEEIK.A	1277.5492	2	3.4878	0.3042	0.08
O75844	K.DIQEDSGMEPR.N	1276.5474	2	3.7453	0.4933	0.22
O75844	K.DIQEDSGMEPR.N	1276.5474	2	2.4397	0.3241	0.66
O75844	K.VYVVEGSK.R	880.4775	1	2.362	0.2611	0.22
Cadherin-related tumor suppressor homolog precursor (Fat protein homolog)						
Q14517	K.VVDLDPCLSKKPLEEK[.P	1816.9856	2	2.2951	0.1722	0.20
Calcium-transporting ATPase type 2C member 1 (EC 3.6.3.8) (ATPase 2C1) (ATP-dependent Ca(2+)						
P98194	K.YISQFK.N	785.4192	1	2.0324	0.2238	0.49
Calnexin precursor (Major histocompatibility complex class I antigen-binding protein p88) (p90)						
P27824	K.AEEDEILNR.S	1088.5218	2	3.0822	0.3175	0.47
P27824	K.AEEDEILNR.S	1088.5218	1	2.0977	0.2533	0.26
P27824	K.AEEDEILNR[.S	1092.5298	2	2.7598	0.3022	0.47
P27824	K.SDAEEDGGTVSQEEEDR.K	1852.7315	2	5.8799	0.6462	1.98
CAMP/cGMP cyclic nucleotide phosphodiesterase 11A3						
Q9GZY7	K.ITRLVQISGASLAEKQEK.H	1971.1233	2	2.3398	0.1161	0.50
Cancer susceptibility candidate gene 5 protein (ALL1-fused gene from chromosome 15q14) (AF15q14)						
Q8NG31	R.TTNEIIKFHSAAMDEK.V	1834.9004	2	2.3774	0.1378	0.07
Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor (EC 6.3.4.16) (Carbamoyl-						
P31327	K.IEFEGQPVDFVDPNK.Q	1733.8381	2	3.9855	0.4449	0.35
Carnitine O-palmitoyltransferase I, mitochondrial liver isoform (EC 2.3.1.21) (CPT I) (CPTI-L)						
P50416	R.SEDPDTSMDSYAK.S	1445.5737	2	3.3997	0.5828	0.29
P50416	R.ILDNTSEPQPGEAR.L	1526.7445	2	3.9601	0.5603	0.41
P50416	R.ILDNTSEPQPGEAR.L	1526.7445	2	3.9075	0.5949	0.93
Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR)						
P11717	R.C*PPETDDGVPCVFPFIFNGK[.S	2243.0278	2	2.2974	0.2538	15.15

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Caveolin-2						
P51636	K.LGFEDVIAEPVTTHSFDK.V	2004.9913	2	5.101	0.5926	0.51
P51636	K.LGFEDVIAEPVTTHSFDK.V	2004.9913	2	4.5376	0.4771	0.51
CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-						
P13987	R.ENELTYYC*C*K.K	1379.5606	2	2.5616	0.5142	11.73
P13987	K.AGLQVYNK.C	892.4887	1	1.9699	0.2073	0.75
P13987	K.FEHC*NFNDVTTR.L	1539.6645	2	3.9196	0.4543	0.50
CDNA FLJ16643 fis, clone TESTI4029528						
Q6ZMV5	K.DIYLFINVIIK.Q	1350.8032	2	2.2609	0.1665	0.24
CDNA PSEC0252 fis, clone NT2RP3003258, highly similar to Likely ortholog of mouse embryonic						
Q8NBI5	R.TFLLMPR.G	877.4964	1	2.098	0.2558	0.59
Q8NBI5	R.TFLLMPR.G	877.4964	1	2.1526	0.2449	0.23
Q8NBI5	R.TFLLMPR.G	877.4964	1	2.0849	0.1085	0.23
Cell cycle checkpoint protein RAD17 (hRad17) (RF-C/activator 1 homolog)						
O75943	R.IVTIEANKNGGKITVPDK.T	1897.0753	2	2.3137	0.2175	0.15
Cell division cycle 5-like protein (Cdc5-like protein) (Pombe cdc5-related protein)						
Q99459	R.YTRANLASK.K	1023.5582	1	2.2662	0.2229	0.28
Q99459	R.YTRANLASK.K	1023.5582	1	2.186	0.1256	0.20
Centaurin-beta 2 (Cnt-b2)						
Q15057	-.MKMTVDFEECLKDSPR.F	1928.8915	2	3.1083	0.0842	0.47
Centrosomal protein 4 (Centrosomal protein of 135 kDa) (Cep135 protein)						
Q66GS9	K.FLNNQYAHKLK[.L	1379.7561	2	2.9719	0.1023	0.30
Centrosome spindle pole associated protein						
Q70F00	K.EEYEAKLEAEMR.T	1497.689	2	2.4526	0.133	0.48
Ceramide glucosyltransferase (EC 2.4.1.80) (Glucosylceramide synthase) (GCS) (UDP-glucose:N-						
Q16739	K.YPNVDARLFIGGKK.V	1577.8798	2	2.2606	0.2006	0.61
Chemokine-binding protein 2 (Chemokine-binding protein D6) (C-C chemokine receptor D6)						
O00590	R.IGCVLVRLR.P	1028.6397	1	2.1349	0.2125	0.55
O00590	R.IGCVLVRLR.P	1028.6397	1	2.2072	0.1398	3.39
Chondroitin sulfate synthase 2 (EC 2.4.1.175) (Glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-						
Q8IZ52	R.NDIVSARPDEWLGR.C	1627.8187	2	3.2042	0.2715	0.34
Chromosome 6 open reading frame 37						
Q5TF85	K.STEDIFPAQLLKLQR[.H	1762.9829	2	2.2582	0.1313	2.59
Q5TF85	K.STEDIFPAQLLKLQR.H	1758.9749	2	2.4863	0.1111	2.59

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
CKLFSF1 protein						
Q6PEV5	R.NISAKTAPR.K	957.5476	1	1.9304	0.312	0.40
Clathrin heavy chain 1 (CLH-17)						
Q00610	R.TSIDAYDNFDNISLAQR.L	1942.9141	2	4.4304	0.5964	0.36
Q00610	K.NNRPSEGPLQTR.L	1368.6979	2	3.2505	0.51	0.98
CMP-sialic acid transporter						
Q5W1L8	R.QDTTSIQQGETASK.E	1493.7078	2	3.9063	0.559	1.43
Coiled-coil-helix-coiled-coil-helix domain containing protein 3						
Q9NX63	R.VAEELALEQAK[.K	1204.655	1	2.949	0.2736	0.51
Q9NX63	R.AAANEQLTR.A	973.5061	1	2.2095	0.2985	0.26
Q9NX63	R.VAEELALEQAK.K	1200.647	2	3.9089	0.4182	0.97
Q9NX63	R.VAEELALEQAK[.K	1204.655	2	3.7789	0.4046	1.05
Q9NX63	R.VTTEQYQK[.A	1000.5077	1	2.0402	0.3325	0.44
Q9NX63	R.VAEELALEQAK.K	1200.647	2	3.9463	0.4423	1.05
Q9NX63	R.VAEELALEQAK[.K	1204.655	2	3.6713	0.3852	0.97
Q9NX63	R.AAANEQLTR.A	973.5061	1	2.0062	0.3575	0.22
Q9NX63	K.AAEEVEAK.F	846.4203	2	2.4348	0.5487	0.13
Q9NX63	R.VAEELALEQAK.K	1200.647	1	2.9626	0.2235	0.51
Q9NX63	R.VAEELALEQAK.K	1200.647	1	2.5216	0.2689	0.46
Q9NX63	R.VAEELALEQAK.K	1200.647	1	2.6397	0.3142	0.51
Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC collagen)						
Q02388	R.GPEASVTQTPVCPR.G	1441.7104	2	2.3273	0.1371	0.44
Q02388	R.GPEASVTQTPVCPR.G	1441.7104	2	2.3084	0.1901	0.44
Q02388	R.GPEASVTQTPVCPR.G	1441.7104	2	2.2432	0.192	0.61
Complement component 1, Q subcomponent binding protein, mitochondrial precursor (Glycoprotein						
Q07021	K.AFVDFLSDEIK.E	1283.6518	2	3.3323	0.4278	0.39
Q07021	K.AFVDFLSDEIK.E	1283.6518	2	3.9924	0.4781	0.38
Q07021	K.VEEQEPELTSTPNFVVEVIK.N	2287.1704	2	4.2113	0.5383	0.68
Core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (EC 2.4.1.122)						
Q9NS00	K.DENTDIAENLYQK[.V	1556.7206	2	3.1352	0.1936	0.30
Coronin-7 (70 kDa WD repeat tumor rejection antigen homolog)						
P57737	K.GLNLTTPGESDGFC*ANKLR.V	2050.0022	2	2.5592	0.1718	0.04
C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-derived factor 1 receptor) (SDF-1						
P61073	K.TSAQHALTSVSR.G	1257.6546	2	3.9244	0.6069	0.16

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Cytochrome c oxidase polypeptide Va, mitochondrial precursor (EC 1.9.3.1)						
P20674	K.GINTLVTYDMVPEPK.I	1676.8564	2	3.6044	0.5217	0.65
P20674	K.IIDAALR.A	771.4723	1	2.0077	0.3061	0.56
Cytochrome c oxidase polypeptide Vb, mitochondrial precursor (EC 1.9.3.1)						
P10606	K.GLDPYNVLAPK.G	1186.6467	2	2.9343	0.6058	0.39
P10606	R.EDPNLVPSISNK.R	1312.6743	2	3.0988	0.5188	0.15
P10606	R.EDPNLVPSISNK.R	1312.6743	2	2.8665	0.4313	0.18
P10606	R.EDPNLVPSISNK.R	1312.6743	1	1.9121	0.5011	0.25
P10606	R.EDPNLVPSISNK.R	1312.6743	2	2.5644	0.2507	1.05
Cytochrome c oxidase polypeptide VIc precursor (EC 1.9.3.1)						
P09669	K.DFEEMR[.K	830.348	1	2.2891	0.2308	0.25
P09669	K.AYADFYR.N	905.4152	1	2.0955	0.1459	0.51
P09669	K.AGIFQSVK[.-	853.4909	2	2.6576	0.142	0.42
P09669	K.AGIFQSVK.-	849.4829	2	2.9165	0.1241	0.42
Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor (EC 1.9.3.1)						
P14406	K.LFQEDDEIPLYLK.G	1622.8312	2	4.2815	0.4045	25.91
P14406	K.GGVADALLYR.A	1034.5629	2	3.4082	0.4721	0.50
P14406	K.GGVADALLYR.A	1034.5629	1	2.4074	0.3751	1.04
P14406	K.GGVADALLYR.A	1034.5629	1	2.5029	0.3865	0.76
Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor (EC 1.9.3.1) (COX IV-1)						
P13073	K.VNPIQGLASK.W	1026.5942	2	2.4411	0.464	0.27
P13073	K.VNPIQGLASK[.W	1030.6022	1	2.5272	0.321	0.83
P13073	K.VNPIQGLASK.W	1026.5942	1	1.913	0.2836	0.83
P13073	K.VNPIQGLASK.W	1026.5942	1	1.9461	0.3887	0.60
Cytochrome c oxidase subunit VIIa-related protein, mitochondrial precursor (COX7a-related protein)						
O14548	K.LTSDSTVYDYAGK.N	1419.6638	2	3.0582	0.561	0.57
O14548	K.LTSDSTVYDYAGK.N	1419.6638	2	3.1374	0.4312	0.57
Cytochrome c1, heme protein, mitochondrial precursor (Cytochrome c-1)						
P08574	K.LFDYFPK.P	929.4767	1	1.9033	0.2839	0.41
P08574	K.PYPNSEAAR.A	1004.4796	1	2.0772	0.1927	0.32
P08574	R.GLLSSLDHTSIR.R	1298.7063	2	2.3526	0.4528	0.27
P08574	R.GLLSSLDHTSIR.R	1298.7063	2	2.4619	0.3589	0.46
P08574	R.GLLSSLDHTSIR.R	1298.7063	2	3.5359	0.5537	0.46
P08574	R.GLLSSLDHTSIR.R	1298.7063	2	3.4453	0.5212	0.46
P08574	K.LFDYFPKPYPNSEAAR.A	1914.9385	2	3.7503	0.5341	1.82

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Cytochrome c-type heme lyase (EC 4.4.1.17) (CCHL) (Holocytochrome c-type synthase)						
P53701	K.GC*PVNTEPSGPTC*EK.K	1632.6992	2	3.1806	0.302	0.40
Cytochrome P450 51A1 (EC 1.14.13.70) (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol						
Q16850	K.DLNLLDR.C	858.468	1	2.1121	0.24	0.36
Cytochrome P450, family 2, subfamily E, polypeptide 2 homolog						
Q6NT55	K.C*REEIQEVMKGR.E	1534.7465	2	2.3643	0.0842	0.19
Cytosolic 5'-nucleotidase 1B (EC 3.1.3.5) (Cytosolic 5'-nucleotidase IB) (cN1B) (cN-IB)						
Q96P26	K.LPSSSTSSR.T	921.4636	1	1.9093	0.2112	0.60
Dapper homolog 1 (hDPR1) (Heptacellular carcinoma novel gene 3 protein)						
Q9NYF0	K.SGGGPEAGVPGRPAGGGHR[.A	1676.8342	2	2.381	0.195	0.22
Death receptor interacting protein splice variant						
Q6YHU2	R.AHGHLQSATDTWENLVSDAR[.I	2212.0508	2	3.0589	0.1926	4.97
Q6YHU2	R.AHGHLQSATDTWENLVSDAR[.I	2212.0508	2	2.7206	0.135	130.58
Q6YHU2	R.AHGHLQSATDTWENLVSDAR[.I	2212.0508	2	3.2826	0.2141	336.49
Dedicator of cytokinesis protein 1 (180 kDa protein downstream of CRK) (DOCK180)						
Q14185	R.PFGVAVMDVTDIINGK[.V	1679.8804	2	2.6455	0.2154	188.67
Defender against cell death 1 (DAD-1)						
P61803	R.FLEEYLSSTPQR.L	1469.7271	2	4.0135	0.4848	0.54
P61803	K.ADFQGISPER.A	1119.5429	2	2.8513	0.3846	0.16
P61803	R.FLEEYLSSTPQR[.L	1473.7351	2	3.3565	0.3075	0.54
Dehydrogenase E1 and transketolase domain containing protein 1						
Q96HY7	R.IGGSVHLIVNNQLGYTTPAER.G	2239.183	2	2.6639	0.0955	1.67
Q96HY7	R.IGGSVHLIVNNQLGYTTPAER.G	2239.183	2	2.8653	0.1268	1.58
Dehydrogenase/reductase SDR family member 8 precursor (EC 1.1.1.-) (17-beta-hydroxysteroid						
Q8NBQ5	R.EDIYSSAK.K	912.4309	1	2.254	0.1894	0.52
Q8NBQ5	R.EDIYSSAK.K	912.4309	1	2.0332	0.3589	0.73
Q8NBQ5	K.FDAVIGYK.M	912.4825	1	2.1658	0.3674	0.08
DEP domain containing 6						
Q8TB45	R.KDDGTFPLDNEVK[.A	1481.7249	2	2.7659	0.1211	0.38
DEP domain containing protein 5						
O75140	R.TRFLLLPAC*VTATK.R	1590.9036	2	2.6356	0.2387	0.17
Dermcidin precursor (Preproteolysin) [Contains: Survival-promoting peptide; DCD-1]						
P81605	K.ENAGEDPGLAR[.Q	1132.536	2	2.7324	0.3503	0.75
P81605	K.ENAGEDPGLAR.Q	1128.528	2	2.8265	0.4668	0.75

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Desmoglein 2, preproprotein						
Q4KKU6	K.SLQEANAEK.V	989.4898	1	2.1814	0.2124	0.08
Q4KKU6	K.VVPSFLPVDQGGSLVGR.N	1726.9486	2	3.3991	0.5838	0.49
Q4KKU6	K.VVPSFLPVDQGGSLVGR.N	1726.9486	2	3.5562	0.53	0.27
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)						
P15924	K.GFFDPNTEENLTYLQLK.E	2028.9913	2	3.0008	0.3241	0.50
DGKG protein						
Q5FWG1	K.YTVHERCVSRNIPGCVK.T	1960.9844	2	2.319	0.2581	0.47
Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20) (Diglyceride acyltransferase) (ACAT-related gene						
O75907	R.LQDSLFSSDSGFSNYR.G	1822.8242	2	4.1123	0.6259	1.91
O75907	R.DAAAGPDVGAAGDAPAPAPNK.D	1832.8773	2	5.7508	0.6877	0.20
Disks large-associated protein 3 (DAP-3) (SAP90/PSD-95-associated protein 3) (SAPAP3) (PSD-						
O95886	R.LPPTLLDQFEK.Q	1300.7147	2	2.2318	0.194	0.37
DNA ligase IV (Ligase IV, DNA, ATP-dependent)						
Q8IY66	K.SLLQLITQSSALEQK[.W	1662.9403	2	3.0547	0.1299	37.85
DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal						
P04053	K.MILDNHALYDKTK.R	1561.8043	2	2.3462	0.1272	0.18
DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1)						
P25205	R.GSSGVGLTAAVTTDQETGER[.R	1939.9334	2	2.3587	0.1379	27.59
DNA-directed RNA polymerase III 62 kDa polypeptide (EC 2.7.7.6) (RNA polymerase C subunit 3)						
Q9BUI4	R.C*YKSIANLIERR.Q	1522.8159	2	2.6957	0.1272	0.66
DNA-directed RNA polymerase, mitochondrial precursor (EC 2.7.7.6) (MtRPOL)						
O00411	R.NVQQIGILK[.P	1016.623	1	1.9334	0.2382	6.29
DnaJ (Hsp40) homolog, subfamily D, member 1 (Growth-inhibiting 22) (DNAJ domain-containing)						
Q5T219	K.DLLETTTK.H	920.4935	1	1.9506	0.103	0.12
Dolichyldiphosphatase 1 (EC 3.6.1.43) (Dolichyl pyrophosphate phosphatase 1)						
Q86YN1	R.PC*GGPHTAVGTK.Y	1181.5732	2	2.7169	0.4702	0.58
Dolichyl-diphosphooligosaccharide-protein glycosyltransferase						
Q5VWA5	R.ELGSEC*GIEFDEEK.T	1641.6949	2	4.4459	0.6128	0.16
Q5VWA5	K.SSLNPILFR.G	1046.5993	1	1.9957	0.221	0.63
Q5VWA5	K.NTLLIAGLQAR.N	1169.7001	1	2.5101	0.4436	0.46
Q5VWA5	R.TLVLLDNLNVR.E	1269.7525	2	2.2677	0.2771	0.20
Q5VWA5	K.SSLNPILFR.G	1046.5993	2	2.3878	0.3122	0.51
Q5VWA5	K.SSLNPILFR[.G	1050.6073	1	2.2722	0.2895	0.63

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q5VWA5	K.TADDPSLSLIK.Y	1159.6205	2	2.954	0.4008	0.27

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor (EC

P04843	R.DISTLNSGK[.K	938.492	1	2.5026	0.3931	0.14
P04843	R.NVESYTK.L	840.4098	1	1.9693	0.3205	0.51
P04843	K.TILPAAAQDVYYR[.D	1484.7875	2	3.1564	0.3788	0.45
P04843	R.SEDLLDYGPFR.D	1311.6216	2	3.6823	0.4585	0.51
P04843	K.TILPAAAQDVYYR.D	1480.7795	2	3.1228	0.4344	0.45
P04843	K.GEDEEENNLEVR[.E	1436.6267	2	3.2205	0.2587	1.00
P04843	R.SEDLLDYGPFR.D	1311.6216	2	2.8926	0.4648	0.48
P04843	R.DISTLNSGK[.K	938.492	1	2.4809	0.3938	0.12
P04843	K.ALTSEIALLQSR.L	1301.7423	1	2.568	0.4251	0.59
P04843	R.DISTLNSGK.K	934.484	1	1.9659	0.4551	0.07
P04843	K.NIEIDSPYEISR.A	1435.7063	1	2.0733	0.4263	0.54
P04843	K.NIEIDSPYEISR.A	1435.7063	2	3.2098	0.3545	0.56
P04843	R.DISTLNSGK.K	934.484	1	2.1562	0.4976	0.14
P04843	R.ATSFLLALEPELEAR.L	1659.8952	2	2.6659	0.3762	0.66
P04843	K.DTYIENEK.L	1011.4629	1	2.2698	0.2897	0.15
P04843	K.GEDEEENNLEVR.E	1432.6187	2	3.5927	0.4242	1.23
P04843	R.SEDLLDYGPFR.D	1311.6216	2	3.8472	0.4858	0.48
P04843	K.VTAEVVLAHLGGGSTSR[.A	1657.8999	2	4.2459	0.5332	1.78
P04843	K.VTAEVVLAHLGGGSTSR.A	1653.8919	2	4.8691	0.6498	1.85
P04843	K.GEDEEENNLEVR[.E	1436.6267	2	3.0347	0.2663	0.85
P04843	K.GEDEEENNLEVR.E	1432.6187	1	2.0113	0.4464	0.96
P04843	R.DISTLNSGK.K	934.484	1	2.1156	0.5067	0.05
P04843	K.NIEIDSPYEISR.A	1435.7063	2	3.4654	0.5549	0.56
P04843	R.TVDLSSHLAK.V	1070.584	2	2.5035	0.4033	0.28
P04843	R.DISTLNSGK.K	934.484	1	2.1385	0.507	0.12
P04843	K.ALTSEIALLQSR.L	1301.7423	2	3.7516	0.274	0.38
P04843	K.DPAAEAR.M	729.3526	2	2.3192	0.3021	0.93
P04843	K.TEGSDLC*DR.V	1052.4313	2	2.5305	0.4017	0.41
P04843	K.DTYIENEK.L	1011.4629	1	2.2946	0.292	0.13
P04843	K.TEGSDLC*DR[.V	1056.4393	2	3.1494	0.387	0.41
P04843	R.NVESYTK[.L	844.4178	1	2.0079	0.3787	0.29
P04843	R.DVPAYSQDTFK.V	1270.595	1	2.4027	0.2556	0.32
P04843	K.LPVALDPGAK[.I	984.5855	1	2.3299	0.4139	0.43
P04843	K.ALTSEIALLQSR.L	1301.7423	2	3.6039	0.355	0.38

