Supplemental Table S-2a. A list of 726 ^{18}O/^{16}O labeled protein-specific peptides quantified by present algorithm, sorted by protein name.

Acc No	Peptide	MH+	z	*f*	H/L ratio
26S proteasome non-ATPase regulatory subunit 1 (26S proteasome regulatory subunit RPN2)					
Q99460	R.NNNTDLMILK.N	1175.609	2	0.769	1.195
Q99460	R.QGALIASALIMIQQTEITC*PK.V	2286.219	2	0.778	0.708
40S ribosomal protein S18 (Ke-3) (Ke3)					
P62269	R.AGELTEDEVER.V	1247.575	2	0.652	0.571
P62269	R.AGELTEDEVER.V	1247.575	1	0.788	0.49
4F2 cell-surface antigen heavy chain (4F2hc) (Lymphocyte activation antigen 4F2 large subunit)					
P08195	R.GENSWFSTQVDTVATK.V	1769.834	2	0.828	0.308
P08195	K.VAEDEAEAAAAAK.F	1245.596	1	0.549	1.461
P08195	K.GQSEDPGSLLSLFR.R	1505.759	2	0.8	0.444
P08195	K.GLVLGPIHK.N	933.588	1	0.685	0.528
P08195	K.VAEDEAEAAAAAK.F	1245.596	1	0.544	1.286
P08195	R.LDYLSSLK.V	938.519	2	0.998	0.177
P08195	K.DLLLTSSYLSDSGSTGEHTK.S	2111.014	2	0.618	0.951
P08195	K.EDFDSLLQSAK.K	1252.606	2	0.346	2.127
P08195	K.EVELNELEPEK.Q	1328.658	2	0.457	1.018
P08195	K.GQSEDPGSLLSLFR.R	1505.759	2	0.708	0.631
P08195	R.LDYLSSLK.V	938.519	1	0.385	0.782
P08195	K.GLVLGPIHK.N	933.588	2	0.544	0.507
P08195	K.ADLLLSTQPGR[.E	1174.656	1	0.544	1.877
P08195	R.LDYLSSLK.V	938.519	1	0.435	0.556
P08195	K.DDVAQTDLLQIDPNFGSK.E	1975.961	2	0.74	0.457
P08195	K.VAEDEAEAAAAAK.F	1245.596	2	0.421	0.891
P08195	K.ADLLLSTQPGREEGSPLELER.L	2310.194	2	0.496	3.484
P08195	K.GQSEDPGSLLSLFR[.R	1509.767	1	0.589	1.07
P08195	R.WC*SWSLSQAR.L	1280.584	2	0.746	0.58
P08195	K.ADLLLSTQPGR.E	1170.648	1	0.591	1.162
P08195	K.EVELNELEPEK.Q	1328.658	1	0.529	0.129
P08195	R.VILDLTPNYR[.G	1207.681	1	0.883	0.424
P08195	K.EDFDSLLQSAK.K	1252.606	2	0.33	1.952
P08195	K.ADLLLSTQPGR.E	1170.648	2	1	0.312
P08195	K.EDFDSLLQSAK.K	1252.606	2	0.403	1.972
P08195	R.EEGSPLELER[.L	1162.572	1	0.557	0.845

Acc No	Peptide	MH+	z	f	H/L ratio
P08195	K.GQSEDPGSLLSLFR.R	1505.759	2	0.831	0.535
P08195	K.EVELNELEPEK.Q	1328.658	1	0.499	0.315
P08195	K.EVELNELEPEK.Q	1328.658	2	0.43	1.091
P08195	R.LDYLSSLK.V	938.519	2	0.498	0.383
P08195	R.LDYLSSLK.V	938.519	2	0.422	0.485
P08195	K.ADLLLSTQPGR.E	1170.648	2	0.83	0.466
P08195	K.GLVLGPIHK.N	933.588	1	0.595	0.656
P08195	K.EDFDSLLQSAK.K	1252.606	1	0.796	0.468
P08195	K.ADLLLSTQPGREEGSPLELER.L	2310.194	2	0.386	2.408
P08195	K.EDFDSLLQSAK.K	1252.606	2	0.533	1.467
P08195	K.SLVTQYLNATGNR.W	1436.749	2	0.738	0.356
P08195	K.ADLLLSTQPGR.E	1170.648	2	0.806	0.562
P08195	K.EVELNELEPEK.Q	1328.658	2	0.438	3.07
P08195	K.EDFDSLLQSAK.K	1252.606	1	0.863	0.333
P08195	K.GLVLGPIHK.N	933.588	2	0.657	0.333
P08195	K.EDFDSLLQSAK.K	1252.606	1	0.98	0.274
P08195	R.IGDLQAFQGHGAGNLAGLK.G	1866.982	3	0.611	0.804
P08195	K.ADLLLSTQPGR.E	1170.648	1	0.565	1.815
60S ribosomal protein L18					
Q07020	K.ILTFDQLALDSPK.G	1460.8	2	0.702	1.487
Q07020	K.ILTFDQLALDSPK.G	1460.8	2	0.688	0.926
60S ribosomal protein L18a					
Q02543	R.DLTTAGAVTQC*YR.D	1455.69	2	0.959	0.362
60S ribosomal protein L23 (Ribosomal protein L17)					
P62829	R.ISLGLPVGAVINC*ADNTGAK.N	1970.037	2	0.691	1.105
60S ribosomal protein L31					
P62899	K.LYTLVTYVPVTTFK.N	1644.925	2	0.557	0.933
60S ribosomal protein L36a (60S ribosomal protein L44) (Migration-inducing gene 6 protein)					
P83881	K.DSLYAQGK.R	881.436	1	0.664	1.149
60S ribosomal protein L4 (L1)					
P36578	R.IEEVPELPLVVEDK.V	1608.873	2	0.548	0.749
78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)					
P11021	K.VLEDSDLK.K	918.478	1	0.513	0.361
P11021	K.NQLTSNPENTVFDAK.R	1677.808	2	0.463	8.479

Acc No	Peptide	MH+	z	f	H/L ratio
Acetyl-coenzyme A transporter 1 (AT-1) (Acetyl-CoA transporter) (Solute carrier family 33 member 1)					
O00400	R.EALLGDTGTGDFLK.A	1436.727	2	0.734	0.605
Adenosine 3'-phospho 5'-phosphosulfate transporter 1 (PAPS transporter 1) (Solute carrier family 35					
Q8TB61	K.ASDEVPLAPR.T	1054.553	1	0.925	1.76
Q8TB61	K.FVSFPTQVLAK.A	1236.699	2	0.79	0.482
Q8TB61	K.ASDEVPLAPR.T	1054.553	2	0.618	0.57
ADP/ATP translocase 1 (Adenine nucleotide translocator 1) (ANT 1) (ADP,ATP carrier protein 1) (Solute					
P12235	K.DFLAGGVAAAVSK.T	1205.652	2	0.648	0.654
ADP/ATP translocase 2 (Adenine nucleotide translocator 2) (ANT 2) (ADP,ATP carrier protein 2) (Solute					
P05141	K.DFLAGGVAAAISK.T	1219.668	1	0.7	1.105
P05141	R.AAYFGIYDTAK.G	1219.599	2	0.597	0.408
P05141	R.AAYFGIYDTAK.G	1219.599	2	0.408	0.738
P05141	R.AAYFGIYDTAK.G	1219.599	2	0.736	0.286
P05141	K.DFLAGGVAAAISK.T	1219.668	2	0.773	0.329
P05141	K.DFLAGGVAAAISK.T	1219.668	2	0.82	0.309
Alkyldihydroxyacetonephosphate synthase, peroxisomal precursor (EC 2.5.1.26) (Alkyl-DHAP synthase)					
O00116	R.GISDPLTVFEQTEAAAR.E	1804.908	2	0.618	1.174
Alpha-1,2-mannosyltransferase ALG9 (EC 2.4.1.-) (Asparagine-linked glycosylation protein 9 homolog)					
Q9H6U8	R.IVPTDMNDQNLEEPSR.Y	1857.865	2	0.976	0.293
Alpha-fetoprotein enhancer binding protein (AT motif-binding factor) (AT-binding transcription factor 1)					
Q15911	R.PHEEPGAAAGSSSK[.K	1328.621	2	0.836	1.926
Aspartyl(Asparaginyl)beta-hydroxylase					
Q9Y4J0	K.EGIESGDPGTDDGR.F	1404.587	2	0.429	0.573
ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14)					
P25705	R.VLSIGDGIAR.V	1000.579	2	0.566	0.682
P25705	K.AVDSLVPIGR.G	1026.594	2	0.907	0.385
P25705	R.FNDGSDEK.K	911.374	1	0.588	0.931
P25705	R.FNDGSDEK.K	911.374	2	0.892	0.616
P25705	R.ELIIGDR[.Q	819.47	1	0.602	0.464
P25705	K.LELAQYR.E	892.489	1	0.673	1.906
P25705	K.TGTAEMSSILEER.I	1423.673	2	0.489	1.226
P25705	R.TGAIVDVPVGEELLGR[.V	1628.899	2	0.546	0.848
P25705	R.EPMQTGIK.A	903.46	1	0.964	1.885
P25705	R.ELIIGDR.Q	815.462	1	0.688	0.421