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P04843	K.LPVALDPGAK.I	980.5775	1	2.0505	0.4176	0.43
P04843	R.NVESYTK.L	840.4098	1	1.9818	0.2973	0.29
P04843	K.LPVALDPGAK.I	980.5775	1	2.1227	0.2662	0.43
P04843	K.LPVALDPGAK.I	980.5775	1	2.3554	0.4127	0.43
P04843	K.NIEIDSPYEISR.A	1435.7063	2	3.2271	0.5658	1.05
P04843	R.SEDLLDYGPFR.D	1311.6216	2	3.9745	0.4076	0.48
P04843	R.SEDLLDYGPFR.D	1311.6216	2	3.1991	0.4623	0.51
P04843	R.SEDLLDYGPFR.D	1311.6216	2	4.0796	0.4632	0.51
P04843	R.DVPAYSQDTFK.V	1270.595	2	2.576	0.5878	0.32
P04843	R.DVPAYSQDTFK.V	1270.595	1	2.625	0.4871	0.32
P04843	K.LPVALDPGAK.I	980.5775	1	1.938	0.2787	0.43
Dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase (EC 2.4.1.-) (Dol-P-Man						
Q92685	R.SGSAAQAEGLC*K.Q	1178.547	1	2.0287	0.4281	0.41
Q92685	R.SGSAAQAEGLC*K.Q	1178.547	2	2.927	0.3783	0.21
Q92685	R.FLPEALFLHR.A	1242.6994	2	2.3995	0.492	0.66
Q92685	R.TGESILSLLR[.D	1092.639	2	4.5	0.3449	0.34
Q92685	R.TGESILSLLR.D	1088.631	2	2.936	0.2122	0.34
Down-regulated in metastasis protein (Key-1A6 protein) (Novel nucleolar protein 73) (NNP73)						
O75691	K.VLYLLELYCEDKQSKIK.E	2085.13	2	2.6055	0.0886	0.31
O75691	K.VLYLLELYCEDKQSKIK.E	2085.13	2	2.6751	0.1311	0.34
DTTR431 (C-type lectin superfamily 4, member G)						
Q6UXB4	K.QTAALGALK[.E	876.528	1	2.103	0.0882	7.38
Dynamin-1-like protein (EC 3.6.5.5) (Dynamin-like protein) (Dnm1p/Vps1p-like protein) (DVLP)						
O00429	R.SQLDINNKK[.S	1063.5873	2	2.4773	0.2641	9.32
O00429	R.SQLDINNKK[.S	1063.5873	2	2.5761	0.2725	8.45
Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2)						
Q13409	K.EGEIQAGAK[.L	906.4658	1	2.076	0.1156	0.83
Dystrophin						
P11532	K.QTNLQWIKVSRALPEK.Q	1911.0811	2	2.2503	0.1952	0.05
Elongation factor 2 (EF-2)						
P13639	K.DLEEDHAC*IPIK.K	1439.6835	2	3.8025	0.3842	0.12
Elongation factor Tu, mitochondrial precursor (EF-Tu) (P43)						
P49411	K.YEEIDNAPEER.A	1364.5965	2	2.7578	0.293	0.58
Elongation of very long chain fatty acids protein 1						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9BW60	R.C*DPVDYSNSPEALR[.M	1626.7195	2	4.8147	0.4528	29.23
Q9BW60	R.C*DPVDYSNSPEALR[.M	1626.7195	2	2.6959	0.2312	26.36
Elongation protein 3 homolog (Hypothetical protein DKFZp761L098)						
Q9BVF7	K.FQHQGFGMLLMEEAER.I	1922.8888	2	2.2588	0.1908	1.13
Ephrin type-A receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ECK) (Epithelial						
P29317	K.TYVDPHTYEDPNQAVLK.F	1989.9552	2	4.7973	0.6248	0.35
P29317	R.VLEDDPEATYTTSGGK.I	1682.7756	2	2.8278	0.3903	0.05
P29317	R.VLEDDPEATYTTSGGK.I	1682.7756	2	4.6428	0.5454	0.10
Epithelial protein lost in neoplasm						
Q9UHB6	K.SEISENTDASGK.I	1237.5543	2	3.8127	0.5536	0.26
Epsin-4 (Epsin-related protein) (EpsinR) (Enthoprotin) (Clathrin interacting protein localized in the						
Q14677	K.ASPDQNASTHTPQSSVK.T	1754.8304	2	4.4169	0.5829	0.45
ERGIC-53 protein precursor (ER-Golgi intermediate compartment 53 kDa protein) (Lectin, mannose-						
P49257	K.NSMSETVR.L	923.4251	1	1.9877	0.3831	0.09
ER-Golgi intermediate compartment 32 kDa protein (ERGIC-32)						
Q969X5	K.IVPTVYEDK.S	1063.567	1	2.0924	0.2103	0.30
Erythrocyte band 7 integral membrane protein (Stomatin) (Protein 7.2b)						
P27105	R.VQNATLAVANITNADSATR.L	1929.9988	2	6.5008	0.7188	0.63
P27105	R.AMAAEAEASR.E	1006.4622	1	2.4012	0.2859	0.22
P27105	R.VQNATLAVANITNADSATR.L	1929.9988	2	6.9561	0.7216	0.58
P27105	R.VQNATLAVANITNADSATR[.L	1934.0068	2	5.4481	0.4908	0.58
P27105	R.VQNATLAVANITNADSATR[.L	1934.0068	2	5.3943	0.4852	0.63
Eukaryotic translation initiation factor 3 subunit 8 (eIF3 p110) (eIF3c)						
Q99613	R.GGVPLVK.E	669.4294	1	1.9433	0.1872	2.26
EVI-5 homolog						
O60447	R.ESNQVVQK[.E	935.4923	2	2.2476	0.0958	0.52
F-actin capping protein alpha-1 subunit (CapZ alpha-1)						
P52907	K.EASDPQPEEADGGLK.S	1542.6918	2	3.6286	0.5988	0.23
Factor for adipocyte differentiation 104 variant (Fragment)						
Q53EP0	K.DLRPATDYHVR.V	1342.6862	1	2.1742	0.1169	0.07
Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein						
Q01469	K.FEETTADGR[.K	1029.4614	2	2.5396	0.4269	1.61
F-box/LRR-repeat protein 19 (F-box and leucine-rich repeat protein 19)						
Q6PCT2	K.VGGDACLLRGSDPGGPGLLPPR.V	2104.0968	2	3.3168	0.4117	0.34

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q6PCT2	K.VGGDACLLRGSDPGGPGLLPPR.V	2104.0968	2	2.5951	0.337	0.41
Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C						
Q9Y5Y0	K.AIPADSPTDQEPK[.T	1372.6722	2	2.2332	0.3266	0.48
FKSG14 protein (Leucine zipper protein AF5alpha) (SoxLZ/Sox6 leucine zipper binding protein)						
Q9BS16	R.QDLEMVLSTK[.E	1167.6057	1	2.3469	0.1143	25.44
FKSG30						
Q9BYX7	K.EITALAPSIMK[.I	1177.6628	2	2.4268	0.3087	180.23
FLJ00086 protein (Fragment)						
Q9H7J3	R.GEWCMVGGCGQPQVGAGR.A	1791.7724	2	2.2246	0.1144	0.18
FLJ00144 protein (Fragment)						
Q8TEP9	R.FFLSSGLIDK.V	1126.6143	2	3.2219	0.5339	0.08
FLJ20625 protein						
Q6IAA8	R.KLLLDPSSPPTK.A	1295.7569	2	2.9839	0.4647	21.79
Flotillin-1						
O75955	R.GEAEAFAIGAR.A	1091.548	1	2.3361	0.4695	0.29
O75955	K.LPQVAEEISGPLTSANK.I	1753.9331	2	5.135	0.6429	0.29
O75955	K.LPQVAEEISGPLTSANK.I	1753.9331	2	4.7986	0.657	0.56
Flotillin-2 (Epidermal surface antigen) (ESA)						
Q14254	K.VDEIVVLSGDNSK.V	1374.7111	2	4.4614	0.6369	1.36
Q14254	K.IGEAEAAVIEAMGK.A	1388.709	2	3.4972	0.5506	0.23
Q14254	K.VDEIVVLSGDNSK.V	1374.7111	2	4.4321	0.6474	3.35
FMI protein						
Q92735	R.C*QPLHHEEPAALSER.S	1773.8337	2	2.2356	0.1454	0.79
Forkhead box protein G1C (Forkhead-related protein FKHL3) (HFK3) (Fragment)						
Q14488	K.LAAFRWCALTSTGLTFMDR[.A	2164.0809	2	2.2597	0.1582	0.49
FP2653 (ELSD1897) (MGC3123 protein)						
Q71RG4	K.FLNDTEELAVARPEDTVGALK[.S	2292.1849	2	2.4276	0.2631	0.63
Q71RG4	K.FLNDTEELAVARPEDTVGALK.S	2288.1769	2	3.9126	0.5593	0.63
Frizzled 6 precursor (Frizzled-6) (Fz-6) (hFz6)						
O60353	R.QYHIPCPYQAKAKAR[.P	1777.9297	2	2.7091	0.1259	0.79
O60353	R.QYHIPCPYQAKAKAR[.P	1777.9297	2	2.6112	0.1744	0.95
FYVE, RhoGEF and PH domain containing protein 6 (Zinc finger FYVE domain containing						
Q6ZV73	K.EFDKNIALLDEQCK[.K	1669.8232	2	2.5204	0.2054	0.81

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
G2/mitotic-specific cyclin-F						
P41002	R.ASSEIVCQLFQASQAVSK.Q	1895.9531	2	2.2679	0.1077	0.85
Gamma crystallin B (Gamma crystallin 1-2)						
P07316	R.GQMSELTDDC*LSVQDR.F	1853.8004	2	2.5033	0.1556	0.31
Gap junction beta-6 protein (Connexin-30) (Cx30)						
O95452	K.DIEDIK.K	732.3774	1	1.9655	0.1352	0.09
Gene rich cluster, C3f gene						
Q6P1A2	K.DQNSLSSEQQK.Y	1263.5811	1	2.193	0.454	0.48
Q6P1A2	K.DQNSLSSEQQK[.Y	1267.5891	2	4.0876	0.3047	0.65
Q6P1A2	K.IPNSIIPALK.R	1065.6667	2	3.2621	0.2043	0.29
General receptor for phosphoinositides 1-associated scaffold protein (GRP1-associated scaffold protein)						
Q7Z6J2	R.KAELEARLQYLK[.Q	1465.8504	2	2.7592	0.1268	1.45
Q7Z6J2	R.KAELEARLQYLK[.Q	1465.8504	2	2.6999	0.103	2.54
Glutamate receptor, ionotropic kainate 1 precursor (Glutamate receptor 5) (GluR-5) (GluR5)						
P39086	K.NNDIEQAFC*FFYGLQC*K.Q	2153.9419	2	2.3114	0.115	0.41
Glutamate--cysteine ligase catalytic subunit (EC 6.3.2.2) (Gamma-glutamylcysteine synthetase)						
P48506	R.EERGLEPLK.N	1070.584	2	2.2392	0.1712	0.57
Glutathione synthetase (EC 6.3.2.3) (Glutathione synthase) (GSH synthetase) (GSH-S)						
P48637	K.EAGKILSNNPSK.G	1257.6797	2	2.2959	0.2139	0.04
P48637	K.EAGKILSNNPSK.G	1257.6797	2	2.3607	0.157	0.08
Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)						
Q5JR58	K.LVITGNLITIFQER.D	1616.937	2	2.2916	0.3599	0.17
Glyceraldehyde-3-phosphate dehydrogenase, liver (EC 1.2.1.12) (GAPDH)						
P04406	R.GALQNIIPASTGAAK[.A	1415.7984	2	3.3202	0.2672	2.09
Glycogen phosphorylase, liver form (EC 2.4.1.1)						
P06737	R.YEYGIFNQKIR[.D	1434.7507	2	2.6672	0.0879	0.42
Glycolipid transfer protein (GLTP)						
Q9NZD2	R.TLQNILEVEK.E	1186.6678	2	2.3418	0.1181	0.48
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-12 subunit						
Q9UBI6	R.SDPLLIGIPTSENPFK.D	1727.9214	2	3.5177	0.5581	0.24
Q9UBI6	R.SDPLLIGIPTSENPFK.D	1727.9214	2	3.255	0.4462	0.19
Q9UBI6	K.TASTNNIAQAR.R	1146.5862	1	1.9232	0.3409	0.09
Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 2 (Transducin beta chain 2) (G						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P62879	K.AC*GDSTLTQITAGLDPVGR.I	1931.9491	2	4.9543	0.5476	0.80
Guanine nucleotide-binding protein G(k), alpha subunit (G(i) alpha-3)						
P08754	R.ISQSNYIPTQQDVLR.T	1761.913	2	4.5407	0.4215	1.04
P08754	R.EYQLNDSASYYLNDLDR.I	2078.9302	2	5.2606	0.5592	0.56
Guanine nucleotide-binding protein, alpha-14 subunit (G-protein alpha subunit 14)						
O95837	R.EYQLSDSAKYYLTDIDR.I	2079.9869	2	2.5646	0.1287	0.16
HCV F-transactivated protein 1						
Q6J203	R.QNFDVRPQSGANGLPK.H	1727.8824	2	2.6047	0.4237	0.44
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)						
P11142	K.SFYPEEVSSMVLTK.M	1616.7876	2	4.0742	0.5523	0.15
P11142	K.SFYPEEVSSMVLTK.M	1616.7876	2	3.4391	0.4761	0.15
P11142	R.FDDAVVQSDMK.H	1254.5671	2	3.9909	0.4977	0.09
P11142	K.DAGTIAGLNVLR[.I	1203.6823	2	3.5952	0.4891	0.83
P11142	K.DAGTIAGLNVLR.I	1199.6743	2	2.3103	0.1894	0.21
P11142	K.NQVAMNPTNTVFDAK.R	1649.7952	2	4.6005	0.5809	0.61
P11142	K.NQVAMNPTNTVFDAK.R	1649.7952	2	3.8641	0.6048	1.91
P11142	K.DAGTIAGLNVLR.I	1199.6743	2	3.7006	0.3522	0.83
P11142	K.EIAEAYLGK.T	993.5251	1	2.1559	0.3759	0.46
Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein						
P04792	K.DGVVEITGK.H	917.4938	1	2.3192	0.4178	1.12
P04792	K.DGVVEITGK[.H	921.5018	1	2.2461	0.3152	1.12
P04792	K.LATQSNEITIPVTFESR.A	1905.9916	2	4.0525	0.5359	0.38
HECT domain and RCC1-like domain protein 3						
Q15034	R.ESPCHVKLLRTQK[.V	1542.8552	2	2.3491	0.2138	2.39
Hermansky-Pudlak syndrome 3 protein						
Q969F9	K.LEPDRFC*GGGRDALFVAAGCK[.V	2243.0827	2	2.557	0.1051	1.38
Histone H1.5 (Histone H1a)						
P16401	K.ATGPPVSELITK.A	1212.6834	2	2.4001	0.2934	0.25
P16401	K.ATGPPVSELITK.A	1212.6834	2	2.896	0.5008	0.25
Histone H4						
P62805	R.DAVTYTEHAK.R	1134.5426	2	3.1649	0.4115	0.52
P62805	R.ISGLIYEETR.G	1180.6208	1	2.7114	0.1047	0.26
P62805	K.TVTAMDVVYALK.R	1310.7025	2	3.694	0.5648	0.44
P62805	K.VFLENVIR.D	989.5778	1	2.0187	0.1861	0.41

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P62805	R.ISGLIYEETR.G	1180.6208	2	3.8161	0.5032	0.23
P62805	R.DNIQGITK[.P	892.4865	1	2.1517	0.3084	0.21
P62805	R.ISGLIYEETR.G	1180.6208	1	2.6018	0.3615	0.33
P62805	R.ISGLIYEETR.G	1180.6208	2	3.9156	0.4682	0.23
P62805	K.VFLENVIR.D	989.5778	1	2.1958	0.0977	0.42
P62805	R.ISGLIYEETR.G	1180.6208	1	2.531	0.3404	0.24
P62805	K.VFLENVIR.D	989.5778	1	2.0674	0.1016	0.72
P62805	K.VFLENVIR[.D	993.5858	2	3.115	0.3665	0.76
P62805	R.ISGLIYEETR.G	1180.6208	1	2.5184	0.3679	0.26
P62805	R.DNIQGITKPAIR.R	1325.7536	2	3.747	0.2322	0.41
P62805	R.DNIQGITKPAIR[.R	1329.7616	2	3.9041	0.4015	0.41
P62805	K.VFLENVIR[.D	993.5858	1	1.9091	0.1283	0.41
P62805	K.VFLENVIR.D	989.5778	2	2.3443	0.3686	0.98
P62805	K.VFLENVIR[.D	993.5858	2	3.1449	0.3968	0.98
P62805	R.ISGLIYEETR.G	1180.6208	2	3.686	0.4716	0.27
P62805	R.DNIQGITK[.P	892.4865	1	1.9591	0.3014	0.18
P62805	K.VFLENVIR.D	989.5778	2	2.5183	0.3155	0.76
P62805	K.VFLENVIR[.D	993.5858	1	2.0548	0.2068	0.42
P62805	R.DNIQGITKPAIR.R	1325.7536	2	3.2434	0.2333	0.36

Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific (EC 2.1.1.43) (H3-K36-

Q96L73	K.QKPLISNSHTDHLMGC*TK[.S	2071.019	2	2.4669	0.3756	0.33

Histone-lysine N-methyltransferase, H3 lysine-9 specific 4 (EC 2.1.1.43) (Histone H3-K9

Q15047	R.MEAEKASTSGLGIK[.D	1425.7385	2	2.3843	0.2471	3.21

HIV GAG protein

GAG_Protein	R.FAVNPGLLETSEGC*R.Q	1649.7952	2	3.5408	0.478	4.92
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	1	2.4639	0.3639	19.06
GAG_Protein	K.ETINEEAAEWDR[.L	1466.6525	2	3.625	0.4912	3.48
GAG_Protein	K.ETINEEAAEWDR.L	1462.6445	2	2.9195	0.4888	3.48
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	2	3.733	0.3525	5.59
GAG_Protein	R.WIILGLNK[.I	960.6008	1	2.1498	0.4029	4.19
GAG_Protein	K.ELYPLASLR[.S	1065.607	1	2.0811	0.3395	1.20
GAG_Protein	R.FGEETTTPSQK.Q	1224.5743	2	3.7155	0.5265	5.59
GAG_Protein	R.AEQASQEVK[.N	993.4978	2	2.7017	0.2092	21.13
GAG_Protein	R.MYSPTSILDIR[.Q	1299.6744	2	3.9451	0.5298	5.53
GAG_Protein	R.AEQASQEVK.N	989.4898	1	2.3137	0.3616	2.28

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
GAG_Protein	K.QEPIDKELYPLASLR[.S	1775.9669	2	3.4511	0.4602	10.18
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	2	3.426	0.3257	6.29
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	1	2.2979	0.3982	19.06
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	2	3.6589	0.3108	4.92
GAG_Protein	R.FAVNPGLLETSEGC*R[.Q	1653.8032	2	4.4563	0.5638	4.92
GAG_Protein	R.FGEETTTPSQK.Q	1224.5743	2	3.7687	0.5458	5.77
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	1	2.4538	0.4499	12.48
GAG_Protein	R.QILGQLQPSLQTGSEELR.S	1997.0662	2	5.7279	0.6476	2.18
GAG_Protein	K.ELYPLASLR[.S	1065.607	1	2.1783	0.3039	2.00
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	2	3.7172	0.3453	5.77
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	1	2.5495	0.4146	12.70
GAG_Protein	R.FGEETTTPSQK[.Q	1228.5823	1	2.2273	0.4178	38.98

HLAT1-3TM

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q8MH63	K.RADGAAPAGEGEGVTLQR.N	1754.878	2	2.6399	0.4779	0.34
Q8MH63	K.RADGAAPAGEGEGVTLQR.N	1754.878	2	3.0186	0.445	0.51

Homeobox protein Cux-2 (Cut-like 2)

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
O14529	R.NPELLSPKEQR[.E	1314.7143	2	2.256	0.1054	6.43

Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q15011	K.VAESTEEPAGSNR.G	1346.6183	2	4.1079	0.504	0.41

Hormonally up-regulated neu tumor-associated kinase (EC 2.7.1.37) (Serine/threonine-protein

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P57058	K.LGYKNSDVINTVLSNR[.A	1796.9632	2	2.6354	0.0978	0.60

Hornerin

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q86YZ3	R.GSGSGQSPSSGQHGTGFGR[.S	1751.7823	2	3.8438	0.5435	3.58

HSPC039 protein (Hypothetical transmembrane protein) (Immediate early response 3 interacting

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9Y5U9	K.NIGWGTDQGIGGFGEEPGIK.S	2031.977	2	5.2517	0.582	0.50

HSPC049

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9NZY6	R.LGDSELAMVC*SQRNASLSQSLR.V	2422.1813	2	2.7365	0.2639	0.04

HSPC121

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9P035	R.LESEGSPETLTNLR.K	1545.7755	2	3.8319	0.5617	0.37
Q9P035	R.QVNITVQK.K	929.5415	1	1.9078	0.1968	0.28
Q9P035	R.QVNITVQK[.K	933.5495	1	2.2021	0.223	0.28
Q9P035	R.QVNITVQK.K	929.5415	1	2.4471	0.2265	0.30
Q9P035	R.LESEGSPETLTNLR.K	1545.7755	2	4.1309	0.5724	0.34

Hydroxyacid oxidase 1 (EC 1.1.3.15) (HAOX1) (Glycolate oxidase) (GOX)