Acc No	Peptide	MH+	z	f	H/L ratio
P25705	K.AVDSLVPIGR.G	1026.594	1	0.986	0.59
ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)					
P06576	R.IMNVIGEPIDER[.G	1389.717	2	0.945	0.515
P06576	K.VALVYGQMNEPPGAR.A	1601.81	2	0.483	0.93
P06576	K.VLDSGAPIKIPVGPETLGR.I	1919.096	2	0.425	1.247
P06576	K.IPVGPETLGR.I	1038.594	1	0.886	0.44
P06576	R.AIAELGIYPAVDPLDSTSR.I	1988.033	2	0.475	1.208
ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14) (ATPase subunit F6)					
P18859	R.QTSGGPVDASSEYQQELER.E	2080.942	2	0.979	0.912
ATP synthase D chain, mitochondrial (EC 3.6.3.14)					
O75947	K.AGLVDDFEK.K	993.489	1	0.528	0.28
O75947	K.AGLVDDFEK.K	993.489	2	0.314	0.757
O75947	K.AGLVDDFEK.K	993.489	1	0.829	0.11
ATP synthase delta chain, mitochondrial precursor (EC 3.6.3.14)					
P30049	K.AQAELVGTADEATR[.A	1435.715	2	0.845	1.069
ATP synthase g chain, mitochondrial (EC 3.6.3.14) (ATPase subunit G)					
O75964	K.IVNSAQTGSFK.Q	1151.605	2	0.378	0.7
O75964	K.IVNSAQTGSFK[.Q	1155.614	1	0.725	0.439
ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14)					
P36542	K.EVMLVGIGDK.I	1060.571	1	0.975	0.122
P36542	K.EVMLVGIGDK.I	1060.571	1	0.978	0.244
ATP synthase O subunit, mitochondrial precursor (EC 3.6.3.14) (Oligomycin sensitivity conferral protein)					
P48047	K.SFLSQGQVLK[.L	1110.628	2	0.813	0.939
P48047	K.SFLSQGQVLK.L	1106.62	2	0.843	1.328
P48047	K.SFLSQGQVLK.L	1106.62	1	0.688	0.466
P48047	K.VAASVLNPYVK.R	1160.667	2	0.941	0.152
ATPase family AAA domain containing protein 1					
Q8NBU5	K.DTVILPIK.K	898.561	1	0.8	0.107
ATP-binding cassette sub-family D member 1 (Adrenoleukodystrophy protein) (ALDP)					
P33897	R.NLLTAAADAIER.I	1257.68	2	0.615	0.311
P33897	K.DAGIALLSITHR.P	1266.717	2	0.453	0.707
P33897	R.TAVLLALAAYGAHK.V	1398.81	2	0.717	0.488
ATP-binding cassette sub-family D member 3 (70 kDa peroxisomal membrane protein) (PMP70)					
P28288	R.DLNFEVR.S	892.452	1	0.632	2.046

Acc No	Peptide	MH+	z	f	H/L ratio
P28288	R.DQVIYPDGR.E	1062.521	2	0.628	0.84
P28288	R.DLNFEVR.S	892.452	2	0.542	0.531
ATP-binding cassette sub-family G member 2 (Placenta-specific ATP-binding cassette transporter) (Breast					
Q9UNQ0	R.VIQELGLDK.V	1014.583	1	0.456	0.242
Q9UNQ0	K.PGLNAILGPTGGGK.S	1251.706	2	0.784	1.167
Q9UNQ0	K.VGTQFIR.G	820.468	1	0.766	1.229
Q9UNQ0	K.VGTQFIR.G	820.468	1	0.866	1.396
Q9UNQ0	K.ATEIIEPSK.Q	987.536	1	0.463	0.38
Q9UNQ0	K.ATEIIEPSK.Q	987.536	1	0.403	0.345
Q9UNQ0	K.SSLLDVLAAR[.K	1048.613	1	0.893	0.525
Q9UNQ0	R.VIQELGLDK.V	1014.583	1	0.659	0.129
Autophagy protein 3-like (APG3-like) (hApg3) (PC3-96 protein)					
Q9NT62	R.TYDLYITYDKYYQTPR[.L	2107.015	2	0.716	0.831
BAG family molecular chaperone regulator 2 (BCL2-associated athanogene 2) (BAG-2)					
O95816	R.LLESLDQLELR.V	1328.742	2	0.61	1.303
O95816	K.TLQQNAESR.F	1046.522	1	0.6	1.825
Bardet-Biedl syndrome 2 protein					
Q9BXC9	R.NYEENAK.A	867.384	1	0.826	0.173
Basigin precursor (CD147 antigen) (Leukocyte activation antigen M6) (Collagenase stimulatory factor)					
P35613	R.FFVSSSQGR.S	1014.5	1	0.573	1.001
P35613	K.EDALPGQK.T	857.436	1	0.801	0.571
P35613	K.EDALPGQK.T	857.436	1	0.719	0.506
B-cell lymphoma/leukemia 11B (B-cell CLL/lymphoma 11B) (Radiation-induced tumor suppressor gene 1					
Q9C0K0	R.GGGFAPGTEPFPGLFPR.K	1703.854	2	0.627	0.404
B-cell receptor-associated protein 29 (BCR-associated protein Bap29)					
Q9UHQ4	K.EYDQLLK.E	908.472	1	0.667	0.425
Q9UHQ4	K.EYDQLLK.E	908.472	1	0.682	0.621
B-cell receptor-associated protein 31 (BCR-associated protein Bap31) (p28 Bap31) (CDM protein) (6C6-AG					
P51572	K.LDVGNAEVK.L	944.505	2	0.58	0.894
P51572	K.LDVGNAEVK[.L	948.513	2	0.553	0.67
P51572	K.LQAAVDGPMDK.K	1144.567	1	0.328	0.361
P51572	K.LDVGNAEVK.L	944.505	2	0.428	1.206
P51572	K.DELASTK[.Q	767.391	1	0.552	1.583
Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3]					