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9UJM8	R.NRFKLPPQLR.M	1268.7586	2	2.5176	0.161	0.05
Hypothetical protein						
Q32M75	K.C*FSKSSALNKHGEIHAR[.E	1945.9792	2	2.3827	0.1997	0.29
Q3MJA4	K.WFMKQNTEESTIGR[.K	1730.8297	2	2.2072	0.0807	0.12
Q4G0N0	R.EVDDSSAQK.G	978.4374	1	2.0976	0.1636	0.24
Q49AJ3	R.FTRSDELQRHSR.T	1531.7724	2	2.5588	0.1587	4.58
Q3B7X4	K.GDTPASATAGDTLSVPAPAVQPEESLK.T	2609.2941	3	4.1185	0.5496	0.51
Q4G0N0	R.EVDDSSAQK.G	978.4374	1	1.9685	0.1426	0.15
Q4G0N0	R.EVDDSSAQK.G	978.4374	1	1.9856	0.1284	1.43
Q6PQ33	R.REISNVSREAR.A	1316.7029	2	2.4854	0.0975	0.53
Q3B7X4	K.GDTPASATAGDTLSVPAPAVQPEESLK.T	2609.2941	2	4.4152	0.4428	0.35
Q3KRF4	R.LFLVAGNFFRIQK[.L	1556.9078	2	2.8268	0.1986	0.50
Hypothetical protein (Novel protein)						
Q8NFQ8	R.LLAPEAGSHPQQTQK.L	1604.8391	2	3.7631	0.5454	1.24
Hypothetical protein C14orf39						
Q8N1H7	K.MNETIFMKFR[.V	1320.657	2	2.3474	0.1055	0.53
Hypothetical protein DKFZp313B047						
Q5H9S5	K.EDVDAAVK.Q	846.4203	1	2.129	0.1948	0.11
Hypothetical protein DKFZp434C011 (RACGAP1 protein)						
Q9H0H5	K.DFEDFR.K	828.3523	1	2.1049	0.17	0.40
Hypothetical protein DKFZP434J0113						
Q8IYM0	R.GIESLTALC*STLIEGQKKR.S	2104.1431	2	2.2579	0.1381	0.28
Q8IYM0	K.RGIESLTALCSTLIEGQKK[.R	2051.1296	2	2.5164	0.2454	0.42
Hypothetical protein DKFZp434P0216 (Fragment)						
Q8NDA2	R.DLRVLALLPC*EASGSPK.P	1825.984	2	2.3639	0.1384	1.30
Hypothetical protein DKFZp686C0394						
Q5HY96	K.DIILTVK.E	801.508	1	2.5469	0.1661	0.06
Hypothetical protein DKFZp686J07132						
Q6MZH2	R.FPSSELK[.N	811.4327	1	2.2037	0.1042	0.05
Hypothetical protein DKFZp686O22167						
Q68DQ6	R.FDNPAAVSPTPTR.Q	1372.6856	2	3.3217	0.5012	0.28
Hypothetical protein DKFZp781B2386						
Q6AHZ3	K.ISEIQLEPNNFPK[.K	1532.8086	1	2.2904	0.0842	32.08
Hypothetical protein DKFZp781D1175						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q5H9U9	K.IMEEKCISEKQADK.C	1651.803	2	2.4299	0.1438	0.13
Hypothetical protein DKFZp781H1112						
Q68DK2	R.CGQDINPQR.V	1030.4735	1	2.0181	0.0906	0.45
Hypothetical protein DKFZp781O2147						
Q6AHZ1	K.NEIVDR.S	745.3839	1	1.9275	0.1445	0.08
Hypothetical protein FAM71B						
Q8TC56	K.MVEKQNIEAKVEK.A	1545.8305	2	2.334	0.1597	0.41
Hypothetical protein FLJ10846						
Q9NVA4	R.DDISEQVR.H	961.4585	1	2.0614	0.3245	0.24
Hypothetical protein FLJ13213						
Q9H8U9	R.QQNRFNDFDHRER.G	1761.8164	2	2.5535	0.1096	0.57
Hypothetical protein FLJ14938 (Hypothetical protein NT2RP2003902) (GK001 protein)						
Q96A33	R.ELLESNFTLVGDDGTNK.E	1851.8971	2	4.5095	0.6331	0.29
Q96A33	K.RQDLLNVLAR.M	1197.7062	2	2.856	0.3409	0.26
Hypothetical protein FLJ16464						
Q6ZN37	R.QLNEVENNIKK.K	1328.7169	1	3.0441	0.1474	0.13
Hypothetical protein FLJ16617						
Q6ZMX2	K.DLWKLLMALNKIK[.I	1589.9578	2	2.9556	0.1396	9.13
Hypothetical protein FLJ20261						
Q9NXG7	R.KVLDDLTMTR.S	1191.6402	2	2.5286	0.0851	0.43
Hypothetical protein FLJ20422 (AVLG582)						
Q9NX61	R.DFLHQPPFGETR.F	1443.7015	2	2.5237	0.3098	1.01
Hypothetical protein FLJ20455 (TPA018) (Ovarian carcinoma immunoreactive antigen) (OCIA						
Q9NX40	R.SVPLAATSMLITQGLISK.G	1830.0405	2	2.9094	0.4803	1.14
Q9NX40	K.NITYEELR.N	1037.5262	1	2.3444	0.1329	0.76
Q9NX40	R.SVPLAATSMLITQGLISK[.G	1834.0485	2	2.2559	0.2798	1.14
Q9NX40	K.LENSPLGEALR.S	1198.6426	2	3.4592	0.4008	0.45
Hypothetical protein FLJ23658						
Q8TEC2	R.PGC*C*VLLHSFTQLPGRR.R	1998.016	2	2.6916	0.1712	1.90
Hypothetical protein FLJ31346						
Q96N66	K.LVSLASEVQDLHLAQR.K	1778.9759	2	4.7227	0.5039	0.27
Hypothetical protein FLJ31359						
Q96N64	K.VFSKNVSKCVTPDGR[.T	1640.8556	2	2.2124	0.1784	5.21

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Hypothetical protein FLJ32363						
Q96MH7	K.ENEFHCQIMK.S	1278.5606	2	2.2819	0.1562	0.14
Hypothetical protein FLJ32786						
Q96M69	K.IKVEEKVSAVNK.Y	1343.7893	2	3.0436	0.085	0.19
Hypothetical protein FLJ37549						
Q8N1U5	R.NPMNVMNVRRPLLVFHR.-	2093.1371	2	2.7983	0.1387	0.36
Hypothetical protein FLJ39430						
Q8N8I4	K.HLREEEEEGEK[.H	1388.6419	2	2.7983	0.132	0.23
Hypothetical protein FLJ41103						
Q6ZWG9	R.TEAGGEGEPGRGTVVPGAALR[.V	1985.0177	2	2.2981	0.232	10.50
Hypothetical protein FLJ42583						
Q6ZVH2	R.PGVGAHACNPSTLGGRGGR[.I	1767.8798	2	2.3894	0.1413	0.36
Hypothetical protein FLJ43035						
Q6ZV38	-.MSAMGSVRPVAGQHSHLR[.A	1924.9723	2	3.0002	0.0914	0.79
Hypothetical protein FLJ44477						
Q6ZTN4	R.GGTRGRHAAAGAGETTEK[.E	1730.8659	2	2.3437	0.0897	7.73
Hypothetical protein FLJ44884						
Q6ZT81	R.WGLWDFIRSWRGSLIK[.K	2024.0996	2	2.2998	0.1283	9.16
Hypothetical protein FLJ45221						
Q6ZST6	R.SESRALAWEGTWRR.I	1704.8565	2	2.7359	0.3526	0.20
Hypothetical protein FLJ46180						
Q6ZRQ5	K.NLDIGVLAEKFSCAFR.E	1782.9207	2	2.4103	0.0849	0.15
Hypothetical protein FLJ46844						
Q6ZQW6	R.MQGPSLPCLGTGTPTLWPHR.C	2149.0681	2	2.3063	0.2458	0.54
Hypothetical protein FP14381						
Q71M32	R.PLPHCFCHKVNALVR[.G	1737.917	2	2.6539	0.1859	0.30
Hypothetical protein gene +108						
Q96S30	R.LGEGGPDSDQAIR.D	1314.6284	2	4.023	0.5884	0.31
Hypothetical protein KIAA1426						
Q96RY5	R.PTCVQAVEGMSRMIVELHR.K	2156.0773	2	2.2651	0.1473	0.17
Hypothetical protein LOC116238						
Q96CP7	R.LPLPVHVR.A	930.5883	2	2.3374	0.3308	6.23
Hypothetical protein LOC133957 (Hypothetical protein FLJ25701)						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q96BQ5	R.TAAFQQDLEAK.Y	1221.611	2	2.2056	0.1616	0.35
Hypothetical protein MGC2731						
Q9BQ15	K.NLNLIFIVLETGR.V	1501.8737	2	2.873	0.331	0.24
Q9BQ15	K.NLNLIFIVLETGR.V	1501.8737	2	2.7548	0.3385	0.34
Q9BQ15	K.NLNLIFIVLETGR.V	1501.8737	2	2.5349	0.2798	0.42
Hypothetical protein MGC33365						
Q8NDZ4	R.FLQLNKCPACFGTSWC*R.R	2030.9398	2	2.3693	0.1635	0.65
Hypothetical protein MGC34713						
Q8IV33	K.EDFNTLCEILAPSSMVK.F	1896.9082	2	2.2604	0.1692	0.12
Hypothetical protein PRO1855						
Q96AG4	K.LTTLPSDFC*GLTHLVK.L	1801.9517	2	3.5702	0.4499	0.39
Q96AG4	K.ATILDLSC*NK.L	1134.5823	2	3.2466	0.4923	0.13
Q96AG4	K.DNPLDPVLAK.V	1081.5888	1	2.7102	0.4805	0.15
Q96AG4	K.DNPLDPVLAK.V	1081.5888	2	2.2248	0.4103	0.46
Q96AG4	K.ATILDLSC*NK.L	1134.5823	1	2.0684	0.3158	0.19
Q96AG4	K.LTTLPSDFC*GLTHLVK.L	1801.9517	2	3.5139	0.5529	0.39
Q96AG4	K.DNPLDPVLAK.V	1081.5888	1	2.1096	0.2368	0.15
IGHG4 protein						
Q8TC63	R.WVLSRLQLQESGPGLLK.P	1924.1015	2	2.242	0.0812	0.32
Import inner membrane translocase subunit TIM50, mitochondrial precursor						
Q3ZCQ8	K.IPDEFDNDPILVQQLR.R	1911.9811	2	5.575	0.6138	0.83
Q3ZCQ8	R.RAPDQAAEIGSR.G	1270.6498	2	2.8218	0.3831	3.28
Inhibitor of nuclear factor kappa-B kinase epsilon subunit (EC 2.7.1.-) (I kappa-B kinase epsilon)						
Q14164	R.C*VVAGMNHLRENGIVHR.D	1961.9909	2	2.2021	0.1815	0.19
Inner membrane protein OXA1L, mitochondrial precursor (Oxidase assembly 1-like protein) (OXA1-						
Q15070	R.QTFTHNPLLQPGK.D	1480.7907	2	2.4827	0.3121	0.45
Q15070	K.DNPPNIPSSSSKPK.S	1467.7438	2	2.6577	0.4429	0.49
Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor) (Type 2						
Q14571	K.GGEEPIEESNILSPVQDGTK.K	2099.0139	2	3.5461	0.4158	0.80
Inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-trisphosphate receptor) (Type 3						
Q14573	R.LFTTTEQDEQGSK.V	1483.6911	2	3.8092	0.4452	0.12
Intraflagellar transport 81 (Carnitine deficiency-associated protein expressed in ventricle 1) (CDV-1						
Q8WYA0	K.KEAKAEELQEAK.E	1373.7271	2	3.2581	0.1047	3.09
ITI-like protein (Inter-alpha (Globulin) inhibitor H5-like)						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q6UXX5	K.NVVFVIDVSSSMFGTK[.M	1733.8909	2	2.5029	0.1343	103.23
Jagunal homolog 1						
Q8N5M9	R.AAGTDGSDFQHR.E	1261.5556	2	3.1465	0.5101	0.32
Ka35 protein						
Q6A163	K.ADLEAQVQSLK.E	1201.6423	2	2.3319	0.1769	0.61
Q6A163	K.ADLEAQVQSLK.E	1201.6423	2	2.2123	0.1351	0.81
Kenae1						
Q86Z20	K.NIEESWIQKYDR.L	1580.7703	2	2.4321	0.1158	0.04
Keratin 10						
Q14664	R.YSSSSKQFSSSR.S	1350.6284	2	4.0119	0.5919	0.17
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14)						
P02533	K.DAEEWFFTK.T	1172.5259	2	3.2831	0.4147	0.81
Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)						
P08779	K.IIAATIENAQPILQIDNAR[.L	2068.1528	2	4.6533	0.5177	1.19
Keratin, type I cytoskeletal 18 (Cytokeratin-18) (CK-18) (Keratin-18) (K18)						
P05783	R.AQIFANTVDNAR.I	1319.6702	2	4.3068	0.5562	0.18
P05783	R.SLGSVQAPSYGAR.P	1292.6593	2	3.2396	0.1684	0.30
P05783	K.VIDDTNITR[.L	1050.5557	2	3.5691	0.4425	0.56
P05783	K.VIDDTNITR.L	1046.5477	2	2.9744	0.4989	0.56
P05783	R.QAQEYEALLNIK.V	1419.7478	2	3.1854	0.5032	0.16
P05783	R.SLGSVQAPSYGAR.P	1292.6593	2	2.7201	0.1162	0.25
P05783	R.TVQSLEIDLDSMR.N	1506.7468	2	3.0801	0.3838	0.18
P05783	K.VIDDTNITR[.L	1050.5557	1	2.4654	0.2468	0.70
P05783	K.VIDDTNITR.L	1046.5477	1	2.1398	0.4776	0.70
P05783	R.AQIFANTVDNAR.I	1319.6702	2	3.69	0.4823	0.82
P05783	R.AQIFANTVDNAR.I	1319.6702	1	2.0332	0.512	0.27
P05783	K.VVSETNDTK.V	992.4895	1	2.2288	0.3185	0.04
P05783	R.AQYDELAR.K	965.4687	1	2.124	0.2363	0.30
P05783	K.VVSETNDTK.V	992.4895	1	2.1202	0.2381	0.04
P05783	R.SLGSVQAPSYGAR[.P	1296.6673	2	3.2809	0.136	0.25
Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)						
P35527	K.VQALEEANNDLENK.I	1586.7657	2	5.1567	0.5173	0.57
P35527	K.STMQELNSR.L	1065.4993	2	2.8872	0.359	0.76
P35527	R.SGGGGGGGLGSGGSIR.S	1232.5978	2	4.7719	0.5984	0.79

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P35527	K.STMQELNSR.L	1065.4993	1	1.9947	0.2413	2.00
P35527	K.STMQELNSR[.L	1069.5073	1	1.9758	0.1664	2.00
P35527	R.QEYEQLIAK[.N	1125.5917	1	2.1675	0.1675	0.98
P35527	K.NYSPYYNTIDDLK.D	1605.7431	2	3.0342	0.4535	0.18
P35527	K.TLLDIDNTR[.M	1064.5713	2	2.8142	0.2921	2.08
P35527	R.FSSSSGYGGGSSR[.V	1239.5367	2	3.1712	0.4541	2.44
P35527	R.FSSSSGYGGGSSR[.V	1239.5367	1	2.3044	0.4027	1.07
P35527	R.QGVDADINGLR.Q	1157.5909	2	3.329	0.4585	0.68
P35527	R.GGSGGSYGGGGSGGGYGGGSGSR.G	1791.7277	2	5.4109	0.7144	0.11
P35527	K.VQALEEANNDLENK[.I	1590.7737	1	3.5649	0.3513	0.84
P35527	K.DQIVDLTVGNNK.T	1315.6852	2	3.722	0.509	0.35
P35527	K.VQALEEANNDLENK.I	1586.7657	2	5.5608	0.522	0.51
P35527	K.VQALEEANNDLENK[.I	1590.7737	2	4.7229	0.4456	0.51
P35527	R.SGGGGGGGLGSGGSIR.S	1232.5978	2	4.4568	0.5561	5.62
P35527	R.FSSSSGYGGGSSR[.V	1239.5367	2	4.0101	0.5716	3.26
P35527	K.DIENQYETQITQIEHEVSSSGQEVQSSAK[.E	3268.5219	3	4.7095	0.5779	0.88
P35527	K.STMQELNSR.L	1065.4993	2	2.8053	0.3349	0.27
P35527	K.DQIVDLTVGNNK[.T	1319.6932	2	3.576	0.2199	0.35
P35527	K.VQALEEANNDLENK[.I	1590.7737	2	3.9878	0.3969	0.57
P35527	R.FSSSSGYGGGSSR.V	1235.5287	1	2.1522	0.5106	1.10
P35527	R.SGGGGGGGLGSGGSIR.S	1232.5978	1	2.3846	0.4367	1.45
P35527	R.SGGGGGGGLGSGGSIR.S	1232.5978	2	4.6212	0.5507	0.88
P35527	R.FSSSSGYGGGSSR.V	1235.5287	1	2.3774	0.4211	1.07
P35527	K.TLLDIDNTR.M	1060.5633	1	2.0577	0.2677	0.44
P35527	K.DQIVDLTVGNNK.T	1315.6852	1	2.5143	0.598	0.23
P35527	K.TLLDIDNTR.M	1060.5633	1	2.267	0.302	0.49
P35527	K.TLLDIDNTR[.M	1064.5713	1	2.3541	0.1691	0.49
P35527	K.TLLDIDNTR[.M	1064.5713	2	3.1063	0.3059	2.35
P35527	K.TLLDIDNTR.M	1060.5633	2	2.8653	0.4155	2.35
P35527	K.VQALEEANNDLENK[.I	1590.7737	2	3.6416	0.2654	1.94
P35527	R.GGSGGSYGGGGSGGGYGGGSGSR.G	1791.7277	2	5.983	0.7035	0.09
P35527	K.TLLDIDNTR.M	1060.5633	2	2.5834	0.4667	2.08
P35527	K.VQALEEANNDLENK.I	1586.7657	1	3.0614	0.3877	0.84
P35527	K.STMQELNSR.L	1065.4993	1	2.2014	0.1947	1.28
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair						
P04264	R.TLLEGEESR.M	1033.516	1	2.1236	0.2193	0.68

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P04264	K.LNDLEDALQQAK[.E	1361.7038	2	5.2156	0.4575	1.68
P04264	R.SLDLDSIIAEVK.A	1302.7151	2	3.9534	0.4468	0.48
P04264	R.TLLEGEESR[.M	1037.524	1	2.196	0.2835	0.84
P04264	R.SLDLDSIIAEVK.A	1302.7151	1	2.4206	0.3851	1.47
P04264	R.SEIDNVKK[.Q	936.5127	2	2.4941	0.213	1.96
P04264	K.LNDLEDALQQAK.E	1357.6958	1	2.7534	0.4007	0.92
P04264	R.TNAENEFVTIK.K	1265.6372	2	3.7776	0.4901	1.90
P04264	K.LNDLEDALQQAK[.E	1361.7038	2	2.6902	0.2472	1.68
P04264	R.GSGGGSSGGSIGGR.G	1092.5028	1	2.0161	0.4463	1.39
P04264	R.TLLEGEESR[.M	1037.524	1	2.285	0.2694	0.68
P04264	R.TLLEGEESR[.M	1037.524	2	2.4905	0.0974	1.20
P04264	R.TLLEGEESR.M	1033.516	2	2.4555	0.389	1.20
P04264	R.TLLEGEESR[.M	1037.524	1	2.101	0.1292	0.68
P04264	R.SLDLDSIIAEVK.A	1302.7151	2	4.215	0.4148	0.40
P04264	R.SLDLDSIIAEVK[.A	1306.7231	1	2.3639	0.1519	1.82
P04264	K.LNDLEDALQQAK[.E	1361.7038	2	4.5826	0.4528	1.68
P04264	R.GSGGGSSGGSIGGR.G	1092.5028	2	3.5633	0.4323	1.37
P04264	R.TNAENEFVTIK.K	1265.6372	1	2.0442	0.3341	1.32
P04264	K.YEELQITAGR.H	1179.6004	1	2.5473	0.4233	0.93
P04264	K.SLNNQFASFIDK.V	1383.6903	2	3.6352	0.4433	0.16
P04264	R.DYQELMNTK.L	1141.5194	1	2.725	0.4052	0.98
P04264	R.DYQELMNTK[.L	1145.5274	1	2.9507	0.3026	0.98
P04264	R.GSGGGSSGGSIGGR.G	1092.5028	2	3.406	0.4606	1.49
P04264	K.AEAESLYQSK[.Y	1129.5502	1	2.4883	0.3629	1.04
P04264	R.GSGGGSSGGSIGGR[.G	1096.5108	1	2.1491	0.3494	1.61
P04264	K.DVDGAYMTK.V	999.4452	2	2.3961	0.5261	1.36
P04264	K.WELLQQVDTSTR[.T	1479.7569	1	2.3154	0.4554	2.68
P04264	K.DVDGAYMTK.V	999.4452	1	2.2965	0.4178	0.68
P04264	R.GSGGGSSGGSIGGR[.G	1096.5108	2	3.7758	0.5108	1.37
P04264	K.LNDLEDALQQAK[.E	1361.7038	2	4.6145	0.4688	1.49
P04264	K.YEELQITAGR[.H	1183.6084	1	2.357	0.2982	0.93
P04264	K.LNDLEDALQQAK[.E	1361.7038	2	4.9394	0.4395	1.49
P04264	K.SLNNQFASFIDK.V	1383.6903	2	3.353	0.4464	0.29
P04264	R.SLDLDSIIAEVK[.A	1306.7231	1	2.5815	0.2976	1.47
P04264	K.YEELQITAGR.H	1179.6004	2	3.9533	0.5144	0.73
P04264	K.WELLQQVDTSTR.T	1475.7489	2	3.9216	0.4606	1.42

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P04264	K.DVDGAYMTK[.V	1003.4532	1	2.2821	0.4562	0.68
P04264	R.DYQELMNTK[.L	1145.5274	1	2.953	0.2983	0.84
P04264	K.LNDLEDALQQAK[.E	1361.7038	1	2.8443	0.3532	0.92
P04264	R.FSSC*GGGGGSFGAGGGFGSR.S	1765.7347	2	4.0077	0.5621	1.42
P04264	R.TLLEGEESR.M	1033.516	2	2.3004	0.3218	1.74
P04264	R.TNAENEFVTIK.K	1265.6372	1	1.9024	0.1641	1.15
P04264	R.TLLEGEESR[.M	1037.524	1	2.0428	0.2232	0.89
P04264	R.TLLEGEESR[.M	1037.524	2	2.8002	0.2354	1.74
P04264	R.TLLEGEESR[.M	1037.524	1	2.2203	0.3296	0.89
P04264	K.SLNNQFASFIDK[.V	1387.6983	1	1.9186	0.1439	0.30
P04264	R.TLLEGEESR[.M	1037.524	2	2.5304	0.1584	1.42
P04264	R.DYQELMNTK.L	1141.5194	1	2.6823	0.4268	0.84
P04264	R.TNAENEFVTIK.K	1265.6372	2	3.5032	0.5286	1.56
P04264	K.AEAESLYQSK.Y	1125.5422	1	2.1397	0.3498	1.04
P04264	R.TNAENEFVTIK[.K	1269.6452	1	2.1071	0.2556	1.15
P04264	R.DYQELMNTK.L	1141.5194	2	2.8724	0.4027	2.10
P04264	K.AEAESLYQSK[.Y	1129.5502	1	2.6723	0.2477	1.04
P04264	K.AEAESLYQSK.Y	1125.5422	2	3.7109	0.5627	0.58
P04264	K.AEAESLYQSK.Y	1125.5422	1	2.6075	0.4011	1.04
P04264	K.AEAESLYQSK[.Y	1129.5502	1	2.7006	0.4227	1.04
P04264	R.TNAENEFVTIK[.K	1269.6452	2	3.6878	0.3814	1.60
P04264	R.TLLEGEESR.M	1033.516	1	2.2731	0.2257	0.89
P04264	K.LNDLEDALQQAK[.E	1361.7038	2	4.527	0.413	1.41
P04264	R.TNAENEFVTIK.K	1265.6372	1	1.9113	0.1416	1.05
P04264	K.WELLQQVDTSTR[.T	1479.7569	2	4.1529	0.3932	0.80
P04264	R.TNAENEFVTIK[.K	1269.6452	1	1.9616	0.1868	1.05
P04264	R.TLLEGEESR[.M	1037.524	1	1.9493	0.1359	0.84
P04264	K.LNDLEDALQQAK[.E	1361.7038	1	2.7186	0.3828	1.28
P04264	R.DYQELMNTK.L	1141.5194	1	2.539	0.4162	0.68
P04264	K.QISNLQQSISDAEQR.G	1716.8511	2	4.6722	0.5926	0.85
P04264	K.QISNLQQSISDAEQR[.G	1720.8591	2	4.7732	0.4017	0.85
P04264	K.WELLQQVDTSTR.T	1475.7489	2	4.0916	0.5042	0.76
P04264	K.SLNNQFASFIDK.V	1383.6903	2	3.6917	0.4499	0.25
P04264	R.SGGGFSSGSAGIINYQR.R	1657.7929	2	4.3161	0.5525	0.69
P04264	K.SISISVAR[.G	836.4967	2	2.3829	0.1808	4.31
P04264	K.QISNLQQSISDAEQR[.G	1720.8591	2	4.5529	0.3851	1.24