Acc No	Peptide	MH+	z	f	H/L ratio
P61769	R.VNHVTLSQPK[.I	1126.635	2	0.742	0.845
Brain acid soluble protein 1 (BASP1 protein) (Neuronal axonal membrane protein NAP-22) (22 kDa					
P80723	K.ETPAATEAPSSTPK.A	1386.675	2	0.686	0.602
P80723	K.APEQEQAAPGPAAGGEAPK.A	1775.856	2	0.646	0.749
P80723	K.ESEPQAAAEPAEAK.E	1427.665	2	0.789	0.309
P80723	K.AEGAATEEEGTPK.E	1289.586	1	0.994	0.122
Brefeldin A-inhibited guanine nucleotide-exchange protein 1 (Brefeldin A-inhibited GEP 1) (p200 ARF-					
Q9Y6D6	K.FPEQKLFAALLIK[.C	1521.917	2	0.789	1.245
C-4 methylsterol oxidase (EC 1.14.13.72) (Methylsterol monooxygenase)					
Q15800	R.IFGTDSQYNAYNEK.R	1649.744	2	0.983	0.485
CAAX prenyl protease 1 homolog (EC 3.4.24.84) (Prenyl protein-specific endoprotease 1) (Farnesylated					
O75844	K.VYVVEGSK.R	880.477	1	0.574	0.654
O75844	K.VYVVEGSK.R	880.477	1	0.488	0.81
Calcium-transporting ATPase type 2C member 1 (EC 3.6.3.8) (ATPase 2C1) (ATP-dependent Ca(2+) pump					
P98194	K.YISQFK.N	785.419	1	0.597	1.027
Calnexin precursor (Major histocompatibility complex class I antigen-binding protein p88) (p90) (IP90)					
P27824	K.AEEDEILNR.S	1088.522	1	0.662	0.509
CAMP/cGMP cyclic nucleotide phosphodiesterase 11A3					
Q9GZY7	K.ITRLVQISGASLAEKQEK.H	1971.123	2	0.324	0.941
Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor (EC 6.3.4.16) (Carbamoyl-phosphate					
P31327	K.IEFEGQPVDFVDPNK.Q	1733.838	2	0.482	0.722
Carnitine O-palmitoyltransferase I, mitochondrial liver isoform (EC 2.3.1.21) (CPT I) (CPTI-L) (Carnitine					
P50416	R.SEDPDTSMDSYAK.S	1445.574	2	0.633	0.495
CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory					
P13987	K.AGLQVYNK.C	892.489	1	0.583	1.979
Cell division cycle 5-like protein (Cdc5-like protein) (Pombe cdc5-related protein)					
Q99459	R.YTRANLASK.K	1023.558	1	0.666	0.431
Centaurin-beta 2 (Cnt-b2)					
Q15057	-.MKMTVDFEECLKDSPR.F	1928.891	2	0.829	0.207
Chemokine-binding protein 2 (Chemokine-binding protein D6) (C-C chemokine receptor D6) (Chemokine					
O00590	R.IGCVLVRLR.P	1028.64	1	0.624	2.239
Chromosome 6 open reading frame 37					
Q5TF85	K.STEDIFPAQLLKLQR[.H	1762.983	2	0.688	5.137

Acc No	Peptide	MH+	z	f	H/L ratio
Clathrin heavy chain 1 (CLH-17)					
Q00610	K.NNRPSEGPLQTR.L	1368.698	2	0.559	2.652
Q00610	R.TSIDAYDNFDNISLAQR.L	1942.914	2	0.421	1.088
CMP-sialic acid transporter					
Q5W1L8	R.QDTTSIQQGETASK.E	1493.708	2	0.865	1.687
Coiled-coil-helix-coiled-coil-helix domain containing protein 3					
Q9NX63	R.VAEELALEQAK.K	1200.647	1	0.75	0.81
Q9NX63	R.VTTEQYQK[.A	1000.508	1	0.567	0.852
Q9NX63	R.VAEELALEQAK[.K	1204.655	1	0.775	0.588
Q9NX63	R.VAEELALEQAK[.K	1204.655	2	0.752	1.382
Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC collagen)					
Q02388	R.GPEASVTQTPVCPR.G	1441.71	2	0.851	0.465
Complement component 1, Q subcomponent binding protein, mitochondrial precursor (Glycoprotein					
Q07021	K.VEEQEPELTSTPNFVVEVIK.N	2287.17	2	0.831	0.706
Q07021	K.AFVDFLSDEIK.E	1283.652	2	0.53	0.191
Q07021	K.AFVDFLSDEIK.E	1283.652	2	0.632	0.227
Core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (EC 2.4.1.122)					
Q9NS00	K.DENTDIAENLYQK[.V	1556.721	2	0.764	0.236
Cytochrome c oxidase polypeptide Va, mitochondrial precursor (EC 1.9.3.1)					
P20674	K.IIDAALR.A	771.472	1	0.711	0.866
Cytochrome c oxidase polypeptide Vb, mitochondrial precursor (EC 1.9.3.1)					
P10606	R.EDPNLVPSISNK.R	1312.674	2	0.327	0.537
P10606	K.GLDPYNVLAPK.G	1186.647	2	0.655	0.576
P10606	R.EDPNLVPSISNK.R	1312.674	2	0.315	1.274
Cytochrome c oxidase polypeptide VIc precursor (EC 1.9.3.1)					
P09669	K.AYADFYR.N	905.415	1	0.734	0.695
P09669	K.DFEEMR[.K	830.348	1	0.516	0.716
P09669	K.AGIFQSVK.-	849.483	2	0.792	0.574
Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor (EC 1.9.3.1) (Cytochrome c					
P14406	K.GGVADALLYR.A	1034.563	1	0.642	0.715
P14406	K.GGVADALLYR.A	1034.563	1	0.507	1.636
Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor (EC 1.9.3.1) (COX IV-1)					
P13073	K.VNPIQGLASK.W	1026.594	2	0.609	0.562
P13073	K.VNPIQGLASK[.W	1030.602	1	0.855	0.87

Acc No	Peptide	MH+	z	f	H/L ratio
P13073	K.VNPIQGLASK.W	1026.594	1	0.567	0.974
Cytochrome c oxidase subunit VIIa-related protein, mitochondrial precursor (COX7a-related protein) (EB1)					
O14548	K.LTSDSTVYDYAGK.N	1419.664	2	0.981	0.271
Cytochrome c1, heme protein, mitochondrial precursor (Cytochrome c-1)					
P08574	K.LFDYFPK.P	929.477	1	0.989	0.159
P08574	K.LFDYFPKPYPNSEAAR.A	1914.938	2	0.89	0.959
P08574	K.PYPNSEAAR.A	1004.48	1	0.536	0.793
Cytochrome c-type heme lyase (EC 4.4.1.17) (CCHL) (Holocytochrome c-type synthase)					
P53701	K.GC*PVNTEPSGPTC*EK.K	1632.699	2	0.737	0.511
Cytosolic 5'-nucleotidase 1B (EC 3.1.3.5) (Cytosolic 5'-nucleotidase IB) (cN1B) (cN-IB) (Autoimmune					
Q96P26	K.LPSSSTSSR.T	921.464	1	0.647	0.904
Defender against cell death 1 (DAD-1)					
P61803	K.ADFQGISPER.A	1119.543	2	0.893	0.164
Dehydrogenase E1 and transketolase domain containing protein 1					
Q96HY7	R.IGGSVHLIVNNQLGYTTPAER.G	2239.183	2	0.45	1.612
Dehydrogenase/reductase SDR family member 8 precursor (EC 1.1.1.-) (17-beta-hydroxysteroid					
Q8NBQ5	K.FDAVIGYK.M	912.482	1	0.423	0.276
Q8NBQ5	R.EDIYSSAK.K	912.431	1	0.759	0.687
DEP domain containing 6					
Q8TB45	R.KDDGTFPLDNEVK[.A	1481.725	2	0.733	0.844
Dermcidin precursor (Preproteolysin) [Contains: Survival-promoting peptide; DCD-1]					
P81605	K.ENAGEDPGLAR[.Q	1132.536	2	0.814	1.183
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)					
P15924	K.GFFDPNTEENLTYLQLK.E	2028.991	2	0.301	2.116
DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal					
P04053	K.MILDNHALYDKTK.R	1561.804	2	0.951	0.363
DnaJ (Hsp40) homolog, subfamily D, member 1 (Growth-inhibiting 22) (DNAJ domain-containing)					
Q5T219	K.DLLETTTK.H	920.494	1	0.352	0.676
Dolichyl-diphosphooligosaccharide-protein glycosyltransferase					
Q5VWA5	R.ELGSEC*GIEFDEEK.T	1641.695	2	0.557	0.507
Q5VWA5	K.SSLNPILFR.G	1046.599	2	0.64	0.471
Q5VWA5	K.SSLNPILFR[.G	1050.607	1	0.547	1.745
Q5VWA5	K.NTLLIAGLQAR.N	1169.7	1	0.849	0.581
Q5VWA5	R.TLVLLDNLNVR.E	1269.752	2	0.489	1.127

Acc No	Peptide	MH+	z	f	H/L ratio
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor (EC 2.4.1.119)					
P04843	R.DVPAYSQDTFK.V	1270.595	1	0.54	0.627
P04843	R.DVPAYSQDTFK.V	1270.595	2	0.794	0.441
P04843	K.GEDEEENNLEVR[.E	1436.627	2	0.833	0.942
P04843	R.DISTLNSGK[.K	938.492	1	0.767	0.2
P04843	K.LPVALDPGAK[.I	984.586	1	0.952	0.331
P04843	R.DISTLNSGK[.K	938.492	1	0.667	0.204
P04843	K.NIEIDSPYEISR.A	1435.706	1	0.631	0.907
P04843	K.NIEIDSPYEISR.A	1435.706	2	0.811	0.587
P04843	K.ALTSEIALLQSR.L	1301.742	1	0.673	0.931
P04843	R.DISTLNSGK.K	934.484	1	0.707	0.285
P04843	K.NIEIDSPYEISR.A	1435.706	2	0.713	0.351
P04843	R.DISTLNSGK.K	934.484	1	0.564	0.222
P04843	R.SEDLLDYGPFR.D	1311.622	2	0.821	0.617
P04843	K.ALTSEIALLQSR.L	1301.742	2	0.917	0.407
P04843	K.GEDEEENNLEVR.E	1432.619	2	0.665	1.744
P04843	K.DTYIENEK.L	1011.463	1	0.627	0.228
P04843	R.ATSFLLALEPELEAR.L	1659.895	2	0.616	0.81
P04843	R.TVDLSSHLAK.V	1070.584	2	0.904	0.38
P04843	K.VTAEVVLAHLGGGSTSR.A	1653.892	2	0.699	2.554
P04843	K.GEDEEENNLEVR.E	1432.619	1	0.567	2.184
P04843	K.LPVALDPGAK.I	980.578	1	0.994	0.347
P04843	K.DPAAEAR.M	729.353	2	0.756	1.331
P04843	K.DTYIENEK.L	1011.463	1	0.748	0.18
Dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase (EC 2.4.1.-) (Dol-P-Man dependent					
Q92685	R.FLPEALFLHR.A	1242.699	2	0.812	0.68
Q92685	R.TGESILSLLR[.D	1092.639	2	0.414	1.521
Down-regulated in metastasis protein (Key-1A6 protein) (Novel nucleolar protein 73) (NNP73)					
O75691	K.VLYLLELYCEDKQSKIK.E	2085.13	2	0.537	0.377
DTTR431 (C-type lectin superfamily 4, member G)					
Q6UXB4	K.QTAALGALK[.E	876.528	1	0.666	48.218
Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2)					
Q13409	K.EGEIQAGAK[.L	906.466	1	0.799	1.212
Elongation factor Tu, mitochondrial precursor (EF-Tu) (P43)					
P49411	K.YEEIDNAPEER.A	1364.597	2	0.537	0.781

Acc No	Peptide	MH+	z	f	H/L ratio
Epithelial protein lost in neoplasm					
Q9UHB6	K.SEISENTDASGK.I	1237.554	2	0.311	1.025
Erythrocyte band 7 integral membrane protein (Stomatin) (Protein 7.2b)					
P27105	R.VQNATLAVANITNADSATR.L	1929.999	2	0.687	0.647
Eukaryotic translation initiation factor 3 subunit 8 (eIF3 p110) (eIF3c)					
Q99613	R.GGVPLVK.E	669.429	1	0.488	7.83
Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog)					
Q01469	K.FEETTADGR[.K	1029.461	2	0.764	2.447
Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor)					
Q9Y5Y0	K.AIPADSPTDQEPK[.T	1372.672	2	0.813	0.352
FKSG30					
Q9BYX7	K.EITALAPSIMK[.I	1177.663	2	0.998	181.065
FLJ00144 protein (Fragment)					
Q8TEP9	R.FFLSSGLIDK.V	1126.614	2	0.806	0.105
Flotillin-1					
O75955	R.GEAEAFAIGAR.A	1091.548	1	0.804	0.418
Flotillin-2 (Epidermal surface antigen) (ESA)					
Q14254	K.IGEAEAAVIEAMGK.A	1388.709	2	0.581	0.796
Q14254	K.VDEIVVLSGDNSK.V	1374.711	2	0.555	2.847
Q14254	K.VDEIVVLSGDNSK.V	1374.711	2	0.534	8.713
FP2653 (ELSD1897) (MGC3123 protein)					
Q71RG4	K.FLNDTEELAVARPEDTVGALK[.S	2292.185	2	0.531	0.748
FYVE, RhoGEF and PH domain containing protein 6 (Zinc finger FYVE domain containing protein 24)					
Q6ZV73	K.EFDKNIALLDEQCK[.K	1669.823	2	0.584	1.949
Gap junction beta-6 protein (Connexin-30) (Cx30)					
O95452	K.DIEDIK.K	732.377	1	0.475	0.378
Gene rich cluster, C3f gene					
Q6P1A2	K.DQNSLSSEQQK[.Y	1267.589	2	0.752	0.555
Glutamate--cysteine ligase catalytic subunit (EC 6.3.2.2) (Gamma-glutamylcysteine synthetase) (Gamma-					
P48506	R.EERGLEPLK.N	1070.584	2	0.74	0.786
Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)					
Q5JR58	K.LVITGNLITIFQER.D	1616.937	2	0.804	0.322
Glyceraldehyde-3-phosphate dehydrogenase, liver (EC 1.2.1.12) (GAPDH)					

Acc No	Peptide	MH+	z	f	H/L ratio
P04406	R.GALQNIIPASTGAAK[.A	1415.798	2	0.779	2.726
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-12 subunit					
Q9UBI6	K.TASTNNIAQAR.R	1146.586	1	0.638	0.169
Guanine nucleotide-binding protein G(k), alpha subunit (G(i) alpha-3)					
P08754	R.ISQSNYIPTQQDVLR.T	1761.913	2	0.695	1.08
Guanine nucleotide-binding protein, alpha-14 subunit (G-protein alpha subunit 14)					
O95837	R.EYQLSDSAKYYLTDIDR.I	2079.987	2	0.506	0.292
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)					
P11142	K.DAGTIAGLNVLR.I	1199.674	2	0.745	0.921
P11142	K.SFYPEEVSSMVLTK.M	1616.788	2	0.771	0.275
Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27)					
P04792	K.DGVVEITGK.H	917.494	1	0.701	1.225
Histone H4					
P62805	R.DNIQGITKPAIR[.R	1329.762	2	0.548	0.781
P62805	R.DAVTYTEHAK.R	1134.543	2	0.405	1.283
P62805	R.ISGLIYEETR.G	1180.621	2	0.988	0.208
P62805	K.VFLENVIR.D	989.578	1	0.665	0.622
P62805	K.VFLENVIR.D	989.578	1	0.533	0.656
P62805	K.VFLENVIR.D	989.578	2	0.837	1.305
P62805	R.DNIQGITKPAIR.R	1325.754	2	0.449	1.067
P62805	K.VFLENVIR.D	989.578	2	0.777	1.15
P62805	R.DNIQGITK[.P	892.487	1	0.465	0.476
P62805	R.ISGLIYEETR.G	1180.621	1	0.44	0.902
P62805	R.ISGLIYEETR.G	1180.621	1	0.411	1.145
HIV GAG protein					
GAG_Protein	R.FGEETTTPSQK.Q	1224.574	2	0.727	7.502
GAG_Protein	R.FGEETTTPSQK[.Q	1228.582	1	0.75	27.479
GAG_Protein	K.ETINEEAAEWDR[.L	1466.652	2	0.336	13.455
GAG_Protein	R.WIILGLNK[.I	960.601	1	0.589	8.763
GAG_Protein	K.ELYPLASLR[.S	1065.607	1	0.474	6.959
GAG_Protein	K.ELYPLASLR[.S	1065.607	1	0.419	5.428
GAG_Protein	R.FGEETTTPSQK[.Q	1228.582	1	0.756	18.584
GAG_Protein	R.FGEETTTPSQK[.Q	1228.582	1	0.773	20.547
GAG_Protein	R.FGEETTTPSQK[.Q	1228.582	2	0.735	8.78
GAG_Protein	R.FGEETTTPSQK[.Q	1228.582	2	0.728	8.376