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P04264	R.DYQELMNTK[.L	1145.5274	1	2.7737	0.3124	0.68
P04264	R.FSSC*GGGGGSFGAGGGFGSR[.S	1769.7427	2	5.518	0.5843	1.42
P04264	K.LNDLEDALQQAK.E	1357.6958	2	4.7501	0.4021	1.49
P04264	K.SLNNQFASFIDK.V	1383.6903	1	3.0498	0.221	0.30
Keratin, type II cytoskeletal 1b						
Q7Z794	K.MEIAELNR[.T	979.5008	1	1.9528	0.0902	0.42
Keratin, type II cytoskeletal 5 (Cytokeratin-5) (CK-5) (Keratin-5) (K5) (58 kDa cytokeratin)						
P13647	K.LAELEEALQK[.A	1147.6336	1	2.5401	0.1063	0.94
P13647	K.YEELQQTAGR[.H	1198.5829	1	2.3668	0.34	1.81
P13647	K.LAELEEALQK.A	1143.6256	1	2.0986	0.2067	0.94
P13647	K.LAELEEALQK.A	1143.6256	2	3.861	0.4078	0.59
P13647	K.LAELEEALQK[.A	1147.6336	2	4.0632	0.3693	0.59
Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin)						
P08729	K.LEAAIAEAEER.G	1201.6059	2	3.763	0.4727	0.27
P08729	R.LDADPSLQR.V	1014.5214	2	2.5173	0.2613	0.79
P08729	R.PGGLGSSSLYGLGASR.P	1478.7598	2	4.9835	0.6427	0.63
P08729	R.LPDIFEAQIAGLR.G	1442.8002	2	2.8126	0.3797	6.34
P08729	R.LPDIFEAQIAGLR.G	1442.8002	2	3.2707	0.5615	0.30
P08729	K.VDALNDEINFLR.T	1418.7274	2	3.8463	0.1854	0.31
Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keraton-8) (K8)						
P05787	R.LQAEIEGLK.G	1000.5673	1	2.3397	0.2474	0.11
P05787	R.LQAEIEGLK.G	1000.5673	1	2.2144	0.3087	0.09
P05787	R.LQAEIEGLK.G	1000.5673	1	2.1364	0.1998	0.09
P05787	R.LQAEIEGLK.G	1000.5673	1	2.2099	0.1119	0.11
P05787	R.LQAEIEGLK.G	1000.5673	2	2.2805	0.3339	0.11
Keratinocyte associated protein 2						
Q6PG45	K.ISSTLYQAAAPVLTPAK.V	1730.9687	2	4.3933	0.623	0.62
KIAA1731 protein (Fragment)						
Q9C0D2	K.HIMEIEEQK[.Q	1160.5747	2	2.7872	0.2339	82.56
KIAA1853 protein (Fragment)						
Q96JH4	R.KPALPSLLGAQR[.L	1254.7659	1	1.9016	0.1159	4.30
Kinectin (Kinesin receptor) (CG-1 antigen)						
Q86UP2	K.ECMAGTSGSEEVK.V	1327.5504	2	2.7165	0.3983	0.42
Kinesin-like protein KIF22 (Kinesin-like DNA-binding protein) (Kinesin-like protein 4)						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q14807	K.ESGAINTSLFVLGK.V	1435.7791	2	2.2944	0.1938	0.58
Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase)						
Q16719	K.FTNLLTSILDSAETK.N	1652.8741	2	2.5024	0.213	0.22
Lanosterol synthase (EC 5.4.99.7) (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol						
P48449	R.DGTAC*AEVSRACDFLLSR.Q	1970.9059	2	2.5154	0.1069	0.33
Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light						
Q01650	K.GDVSNLDPNFSFEGTK.L	1726.7919	2	4.5152	0.4742	0.30
Q01650	K.GDVSNLDPNFSFEGTK.L	1726.7919	2	4.3905	0.4535	0.09
Q01650	K.GDVSNLDPNFSFEGTK.L	1726.7919	2	4.8914	0.4606	0.17
Q01650	K.GDVSNLDPNFSFEGTK.L	1726.7919	1	3.1466	0.5864	0.55
Q01650	K.GDVSNLDPNFSFEGTK.L	1726.7919	2	4.7619	0.4589	0.22
Q01650	K.GDVSNLDPNFSFEGTK[.L	1730.7999	2	4.1296	0.4493	0.20
Leucine zipper transcription factor-like 1						
Q8TC61	K.TLNDKTENQK[.S	1194.6092	2	2.3321	0.1018	8.93
Leucine zipper-EF-hand containing transmembrane protein 1, mitochondrial precursor						
O95202	K.VAEVEGEQVDNK.A	1316.6329	2	4.1886	0.4187	0.27
Leukocyte immunoglobulin-like receptor subfamily B member 4 precursor (Leukocyte						
Q8NHJ6	R.QNPLEPKNKAR.F	1294.7226	2	2.2883	0.1133	1.03
LLGL protein						
O00188	R.PQVHYSCIR.K	1102.5462	2	2.2057	0.1018	0.52
LOC389203 protein (Fragment)						
Q8N5G0	R.AGIVQEDVQPPGLK.V	1450.79	2	3.5312	0.5692	0.17
LOC51234 protein						
Q9BUI5	R.GSGQGDSLYPVGYLDK.Q	1655.7911	2	3.5465	0.5607	0.54
Long-chain fatty acid transport protein 1 (EC 6.2.1.-) (Fatty acid transport protein 1) (FATP-1)						
Q6PCB7	K.TARRDLFGLSVLIR.V	1616.9595	2	2.7476	0.1507	0.10
Lysosome membrane protein II (LIMP II) (Scavenger receptor class B member 2) (85 kDa lysosomal						
Q14108	R.DQSVGDPK.I	845.3999	1	1.9061	0.1408	0.20
Q14108	R.VEEVGPYTYR.E	1212.5895	2	3.0808	0.4384	0.31
Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1)						
P14174	-.PMFIVNTNVPR.A	1287.6878	2	3.2464	0.5796	0.41
MBC3205 (Hypothetical protein UNQ501)						
Q6UW68	R.HTFGLVQSK.L	1016.5524	2	2.2252	0.5907	0.47

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Mcd4p homolog						
O95427	K.GWKENPVEFDSLFNESK.Y	2025.9552	2	2.3328	0.1254	0.34
Membrane associated progesterone receptor component 1 (mPR)						
O00264	K.FYGPEGPYGVFAGR.D	1516.7219	2	4.1382	0.6447	0.98
O00264	R.GDQPAASGDSDDDEPPPLPR.L	2035.8839	2	4.8741	0.7283	0.22
O00264	R.FDGVQDPR.I	933.4425	2	2.263	0.1976	0.27
O00264	R.GDQPAASGDSDDDEPPPLPR.L	2035.8839	2	5.09	0.7424	0.34
O00264	K.EGEEPTVYSDEEEPK.D	1737.7337	2	3.6372	0.4999	0.24
Membrane associated progesterone receptor component 2 (Progesterone membrane binding protein)						
O15173	R.GLGAGAGAGEESPATSLPR[.M	1701.8533	2	4.0244	0.5094	2.31
O15173	R.GLGAGAGAGEESPATSLPR.M	1697.8453	2	5.0456	0.5325	2.31
O15173	R.DFSLEQLR.Q	1007.5156	2	2.4383	0.4273	0.38
O15173	R.DFSLEQLR.Q	1007.5156	1	1.9925	0.2555	0.35
Membrane protein (STMF151) (LOC54499) (Xenogeneic cross-immune protein)						
Q9UM00	K.QAGGFLGPPPPSGK.F	1309.6899	2	3.7699	0.467	0.55
Q9UM00	K.ETITESAGR.Q	963.4742	1	2.1412	0.3293	0.31
Q9UM00	R.DLSMVR.M	720.3709	1	2.0548	0.1373	0.24
MGC13159 protein						
Q5BJH2	R.EGDAGPETSTAVEK.K	1390.6332	2	3.105	0.5823	0.28
Microsomal glutathione S-transferase 1 (EC 2.5.1.18) (Microsomal GST-1) (Microsomal GST-I)						
P10620	R.KVFANPEDC*VAFGK.G	1581.773	2	2.2763	0.3087	0.67
P10620	R.KVFANPEDC*VAFGK.G	1581.773	2	3.4597	0.4158	0.65
P10620	K.VFANPEDC*VAFGK.G	1453.678	2	3.4745	0.5199	0.36
P10620	K.VFANPEDC*VAFGK.G	1453.678	2	3.5678	0.6443	0.54
P10620	R.KVFANPEDC*VAFGK[.G	1585.781	2	2.4376	0.2285	0.67
Migration-inducing protein 7						
Q5J9I5	R.WIPSSWFPRVILKQC*K.R	2045.1153	2	2.438	0.2145	0.47
Minor histocompatibility antigen H13 (EC 3.4.99.-) (Signal peptide peptidase) (Presenilin-like						
Q8TCT9	K.NASDMPETITSR.D	1321.6053	2	2.3375	0.3832	0.25
Q8TCT9	K.LVFPQDLLEK.G	1201.6827	2	2.3541	0.5317	0.40
Q8TCT9	K.DPAAVTESK[.E	921.4655	1	3.1334	0.3983	0.24
Q8TCT9	K.DPAAVTESK.E	917.4575	1	2.4939	0.5319	0.24
Q8TCT9	K.NASDMPETITSR.D	1321.6053	2	2.7894	0.3659	0.24
Q8TCT9	R.QYQLLFTQGSGENK.E	1612.7966	2	4.4811	0.5834	0.27

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q8TCT9	K.DPAAVTESK.E	917.4575	2	2.834	0.3563	0.31
Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP) (Solute carrier family 25 member 11)						
Q02978	K.NVFNALIR.I	946.5469	1	2.0559	0.191	0.27
Q02978	K.NVFNALIR.I	946.5469	2	2.2729	0.192	0.13
Mitochondrial aspartate-glutamate carrier protein						
Q546F9	R.YLNIFGESQPNPK.T	1506.7587	2	4.2025	0.4866	0.42
Q546F9	K.DVEVTKEEFVLAAQK.F	1705.9007	2	4.5912	0.5487	2.53
Q546F9	K.TVELLSGVVDQTK.D	1388.7631	2	3.5537	0.4449	0.29
Q546F9	R.PVLLQVAESAYR.F	1345.7474	2	3.9677	0.529	0.19
Mitochondrial carrier homolog 2 (Met-induced mitochondrial protein)						
Q9Y6C9	K.VLIQVGYEPLPPTIGR.N	1752.0054	2	3.942	0.4814	0.43
Q9Y6C9	K.EVSSSFDHVIK.E	1247.6266	2	2.8835	0.4666	0.16
Q9Y6C9	R.GLFTGLTPR.L	961.5465	1	1.9989	0.3553	0.11
Q9Y6C9	K.EVSSSFDHVIK.E	1247.6266	2	2.5718	0.2701	0.13
Q9Y6C9	K.VLIQVGYEPLPPTIGR.N	1752.0054	2	3.7804	0.4486	0.43
Q9Y6C9	R.LC*SGVLGTVVHGK.V	1326.7198	2	3.6002	0.5512	0.38
Q9Y6C9	R.GLFTGLTPR.L	961.5465	2	2.6393	0.4582	0.10
Q9Y6C9	R.GLFTGLTPR.L	961.5465	1	2.5825	0.4204	0.13
Q9Y6C9	K.GEELGPGNVQK.E	1127.5691	2	3.4874	0.479	0.24
Q9Y6C9	R.GLFTGLTPR.L	961.5465	1	2.1371	0.2995	0.13
Mitochondrial dicarboxylate carrier						
Q9UBX3	K.GSQGPLPFHEK.V	1196.6058	2	2.7728	0.1758	0.04
Q9UBX3	K.VHLQTQQEVK.L	1209.6586	2	2.2906	0.457	0.25
Mitochondrial import inner membrane translocase subunit Tim17-B						
O60830	R.YTAQQFR.N	913.4526	1	1.959	0.3393	0.31
Mitochondrial import receptor subunit TOM20 homolog (Mitochondrial 20 kDa outer membrane						
Q15388	K.DAEAVQK.F	760.3836	1	2.2092	0.2616	0.19
Mitochondrial import receptor subunit TOM22 homolog (Translocase of outer membrane 22 kDa						
Q9NS69	K.LQMEQQQQLQQR.Q	1557.7802	2	3.7997	0.4405	0.15
Mitochondrial inner membrane protein (Mitofilin) (p87/89) (Proliferation-inducing gene 4 protein)						
Q16891	K.SEFEQNLSEK.L	1210.5586	2	3.3158	0.4258	0.40
Q16891	R.SEIQAEQDR.K	1075.5014	2	2.2663	0.2066	0.13
Q16891	K.LSEQELQFR[.R	1153.5979	2	3.9689	0.2852	1.23
Q16891	K.PHITAAEGK.L	923.4945	1	2.514	0.378	0.43

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q16891	K.SVIENAK[.K	764.4279	1	2.1098	0.1267	0.20
Q16891	K.EVAGAKPHITAAEGK.L	1478.7962	2	3.719	0.4542	0.42
Q16891	K.SVIENAK[.K	764.4279	1	2.1232	0.1273	0.19
Q16891	R.SEIQAEQDR.K	1075.5014	1	2.0403	0.2972	0.31
Q16891	R.ELDSITPEVLPGWK.G	1583.8316	2	3.4771	0.4313	1.19
Q16891	R.SEIQAEQDR.K	1075.5014	2	2.9137	0.3426	0.13
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	4.2104	0.5293	0.36
Q16891	K.TSSAETPTIPLGSAVEAIK[.A	1876.004	2	3.9432	0.4168	0.36
Q16891	K.VQAAQSEAK.V	931.4843	1	2.3452	0.2931	0.25
Q16891	K.EVAGAKPHITAAEGK[.L	1482.8042	2	3.756	0.5069	0.35
Q16891	K.AVDEAADALLK.A	1115.5943	2	3.0516	0.3712	0.31
Q16891	K.AAMDNSEIAGEK.K	1235.5572	1	2.1295	0.4264	0.26
Q16891	K.LSEQELQFR.R	1149.5899	1	2.2882	0.3175	0.56
Q16891	K.AAMDNSEIAGEK.K	1235.5572	2	3.4135	0.4217	0.51
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	4.4692	0.5668	0.31
Q16891	K.EVAGAKPHITAAEGK[.L	1482.8042	2	3.2593	0.5085	0.42
Q16891	K.LSEQELQFR.R	1149.5899	2	2.8773	0.3792	0.53
Q16891	K.PHITAAEGK.L	923.4945	1	2.1986	0.1947	0.43
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	4.7236	0.5635	0.51
Q16891	K.AAMDNSEIAGEK.K	1235.5572	1	2.0966	0.2674	0.26
Q16891	R.SEIQAEQDR.K	1075.5014	2	2.7227	0.3811	0.18
Q16891	K.AVDEAADALLK.A	1115.5943	2	2.4499	0.3086	0.19
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	4.9766	0.5501	0.28
Q16891	K.EVAGAKPHITAAEGK.L	1478.7962	2	3.7759	0.4994	0.35
Q16891	K.AVDEAADALLK[.A	1119.6023	2	2.5856	0.3267	0.19
Q16891	K.LSEQELQFR.R	1149.5899	2	3.6387	0.3417	1.23
Q16891	R.SEIQAEQDR.K	1075.5014	2	2.784	0.4	0.36
Q16891	K.TSSAETPTIPLGSAVEAIK[.A	1876.004	2	3.7785	0.4203	0.28
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	5.0433	0.487	0.31

Mitochondrial precursor proteins import receptor (Translocase of outer membrane TOM70)

O94826	R.LRPESALAQAQK.C	1311.7379	2	3.1197	0.4491	0.22

Mitogen-activated protein kinase kinase kinase 15 (Fragment)

Q5JPR4	K.ETLLNDIRKAR[.E	1332.7725	2	2.3501	0.0953	7.98

Mitsugumin-23 precursor (Mg23)

Q9BVC6	R.EAPVDVLTQIGR.S	1297.711	2	3.4176	0.4558	0.72

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9BVC6	R.EAPVDVLTQIGR.S	1297.711	2	2.2924	0.2059	0.72
Q9BVC6	R.RDFAPPGQQK.R	1143.5905	2	2.2499	0.2385	0.06

Monocarboxylate transporter 1 (MCT 1)

P53985	K.EEETSIDVAGKPNEVTK.A	1845.9076	2	3.4324	0.5421	0.67
P53985	K.EEETSIDVAGKPNEVTK[.A	1849.9156	2	3.5281	0.4131	0.67
P53985	K.EEETSIDVAGKPNEVTK.A	1845.9076	2	4.3592	0.5919	0.71
P53985	K.EEETSIDVAGKPNEVTK[.A	1849.9156	2	4.2247	0.499	0.71
P53985	K.EEETSIDVAGKPNEVTK[.A	1849.9156	2	4.2388	0.4297	0.70
P53985	K.EEETSIDVAGKPNEVTK.A	1845.9076	2	4.3487	0.5748	0.70

Monocarboxylate transporter 4 (MCT 4) (MCT 3)

O15427	K.DLGVPDTK.A	844.4411	1	2.0253	0.3273	0.13
O15427	R.PLVVTAQPGSGPPRPSR.R	1715.9551	2	2.8257	0.4389	0.22
O15427	K.EPQPEVAAAEEEK.L	1426.6696	2	2.4532	0.3695	0.19
O15427	R.LLDLSVFR.D	962.5669	2	2.8892	0.2564	0.24
O15427	K.EPQPEVAAAEEEK.L	1426.6696	2	2.5578	0.6089	0.21
O15427	R.LLDLSVFR.D	962.5669	1	1.9514	0.1744	0.23
O15427	K.EPQPEVAAAEEEK.L	1426.6696	1	2.6052	0.4982	0.30
O15427	K.EPQPEVAAAEEEK[.L	1430.6776	2	2.2006	0.1063	0.21
O15427	R.PAAGFVAGLGK.V	987.5622	2	3.6758	0.5098	0.12
O15427	K.EPQPEVAAAEEEK.L	1426.6696	1	2.1808	0.5655	0.24
O15427	K.EPQPEVAAAEEEK.L	1426.6696	2	2.2903	0.5432	0.20
O15427	R.LLDLSVFR.D	962.5669	1	2.7316	0.2607	0.29

MOP-3

Q9H3T8	R.GVGAMEIVAMDMKLRGMYIAR.Q	2312.1746	2	2.2404	0.1871	0.21

mRNA decapping enzyme 1B (EC 3.-.-.-)

Q8IZD4	K.FPVLAQSSGTGK.P	1191.6368	2	2.2061	0.11	0.12

Myb-related protein B (B-Myb)

P10244	R.SEAGIELIIEDDIRPEK.Q	1927.0019	2	2.4535	0.1217	0.18

Myosin Ib (Myosin I alpha) (MMI-alpha) (MMIa) (MYH-1c)

O43795	R.DQFTDQQK.L	1009.4585	2	2.3044	0.1586	0.27
O43795	K.LEASELFK.D	936.5037	1	1.9265	0.257	8.13
O43795	K.EIC*ELTGIDQSVLER.A	1761.8687	2	4.8128	0.4903	1.17
O43795	K.EIC*ELTGIDQSVLER[.A	1765.8767	2	4.1355	0.22	1.17

Myosin IE

Q4KMR3	K.QGLFPNNYVTK.I	1280.6634	2	3.1048	0.2986	0.41

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Myosin-10 (Myosin heavy chain, nonmuscle IIb) (Nonmuscle myosin heavy chain IIb) (NMMHC II-						
P35580	R.LQQELDDLTVDLDHQR.Q	1937.9563	2	5.0668	0.635	2.03
P35580	K.TELEDTLDTTAAQQELR.T	1933.9349	2	4.8129	0.5581	0.35
P35580	K.DLEAQIEAANK.A	1201.6059	2	4.0827	0.277	0.06
Myosin-9 (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMMHC II-a)						
P35579	R.ELEDATETADAMNR.E	1565.6748	2	4.2086	0.6222	0.43
P35579	K.TELEDTLDSTAAQQELR.S	1919.9193	2	6.2004	0.6192	0.77
P35579	K.KVEAQLQELQVK.F	1412.8108	2	4.0835	0.4345	0.49
P35579	R.EQLEEEEEAK.H	1233.5481	1	3.1224	0.2407	0.20
P35579	K.DLEGLSQR[.H	921.4767	1	2.0605	0.1966	0.42
P35579	R.VEEEAAQK.N	903.4418	1	2.2208	0.1887	0.31
P35579	R.VEEEAAQK.N	903.4418	2	2.7042	0.0819	0.29
P35579	R.ELESQISELQEDLESER.A	2033.9509	2	3.1075	0.3622	0.75
P35579	R.EQEVNILK.K	972.536	1	1.9564	0.1375	0.37
P35579	R.VEEEAAQK.N	903.4418	2	2.9283	0.3132	0.29
P35579	K.KVEAQLQELQVK[.F	1416.8188	2	2.6774	0.1105	0.49
P35579	R.ELEDATETADAMNR[.E	1569.6828	2	3.5661	0.4057	0.43
P35579	R.EQLEEEEEAK.H	1233.5481	2	2.5149	0.4413	0.25
P35579	K.LEEEQIILEDQNC*K.L	1760.8371	2	4.3693	0.2671	0.33
Myotubularin (EC 3.1.3.48)						
Q13496	R.VATFRSRNR.I	1106.6177	2	2.2556	0.3396	0.56
N-acetylgalactosaminyltransferase						
Q76KP1	R.GSDHVEVGWRAFLPGLK.F	1867.9813	2	2.68	0.0993	0.16
Q76KP1	R.FLLELELQERGGGR.L	1616.8755	2	2.3271	0.1548	0.03
N-acetylgalactosaminyltransferase 7 (EC 2.4.1.-) (Protein-UDP acetylgalactosaminyltransferase 7)						
Q86SF2	R.DVNDPMPNR.G	1057.4731	2	2.3399	0.4454	0.09
NAD(P) transhydrogenase, mitochondrial precursor (EC 1.6.1.2) (Pyridine nucleotide						
Q13423	K.AVVLAANHFGR.F	1154.6429	2	3.4126	0.4978	0.53
NAD-dependent deacetylase sirtuin-5 (EC 3.5.1.-) (SIR2-like protein 5)						
Q9NXA8	R.RVVVITQNIDELHRK[.A	1824.0581	2	3.4157	0.1708	0.86
NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R) (Diaphorase-1) (Cytochrome b5 reductase 3)						
P00387	R.STPAITLESPDIK.Y	1371.7366	2	2.9313	0.429	0.11
P00387	R.STPAITLESPDIK.Y	1371.7366	2	2.9083	0.3975	0.08
P00387	R.STPAITLESPDIK.Y	1371.7366	1	2.1783	0.4798	0.22