Acc No	Peptide	MH+	z	f	H/L ratio
GAG_Protein	R.QILGQLQPSLQTGSEELR.S	1997.066	2	0.309	4.06
HLAT1-3TM					
Q8MH63	K.RADGAAPAGEGEGVTLQR.N	1754.878	2	0.993	0.795
Hormonally up-regulated neu tumor-associated kinase (EC 2.7.1.37) (Serine/threonine-protein kinase					
P57058	K.LGYKNSDVINTVLSNR[.A	1796.963	2	0.427	1.266
HSPC121					
Q9P035	R.QVNITVQK.K	929.542	1	0.864	0.488
Q9P035	R.LESEGSPETLTNLR.K	1545.776	2	0.32	0.93
Q9P035	R.QVNITVQK[.K	933.549	1	0.759	0.475
Hypothetical protein					
Q6PQ33	R.REISNVSREAR.A	1316.703	2	0.946	1.18
Q4G0N0	R.EVDDSSAQK.G	978.437	1	0.344	1.443
Hypothetical protein (Novel protein)					
Q8NFQ8	R.LLAPEAGSHPQQTQK.L	1604.839	2	0.654	0.894
Hypothetical protein C14orf39					
Q8N1H7	K.MNETIFMKFR[.V	1320.657	2	0.681	1.165
Hypothetical protein DKFZp313B047					
Q5H9S5	K.EDVDAAVK.Q	846.42	1	0.922	0.202
Hypothetical protein FLJ10846					
Q9NVA4	R.DDISEQVR.H	961.458	1	0.564	0.473
Hypothetical protein FLJ14938 (Hypothetical protein NT2RP2003902) (GK001 protein)					
Q96A33	K.RQDLLNVLAR.M	1197.706	2	0.74	0.557
Hypothetical protein FLJ16464					
Q6ZN37	R.QLNEVENNIKK.K	1328.717	1	0.534	0.287
Hypothetical protein FLJ20422 (AVLG582)					
Q9NX61	R.DFLHQPPFGETR.F	1443.702	2	0.673	1.635
Hypothetical protein FLJ20455 (TPA018) (Ovarian carcinoma immunoreactive antigen) (OCIA domain					
Q9NX40	K.LENSPLGEALR.S	1198.643	2	0.998	0.293
Hypothetical protein FLJ39430					
Q8N8I4	K.HLREEEEEGEK[.H	1388.642	2	0.68	0.321
Hypothetical protein FLJ46844					
Q6ZQW6	R.MQGPSLPCLGTGTPTLWPHR.C	2149.068	2	0.573	1.135
Hypothetical protein FP14381					

Acc No	Peptide	MH+	z	f	H/L ratio
Q71M32	R.PLPHCFCHKVNALVR[.G	1737.917	2	0.654	0.453
Hypothetical protein KIAA1426					
Q96RY5	R.PTCVQAVEGMSRMIVELHR.K	2156.077	2	0.698	0.373
Hypothetical protein LOC133957 (Hypothetical protein FLJ25701)					
Q96BQ5	R.TAAFQQDLEAK.Y	1221.611	2	0.736	0.506
Hypothetical protein MGC2731					
Q9BQ15	K.NLNLIFIVLETGR.V	1501.874	2	0.621	0.595
Q9BQ15	K.NLNLIFIVLETGR.V	1501.874	2	0.831	0.32
Q9BQ15	K.NLNLIFIVLETGR.V	1501.874	2	0.709	0.621
Hypothetical protein PRO1855					
Q96AG4	K.DNPLDPVLAK.V	1081.589	2	0.854	0.649
IGHG4 protein					
Q8TC63	R.WVLSRLQLQESGPGLLK.P	1924.101	2	0.563	1.219
Inner membrane protein OXA1L, mitochondrial precursor (Oxidase assembly 1-like protein) (OXA1-like					
Q15070	K.DNPPNIPSSSSKPK.S	1467.744	2	0.584	0.987
Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor) (Type 2 InsP3					
Q14571	K.GGEEPIEESNILSPVQDGTK.K	2099.014	2	0.683	1.013
Intraflagellar transport 81 (Carnitine deficiency-associated protein expressed in ventricle 1) (CDV-1 protein)					
Q8WYA0	K.KEAKAEELQEAK.E	1373.727	2	0.321	5.761
Ka35 protein					
Q6A163	K.ADLEAQVQSLK.E	1201.642	2	0.591	1.109
Keratin, type I cytoskeletal 18 (Cytokeratin-18) (CK-18) (Keratin-18) (K18)					
P05783	R.AQYDELAR.K	965.469	1	0.85	0.506
P05783	R.SLGSVQAPSYGAR[.P	1296.667	2	0.883	0.262
P05783	R.AQIFANTVDNAR.I	1319.67	2	0.737	1.245
P05783	R.AQIFANTVDNAR.I	1319.67	1	0.611	0.567
P05783	K.VIDDTNITR.L	1046.548	1	0.693	1.206
P05783	K.VIDDTNITR.L	1046.548	2	0.981	0.548
P05783	R.TVQSLEIDLDSMR.N	1506.747	2	0.897	0.275
P05783	R.AQIFANTVDNAR.I	1319.67	2	0.559	0.346
P05783	R.SLGSVQAPSYGAR.P	1292.659	2	0.787	0.454
P05783	R.QAQEYEALLNIK.V	1419.748	2	0.691	0.313
Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)					
P35527	R.FSSSSGYGGGSSR[.V	1239.537	2	0.741	8.506

Acc No	Peptide	MH+	z	f	H/L ratio
P35527	K.VQALEEANNDLENK.I	1586.766	2	0.443	1.187
P35527	K.TLLDIDNTR[.M	1064.571	2	0.738	3.961
P35527	K.TLLDIDNTR[.M	1064.571	2	0.752	3.539
P35527	R.SGGGGGGGLGSGGSIR.S	1232.598	1	0.721	2.574
P35527	R.FSSSSGYGGGSSR.V	1235.529	1	0.614	1.682
P35527	K.TLLDIDNTR.M	1060.563	1	0.672	1.013
P35527	K.TLLDIDNTR.M	1060.563	1	0.614	1.106
P35527	K.DQIVDLTVGNNK.T	1315.685	2	0.629	0.5
P35527	K.STMQELNSR.L	1065.499	1	0.687	2.288
P35527	K.DIENQYETQITQIEHEVSSSGQEVQSSAK[.E	3268.522	3	0.831	2.946
P35527	R.FSSSSGYGGGSSR[.V	1239.537	2	0.719	8.239
P35527	R.FSSSSGYGGGSSR.V	1235.529	1	0.588	1.735
P35527	K.STMQELNSR.L	1065.499	2	0.788	1.571
P35527	K.NYSPYYNTIDDLK.D	1605.743	2	0.46	0.531
P35527	R.QEYEQLIAK[.N	1125.592	1	0.697	1.818
P35527	R.SGGGGGGGLGSGGSIR.S	1232.598	2	0.799	3.669
P35527	K.STMQELNSR[.L	1069.507	1	0.601	4.408
P35527	R.QGVDADINGLR.Q	1157.591	2	0.47	0.971

Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha

P04264	R.DYQELMNTK[.L	1145.527	1	0.719	1.395
P04264	R.SLDLDSIIAEVK.A	1302.715	1	0.649	2.823
P04264	R.TLLEGEESR.M	1033.516	1	0.828	1.188
P04264	K.AEAESLYQSK[.Y	1129.55	1	0.874	1.221
P04264	R.GSGGGSSGGSIGGR[.G	1096.511	1	0.618	2.529
P04264	K.DVDGAYMTK.V	999.445	2	0.639	2.438
P04264	K.YEELQITAGR[.H	1183.608	1	0.597	1.698
P04264	R.TLLEGEESR.M	1033.516	2	0.794	2.398
P04264	R.GSGGGSSGGSIGGR.G	1092.503	2	0.663	3.152
P04264	R.FSSC*GGGGGSFGAGGGFGSR[.S	1769.743	2	0.802	1.716
P04264	K.SLNNQFASFIDK.V	1383.69	2	0.375	0.634
P04264	K.YEELQITAGR.H	1179.6	2	0.574	2.218
P04264	K.SLNNQFASFIDK.V	1383.69	2	0.394	1.177
P04264	R.SGGGFSSGSAGIINYQR.R	1657.793	2	0.344	2.024
P04264	R.SEIDNVKK[.Q	936.513	2	0.852	3.68
P04264	R.TNAENEFVTIK.K	1265.637	1	0.564	2.245
P04264	R.SLDLDSIIAEVK.A	1302.715	2	0.629	0.95

Acc No	Peptide	MH+	z	f	H/L ratio
P04264	K.WELLQQVDTSTR[.T	1479.757	1	0.68	4.62
P04264	R.GSGGGSSGGSIGGR.G	1092.503	1	0.639	2.448
P04264	K.WELLQQVDTSTR.T	1475.749	2	0.721	2.285
P04264	K.LNDLEDALQQAK[.E	1361.704	1	0.832	1.631
P04264	K.LNDLEDALQQAK[.E	1361.704	2	0.705	2.318
P04264	R.TLLEGEESR[.M	1037.524	2	0.786	2.065
P04264	R.DYQELMNTK.L	1141.519	2	0.659	4.344
P04264	K.AEAESLYQSK[.Y	1129.55	1	0.811	1.379
P04264	K.WELLQQVDTSTR[.T	1479.757	2	0.83	1.822
P04264	R.SLDLDSIIAEVK[.A	1306.723	1	0.648	2.736
P04264	R.TLLEGEESR[.M	1037.524	1	0.788	1.139
P04264	R.TNAENEFVTIK[.K	1269.645	1	0.554	2.53
P04264	K.LNDLEDALQQAK[.E	1361.704	1	0.743	1.444
P04264	R.GSGGGSSGGSIGGR.G	1092.503	2	0.645	3.079
P04264	K.LNDLEDALQQAK[.E	1361.704	2	0.711	2.124
P04264	R.TNAENEFVTIK.K	1265.637	1	0.551	2.197
P04264	R.TNAENEFVTIK.K	1265.637	2	0.6	2.648
P04264	K.SLNNQFASFIDK[.V	1387.698	1	0.405	1.463
P04264	K.LNDLEDALQQAK[.E	1361.704	2	0.693	2.608
P04264	R.TLLEGEESR.M	1033.516	2	0.752	2.164
P04264	R.TLLEGEESR[.M	1037.524	1	0.815	0.879
P04264	K.QISNLQQSISDAEQR[.G	1720.859	2	0.992	1.157
P04264	R.SLDLDSIIAEVK.A	1302.715	2	0.614	0.812
P04264	R.DYQELMNTK[.L	1145.527	1	0.702	1.309

Keratin, type II cytoskeletal 1b

Q7Z794	K.MEIAELNR[.T	979.501	1	0.342	0.94

Keratin, type II cytoskeletal 5 (Cytokeratin-5) (CK-5) (Keratin-5) (K5) (58 kDa cytokeratin)

P13647	K.LAELEEALQK.A	1143.626	2	0.585	1.521
P13647	K.YEELQQTAGR[.H	1198.583	1	0.781	2.501
P13647	K.LAELEEALQK[.A	1147.634	1	0.762	1.492

Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin)

P08729	K.LEAAIAEAEER.G	1201.606	2	0.704	0.618
P08729	R.LDADPSLQR.V	1014.521	2	0.627	1.228

Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keraton-8) (K8)

P05787	R.LQAEIEGLK.G	1000.567	1	0.551	0.218

Acc No	Peptide	MH+	z	f	H/L ratio
Keratinocyte associated protein 2					
Q6PG45	K.ISSTLYQAAAPVLTPAK.V	1730.969	2	0.833	0.785
Lanosterol synthase (EC 5.4.99.7) (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol					
P48449	R.DGTAC*AEVSRACDFLLSR.Q	1970.906	2	0.881	0.636
Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light chain)					
Q01650	K.GDVSNLDPNFSFEGTK.L	1726.792	1	0.707	0.283
Leucine zipper-EF-hand containing transmembrane protein 1, mitochondrial precursor					
O95202	K.VAEVEGEQVDNK.A	1316.633	2	0.467	0.483
Lysosome membrane protein II (LIMP II) (Scavenger receptor class B member 2) (85 kDa lysosomal					
Q14108	R.DQSVGDPK.I	845.4	1	0.95	0.205
Mcd4p homolog					
O95427	K.GWKENPVEFDSLFNESK.Y	2025.955	2	0.484	0.59
Membrane associated progesterone receptor component 1 (mPR)					
O00264	K.EGEEPTVYSDEEEPK.D	1737.734	2	0.802	0.204
O00264	R.GDQPAASGDSDDDEPPPLPR.L	2035.884	2	0.816	0.602
Membrane associated progesterone receptor component 2 (Progesterone membrane binding protein) (Steroid					
O15173	R.DFSLEQLR.Q	1007.516	2	0.753	0.45
O15173	R.DFSLEQLR.Q	1007.516	1	0.542	0.691
O15173	R.GLGAGAGAGEESPATSLPR.M	1697.845	2	0.729	1.333
Membrane protein (STMF151) (LOC54499) (Xenogeneic cross-immune protein)					
Q9UM00	K.ETITESAGR.Q	963.474	1	0.865	0.39
Q9UM00	K.QAGGFLGPPPPSGK.F	1309.69	2	0.668	0.761
MGC13159 protein					
Q5BJH2	R.EGDAGPETSTAVEK.K	1390.633	2	0.487	0.89
Microsomal glutathione S-transferase 1 (EC 2.5.1.18) (Microsomal GST-1) (Microsomal GST-I)					
P10620	K.VFANPEDC*VAFGK.G	1453.678	2	0.719	1.127
P10620	K.VFANPEDC*VAFGK.G	1453.678	2	0.751	0.837
Minor histocompatibility antigen H13 (EC 3.4.99.-) (Signal peptide peptidase) (Presenilin-like protein 3)					
Q8TCT9	R.QYQLLFTQGSGENK.E	1612.797	2	0.512	0.531
Q8TCT9	K.DPAAVTESK[.E	921.466	1	0.614	0.454
Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP) (Solute carrier family 25 member 11)					
Q02978	K.NVFNALIR.I	946.547	2	0.713	0.287
Mitochondrial aspartate-glutamate carrier protein					

Acc No	Peptide	MH+	z	f	H/L ratio
Q546F9	K.TVELLSGVVDQTK.D	1388.763	2	0.363	0.643
Q546F9	R.YLNIFGESQPNPK.T	1506.759	2	0.809	0.524
Mitochondrial carrier homolog 2 (Met-induced mitochondrial protein)					
Q9Y6C9	R.GLFTGLTPR.L	961.547	2	0.557	0.215
Q9Y6C9	K.VLIQVGYEPLPPTIGR.N	1752.005	2	0.851	0.413
Q9Y6C9	K.GEELGPGNVQK.E	1127.569	2	0.857	0.287
Q9Y6C9	R.GLFTGLTPR.L	961.547	1	0.496	0.291
Q9Y6C9	K.EVSSSFDHVIK.E	1247.627	2	0.356	0.345
Q9Y6C9	R.GLFTGLTPR.L	961.547	1	0.863	0.161
Mitochondrial dicarboxylate carrier					
Q9UBX3	K.VHLQTQQEVK.L	1209.659	2	0.612	0.53
Mitochondrial import inner membrane translocase subunit Tim17-B					
O60830	R.YTAQQFR.N	913.453	1	0.39	1.14
Mitochondrial import receptor subunit TOM20 homolog (Mitochondrial 20 kDa outer membrane protein)					
Q15388	K.DAEAVQK.F	760.384	1	0.486	0.524
Mitochondrial inner membrane protein (Mitofilin) (p87/89) (Proliferation-inducing gene 4 protein)					
Q16891	K.TSSAETPTIPLGSAVEAIK[.A	1876.004	2	0.426	0.639
Q16891	K.LSEQELQFR.R	1149.59	2	0.652	1.255
Q16891	K.EVAGAKPHITAAEGK.L	1478.796	2	0.795	0.299
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	0.5	0.653
Q16891	K.LSEQELQFR.R	1149.59	1	0.552	1.293
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	0.47	0.524
Q16891	K.PHITAAEGK.L	923.495	1	0.622	0.537
Q16891	K.SEFEQNLSEK.L	1210.559	2	0.517	0.862
Q16891	K.VQAAQSEAK.V	931.484	1	0.574	0.737
Q16891	K.TSSAETPTIPLGSAVEAIK.A	1871.996	2	0.361	1.15
Q16891	R.SEIQAEQDR.K	1075.501	2	0.464	0.852
Q16891	K.LSEQELQFR[.R	1153.598	2	0.623	2.215
Q16891	R.SEIQAEQDR.K	1075.501	2	0.384	0.715
Q16891	K.EVAGAKPHITAAEGK[.L	1482.804	2	0.824	0.378
Q16891	K.AAMDNSEIAGEK.K	1235.557	2	0.606	0.772
Mitsugumin-23 precursor (Mg23)					
Q9BVC6	R.EAPVDVLTQIGR.S	1297.711	2	0.658	0.71
Monocarboxylate transporter 1 (MCT 1)					
P53985	K.EEETSIDVAGKPNEVTK[.A	1849.916	2	0.879	0.747