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC						
O75489	R.VVAEPVELAQEFR.K	1486.79	2	3.3041	0.5148	0.53
NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC						
P49821	K.YLVVNADEGEPGTC*K.D	1651.7632	2	3.8426	0.5585	1.25
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC						
P28331	R.ALSEIAGMTLPYDTLDQVR.N	2093.0583	2	3.0366	0.1693	0.46
NADH-ubiquinone oxidoreductase B12 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B12) (CI-						
O43676	K.IEGTPLETIQK.K	1228.6783	2	2.6809	0.3911	0.49
NADH-ubiquinone oxidoreductase B17 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B17) (CI-						
O95139	R.IFPGDTILETGEVIPPMK.E	1957.0351	2	3.1985	0.4154	0.17
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3) (NADH dehydrogenase subunit 4)						
P03905	R.LTLILNPLTK.H	1125.7242	1	3.0054	0.3532	0.20
NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3) (NADH dehydrogenase subunit 6)						
P03923	R.EDPIGAGALYDYGR.W	1496.7016	2	3.1943	0.5484	0.31
NADH-ubiquinone oxidoreductase flavoprotein 3, isoform a						
Q8WU60	R.GGTQEPAPVPAEPFDNTTYK.N	2118.9978	2	3.4295	0.436	0.50
NADPH--cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)						
P16435	K.RLEQLGAQR.I	1070.6065	2	3.6916	0.3553	0.40
P16435	R.ESSFVEK[.M	829.4069	1	1.9233	0.2847	0.74
P16435	K.RLEQLGAQR[.I	1074.6145	2	3.0428	0.1786	0.40
P16435	R.YESGDHVAVYPANDSALVNQLGK.I	2447.1837	2	4.0928	0.6485	0.85
P16435	R.SDEDYLYR.E	1060.4582	2	2.4296	0.3121	0.40
P16435	R.YYSIASSSK.V	1005.4888	1	2.1621	0.45	1.17
P16435	K.NPFLAAVTTNR.K	1203.648	2	3.8385	0.3528	0.43
P16435	R.SDEDYLYR.E	1060.4582	1	1.9807	0.4665	0.27
P16435	R.SDEDYLYR.E	1060.4582	2	2.8687	0.4211	0.40
P16435	R.SDEDYLYR.E	1060.4582	1	1.9918	0.3112	0.27
P16435	R.YYSIASSSK.V	1005.4888	1	2.102	0.403	1.17
P16435	R.ESSFVEK.M	825.3989	1	2.0203	0.1408	1.37
P16435	K.NPFLAAVTTNR.K	1203.648	1	2.7688	0.4003	0.42
P16435	R.DGALTQLNVAFSR[.E	1395.7358	2	3.6047	0.416	2.95
P16435	K.FAVFGLGNK.T	952.5251	2	3.0185	0.3573	0.19
P16435	K.NPFLAAVTTNR.K	1203.648	2	2.8596	0.3246	0.34
P16435	K.NPFLAAVTTNR.K	1203.648	2	4.1988	0.3375	0.34

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P16435	K.NPFLAAVTTNR.K	1203.648	2	4.1982	0.3418	0.34
P16435	K.IQTLTSSVR.E	1004.5735	2	2.5423	0.4131	0.93
P16435	K.NPFLAAVTTNR.K	1203.648	1	2.5248	0.3113	0.42
P16435	K.FAVFGLGNK.T	952.5251	1	1.93	0.2953	0.09
P16435	R.YYSIASSSK[.V	1009.4968	1	1.9396	0.3669	1.17
Nascent polypeptide-associated complex alpha subunit (NAC-alpha) (Alpha-NAC) (Hom s 2.02)						
Q13765	K.IEDLSQQAQLAAAEKFK.V	1889.9967	2	2.4682	0.1198	0.67
NEDD4-binding protein 2 (EC 3.-.-.-) (N4BP2) (BCL-3-binding protein)						
Q86UW6	K.LQATDKSENEQIEMVAVK.G	2033.0219	2	2.4669	0.1064	0.18
NEDD4-like ubiquitin ligase 1						
Q9HCC7	R.GGYHDGHLVIRWFWAAVER[.F	2273.1494	2	2.5145	0.1057	0.81
Neighbor of COX4						
O43402	K.DASPNQVAEK.V	1058.5113	2	2.4645	0.4383	0.26
Neural cell adhesion molecule L1 precursor (N-CAM L1) (CD171 antigen)						
P32004	K.VGEEDDGEYR[.C	1172.4833	2	3.1524	0.2933	0.50
P32004	K.VGEEDDGEYR.C	1168.4753	2	3.378	0.4747	0.50
P32004	R.LVVFPTDDISLK.C	1346.7566	2	2.8663	0.4386	0.13
Neuromodulin (Axonal membrane protein GAP-43) (Growth associated protein 43) (PP46) (Neural						
P17677	K.DDVQAAEAEANKK[.D	1392.6732	2	2.3081	0.1766	2.99
Neuronal acetylcholine receptor protein, alpha-5 subunit precursor						
P30532	R.CGLAGAAGGAQRGLSEPSSIAK[.H	2005.0262	2	2.2004	0.0884	0.40
Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II alpha subunit)						
Q14697	K.DPAEGDGAQPEETPR.D	1568.6823	2	4.8685	0.5524	0.49
Neutral amino acid transporter B(0) (ATB(0)) (Sodium-dependent neutral amino acid transporter						
Q15758	R.STEPELIQVK.S	1143.6256	2	2.5996	0.4116	0.35
Q15758	R.GPAGDATVASEK.E	1102.5375	1	2.2702	0.2211	0.88
Q15758	R.GPAGDATVASEK.E	1102.5375	2	3.6564	0.4989	0.69
Q15758	K.SELPLDPLPVPTEEGNPLLK.H	2158.1642	2	4.1944	0.6634	0.83
Q15758	R.GPAGDATVASEK.E	1102.5375	1	2.858	0.3166	0.88
Q15758	K.EVLDSFLDLAR.N	1277.6736	2	3.1261	0.4101	0.27
NGT						
Q9H2Q2	K.LGEQVFGTTGK.F	1136.5946	2	3.5596	0.5041	2.62
Q9H2Q2	R.SSLFELAK.K	894.4931	2	2.2332	0.3242	0.33
Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS type I) (Neuronal NOS) (N-NOS) (nNOS)						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P29475	R.SAITIFPQRTDGKHDFR[.V	1993.0381	2	2.4948	0.1897	23.46
Novel protein						
Q5SWH9	R.PSSTITYLTDSPK.P	1409.7159	2	3.2721	0.5295	0.33
Q5JP08	R.EFDSSTLNESVR.N	1383.6387	2	3.1381	0.5797	0.22
Q5VZP5	R.TPESSEREESPEPQR.P	1757.7937	2	2.2058	0.1158	0.24
Nuclear protein 5qNCA						
Q7LBC6	K.PEAFSQEFGDQDVDLVNC*R[.N	2229.9848	2	3.1081	0.2074	1.39
Nuclear RNA export factor 2 (TAP-like protein 2) (TAPL-2)						
Q9GZY0	R.DNFDK.R	638.278	1	1.9583	0.1557	0.01
Q9GZY0	R.DNFDK.R	638.278	1	1.9754	0.1449	0.01
Nuclease sensitive element binding protein 1 (Y-box binding protein 1) (Y-box transcription factor)						
P67809	K.NEGSESAPEGQAQQR.R	1587.6994	2	4.2656	0.5715	0.82
Nucleolar RNA helicase 2 (EC 3.6.1.-) (Nucleolar RNA helicase II) (Nucleolar RNA helicase Gu)						
Q9NR30	K.DFSDITK.K	825.3989	1	1.947	0.3049	0.92
Q9NR30	K.DFSDITK[.K	829.4069	1	2.1349	0.2803	0.92
OK/SW-CL.16						
Q8NI70	R.RALAPNR.H	797.474	1	2.086	0.2322	0.28
Olfactory receptor 2T1 (Olfactory receptor 1-25) (OR1-25) (Olfactory receptor OR1-61)						
O43869	R.YVAIC*NPLRYPVLMSR.R	1952.0245	2	2.4039	0.1944	0.05
OTTHUMP00000016784						
Q5TFD7	R.KMIPAMDR[.R	965.5038	1	2.1279	0.0933	4.20
OTTHUMP00000017314 (Fragment)						
Q5JUJ7	K.EQETVLQAQVRPGGR.G	1667.8824	2	2.5217	0.1577	0.25
OTTHUMP00000017471						
Q5VYA5	K.VPAEDCSEPVQLLR[.Y	1559.7865	2	3.0724	0.341	0.30
OTTHUMP00000021035						
Q4VXA4	R.AGDNILAVLK.H	1013.599	2	3.6396	0.4051	0.24
OTTHUMP00000031372						
Q9NQJ4	R.PPSAFFLFC*SEYHPK[.I	1830.8651	2	2.3962	0.2236	0.53
Oxygen-regulated protein 1 (Retinitis pigmentosa RP1 protein) (Retinitis pigmentosa 1 protein)						
P56715	R.KSQVCPYNSVEFQCSR.K	1874.8524	2	2.3995	0.2541	0.49
Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin B) (S-						
P23284	K.DTNGSQFFITTVK.T	1457.7271	2	3.6144	0.4579	5.38

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P23284	R.VIFGLFGK.T	880.5291	1	1.9476	0.211	0.34
Peptidyl-tRNA hydrolase 2, mitochondrial precursor (EC 3.1.1.29) (PTH 2) (Bcl-2 inhibitor of						
Q9Y3E5	R.TQIAPGSQTVLGIGPGPADLIDK.V	2248.2183	2	6.4517	0.6197	0.29
Pericentrin (Pericentrin B) (Kendrin)						
O95613	K.RLEEMNINIRK.K	1415.7787	2	2.3369	0.1181	0.65
Phosphate carrier protein, mitochondrial precursor (PTP)						
Q00325	R.LPRPPPPEMPESLK.K	1587.8563	2	2.7007	0.4776	0.12
Q00325	R.LPRPPPPEMPESLK.K	1587.8563	2	2.3777	0.2484	0.26
Q00325	R.IQTQPGYANTLR.D	1361.7172	2	3.3397	0.4556	0.41
Q00325	R.IQTQPGYANTLR.D	1361.7172	2	2.6054	0.3754	0.41
Q00325	R.IQTQPGYANTLR.D	1361.7172	1	2.4748	0.3804	0.39
Q00325	R.IQTQPGYANTLR.D	1361.7172	2	2.5052	0.4311	0.47
Q00325	R.LPRPPPPEMPESLK.K	1587.8563	2	3.0095	0.4885	0.17
Q00325	R.IQTQPGYANTLR.D	1361.7172	2	2.9482	0.4421	0.43
Q00325	R.IQTQPGYANTLR.D	1361.7172	2	3.1475	0.4721	0.47
Q00325	R.IQTQPGYANTLR.D	1361.7172	1	2.4619	0.3343	0.37
Q00325	R.IQTQPGYANTLR[.D	1365.7252	2	3.0252	0.3757	0.34
Q00325	R.IQTQPGYANTLR.D	1361.7172	2	2.9208	0.4485	0.34
Q00325	R.IQTQPGYANTLR.D	1361.7172	2	3.7336	0.5275	0.41
Phosphatidate cytidylyltransferase 2 (EC 2.7.7.41) (CDP-diglyceride synthetase 2) (CDP-diglyceride						
O95674	R.AESAPLPVSADDTPEVLNR[.A	1984.9953	2	4.0806	0.4684	0.63
O95674	R.AESAPLPVSADDTPEVLNR[.A	1984.9953	2	4.1665	0.5085	0.83
O95674	R.AESAPLPVSADDTPEVLNR.A	1980.9873	2	4.7993	0.6301	0.84
O95674	K.VDGETASDSESR.A	1252.5288	2	3.8741	0.5614	1.07
O95674	K.VDGETASDSESR.A	1252.5288	2	3.5686	0.5155	0.96
O95674	R.AESAPLPVSADDTPEVLNR.A	1980.9873	2	5.195	0.6303	0.63
Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing beta polypeptide (EC 2.7.1.154)						
O00750	R.THTLKSSGRISDVFLC*R.H	1977.0335	2	2.3782	0.3012	0.86
Phosphatidylserine synthase 1 (EC 2.7.8.-) (PtdSer synthase 1) (PSS-1) (Serine-exchange enzyme I)						
P48651	R.AVLQFTPASWTYVR.W	1638.8639	2	2.2013	0.2798	0.62
P48651	R.ILFIGGITAPTVR.Q	1357.8202	2	2.8455	0.1883	1.03
Phosphatidylserine synthase 2 (EC 2.7.8.-) (PtdSer synthase 2) (PSS-2) (Serine-exchange enzyme II)						
Q9BVG9	R.ASLEEPPDGPSAGQATGPGEGR.R	2079.9578	2	4.4981	0.6294	0.44
Q9BVG9	R.ASLEEPPDGPSAGQATGPGEGR.R	2079.9578	2	4.6045	0.6309	0.35
Q9BVG9	R.DAGGPRPESPVPAGR[.A	1466.7477	2	2.2668	0.2242	0.38

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9BVG9	R.DAGGPRPESPVPAGR.A	1462.7397	2	2.3989	0.3222	0.38
Photolyase (Cryptochrome 1)						
Q16526	K.LSIEYDSEPFGK[.E	1388.6711	2	2.4412	0.2794	0.21
Q16526	K.LSIEYDSEPFGK.E	1384.6631	2	2.3685	0.0899	0.17
Q16526	K.LSIEYDSEPFGK[.E	1388.6711	2	2.3524	0.2055	0.17
Q16526	K.LSIEYDSEPFGK[.E	1388.6711	2	2.2971	0.344	0.17
Q16526	K.LSIEYDSEPFGK.E	1384.6631	2	2.5035	0.1473	0.17
Q16526	K.LSIEYDSEPFGK.E	1384.6631	2	2.4291	0.1119	0.21
PIK3CA variant protein (Fragment)						
Q4LE51	K.LDKGQIIVVIWVIVSPNNDK.Q	2250.2856	2	3.1205	0.2024	0.21
Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Domain-rich serine protein)						
Q9H307	K.LTEVPVEPVLTVHPESK[.S	1878.035	2	3.8937	0.5235	1.09
Q9H307	R.DLEGAVSR.L	846.4316	1	1.9054	0.1539	0.28
Q9H307	K.LTEVPVEPVLTVHPESK.S	1874.027	2	4.3495	0.5555	1.09
Q9H307	R.VESVEPSENEASK.E	1404.6489	2	2.8078	0.4983	0.43
Q9H307	K.KPALQSSVVATSK.E	1315.758	2	3.6359	0.5757	0.51
Q9H307	R.DLIQDQNMDEK.G	1348.6049	2	3.1835	0.493	0.20
Plasma membrane calcium-transporting ATPase 1 (EC 3.6.3.8) (PMCA1) (Plasma membrane						
P20020	K.TSPNEGLSGNPADLER.R	1656.7824	2	4.4914	0.4905	0.24
Plexin D1 precursor						
Q9Y4D7	R.KGFAELQTDMTDLTKELNR[.S	2214.1202	2	3.2283	0.1256	2.68
PNAS-117						
Q9HB66	K.NDDIPEQDSLGLSNLQK.S	1885.9138	2	4.5477	0.3192	0.40
Q9HB66	K.NDDIPEQDSLGLSNLQK.S	1885.9138	2	4.7045	0.4146	0.35
Polymerase I and transcript release factor (PTRF protein)						
Q6NZI2	K.IIGAVDQIQLTQAQLEER.Q	2025.0975	2	5.3118	0.6507	0.15
Polypeptide N-acetylgalactosaminyltransferase 2 (EC 2.4.1.41) (Protein-UDP						
Q10471	K.FNQVESDK.L	966.4527	1	2.1056	0.1695	0.16
Q10471	R.NVPYGNIQSR.L	1147.5854	2	2.203	0.3706	1.07
Possible integral membrane						
Q96S06	R.LPQHTPTSR[.I	1040.5614	2	2.6534	0.2749	10.90
Postreplication repair protein RAD18 (hRAD18) (hHR18) (RING finger protein 73)						
Q9NS91	K.NLAVKVYTPVASRQSLK[.Q	1878.0938	2	2.3609	0.1597	0.11
Potassium channel tetramerization domain-containing 1 (KCTD1 protein)						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q719H9	R.IGRLFDGTEPIVLDSLK[.Q	1877.0509	2	2.5513	0.0895	0.22
Prickle-like protein 1 (REST/NRSF-interacting LIM domain protein 1)						
Q96MT3	K.FPGLSGNADDTLSRK.L	1577.7918	2	2.4133	0.269	1.17
PRKR interacting protein 1 (IL11 inducible)						
Q96CF8	K.NAAEEQKLKLER.L	1428.7805	2	2.7991	0.1283	1.05
PRO0756						
Q9H375	R.MLPFSLQKNVLLKGEK[.A	1849.0747	2	2.2927	0.2034	68.93
Q9H375	R.MLPFSLQKNVLLKGEK[.A	1849.0747	2	2.6792	0.2829	62.82
Probable cation-transporting ATPase 13A1 (EC 3.6.3.-)						
Q9HD20	R.SPQENLVPC*DVLLLR.G	1752.9313	2	3.8592	0.5079	0.58
Q9HD20	K.EFVITSLK.E	936.5401	1	1.9539	0.2717	0.25
Q9HD20	K.EPIEDLSPDR.V	1170.5637	2	2.4021	0.4054	0.65
Q9HD20	R.SPQENLVPC*DVLLLR.G	1752.9313	2	3.9313	0.4637	0.58
Q9HD20	K.EVTPVSSIPVETHR.A	1550.8173	2	3.3628	0.5533	0.81
Q9HD20	K.EVTPVSSIPVETHR[.A	1554.8253	2	2.3583	0.1707	0.81
Probable endonuclease KIAA0830 precursor (EC 3.1.30.-)						
O94919	R.STLLPPEASEGSSSFLGK[.L	1810.92	2	2.9699	0.3137	0.48
O94919	R.STLLPPEASEGSSSFLGK.L	1806.912	2	3.3337	0.5847	0.48
Probable G-protein coupled receptor 125 precursor						
Q8IWK6	K.STGFTGMTCTVFQKVAASDR.T	2106.9947	2	2.6695	0.1094	0.15
Probable mitochondrial import receptor subunit TOM40 homolog (Translocase of outer membrane						
O96008	K.MAIQTQQSK[.F	1038.5379	1	2.3228	0.4288	0.25
O96008	R.TPGAATASASGAAEDGAC*GC*LPNPGTFEEC*HR.K	3219.3524	3	5.807	0.4507	1.52
O96008	K.ELFPIQMEGVK.L	1290.6762	2	2.4929	0.4133	0.36
O96008	K.ELFPIQMEGVK.L	1290.6762	1	2.6784	0.279	0.10
O96008	R.RPGEEGTVMSLAGK.Y	1431.726	2	3.9363	0.589	0.36
O96008	K.MAIQTQQSK.F	1034.5299	1	2.158	0.3864	0.25
O96008	K.MAIQTQQSK.F	1034.5299	1	2.0775	0.3786	0.23
Probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (hOSGEP)						
Q9NPF4	R.IFGETIDIAVGNC*LDR[.F	1796.8978	2	2.289	0.1109	1.62
Probable palmitoyltransferase ZDHHC13 (EC 2.3.1.-) (Zinc finger DHHC domain-containing						
Q8IUH4	R.YGICAHENKELANAR.E	1688.8173	2	2.2778	0.0831	0.03
Probable palmitoyltransferase ZDHHC6 (EC 2.3.1.-) (Zinc finger DHHC domain-containing protein						
Q9H6R6	R.KCVEKC*PC*DAETDQAPEGEK.K	2293.9734	2	2.2452	0.0983	0.16

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Programmed cell death 6-interacting protein (PDCD6-interacting protein) (ALG-2 interacting protein						
Q8WUM4	R.LLDEEEATDNDLR.A	1532.7075	2	3.9021	0.5076	0.27
Prohibitin						
P35232	R.NVPVITGSK.D	914.5306	1	2.4242	0.2894	0.27
P35232	R.NVPVITGSK.D	914.5306	1	2.2653	0.2747	0.18
P35232	R.NVPVITGSK[.D	918.5386	1	2.7473	0.4074	0.18
P35232	K.AAIISAEGDSK.A	1061.5473	1	2.5733	0.482	0.24
P35232	R.NVPVITGSK.D	914.5306	1	2.3866	0.4897	0.18
P35232	R.IFTSIGEDYDER.V	1444.6591	2	3.4318	0.5372	0.42
P35232	R.NVPVITGSK.D	914.5306	1	2.4367	0.4559	0.98
P35232	K.AAIISAEGDSK.A	1061.5473	2	2.5201	0.4367	1.02
P35232	R.IFTSIGEDYDER.V	1444.6591	1	2.9541	0.4858	0.63
P35232	K.AAELIANSLATAGDGLIELR.K	1998.0866	2	3.2885	0.2888	0.72
P35232	K.AAIISAEGDSK.A	1061.5473	1	2.6525	0.5996	0.24
P35232	R.ILFRPVASQLPR.I	1396.8423	2	3.3418	0.3283	0.19
P35232	K.AAELIANSLATAGDGLIELR.K	1998.0866	2	5.7314	0.5539	0.72
P35232	R.IFTSIGEDYDER.V	1444.6591	2	3.4144	0.5728	0.37
P35232	R.PVASQLPR.I	867.5047	1	2.2335	0.2367	0.18
P35232	R.IFTSIGEDYDER.V	1444.6591	2	3.2341	0.5421	0.43
P35232	R.NVPVITGSK[.D	918.5386	1	2.836	0.3548	0.27
P35232	R.NVPVITGSK.D	914.5306	1	2.2824	0.4663	0.27
P35232	R.NVPVITGSK.D	914.5306	1	2.3367	0.4579	0.35
P35232	R.NVPVITGSK[.D	918.5386	1	2.3683	0.3487	0.27
P35232	R.IFTSIGEDYDER[.V	1448.6671	2	3.3474	0.3944	0.37
P35232	K.AAIISAEGDSK.A	1061.5473	1	2.5552	0.5935	0.76
P35232	R.IFTSIGEDYDER.V	1444.6591	2	3.4818	0.5758	0.63
P35232	R.ILFRPVASQLPR.I	1396.8423	2	3.3026	0.295	0.25
P35232	R.PVASQLPR.I	867.5047	2	2.8749	0.5158	0.31
Prohibitin-2 (B-cell receptor-associated protein BAP37) (Repressor of estrogen receptor activity) (D-						
Q99623	R.LPAGPR.G	610.3671	1	2.0245	0.1893	0.41
Q99623	K.FNASQLITQR.A	1177.6324	2	2.7649	0.1844	0.56
Q99623	R.LGLDYEER.V	994.484	2	2.7275	0.5726	0.92
Q99623	R.EYTAAVEAK.Q	981.4888	1	2.454	0.4369	0.55
Q99623	K.IVQAEGEAEAAK.M	1215.6216	1	2.7522	0.459	0.23
Q99623	K.FNASQLITQR.A	1177.6324	2	3.6826	0.3975	0.56

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q99623	R.LGLDYEER.V	994.484	1	1.9554	0.2258	0.39
Q99623	R.EYTAAVEAK.Q	981.4888	1	2.3006	0.3953	1.97
Q99623	K.DLQMVNISLR.V	1188.6405	1	2.9318	0.3804	0.48
Q99623	R.EYTAAVEAK.Q	981.4888	1	2.1682	0.3664	0.63
Q99623	R.EYTAAVEAK[.Q	985.4968	1	2.1542	0.3942	0.86
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.9868	2	4.8911	0.6622	0.93
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.9868	3	5.0193	0.5312	0.81
Q99623	R.EYTAAVEAK.Q	981.4888	1	2.1864	0.3865	0.86
Q99623	K.IVQAEGEAEAAK.M	1215.6216	1	2.2104	0.3304	0.26
Q99623	R.LGLDYEER.V	994.484	2	2.698	0.5457	0.81
Q99623	K.DLQMVNISLR[.V	1192.6485	1	3.1093	0.3055	0.48
Q99623	K.IVQAEGEAEAAK.M	1215.6216	1	2.4481	0.4154	0.26
Q99623	R.LGLDYEER.V	994.484	1	2.4381	0.2708	0.47
Q99623	R.VLPSIVNEVLK.S	1210.7406	1	2.3817	0.2189	0.51
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.9868	3	5.5359	0.5356	0.81
Q99623	R.VLPSIVNEVLK.S	1210.7406	1	2.2574	0.4405	0.51
Q99623	K.IVQAEGEAEAAK.M	1215.6216	1	2.3345	0.3185	0.23
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.9868	3	5.2111	0.492	0.83
Q99623	K.FNASQLITQR.A	1177.6324	2	4.1623	0.2921	0.56
Q99623	K.FNASQLITQR.A	1177.6324	1	2.1495	0.2198	0.66
Q99623	R.AQVSLLIR.R	899.5673	1	1.9812	0.1433	0.36
Q99623	K.QVAQQEAQR.A	1057.5385	2	2.3132	0.3205	1.98
Q99623	R.LPAGPR.G	610.3671	1	2.0032	0.204	0.43
Q99623	K.IVQAEGEAEAAK.M	1215.6216	2	4.1972	0.5317	0.36
Q99623	R.VLPSIVNEVLK.S	1210.7406	1	2.1481	0.3187	0.56
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.9868	2	5.2079	0.6309	0.61
Q99623	K.QVAQQEAQR.A	1057.5385	1	2.0388	0.2271	0.79
Q99623	R.PNAQELPSMYQR.L	1433.6842	2	3.4478	0.4543	0.27
Q99623	R.IGGVQQDTILAEGLHFR[.I	1857.9948	2	4.6698	0.4989	0.61
Q99623	R.VLPSIVNEVLK.S	1210.7406	2	2.3114	0.3961	0.71
Q99623	R.IGGVQQDTILAEGLHFR[.I	1857.9948	2	4.3597	0.5326	0.93
Q99623	K.FNASQLITQR[.A	1181.6404	1	2.2056	0.3516	0.66
Q99623	K.LLLGAGAVAYGVR.E	1259.747	2	4.5682	0.4336	0.34
Q99623	R.EYTAAVEAK[.Q	985.4968	1	1.9899	0.3254	0.63
Q99623	K.LLLGAGAVAYGVR.E	1259.747	2	4.3639	0.5535	0.34
Q99623	K.DLQMVNISLR.V	1188.6405	2	3.2316	0.2523	0.15

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q99623	R.EYTAAVEAK.Q	981.4888	1	2.027	0.1709	0.63
Q99623	K.DLQMVNISLR.V	1188.6405	2	2.9378	0.3448	0.15

Prolactin regulatory element-binding protein (Mammalian guanine nucleotide exchange factor

Q9HCU5	R.VENLQAVQTDFSSDPLQK.V	2019.0029	2	4.4406	0.6179	1.02

Prostaglandin E synthase (EC 5.3.99.3) (Microsomal glutathione S-transferase 1-like 1) (MGST1-L1)

O14684	K.AFANPEDALR.H	1103.548	2	2.7751	0.3101	0.10
O14684	K.AFANPEDALR.H	1103.548	1	2.2763	0.3106	0.47

Protein C10orf70

Q9NZ45	K.IVHAFDMEDLGDK.A	1489.6992	2	3.8181	0.5756	0.78

Protein C14orf106 (P243)

Q6P0N0	K.LKIGERTNER.I	1215.6804	1	2.2871	0.2464	0.18
Q6P0N0	K.LKIGERTNER.I	1215.6804	1	2.2281	0.231	0.10
Q6P0N0	K.YMAINQK.K	867.4393	1	2.069	0.1062	0.92

Protein C19orf21

Q8IVT2	R.ALSSDSILSPAPDAR.A	1499.77	2	3.5061	0.5135	0.33
Q8IVT2	R.DIVQETQR.E	988.5058	1	2.2515	0.2293	0.52
Q8IVT2	R.QQFLSLEQANK.G	1305.6797	2	2.9861	0.3935	0.64

Protein C2orf17

Q8NC44	R.QALDSEEEEEDVAAK.E	1662.7341	2	2.7165	0.4434	0.44

Protein C9orf5 (Protein CG-2)

Q9H330	R.ALNSAANNVYQYGR.E	1540.7503	2	3.2343	0.5542	0.08

Protein expressed in T-cells and eosinophils in atopic dermatitis (ETEA)

Q96CS3	R.DLTQEQTEK.L	1091.5215	1	2.5438	0.3297	0.18
Q96CS3	R.DLTQEQTEK.L	1091.5215	2	2.207	0.4332	0.25

Protein KIAA0152 precursor

Q14165	R.SNPEDQILYQTER.Y	1592.7551	2	4.1116	0.4485	0.32
Q14165	K.FAEVYFAQSQQK.V	1445.706	2	3.96	0.5791	0.31

Protein KIAA0406

O43156	K.ALVGLVNDESPEIQAQCNK.V	2028.0066	2	2.3052	0.0827	0.66

Protein KIAA0841

O94927	K.LELEAAVTRLR[.A	1274.7558	2	2.3829	0.0988	3.39

Protein KIAA1045

Q9UPV7	K.EAEAGTSVVQEESSAGRAAWER.L	2320.08	2	2.7614	0.2753	0.10

Protein KIAA1849

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q96JH8	K.RQSQLLSSMLSRTLSYK.Y	1998.0801	2	2.4674	0.1863	1.34
Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon)						
Q02156	K.RCHELIITKCAGLK.K	1584.8713	2	2.6171	0.2296	0.21
Protein kinase, D1 type (EC 2.7.1.-) (nPKC-D1) (Protein kinase D) (Protein kinase C, mu type)						
Q15139	K.EISHEAIDLINNLLQVKMR[.K	2240.2198	2	3.0606	0.13	10.13
Protein LYRIC (Lysine-rich CEACAM1 co-isolated protein) (3D3/lyric) (Metastasis adhesion protein)						
Q86UE4	K.QGEDNSTAQDTEELEK.E	1793.7672	2	4.2338	0.4873	0.79
Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1)						
P61619	K.AFSPTTVNTGR.G	1150.5851	2	2.2888	0.4432	0.38
P61619	R.GQYNTYPIK.L	1083.5469	2	2.7349	0.4982	0.16
P61619	R.GQYNTYPIK.L	1083.5469	1	1.9608	0.2614	0.15
Protein transport protein Sec61 beta subunit						
P60468	-.PGPTPSGTNVGSSGR.S	1370.6659	1	3.0787	0.4558	0.28
P60468	-.PGPTPSGTNVGSSGR.S	1370.6659	2	3.4054	0.5391	0.07
P60468	R.FYTEDSPGLK.V	1156.5521	2	2.6953	0.4152	0.31
P60468	R.FYTEDSPGLK.V	1156.5521	1	1.9679	0.4198	0.21
P60468	R.FYTEDSPGLK.V	1156.5521	1	1.9888	0.2349	0.21
P60468	-.PGPTPSGTNVGSSGR.S	1370.6659	2	3.4285	0.5653	0.16
P60468	R.FYTEDSPGLK.V	1156.5521	1	1.9776	0.392	0.24
P60468	-.PGPTPSGTNVGSSGR[.S	1374.6739	2	3.3124	0.5229	0.07
P60468	-.PGPTPSGTNVGSSGR.S	1370.6659	2	3.3433	0.4605	0.10
P60468	R.FYTEDSPGLK.V	1156.5521	2	2.2057	0.3212	3.41
P60468	-.PGPTPSGTNVGSSGR.S	1370.6659	2	3.4365	0.5589	0.12
P60468	R.FYTEDSPGLK.V	1156.5521	2	2.2895	0.3406	0.31
Protein tyrosine phosphatase-like member b (Protein tyrosine phosphatase-like (Proline instead of						
Q6Y1H2	R.QAGLYSISLPNK.Y	1290.7052	2	3.4504	0.4369	0.15
Protein-S-isoprenylcysteine O-methyltransferase (EC 2.1.1.100) (Isoprenylcysteine						
O60725	K.AAMFTAGSNFNHVVQNEK.S	1964.9283	2	4.3159	0.5319	0.10
Protocadherin beta 3 precursor (PCDH-beta3)						
Q9Y5E6	K.EKGFLIANLAK.D	1203.7096	2	2.3369	0.1367	0.44
Pumilio homolog 2 (Pumilio-2)						
Q8TB72	R.IRGHVLPLALQMYGCR.V	1826.988	2	2.2556	0.2179	0.53
Putative 40-9-1 protein						
Q96QD8	K.TANEGGSLLYEQLGYK[.A	1746.8676	2	4.0876	0.3674	0.60

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q96QD8	K.TANEGGSLLYEQLGYK.A	1742.8596	2	5.0822	0.5709	0.60
Q96QD8	R.FSISPDEDSSSYSSNSDFNYSYPTK[.Q	2828.1824	2	2.6276	0.3312	3.01
Putative Polycomb group protein ASXL1 (Additional sex combs-like protein 1)						
Q8IXJ9	K.QESEQAGVAK.D	1046.5113	2	2.3035	0.1027	0.11
Q8IXJ9	K.QESEQAGVAK.D	1046.5113	1	2.0642	0.0918	0.17
Rap guanine nucleotide exchange factor 2 (PDZ domain containing guanine nucleotide exchange						
Q9Y4G8	K.INQGLQVPAVSLYPSRKK[.V	2002.1575	2	2.8228	0.1439	1.42
Ras GTPase-activating-like protein IQGAP1 (p195)						
P46940	K.EELQSGVDAANSAAQQYQR.R	2064.9581	2	5.2402	0.6484	0.35
Ras-related protein Rab-10						
P61026	K.SFENISK.W	824.4149	1	2.0492	0.1262	0.52
Ras-related protein Rab-14						
P61106	R.LTSEPQPQR[.E	1059.556	1	2.3689	0.2533	0.26
P61106	R.LTSEPQPQR.E	1055.548	2	2.4753	0.2133	2.85
Ras-related protein Rab-1A (YPT1-related protein)						
P62820	R.MGPGATAGGAEK.S	1046.4935	1	2.0274	0.4853	0.44
Ras-related protein Rab-1B						
Q9H0U4	R.MGPGAASGGERPNLK.I	1441.7216	2	2.6893	0.2522	0.17
Ras-related protein Rab-2A						
P61019	K.TASNVEEAFINTAK[.E	1498.7515	2	4.0693	0.4484	0.72
P61019	K.IQEGVFDINNEANGIK.I	1760.8814	2	3.7215	0.5149	0.53
P61019	K.IQEGVFDINNEANGIK.I	1760.8814	2	5.2855	0.5888	0.35
Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah)						
Q9BZG1	R.INSDDSNLYLTASK.K	1540.7489	2	3.9536	0.5717	0.18
Ras-related protein Rab-5C (RAB5L) (L1880)						
P51148	R.GVDLQENNPASR.S	1299.6288	2	3.8066	0.4796	0.47
P51148	K.NEPQNATGAPGR.N	1211.5763	2	2.989	0.503	0.29
P51148	R.QASPNIVIALAGNK.A	1395.7954	2	3.3616	0.6047	0.25
P51148	R.QASPNIVIALAGNK.A	1395.7954	2	2.5913	0.357	0.25
Ras-related protein Rab-7						
P51149	R.DEFLIQASPR.D	1175.6055	1	2.3641	0.314	0.47
P51149	R.FQSLGVAFYR.G	1187.6208	2	3.6992	0.3001	0.41
P51149	K.TSLMNQYVNK.K	1197.5932	1	1.913	0.2837	0.31
P51149	K.EAINVEQAFQTIAR.N	1589.8282	2	4.4261	0.5135	0.85

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P51149	R.DEFLIQASPR.D	1175.6055	2	3.2517	0.2607	0.58
P51149	K.VIILGDSGVGK.T	1057.6252	2	2.5549	0.2492	3.46
P51149	K.VIILGDSGVGK.T	1057.6252	1	2.5475	0.4624	2.72
P51149	K.ATIGADFLTK.E	1036.5673	1	1.9632	0.3095	0.36
P51149	K.ATIGADFLTK.E	1036.5673	2	2.3056	0.4205	0.30
P51149	K.NNIPYFETSAK.E	1283.6266	2	2.3917	0.2554	1.54
P51149	R.DEFLIQASPR.D	1175.6055	2	2.8781	0.2266	0.58
P51149	R.LVTMQIWDTAGQER.F	1647.8159	2	4.3503	0.4718	2.46
P51149	K.TSLMNQYVNK[.K	1201.6012	2	2.5096	0.2164	0.20
P51149	K.NNIPYFETSAK[.E	1287.6346	2	2.5455	0.2408	1.54
P51149	K.TSLMNQYVNK.K	1197.5932	2	3.6566	0.5775	0.20
P51149	R.DPENFPFVVLGNK.I	1475.7529	2	4.089	0.5257	0.36
P51149	K.QETEVELYNEFPEPIK.L	1964.9488	2	4.6438	0.5416	0.25
Ras-related protein Rab-8A (Oncogene c-mel)						
P61006	K.KLEGNSPQGSNQGVK.I	1542.7871	2	4.9805	0.5607	0.51
P61006	K.LEGNSPQGSNQGVK.I	1414.6921	1	2.5717	0.5383	0.33
Ras-related protein Rab-9A (Rab-9)						
P51151	K.EPESFPFVILGNK.I	1476.7733	2	2.7072	0.4167	0.23
Relaxin-like factor b						
Q6YNB5	R.WDLACSPCPR.P	1147.5023	1	2.2258	0.1692	0.12
Retinoblastoma binding protein 2 homolog 1						
O95811	K.LLSPLQDVDIKIC*LC*R.K	1943.0453	2	2.258	0.1567	0.10
Retinoic acid-induced protein 3 (G-protein coupled receptor family C group 5 member A) (Retinoic						
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.7383	2	2.9327	0.5327	0.89
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.7383	2	3.6815	0.6224	1.44
Q8NFJ5	R.TNVNVFSELSAPR[.R	1437.7463	2	3.3654	0.3187	1.44
Q8NFJ5	R.NPMDYPVEDAFC*KPQLVK[.K	2155.0329	2	3.4195	0.2767	0.54
Q8NFJ5	K.DYEVK[.K	657.3221	1	1.9518	0.1645	0.26
Q8NFJ5	R.TNVNVFSELSAPR[.R	1437.7463	2	4.6092	0.4187	0.78
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.7383	2	3.6096	0.6229	0.90
Q8NFJ5	R.TNVNVFSELSAPR[.R	1437.7463	2	3.3555	0.3313	0.90
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.7383	2	4.0441	0.621	0.78
Q8NFJ5	R.NPMDYPVEDAFC*KPQLVK.K	2151.0249	2	4.4846	0.6699	0.54
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.7383	1	2.9327	0.4088	0.45
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.7383	1	2.3065	0.2831	0.45

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Rhophilin-2 (GTP-Rho binding protein 2) (76 kDa RhoB effector protein) (p76RBE)						
Q8IUC4	R.AMAHHEESVREASLC*K.K	1854.8585	2	2.49	0.3106	0.04
Rho-related GTP-binding protein RhoG						
P84095	K.EYIPTVFDNYSAQSAVDGR.T	2131.9931	2	4.6037	0.6646	0.53
Ribosome-binding protein 1 (Ribosome receptor protein) (180 kDa ribosome receptor homolog)						
Q9P2E9	R.DAQDVQASQAEADQQQTR.L	1988.8904	2	6.1558	0.6401	0.80
RNA-binding protein 28 (RNA-binding motif protein 28)						
Q9NW13	K.C*LLAASPENEAGGLKLDGR.Q	1970.9964	2	2.3755	0.1999	0.15
RNA-binding protein with serine-rich domain 1 (SR-related protein LDC2)						
Q15287	K.GYAYVEFENPDEAEK.A	1760.765	2	4.9327	0.698	0.28
RPS27L protein						
Q49A11	R.DLLHPSLEEEK.K	1309.6634	2	2.7603	0.3206	0.13
Ryanodine receptor 3 (Brain-type ryanodine receptor) (RyR3) (RYR-3) (Brain ryanodine receptor-						
Q15413	K.MSKAMQVKSGGQDQER.K	1779.8476	2	2.3961	0.1763	0.16
Q15413	K.KYDPDLFR.M	1053.5364	2	2.2301	0.0896	2.05
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (EC 3.6.3.8) (Calcium pump 2) (SERCA2)						
P16615	K.MNVFDTELK.G	1096.5343	2	2.9439	0.484	0.07
P16615	R.IGIFGQDEDVTSK.A	1408.6955	2	4.0796	0.4391	0.30
P16615	R.IGIFGQDEDVTSK.A	1408.6955	2	3.3442	0.4091	0.30
P16615	K.VPMTSGVK.Q	818.4441	1	1.9945	0.3089	0.21
P16615	K.MNVFDTELK.G	1096.5343	1	2.2954	0.3004	0.11
P16615	R.EEMHLEDSANFIK[.Y	1566.7235	2	2.6852	0.2799	0.36
P16615	K.MNVFDTELK.G	1096.5343	1	2.2648	0.1448	0.11
P16615	R.IEVASSVK.L	832.4775	1	1.936	0.3427	0.24
P16615	K.MNVFDTELK.G	1096.5343	1	2.093	0.2946	0.18
P16615	R.IEVASSVK.L	832.4775	1	1.9244	0.3076	1.96
P16615	R.IGIFGQDEDVTSK.A	1408.6955	2	3.7225	0.3969	0.46
P16615	R.NYLEPGK.E	820.4199	1	1.9865	0.2055	0.19
P16615	R.EFDELNPSAQR[.D	1309.615	2	3.4506	0.3085	0.35
P16615	R.EFDELNPSAQR.D	1305.607	2	3.8361	0.4376	0.35
P16615	R.EEMHLEDSANFIK.Y	1562.7155	2	3.4928	0.542	0.36
P16615	R.IGIFGQDEDVTSK.A	1408.6955	2	3.816	0.4192	0.29
P16615	R.DEMVATEQER.T	1207.5259	2	3.1359	0.4912	0.63
P16615	R.EFDELNPSAQR.D	1305.607	2	3.6777	0.4293	0.52