Acc No	Peptide	MH+	z	f	H/L ratio
P53985	K.EEETSIDVAGKPNEVTK[.A	1849.916	2	0.826	0.882
P53985	K.EEETSIDVAGKPNEVTK.A	1845.908	2	0.856	0.869
Monocarboxylate transporter 4 (MCT 4) (MCT 3)					
O15427	K.EPQPEVAAAEEEK.L	1426.67	1	0.494	0.716
O15427	K.DLGVPDTK.A	844.441	1	0.347	0.558
O15427	K.EPQPEVAAAEEEK.L	1426.67	2	0.436	0.494
O15427	R.LLDLSVFR.D	962.567	1	1	0.171
O15427	K.EPQPEVAAAEEEK.L	1426.67	2	0.482	0.434
O15427	R.LLDLSVFR.D	962.567	2	0.952	0.217
O15427	R.LLDLSVFR.D	962.567	1	0.888	0.253
mRNA decapping enzyme 1B (EC 3.-.-.-)					
Q8IZD4	K.FPVLAQSSGTGK.P	1191.637	2	0.751	0.312
Myb-related protein B (B-Myb)					
P10244	R.SEAGIELIIEDDIRPEK.Q	1927.002	2	0.429	0.403
Myosin Ib (Myosin I alpha) (MMI-alpha) (MMIa) (MYH-1c)					
O43795	K.EIC*ELTGIDQSVLER[.A	1765.877	2	0.769	0.933
O43795	R.DQFTDQQK.L	1009.458	2	0.565	0.784
O43795	K.LEASELFK.D	936.504	1	0.509	23.594
Myosin IE					
Q4KMR3	K.QGLFPNNYVTK.I	1280.663	2	0.871	0.582
Myosin-10 (Myosin heavy chain, nonmuscle IIb) (Nonmuscle myosin heavy chain IIb) (NMMHC II-b)					
P35580	R.LQQELDDLTVDLDHQR.Q	1937.956	2	0.967	1.13
P35580	K.TELEDTLDTTAAQQELR.T	1933.935	2	0.386	1.147
Myosin-9 (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMMHC II-a)					
P35579	K.TELEDTLDSTAAQQELR.S	1919.919	2	0.46	1.779
P35579	K.KVEAQLQELQVK.F	1412.811	2	0.524	1.011
P35579	R.EQEVNILK.K	972.536	1	0.899	0.42
P35579	R.EQLEEEEEAK.H	1233.548	2	0.994	0.259
P35579	K.DLEGLSQR[.H	921.477	1	0.692	0.566
P35579	R.VEEEAAQK.N	903.442	1	0.612	0.622
P35579	R.VEEEAAQK.N	903.442	2	0.555	0.606
Myotubularin (EC 3.1.3.48)					
Q13496	R.VATFRSRNR.I	1106.618	2	0.94	0.606
N-acetylgalactosaminyltransferase					

Acc No	Peptide	MH+	z	f	H/L ratio
Q76KP1	R.GSDHVEVGWRAFLPGLK.F	1867.981	2	0.751	0.228
NAD(P) transhydrogenase, mitochondrial precursor (EC 1.6.1.2) (Pyridine nucleotide transhydrogenase)					
Q13423	K.AVVLAANHFGR.F	1154.643	2	0.6	0.408
NAD-dependent deacetylase sirtuin-5 (EC 3.5.1.-) (SIR2-like protein 5)					
Q9NXA8	R.RVVVITQNIDELHRK[.A	1824.058	2	0.881	1.065
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3)					
P28331	R.ALSEIAGMTLPYDTLDQVR.N	2093.058	2	0.309	2.587
NADH-ubiquinone oxidoreductase B12 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B12) (CI-B12)					
O43676	K.IEGTPLETIQK.K	1228.678	2	0.835	0.259
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3) (NADH dehydrogenase subunit 4)					
P03905	R.LTLILNPLTK.H	1125.724	1	0.877	0.469
NADPH--cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)					
P16435	R.ESSFVEK.M	825.399	1	0.836	1.3
P16435	K.IQTLTSSVR.E	1004.573	2	0.392	0.674
P16435	R.YESGDHVAVYPANDSALVNQLGK.I	2447.184	2	0.598	2.038
P16435	K.FAVFGLGNK.T	952.525	1	0.891	0.114
P16435	R.SDEDYLYR.E	1060.458	2	0.693	0.535
P16435	K.RLEQLGAQR.I	1070.606	2	0.737	0.564
P16435	R.YYSIASSSK[.V	1009.497	1	0.833	1.51
P16435	R.ESSFVEK[.M	829.407	1	0.765	1.103
P16435	K.FAVFGLGNK.T	952.525	2	0.761	0.425
P16435	R.SDEDYLYR.E	1060.458	1	0.697	0.316
P16435	K.NPFLAAVTTNR.K	1203.648	1	0.881	0.412
Nascent polypeptide-associated complex alpha subunit (NAC-alpha) (Alpha-NAC) (Hom s 2.02)					
Q13765	K.IEDLSQQAQLAAAEKFK.V	1889.997	2	0.473	0.976
NEDD4-like ubiquitin ligase 1					
Q9HCC7	R.GGYHDGHLVIRWFWAAVER[.F	2273.149	2	0.811	0.78
Neural cell adhesion molecule L1 precursor (N-CAM L1) (CD171 antigen)					
P32004	K.VGEEDDGEYR[.C	1172.483	2	0.563	1.322
P32004	R.LVVFPTDDISLK.C	1346.757	2	0.927	0.139
Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II alpha subunit)					
Q14697	K.DPAEGDGAQPEETPR.D	1568.682	2	0.43	1.208
Neutral amino acid transporter B(0) (ATB(0)) (Sodium-dependent neutral amino acid transporter type 2)					
Q15758	R.STEPELIQVK.S	1143.626	2	0.407	0.931

Acc No	Peptide	MH+	z	f	H/L ratio
Q15758	R.GPAGDATVASEK.E	1102.537	2	0.357	1.484
Q15758	R.GPAGDATVASEK.E	1102.537	1	0.709	0.744
Q15758	K.SELPLDPLPVPTEEGNPLLK.H	2158.164	2	0.817	1.032
Q15758	K.EVLDSFLDLAR.N	1277.674	2	0.629	0.45

NGT

Acc No	Peptide	MH+	z	f	H/L ratio
Q9H2Q2	R.SSLFELAK.K	894.493	2	0.708	0.569

Novel protein

Acc No	Peptide	MH+	z	f	H/L ratio
Q5JP08	R.EFDSSTLNESVR.N	1383.639	2	0.91	0.261
Q5VZP5	R.TPESSEREESPEPQR.P	1757.794	2	0.332	0.675

Nucleolar RNA helicase 2 (EC 3.6.1.-) (Nucleolar RNA helicase II) (Nucleolar RNA helicase Gu) (RH

Acc No	Peptide	MH+	z	f	H/L ratio
Q9NR30	K.DFSDITK.K	825.399	1	0.809	0.779

OK/SW-CL.16

Acc No	Peptide	MH+	z	f	H/L ratio
Q8NI70	R.RALAPNR.H	797.474	1	0.678	0.371

OTTHUMP00000017314 (Fragment)

Acc No	Peptide	MH+	z	f	H/L ratio
Q5JUJ7	K.EQETVLQAQVRPGGR.G	1667.882	2	0.469	0.932

OTTHUMP00000021035

Acc No	Peptide	MH+	z	f	H/L ratio
Q4VXA4	R.AGDNILAVLK.H	1013.599	2	0.785	0.435

Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin B) (S-

Acc No	Peptide	MH+	z	f	H/L ratio
P23284	R.VIFGLFGK.T	880.529	1	0.594	0.753

Pericentrin (Pericentrin B) (Kendrin)