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Scavenger receptor class B member 1 (SRB1) (SR-BI) (CD36 antigen-like 1) (CD36 and LIMPII						
Q8WTV0	K.SVAGIGQTGK[.I	921.5131	1	1.9482	0.1622	0.39
Q8WTV0	K.SVAGIGQTGK.I	917.5051	1	2.1506	0.4401	0.39
Q8WTV0	K.SVAGIGQTGK.I	917.5051	1	2.001	0.278	0.56
SCO1 protein homolog, mitochondrial precursor						
O75880	R.EEVDQVAR[.A	949.4716	1	2.3991	0.234	0.55
Secretory carrier membrane protein 3						
Q4VX17	R.QYATLDVYNPFETR.E	1716.8228	2	4.261	0.5863	0.30
Separin (EC 3.4.22.49) (Separase) (Caspase-like protein ESPL1) (Extra spindle poles-like 1 protein)						
Q14674	R.DQLLDDK.A	846.4203	1	1.9929	0.1945	0.36
Sequestosome-1 (Phosphotyrosine-independent ligand for the Lck SH2 domain of 62 kDa)						
Q13501	R.PGPTAESASGPSEDPSVNFLK.N	2086.9928	2	5.358	0.6261	0.68
Q13501	R.PGPTAESASGPSEDPSVNFLK[.N	2091.0008	2	5.013	0.4873	0.68
Serpin B10 (Bomapin) (Protease inhibitor 10)						
P48595	R.IRVPSIEFNANHPFLFFIR.H	2317.2604	2	2.2109	0.2243	0.44
SH3-binding kinase						
Q52WX2	R.EVSITNSLSSSPFIIK.V	1721.932	2	2.4752	0.1393	0.18
Sideroflexin-1 (Tricarboxylate carrier protein) (TCC)						
Q9H9B4	R.NILLTNEQLESAR[.K	1504.8096	2	3.3519	0.1907	1.27
Q9H9B4	K.VGIPVTDENGNR.L	1270.6386	2	2.5311	0.4249	0.78
Q9H9B4	R.NILLTNEQLESAR[.K	1504.8096	2	3.3106	0.2709	0.99
Q9H9B4	K.SSMSVTSLEAELQAK.I	1580.7836	2	3.1573	0.4974	0.40
Q9H9B4	K.QAITQVVVSR.I	1100.6422	1	2.0145	0.1818	0.22
Q9H9B4	R.NILLTNEQLESAR.K	1500.8016	2	4.3144	0.5801	0.99
Signal peptidase complex subunit 1 (EC 3.4.-.-) (Microsomal signal peptidase 12 kDa subunit)						
Q9Y6A9	K.WLPVQESSTDDK.K	1404.6642	2	3.0364	0.5333	0.16
Signal peptidase complex subunit 2 (EC 3.4.-.-) (Microsomal signal peptidase 25 kDa subunit)						
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR[.S	1861.7279	2	4.773	0.5789	0.43
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR.S	1857.7199	2	2.906	0.6059	0.39
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR[.S	1861.7279	2	3.8085	0.5425	0.84
Q15005	K.NSLDDSAK.K	849.3949	1	2.1771	0.2974	0.22
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR[.S	1861.7279	2	4.416	0.5611	0.39
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR.S	1857.7199	2	4.5643	0.7219	0.43
Signal peptidase complex subunit 3 (EC 3.4.-.-) (Microsomal signal peptidase 23 kDa subunit)						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P61009	K.NVEDFTGPR.E	1034.4901	1	2.2725	0.4021	0.29
P61009	K.NVEDFTGPR.E	1034.4901	1	2.3486	0.302	0.40
P61009	K.NVEDFTGPR.E	1034.4901	1	2.4113	0.2531	0.19
P61009	K.NNALNQVVLWDK.I	1413.7485	2	3.7133	0.5417	0.69
P61009	K.YFFFDDGNGLK.G	1322.6052	2	3.0908	0.536	0.11
Signal recognition particle receptor beta subunit (SR-beta) (Protein APMCF1)						
Q9Y5M8	R.DTQTSITDSC*AVYR.V	1616.7221	2	3.2276	0.5349	0.35
Q9Y5M8	R.VADGGGAGGTFQPYLDTLR.Q	1894.9294	2	5.1032	0.635	0.42
Q9Y5M8	R.DTQTSITDSC*AVYR.V	1616.7221	2	3.6173	0.5231	0.35
Q9Y5M8	R.SAAPSTLDSSSTAPAQLGK.K	1788.8974	2	4.3914	0.5684	0.18
Signal transducer and activator of transcription 3 (Acute-phase response factor)						
P40763	R.IVELFRNLMK.S	1262.7289	2	2.2679	0.1517	0.14
P40763	R.IVELFRNLMK.S	1262.7289	2	2.2298	0.2362	0.22
Similar to flotillin 2						
Q9BTI6	K.IGEAEATVIEAMGK.A	1418.7196	2	4.0903	0.651	0.38
Similar to mouse 1500009M05Rik protein						
Q8N5K1	K.DSLINLK.I	802.4669	1	1.9142	0.1539	0.44
Q8N5K1	R.LPVPESITGFAR.L	1286.7103	2	2.8836	0.3982	0.23
Q8N5K1	K.VVNEINIEDLC*LTK.A	1659.8622	2	4.8576	0.4728	0.82
Q8N5K1	R.LPVPESITGFAR.L	1286.7103	2	3.1818	0.4103	0.20
Single-stranded DNA-binding protein, mitochondrial precursor (Mt-SSB) (MtSSB) (PWP1-						
Q04837	R.SGDSEVYQLGDVSQK.T	1611.7497	2	4.7945	0.5378	0.68
Small glutamine-rich tetratricopeptide repeat-containing protein B (Small glutamine-rich protein						
Q96EQ0	K.FEEAVTSYQK.A	1201.5735	1	2.2316	0.195	0.64
Small proline-rich protein 4						
Q96PI1	K.QPC*QPPPVKCQETCAPK.T	1910.8921	2	2.2662	0.1833	0.16
Sodium/potassium-transporting ATPase alpha-1 chain precursor (EC 3.6.3.9) (Sodium pump 1)						
P05023	K.IVEIPFNSTNK.Y	1261.6787	2	2.3357	0.3432	0.23
P05023	R.AVFQANQENLPILK.R	1584.8744	2	3.3275	0.4025	0.30
P05023	R.SPDFTNENPLETR[.N	1523.7103	2	3.7079	0.451	0.65
P05023	R.SPDFTNENPLETR.N	1519.7023	2	4.3618	0.6122	0.65
Sodium/potassium-transporting ATPase beta-2 chain (Sodium/potassium-dependent ATPase beta-2						
P14415	K.FLEPYNDSMQAQKNDVC*R[.P	2218.9987	2	2.889	0.1852	0.09
Sodium/potassium-transporting ATPase beta-3 chain (Sodium/potassium-dependent ATPase beta-3						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P54709	K.LFIYNPTTGEFLGR.T	1627.8479	2	4.5382	0.5445	0.40
P54709	R.IIGLKPEGVPR.I	1178.7256	2	2.52	0.4084	0.12
Sodium-dependent multivitamin transporter (Na(+)-dependent multivitamin transporter)						
Q9Y289	R.ISGFELDPDPFVR.H	1491.7478	2	3.6018	0.5006	0.36
Q9Y289	R.SLNPATIYPVLPK.L	1412.8148	2	3.0861	0.532	0.76
Solute carrier family 2, facilitated glucose transporter member 1 (Glucose transporter type 1,						
P11166	R.TFDEIASGFR.Q	1142.5477	2	2.6797	0.4569	0.46
P11166	R.TFDEIASGFR.Q	1142.5477	2	2.8181	0.5223	0.77
Solute carrier family 25 member 24, isoform 1						
Q6NUK1	R.NLGIPLGQDAEEK.I	1383.7114	2	2.2129	0.3718	0.23
Sorting and assembly machinery component 50 homolog						
Q9Y512	R.FYLGGPTSVR.G	1096.5786	2	2.33	0.4691	0.21
Q9Y512	K.VNQELAGYTGGDVSFIK.E	1797.9018	2	5.748	0.7144	1.23
Q9Y512	R.FYLGGPTSVR.G	1096.5786	2	2.8414	0.3953	0.21
Q9Y512	K.NLIEVMR.K	874.4815	1	2.1447	0.1344	0.46
Q9Y512	R.NSSILPR.R	786.4468	1	2.2509	0.0813	0.48
Q9Y512	K.QEILENK.D	873.4676	1	2.4487	0.1935	0.16
Q9Y512	K.VTGQFPWSSLR.E	1277.6637	2	4.0182	0.4287	0.35
Q9Y512	R.NSSILPR.R	786.4468	1	2.2391	0.1429	0.39
Q9Y512	R.FYLGGPTSVR.G	1096.5786	2	2.5947	0.485	0.21
Q9Y512	K.VTGQFPWSSLR.E	1277.6637	2	3.2121	0.396	0.35
Source of immunodominant MHC-associated peptides						
Q8TCJ2	R.ESDYFTPQGEFR.V	1475.6437	2	2.5973	0.4507	0.50
Q8TCJ2	R.ESDYFTPQGEFR[.V	1479.6517	2	2.6445	0.417	0.50
Q8TCJ2	R.NQGNLYDK.A	951.453	1	2.0326	0.24	0.05
Q8TCJ2	R.ENPPVEDSSDEDDK.R	1575.6293	2	2.338	0.4462	0.47
Q8TCJ2	R.ENPPVEDSSDEDDKR.N	1731.7304	2	3.4646	0.5706	0.56
Q8TCJ2	R.NQGNLYDK.A	951.453	1	1.9164	0.1768	0.02
Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha						
Q13813	R.EANQQQQFNR.N	1262.5872	1	2.0913	0.2975	0.32
Q13813	K.VNSLGETAER.L	1075.5378	2	2.8152	0.4563	0.40
Q13813	R.DLAALGDK.V	802.4305	1	2.1979	0.2735	0.87
Q13813	K.VLETAEDIQER.R	1302.6536	2	3.2176	0.5554	0.04
Q13813	K.ITALDEFATK.L	1108.5885	2	2.8048	0.3662	0.40
Q13813	K.LGESQTLQQFSR.D	1393.707	2	3.7406	0.5211	0.20

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q13813	K.LQTASDESYKDPTNIQSK.H	2024.9771	2	5.0244	0.6586	0.39
Q13813	K.DLTNVQNLQK.K	1172.627	2	3.3978	0.3531	0.29
Q13813	K.LQTASDESYKDPTNIQSK[.H	2028.9851	2	3.7674	0.4615	0.39
Q13813	K.AINVQEEK.I	930.4891	1	2.1849	0.2852	0.64
Q13813	R.QEQIDNQTR.I	1131.5389	2	2.4436	0.1569	0.13
Q13813	K.DLTNVQNLQK[.K	1176.635	2	2.4484	0.1226	0.29
Q13813	K.AINVQEEK.I	930.4891	1	2.1487	0.2573	2.35
Q13813	K.VLETAEDIQER.R	1302.6536	2	3.6464	0.525	0.04
Q13813	K.LQIASDENYKDPTNLQGK.L	2034.0138	2	5.3698	0.5338	0.70
Q13813	K.DLTNVQNLQK.K	1172.627	1	2.1133	0.3127	0.30
Q13813	K.LLEAQSHFR[.K	1104.5927	2	2.7204	0.1914	1.21
Q13813	R.DLAALEDK.V	874.4516	1	2.4599	0.4036	0.31
Q13813	R.DLAALGDK.V	802.4305	1	2.6729	0.2786	0.10
Q13813	K.KGDILTLLNSTNK.D	1416.8057	2	4.3926	0.5955	0.22
Q13813	R.SQLLGSAHEVQR.F	1324.6968	2	3.4134	0.4658	0.26
Q13813	K.VLETAEDIQER.R	1302.6536	2	3.7843	0.5934	0.05
Q13813	R.QQVAPTDDETGK.E	1288.6016	2	2.292	0.4175	0.53
Q13813	R.DLSSVQTLLTK.Q	1204.6783	2	3.0673	0.4858	0.20
Q13813	K.DLASVNNLLK.K	1086.6153	2	2.4377	0.4062	0.68
Q13813	K.GRELPTAFDYVEFTR.S	1800.8915	2	2.4411	0.3508	0.29

Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II spectrin) (Fodrin beta

Q01082	R.AQTLPTSVVTITSESSPGK.R	1903.0019	2	4.9402	0.7293	0.31
Q01082	K.TALPAQSAATLPAR.T	1367.7641	1	2.4248	0.494	0.27

SPFH domain protein 1 precursor (Protein KE04)

O75477	K.EALEPSGENVIQNK.E	1527.7649	2	3.5772	0.4748	0.98

SPFH domain protein 2 precursor

O94905	K.LSFGLEDEPLETATK[.E	1653.8349	2	4.0814	0.3665	0.34
O94905	K.LSFGLEDEPLETATK[.E	1653.8349	2	4.4545	0.3226	0.49
O94905	K.LSFGLEDEPLETATK.E	1649.8269	2	5.4623	0.5881	0.34
O94905	K.LSFGLEDEPLETATK.E	1649.8269	2	4.6701	0.5606	0.49

Sphingosine kinase 2 (EC 2.7.1.-) (SK 2) (SPK 2)

Q9NRA0	R.LLLLVNPFGGRGLAWQWC*K.N	2228.2161	2	2.5574	0.1128	0.26

Splicing coactivator subunit SRm300

Q9UHA8	R.SPVPSAFSDQSR.C	1277.6121	1	2.4161	0.4435	0.68
Q9UHA8	R.SPVPSAFSDQSR.C	1277.6121	2	2.459	0.4556	0.21

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9UHA8	R.AAFGISDSYVDGSSFDPQR.R	2018.909	2	4.4317	0.49	0.64
Q9UHA8	R.AAFGISDSYVDGSSFDPQR[.R	2022.917	2	4.6009	0.5345	0.64
Stabilin-1 precursor (FEEL-1 protein) (MS-1 antigen)						
Q9NY15	R.VFLQLRVAVAMMDQGCR[.E	1940.9998	2	2.2654	0.0918	149.47
Stanniocalcin-1 precursor (STC-1)						
P52823	K.SRVAAQNSAEVVR.C	1386.7448	2	2.4582	0.1297	0.01
Steroid dehydrogenase homolog (Fragment)						
Q53GQ0	R.TIAVDFASEDIYDK.I	1586.7584	2	3.1431	0.4792	0.30
Stomatin-like protein 2 (SLP-2) (EPB72-like 2)						
Q9UJZ1	K.APVPGTPDSLSSGSSR.D	1514.7445	2	3.3336	0.5386	0.52
Stress-70 protein, mitochondrial precursor (75 kDa glucose regulated protein) (GRP 75) (Peptide-						
P38646	K.DDIENMVK.N	963.4452	1	1.9977	0.2849	0.31
Supervillin (Archvillin) (p205/p250)						
O95425	R.SNEEEETSDSSLEK.Q	1583.6555	2	4.8573	0.5364	0.75
O95425	R.YQTQPVTLGEVEQVQSGK.L	1991.008	2	4.4792	0.527	0.17
O95425	K.ELAEQGEPDSSTLSLAEK[.L	1907.9211	2	3.5874	0.3986	0.26
Synaptic glycoprotein SC2						
Q9NZ01	R.LLETLFVHR.F	1127.6572	2	2.9502	0.4137	0.26
Q9NZ01	K.DEDVLQK.L	846.4203	1	2.3793	0.3533	0.24
Q9NZ01	K.DEDVLQK.L	846.4203	1	2.2566	0.3105	0.72
Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog)						
Q5UIP0	K.LIVKVIYSFHTLSFK.E	1795.0517	2	2.3727	0.3122	0.07
Tetratricopeptide repeat protein KIAA0103						
Q15006	R.ILQEDPTNTAAR[.K	1332.6885	2	3.5062	0.2661	0.64
Q15006	R.ILQEDPTNTAAR.K	1328.6805	2	4.0791	0.4798	0.64
Q15006	R.ILQEDPTNTAAR.K	1328.6805	2	3.9354	0.4612	0.39
TGF-beta receptor type II precursor (EC 2.7.1.37) (TGFR-2) (TGF-beta type II receptor)						
P37173	K.NDENITLETVCHDPK[.L	1731.7985	2	2.708	0.1694	0.11
P37173	K.NDENITLETVCHDPK[.L	1731.7985	2	2.7446	0.2058	0.20
THAP domain-containing protein 2						
Q9H0W7	K.ILEQDQQDKTLLSLNLK.Q	1999.107	2	2.9009	0.2384	0.23
Q9H0W7	K.ILEQDQQDKTLLSLNLK.Q	1999.107	2	3.4072	0.2297	0.27
Q9H0W7	K.ILEQDQQDKTLLSLNLK.Q	1999.107	2	2.8931	0.2179	0.24
Q9H0W7	K.ILEQDQQDKTLLSLNLK.Q	1999.107	2	3.3653	0.2133	0.29

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q9H0W7	K.ILEQDQQDKTLLSLNLK.Q	1999.107	2	2.8417	0.2812	0.45
Thioredoxin domain-containing protein 1 precursor (Transmembrane Trx-related protein)						
Q9H3N1	K.VDVTEQPGLSGR.F	1257.6434	2	4.5636	0.5268	0.30
Thioredoxin reductase 2 intronic transcript 1						
Q6F5E7	K.VFGQGFPSPLEEIKR[.L	1707.9195	2	2.2273	0.1405	0.22
Thyroid hormone receptor-associated protein complex 95 kDa component (Trap95) (Thyroid hormone						
Q9Y2X0	R.APGQPKIDHLRR.L	1387.7917	1	1.9565	0.1847	0.16
Thyroid receptor-interacting protein 11 (TRIP-11) (Golgi-associated microtubule-binding protein 210)						
Q15643	R.EKEFECHSMKEK.A	1524.6821	2	2.6467	0.1687	0.19
TNF receptor-associated factor 5 (RING finger protein 84)						
O00463	R.FVAHSVLENAKNAYIK.D	1803.9752	2	2.4046	0.1963	0.27
Transcription elongation factor A (SII)-like 3 (MSTP072) (Hypothetical protein FLJ25628)						
Q969E4	K.SDEEEKPDVEGKTECEGK.R	2008.8652	2	2.3771	0.1167	0.37
Transcription elongation factor B polypeptide 1 (RNA polymerase II transcription factor SIII						
Q15369	K.AMLSGPGQFAENETNEVNFR.E	2211.0135	2	2.6363	0.1214	0.46
Transcription factor 20 (Stromelysin 1 PDGF-responsive element-binding protein) (SPRE-binding						
Q9UGU0	R.SASSNSAEAGGDTVTLDDILSLK[.S	2255.1016	2	3.2275	0.1769	2.37
Transcription termination factor, mitochondrial precursor (mTERF) (Mitochondrial transcription						
Q99551	K.NEDLLKNLLTMGVDIDMARK.R	2289.1941	2	2.8265	0.3701	0.44
Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 antigen) (T9) (p90)						
P02786	R.YNSQLLSFVR.D	1226.6528	2	3.342	0.3071	1.42
P02786	R.EEPGEDFPAAR.R	1217.5433	2	2.3099	0.4627	0.46
P02786	R.SSGLPNIPVQTISR.A	1468.8118	2	3.9584	0.4588	1.27
P02786	K.DSAQNSVIIVDK.N	1288.6743	2	3.7757	0.4535	0.96
P02786	R.SSGLPNIPVQTISR[.A	1472.8198	2	3.0067	0.3229	1.27
P02786	K.GFVEPDHYVVVGAQR.D	1672.8442	2	4.4845	0.5113	0.56
P02786	K.LAVDEEENADNNTK.A	1561.6976	2	4.3373	0.5761	0.28
P02786	R.YNSQLLSFVR.D	1226.6528	2	2.4271	0.2281	1.42
P02786	K.VSASPLLYTLIEK[.T	1437.833	2	3.5023	0.4846	0.32
P02786	K.VSASPLLYTLIEK.T	1433.825	2	3.7562	0.6031	0.32
P02786	K.LAVDEEENADNNTK.A	1561.6976	2	4.7406	0.5471	0.34
Transformation/transcription domain-associated protein (350/400 kDa PCAF-associated factor)						
Q9Y4A5	K.YLQFVAALTDVNTPDETKLK[.M	2270.2045	2	3.2329	0.2754	0.88
Translocation associated membrane protein 1						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Q15629	K.LDFSTGNFNVLAVR.I	1552.8118	2	4.1592	0.6036	0.30
Q15629	R.EHSAFQAPAVK[.K	1188.6138	2	2.4652	0.4122	0.79
Q15629	K.LDFSTGNFNVLAVR[.I	1556.8198	2	3.7467	0.2688	0.30
Q15629	K.LDFSTGNFNVLAVR.I	1552.8118	2	4.8019	0.5938	0.30
Q15629	R.EHSAFQAPAVK.K	1184.6058	2	2.7179	0.4799	0.79

Translocation protein SEC63 homolog

Q9UGP8	K.DATSRPTDNILIPQLIR[.E	1927.0738	2	4.2116	0.3845	2.08
Q9UGP8	K.DATSRPTDNILIPQLIR.E	1923.0658	2	3.8648	0.3894	2.08

Translocon-associated protein alpha subunit precursor (TRAP-alpha) (Signal sequence receptor

P43307	K.GEDFPANNIVK[.F	1207.6084	1	2.0241	0.2379	1.33

Translocon-associated protein delta subunit precursor (TRAP-delta) (Signal sequence receptor delta

P51571	R.FFDEESYSLLR.K	1405.6634	2	3.4382	0.5907	0.26
P51571	R.FFDEESYSLLR.K	1405.6634	2	2.6362	0.2989	0.26
P51571	R.FFDEESYSLLR.K	1405.6634	2	3.5248	0.5797	0.40
P51571	R.FFDEESYSLLR.K	1405.6634	2	4.0895	0.4615	0.40
P51571	R.FFDEESYSLLR.K	1405.6634	2	3.2839	0.4057	0.40

Translocon-associated protein gamma subunit (TRAP-gamma) (Signal sequence receptor gamma

Q9UNL2	K.QQSEEDLLLQDFSR.N	1707.8184	2	4.2575	0.5617	0.14
Q9UNL2	K.QQSEEDLLLQDFSR.N	1707.8184	2	4.2119	0.5428	0.22

Transmembrane 9 superfamily protein member 2 precursor (p76)

Q99805	R.PSENLGQVLFGER.I	1445.7383	2	3.3831	0.4564	0.65

Transmembrane anchor protein 1

P84157	R.QEEEQDLDGEK.G	1319.5597	2	2.751	0.4445	0.69
P84157	R.QEEEQDLDGEK.G	1319.5597	2	2.4951	0.4104	0.19
P84157	R.QEEEQDLDGEK.G	1319.5597	2	2.6205	0.1545	0.19

Transmembrane emp24 domain containing protein 10 precursor (Transmembrane protein Tmp21)

P49755	R.IPDQLVILDMK.H	1284.7232	2	3.8634	0.5017	0.36
P49755	R.IPDQLVILDMK.H	1284.7232	2	3.8245	0.4835	0.26
P49755	K.NYEEIAK.V	866.4254	1	2.274	0.1579	0.69
P49755	R.LEDLSESIVNDFAYMK[.K	1877.8968	2	3.0124	0.3612	0.74
P49755	R.IPDQLVILDMK.H	1284.7232	1	2.569	0.3976	0.03
P49755	K.ITDSAGHILYSK.E	1304.6845	2	4.2997	0.6456	0.24
P49755	R.LEDLSESIVNDFAYMK.K	1873.8888	2	4.414	0.6094	0.76
P49755	K.NYEEIAK.V	866.4254	1	2.1541	0.1314	0.50
P49755	R.IPDQLVILDMK.H	1284.7232	2	3.8301	0.4532	0.36

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P49755	K.NYEEIAK.V	866.4254	1	2.0762	0.1229	4.48
P49755	R.LEDLSESIVNDFAYMK[.K	1877.8968	2	3.9864	0.3694	0.76
P49755	R.LEDLSESIVNDFAYMK.K	1873.8888	2	3.5671	0.5767	0.74
P49755	K.NYEEIAK[.V	870.4334	1	2.0881	0.089	0.69
Transmembrane emp24 domain containing protein 4 precursor						
Q7Z7H5	R.LTSESTNQR.V	1035.5065	1	2.3652	0.2339	0.65
Q7Z7H5	R.LTSESTNQR[.V	1039.5145	1	2.1174	0.3237	0.69
Q7Z7H5	R.LTSESTNQR.V	1035.5065	1	2.323	0.2994	0.69
Q7Z7H5	R.LTSESTNQR[.V	1039.5145	1	1.983	0.3048	0.65
Transmembrane emp24 domain containing protein 5 precursor						
Q9Y3A6	R.NIQESNFDR.V	1122.5174	1	2.6434	0.3189	0.23
Transmembrane emp24 domain containing protein 9 precursor (Glycoprotein 25L2)						
Q9BVK6	R.TQLYDK.Q	767.3934	1	1.9252	0.1863	0.08
Q9BVK6	R.QLVEQVEQIQK.E	1341.7373	2	4.2436	0.1543	0.88
Transmembrane protein 11 (Protein PM1)						
P17152	R.LGPGSSGGSAR.E	945.4748	1	1.974	0.4318	1.22
P17152	R.LPLHTLTSSTPVVLVR[.K	1737.04	2	3.3827	0.3245	2.82
Transmembrane protein 33 (DB83 protein)						
P57088	R.ALLANALTSALR.L	1213.7263	2	3.8985	0.5337	0.58
P57088	R.ALLANALTSALR.L	1213.7263	2	4.616	0.5403	0.27
P57088	K.LSANQQNILK.F	1128.6371	2	2.9515	0.3854	0.76
P57088	K.LSANQQNILK.F	1128.6371	2	2.8644	0.3869	0.43
P57088	R.ALLANALTSALR.L	1213.7263	2	2.9714	0.5024	0.58
P57088	R.ALLANALTSALR.L	1213.7263	2	4.8652	0.5323	0.27
P57088	R.ALLANALTSALR[.L	1217.7343	2	3.852	0.4742	0.27
P57088	R.GSNSLPLLR.S	956.5524	2	2.7672	0.346	0.36
Transmembrane protein 49 (TDC1)						
Q96GC9	K.PFQEYLEAQR.Q	1280.627	2	3.3822	0.372	0.41
Transmembrane protein PT27 (TPA regulated locus)						
Q9HC07	R.NKEPPAPAQQLQPQPVAVQGPEPAR.V	2647.3951	3	4.6944	0.5976	0.69
Q9HC07	K.DEEFQR.T	823.3581	1	2.0009	0.1065	0.42
Q9HC07	K.LLNGPGDVETGTSITVPQK.K	1926.0178	2	4.7028	0.5605	0.27
Q9HC07	K.LLNGPGDVETGTSITVPQK[.K	1930.0258	2	2.9682	0.2141	0.27
Q9HC07	K.LLNGPGDVETGTSITVPQK.K	1926.0178	2	3.7274	0.433	0.30

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Tricarboxylate transport protein, mitochondrial precursor (Citrate transport protein) (CTP)						
P53007	K.TQLQLDER.S	1002.5214	1	2.3416	0.2598	0.42
P53007	R.GLSSLLYGSIPK.A	1234.7042	2	3.3004	0.4493	0.34
P53007	K.FIHDQTSPNPK[.Y	1287.6459	2	3.0615	0.3122	0.67
P53007	K.FIHDQTSPNPK.Y	1283.6379	2	3.0756	0.4471	0.67
Triggering receptor expressed on myeloid cells 5						
Q8N6D1	R.WDTC*KILIETR.G	1434.741	2	2.2087	0.2404	0.23
Tripartite motif protein 10 (RING finger protein 9) (B30-RING finger protein)						
Q9UDY6	R.YC*EIPGPDLEESPTC*PLC*K.E	2264.9872	2	2.3257	0.2602	0.74
Tryptophan/serine protease						
Q6UWB4	K.LTKNMLCAGYKNESYDACK[.G	2155.9952	2	2.4882	0.2326	0.68
Tubulin alpha-1 chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha)						
P68366	K.TIGGGDDSFTTFFC*ETGAGK.H	2067.8964	2	3.7669	0.6131	0.27
P68366	K.TIGGGDDSFTTFFCETGAGK[.H	2014.8829	2	2.6482	0.2167	0.16
Tubulin tyrosine ligase-like protein 4						
Q14679	K.LLRWKMSTVTPNIVK.Q	1786.0408	2	2.3915	0.1616	0.34
Tumor necrosis factor ligand superfamily member 4 (OX40 ligand) (OX40L) (Glycoprotein GP34)						
P23510	R.VQPLEENVGNAARPRFER[.N	2086.0919	2	2.2602	0.1601	1.83
Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF						
Q96RJ3	R.GASSAEAPDGDKDAPEPLDK.V	1969.8985	2	2.5893	0.101	0.65
TXNDC14 protein						
Q561W0	K.AGDNIPEEQPVASTPTTVSDGENK.K	2456.1423	2	3.572	0.573	0.35
Q561W0	K.AGDNIPEEQPVASTPTTVSDGENK.K	2456.1423	3	4.3747	0.3788	0.20
Q561W0	K.AGDNIPEEQPVASTPTTVSDGENK.K	2456.1423	3	3.3276	0.4221	0.20
Q561W0	K.AGDNIPEEQPVASTPTTVSDGENK.K	2456.1423	2	4.1099	0.6249	0.48
Q561W0	K.AGDNIPEEQPVASTPTTVSDGENK.K	2456.1423	2	3.7205	0.607	0.40
Type I inositol-3,4-bisphosphate 4-phosphatase (EC 3.1.3.66) (Inositol polyphosphate 4-phosphatase						
Q96PE3	R.LHGEGC*EDVFPC*AGSC*TSK.K	2110.8627	2	2.8718	0.334	0.14
Q96PE3	R.LHGEGC*EDVFPC*AGSC*TSK.K	2110.8627	2	2.343	0.2648	0.24
Q96PE3	R.LHGEGC*EDVFPC*AGSC*TSK.K	2110.8627	2	2.8263	0.4126	0.18
Type-1 angiotensin II receptor-associated protein (AT1 receptor-associated protein)						
Q6RW13	R.SAYQTIDSAEAPADPFAVPEGR.S	2292.0779	2	2.2771	0.3853	0.94
Tyrosine-protein phosphatase, non-receptor type 1 (EC 3.1.3.48) (Protein-tyrosine phosphatase 1B)						
P18031	K.DPSSVDIK.K	860.436	1	2.0716	0.3591	0.49

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P18031	K.EFEQIDK.S	908.436	1	2.2065	0.104	0.10
Tyrosine-protein phosphatase, non-receptor type 4 (EC 3.1.3.48) (Protein-tyrosine phosphatase						
P29074	K.LENEPDFQYIPEK[.A	1625.7824	2	2.2971	0.0855	0.57
U5 small nuclear ribonucleoprotein 200 kDa helicase (EC 3.6.1.-) (U5 snRNP-specific 200 kDa						
O75643	K.TLNLCKMIDK.R	1178.6272	2	2.5072	0.1382	0.04
Ubiquinol-cytochrome c reductase complex 7.2 kDa protein (EC 1.10.2.2) (Cytochrome C1, nonheme						
Q9UDW1	R.AFDQGADAIYDHINEGK[.L	1867.8588	2	2.9046	0.3457	3.46
Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C (EC 1.10.2.2)						
O14949	K.NPAAYENDK.-	1021.4585	1	2.8347	0.4387	0.07
O14949	K.NPAAYENDK.-	1021.4585	1	2.7782	0.4143	0.24
O14949	K.NPAAYENDK.-	1021.4585	1	2.9124	0.4145	0.61
Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (EC 1.10.2.2)						
P22695	R.GGLGLSGAK[.A	763.4439	1	2.1533	0.1986	0.84
P22695	R.GGLGLSGAK[.A	763.4439	1	1.9037	0.3147	0.71
P22695	K.ATAAPAGAPPQPQDLEFTK[.L	1913.9734	2	3.389	0.4086	0.71
P22695	K.ATAAPAGAPPQPQDLEFTK.L	1909.9654	2	4.1517	0.659	0.71
P22695	K.ATAAPAGAPPQPQDLEFTK[.L	1913.9734	2	3.701	0.4898	0.64
P22695	K.TIAQGNLSNTDVQAAK.N	1630.8395	2	4.6302	0.6573	0.41
P22695	K.TIAQGNLSNTDVQAAK.N	1630.8395	2	4.399	0.6798	0.41
P22695	K.ATAAPAGAPPQPQDLEFTK.L	1909.9654	2	4.1469	0.6341	0.64
P22695	K.TIAQGNLSNTDVQAAK.N	1630.8395	2	4.3813	0.6557	0.35
P22695	R.NALANPLYC*PDYR.I	1566.7369	2	3.9337	0.514	0.68
Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (EC 1.10.2.2)						
P31930	K.AVELLGDIVQNC*SLEDSQIEK.E	2360.165	2	5.0826	0.7366	1.59
P31930	R.IAEVDASVVR.E	1058.584	1	2.4805	0.4254	0.28
P31930	R.MVLAAAGGVEHQQLLDLAQK.H	2092.1219	3	4.2835	0.4343	0.07
P31930	R.IAEVDASVVR.E	1058.584	2	3.0036	0.3916	0.19
P31930	R.NALVSHLDGTTPVC*EDIGR.S	2053.9971	2	5.0945	0.6132	0.78
P31930	R.NALVSHLDGTTPVC*EDIGR[.S	2058.0051	2	4.8678	0.4621	0.78
Ubiquitin carboxyl-terminal hydrolase 3 (EC 3.1.2.15) (Ubiquitin thiolesterase 3) (Ubiquitin-specific						
Q9Y6I4	R.KLLENSTLNSKLLK.V	1600.9632	2	2.281	0.1271	0.18
Ubiquitin carboxyl-terminal hydrolase 37 (EC 3.1.2.15) (Ubiquitin thiolesterase 37) (Ubiquitin-						
Q86T82	K.REQFNDLSIDLPRR[.K	1762.9326	2	2.8426	0.1413	15.67
Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) (Ubiquitin thiolesterase 5) (Ubiquitin-specific						

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P45974	R.VTSAVEALLSADSASR.K	1576.8177	2	2.5262	0.2641	1.60
Ubiquitin ligase protein CHFR (EC 6.3.2.-) (Checkpoint with forkhead and RING finger domains						
Q96EP1	R.NKITQDMLQPK[.V	1319.7118	2	2.232	0.1669	1.38
Ubiquitin ligase protein MIB1 (EC 6.3.2.-) (Mind bomb homolog 1) (DAPK-interacting protein 1)						
Q86YT6	R.QTPLHIAVNK.G	1120.6473	1	1.925	0.1512	0.65
Ubiquitin-conjugating enzyme E2 J1 (EC 6.3.2.19) (Non-canonical ubiquitin-conjugating enzyme 1)						
Q9Y385	K.SGSDSSQADQEAK.E	1309.5502	2	2.4156	0.3449	0.27
UBX domain-containing protein 6 (Rep-8 protein) (Reproduction 8 protein)						
O00124	K.LGGDEGTSQTSFETSNR.E	1785.7886	2	4.9921	0.6723	0.64
UPF0198 protein CGI-141						
Q9Y3E0	R.VPVLGSLLNLPGIR.S	1447.8995	2	3.0276	0.4299	0.31
UPF0347 protein LOC55831						
Q9P0I2	R.SIYSLILGQDNAADQSR.M	1850.9243	2	4.526	0.5829	0.19
Q9P0I2	K.LTQEQVSDSQVLIR.S	1615.865	2	4.169	0.5339	0.35
Vacuolar ATP synthase subunit d (EC 3.6.3.14) (V-ATPase d subunit) (Vacuolar proton pump d						
P61421	R.LYPEGLAQLAR.A	1230.6841	2	2.8007	0.4127	0.36
P61421	K.LLFEGAGSNPGDK.T	1304.6481	1	2.6469	0.434	0.13
P61421	K.LLFEGAGSNPGDK.T	1304.6481	2	3.9772	0.4262	0.12
Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 (V-ATPase 116-kDa isoform a1)						
Q93050	R.IDDLQMVLNQTEDHR.Q	1826.8701	2	4.642	0.5548	1.20
Q93050	R.IDDLQMVLNQTEDHR[.Q	1830.8781	2	3.8172	0.1278	1.12
Vesicle trafficking protein SEC22b (SEC22 vesicle trafficking protein-like 1)						
O75396	R.DLQQYQSQAK.Q	1208.5906	1	2.8484	0.4203	0.36
O75396	R.NLGSINTELQDVQR.I	1586.8133	2	4.4457	0.5712	0.35
O75396	R.VADGLPLAASMQEDEQSGR.D	1973.9233	2	4.9987	0.6422	0.33
O75396	R.VADGLPLAASMQEDEQSGR.D	1973.9233	2	4.8354	0.6494	0.85
O75396	R.VADGLPLAASMQEDEQSGR[.D	1977.9313	2	4.1826	0.3608	0.33
O75396	R.NLGSINTELQDVQR.I	1586.8133	2	3.3534	0.4227	0.35
O75396	R.VADGLPLAASMQEDEQSGR[.D	1977.9313	2	3.8642	0.3687	0.36
O75396	R.DLQQYQSQAK.Q	1208.5906	2	3.5222	0.4705	1.19
O75396	R.DLQQYQSQAK[.Q	1212.5986	2	3.5281	0.4182	1.19
O75396	R.NLGSINTELQDVQR.I	1586.8133	2	4.7569	0.5047	0.40
O75396	R.NLGSINTELQDVQR.I	1586.8133	2	5.0026	0.5246	0.40
O75396	R.NLGSINTELQDVQR.I	1586.8133	2	4.3387	0.5368	0.38

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
O75396	R.IMVANIEEVLQR[.G	1418.7803	2	4.079	0.2911	0.88
O75396	R.IMVANIEEVLQR.G	1414.7723	2	3.9952	0.4346	0.88
O75396	R.NLGSINTELQDVQR.I	1586.8133	2	2.6135	0.434	0.38
O75396	R.VADGLPLAASMQEDEQSGR.D	1973.9233	2	5.1224	0.6812	0.36
O75396	K.LNEQSPTR.C	944.4796	1	2.109	0.2013	0.29
O75396	R.DLQQYQSQAK.Q	1208.5906	1	2.7512	0.2534	0.36
Vesicle-associated membrane protein-associated protein A (VAMP-associated protein A) (VAMP-A)						
Q9P0L0	K.FKGPFTDVVTTNLK[.L	1570.8606	2	4.0273	0.4319	0.39
Q9P0L0	R.C*VFEMPNENDK.L	1382.5715	2	2.9982	0.3465	0.09
Q9P0L0	K.PHSVSLNDTETR.K	1355.655	2	2.7754	0.4547	0.33
Q9P0L0	K.PHSVSLNDTETR[.K	1359.663	2	2.4744	0.2604	0.33
Q9P0L0	K.FKGPFTDVVTTNLK.L	1566.8526	2	4.3567	0.487	0.39
Vesicular integral-membrane protein VIP36 precursor (GP36b glycoprotein) (Lectin, mannose-						
Q12907	K.DNVDDPTGNFR.S	1249.5444	2	3.7121	0.5005	0.39
Q12907	K.DNVDDPTGNFR[.S	1253.5524	2	3.4717	0.3996	0.39
Vimentin						
P08670	R.ETNLDSLPLVDTHSK.R	1668.8439	2	3.9176	0.5678	0.31
P08670	R.ETNLDSLPLVDTHSK.R	1668.8439	2	4.4025	0.5865	0.43
P08670	R.ETNLDSLPLVDTHSK[.R	1672.8519	2	3.6571	0.4467	0.31
Vitamin K epoxide reductase complex subunit 1 (EC 1.1.4.1) (Vitamin K1 2,3-epoxide reductase						
Q9BQB6	R.ALC*DVGTAISC*SR.V	1409.6512	2	3.4277	0.5895	0.37
Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial						
P21796	R.VTQSNFAVGYK[.T	1217.6292	2	2.7457	0.4203	0.49
P21796	K.YQIDPDAC*FSAK.V	1414.6307	2	2.7559	0.5283	0.79
P21796	K.LTFDSSFSPNTGK.K	1400.6692	2	3.63	0.6896	0.29
P21796	K.LTFDSSFSPNTGK.K	1400.6692	1	2.27	0.5709	0.44
P21796	K.YQIDPDAC*FSAK[.V	1418.6387	2	2.8992	0.318	1.38
P21796	K.VNNSSLIGLGYTQTLKPGIK.L	2103.1808	2	4.4061	0.4096	1.11
P21796	K.SENGLEFTSSGSANTETTK.V	1959.8778	2	5.6904	0.7143	0.40
P21796	K.LTFDSSFSPNTGK.K	1400.6692	2	3.4681	0.5916	0.33
P21796	R.VTQSNFAVGYK[.T	1217.6292	1	2.2742	0.2782	0.38
P21796	K.LTFDSSFSPNTGKK.N	1528.7642	2	3.3036	0.5526	0.94
P21796	K.LTFDSSFSPNTGK.K	1400.6692	1	2.3297	0.4067	0.44
P21796	K.LTFDSSFSPNTGKK[.N	1532.7722	2	3.0842	0.4171	0.94
P21796	K.VNNSSLIGLGYTQTLKPGIK[.L	2107.1888	2	3.7421	0.425	0.85

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
P21796	K.YQIDPDAC*FSAK.V	1414.6307	2	2.726	0.4691	1.38
P21796	R.VTQSNFAVGYK.T	1213.6212	2	3.4903	0.5564	0.57
P21796	K.WNTDNTLGTEITVEDQLAR.G	2176.0517	2	5.2157	0.5647	0.38
P21796	R.VTQSNFAVGYK.T	1213.6212	2	3.1127	0.4379	0.49
P21796	R.VTQSNFAVGYK[.T	1217.6292	2	3.5477	0.5264	0.52
P21796	K.VNNSSLIGLGYTQTLKPGIK.L	2103.1808	2	5.2379	0.4062	0.85
P21796	K.LTFDSSFSPNTGK[.K	1404.6772	2	3.2434	0.4515	0.33
P21796	K.SENGLEFTSSGSANTETTK.V	1959.8778	2	5.5376	0.6256	0.96
P21796	K.WNTDNTLGTEITVEDQLAR[.G	2180.0597	2	3.7986	0.3731	0.38
P21796	K.LTFDSSFSPNTGK[.K	1404.6772	1	2.2967	0.3949	0.55
P21796	K.LTFDSSFSPNTGK.K	1400.6692	1	2.6134	0.6054	0.32
P21796	K.LTFDSSFSPNTGK.K	1400.6692	2	3.6343	0.6689	0.23
P21796	R.VTQSNFAVGYK.T	1213.6212	1	2.0013	0.1376	0.25
P21796	R.VTQSNFAVGYK.T	1213.6212	2	3.333	0.568	0.52
P21796	K.VNNSSLIGLGYTQTLKPGIK[.L	2107.1888	2	3.2799	0.4102	1.11
P21796	K.LTFDSSFSPNTGK.K	1400.6692	2	3.5116	0.6566	0.34
P21796	R.VTQSNFAVGYK.T	1213.6212	1	2.2332	0.3041	0.38
P21796	R.VTQSNFAVGYK.T	1213.6212	1	2.2651	0.3022	0.38
P21796	K.LTFDSSFSPNTGK.K	1400.6692	1	2.2	0.5936	0.55

Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3) (Outer mitochondrial

Q9Y277	K.VC*NYGLTFTQK.W	1330.646	1	2.2209	0.4222	0.54
Q9Y277	K.LTLDTIFVPNTGK[.K	1422.797	2	3.9745	0.348	0.26
Q9Y277	K.VNNASLIGLGYTQTLR.P	1719.9388	2	5.1189	0.5767	0.94
Q9Y277	K.LTLDTIFVPNTGK[.K	1422.797	2	3.5365	0.264	0.17
Q9Y277	K.LTLDTIFVPNTGK.K	1418.789	2	3.6945	0.539	0.17
Q9Y277	K.LTLDTIFVPNTGK.K	1418.789	2	3.6279	0.5028	0.26
Q9Y277	K.LTLDTIFVPNTGK.K	1418.789	2	3.1755	0.4425	0.51
Q9Y277	K.LTLDTIFVPNTGK.K	1418.789	1	2.757	0.6034	0.15
Q9Y277	K.LSQNNFALGYK.A	1254.6477	2	2.6678	0.0808	0.14
Q9Y277	K.LSQNNFALGYK.A	1254.6477	2	3.6885	0.4494	0.15
Q9Y277	K.VC*NYGLTFTQK.W	1330.646	2	3.6642	0.2947	0.16
Q9Y277	K.LSQNNFALGYK.A	1254.6477	2	3.0308	0.5123	0.19
Q9Y277	K.VNNASLIGLGYTQTLRPGVK.L	2101.1764	2	3.1695	0.4047	3.69
Q9Y277	K.LSQNNFALGYK.A	1254.6477	2	3.5109	0.5076	0.27

WD-repeat protein 67

Q96DN5	R.NKCYQEVAKLLR.E	1464.7991	2	2.3538	0.2611	0.04

Acc #	Peptide	MH+	z	XC	DCN	H/L ratio
Wee1-like protein kinase (EC 2.7.1.112) (WEE1hu)						
P30291	K.ADIFALALTVVC*AAGAEPLPR.N	2155.158	2	2.2076	0.1183	0.07
Wnt-4 protein precursor						
P56705	R.ALVPRNAQFK[.P	1147.6713	1	1.9706	0.1266	0.27
YLP motif containing protein 1 (Nuclear protein ZAP3) (ZAP113)						
P49750	K.GPVVAKDTPEPVK[.E	1340.7551	1	2.0509	0.0962	105.27
ZDHHC8 protein						
Q96GI9	-.MDRGTQGPHR.P	1154.5483	1	1.9212	0.0984	0.08
Zinc finger CCCH type antiviral protein 1 (Zinc finger CCCH type domain containing protein 2)						
Q7Z2W4	R.VALVNDSLSDVTSTTSSR.V	1851.9294	2	5.6798	0.6334	1.06
Zinc finger FYVE domain-containing protein 16 (Endofin) (Endosome-associated FYVE domain						
Q7Z3T8	K.YIENLDNITFTESFLSSK.D	2121.0386	2	2.485	0.1245	0.11
Zinc finger protein 263 (Zinc finger protein FPM315)						
O14978	K.CLECGKCFSQNTHLTR[.H	1843.8379	2	2.6501	0.1485	0.47
Zinc finger protein 300						
Q96RE9	K.GVTRDGSLC*SILK.V	1405.7468	2	2.3629	0.0918	0.10
Zinc finger protein 317						
Q96PQ6	R.GAHQGACADWETPSKTK[.W	1790.8257	2	2.3088	0.2492	20.40
Zinc finger protein 510						
Q9Y2H8	K.PFQCNKCGKTFGQK.S	1585.7614	2	2.5468	0.1941	0.02
Zinc finger protein 512						
Q96ME7	R.QQPGIELPETELSLR.V	1709.9068	2	2.3206	0.2241	0.27
Zinc transporter 1 (ZnT-1) (Solute carrier family 30 member 1)						
Q9Y6M5	K.ESALILLQTVPK.Q	1311.7882	2	3.2085	0.3863	0.30