Acc No	Peptide	MH+	z	f	H/L ratio
O95613	K.RLEEMNINIRK.K	1415.779	2	0.996	0.997

Phosphate carrier protein, mitochondrial precursor (PTP)

Acc No	Peptide	MH+	z	f	H/L ratio
Q00325	R.IQTQPGYANTLR.D	1361.717	2	0.58	0.498
Q00325	R.IQTQPGYANTLR.D	1361.717	1	0.647	0.655
Q00325	R.IQTQPGYANTLR.D	1361.717	1	0.664	0.717

Phosphatidate cytidylyltransferase 2 (EC 2.7.7.41) (CDP-diglyceride synthetase 2) (CDP-diglyceride

Acc No	Peptide	MH+	z	f	H/L ratio
O95674	R.AESAPLPVSADDTPEVLNR.A	1980.987	2	0.701	0.622
O95674	K.VDGETASDSESR.A	1252.529	2	0.348	2.667
O95674	K.VDGETASDSESR.A	1252.529	2	0.419	3.035
O95674	R.AESAPLPVSADDTPEVLNR[.A	1984.995	2	0.709	0.528

Phosphatidylserine synthase 2 (EC 2.7.8.-) (PtdSer synthase 2) (PSS-2) (Serine-exchange enzyme II)

Acc No	Peptide	MH+	z	f	H/L ratio
Q9BVG9	R.ASLEEPPDGPSAGQATGPGEGR.R	2079.958	2	0.863	0.752
Q9BVG9	R.ASLEEPPDGPSAGQATGPGEGR.R	2079.958	2	0.857	0.456
Q9BVG9	R.DAGGPRPESPVPAGR[.A	1466.748	2	0.552	0.982

Acc No	Peptide	MH+	z	f	H/L ratio
Photolyase (Cryptochrome 1)					
Q16526	K.LSIEYDSEPFGK.E	1384.663	2	0.545	0.306
Q16526	K.LSIEYDSEPFGK.E	1384.663	2	0.674	0.233
Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Domain-rich serine protein) (DRS-					
Q9H307	K.LTEVPVEPVLTVHPESK.S	1874.027	2	0.659	1.307
Q9H307	K.KPALQSSVVATSK.E	1315.758	2	0.81	0.757
PNAS-117					
Q9HB66	K.NDDIPEQDSLGLSNLQK.S	1885.914	2	0.762	0.338
Q9HB66	K.NDDIPEQDSLGLSNLQK.S	1885.914	2	0.627	0.524
Polymerase I and transcript release factor (PTRF protein)					
Q6NZI2	K.IIGAVDQIQLTQAQLEER.Q	2025.098	2	0.695	0.55
Postreplication repair protein RAD18 (hRAD18) (hHR18) (RING finger protein 73)					
Q9NS91	K.NLAVKVYTPVASRQSLK[.Q	1878.094	2	0.696	0.178
PRKR interacting protein 1 (IL11 inducible)					
Q96CF8	K.NAAEEQKLKLER.L	1428.781	2	0.572	1.006
Probable cation-transporting ATPase 13A1 (EC 3.6.3.-)					
Q9HD20	R.SPQENLVPC*DVLLLR.G	1752.931	2	0.679	0.549
Q9HD20	K.EFVITSLK.E	936.54	1	0.598	0.635
Q9HD20	K.EPIEDLSPDR.V	1170.564	2	0.811	0.774
Probable endonuclease KIAA0830 precursor (EC 3.1.30.-)					
O94919	R.STLLPPEASEGSSSFLGK.L	1806.912	2	0.675	0.916
Probable mitochondrial import receptor subunit TOM40 homolog (Translocase of outer membrane 40 kDa					
O96008	R.RPGEEGTVMSLAGK.Y	1431.726	2	0.772	0.62
O96008	K.MAIQTQQSK.F	1034.53	1	0.839	0.264
Programmed cell death 6-interacting protein (PDCD6-interacting protein) (ALG-2 interacting protein 1)					
Q8WUM4	R.LLDEEEATDNDLR.A	1532.708	2	0.402	0.558
Prohibitin					
P35232	R.IFTSIGEDYDER.V	1444.659	1	0.674	0.461
P35232	R.NVPVITGSK.D	914.531	1	0.995	0.358
P35232	R.PVASQLPR.I	867.505	1	0.795	0.256
P35232	R.IFTSIGEDYDER[.V	1448.667	2	0.982	0.4
P35232	K.AAIISAEGDSK.A	1061.547	2	0.945	1.36
P35232	R.IFTSIGEDYDER.V	1444.659	2	0.848	0.726
P35232	K.AAIISAEGDSK.A	1061.547	1	0.926	0.252

Acc No	Peptide	MH+	z	f	H/L ratio
P35232	R.NVPVITGSK[.D	918.539	1	0.852	0.318
P35232	R.ILFRPVASQLPR.I	1396.842	2	0.62	0.385
Prohibitin-2 (B-cell receptor-associated protein BAP37) (Repressor of estrogen receptor activity) (D-					
Q99623	R.IGGVQQDTILAEGLHFR[.I	1857.995	2	0.76	0.872
Q99623	R.LGLDYEER.V	994.484	1	0.717	0.706
Q99623	R.LGLDYEER.V	994.484	2	0.532	0.848
Q99623	R.EYTAAVEAK[.Q	985.497	1	0.88	0.646
Q99623	K.QVAQQEAQR.A	1057.538	2	0.983	1.398
Q99623	R.VLPSIVNEVLK.S	1210.741	2	0.338	2.843
Q99623	K.QVAQQEAQR.A	1057.538	1	0.63	1.019
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.987	3	0.597	1.678
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.987	3	0.516	1.182
Q99623	R.LPAGPR.G	610.367	1	0.956	0.468
Q99623	K.FNASQLITQR.A	1177.632	2	0.397	0.62
Q99623	K.IVQAEGEAEAAK.M	1215.622	1	0.453	0.797
Q99623	R.IGGVQQDTILAEGLHFR.I	1853.987	3	0.859	0.626
Q99623	R.AQVSLLIR.R	899.567	1	0.695	0.506
Q99623	R.VLPSIVNEVLK.S	1210.741	1	0.517	1.111
Q99623	K.IVQAEGEAEAAK.M	1215.622	2	0.408	1.083
Q99623	R.EYTAAVEAK[.Q	985.497	1	0.995	0.836
Q99623	R.LGLDYEER.V	994.484	2	0.606	0.636
Q99623	R.IGGVQQDTILAEGLHFR[.I	1857.995	2	0.856	0.791
Q99623	R.VLPSIVNEVLK.S	1210.741	1	0.491	1.301
Q99623	R.LPAGPR.G	610.367	1	0.926	0.466
Q99623	K.LLLGAGAVAYGVR.E	1259.747	2	0.732	0.675
Q99623	K.FNASQLITQR[.A	1181.64	1	0.631	0.995
Q99623	K.IVQAEGEAEAAK.M	1215.622	1	0.497	0.747
Q99623	R.LGLDYEER.V	994.484	1	0.734	0.714
Prolactin regulatory element-binding protein (Mammalian guanine nucleotide exchange factor mSec12)					
Q9HCU5	R.VENLQAVQTDFSSDPLQK.V	2019.003	2	0.544	0.917
Prostaglandin E synthase (EC 5.3.99.3) (Microsomal glutathione S-transferase 1-like 1) (MGST1-L1) (p53-					
O14684	K.AFANPEDALR.H	1103.548	2	0.554	0.201
Protein C14orf106 (P243)					
Q6P0N0	K.YMAINQK.K	867.439	1	0.998	0.667
Protein C19orf21					

Acc No	Peptide	MH+	z	f	H/L ratio
Q8IVT2	R.ALSSDSILSPAPDAR.A	1499.77	2	0.672	0.717
Protein expressed in T-cells and eosinophils in atopic dermatitis (ETEA)					
Q96CS3	R.DLTQEQTEK.L	1091.521	1	0.843	0.229
Protein KIAA0152 precursor					
Q14165	R.SNPEDQILYQTER.Y	1592.755	2	0.398	0.835
Protein KIAA1045					
Q9UPV7	K.EAEAGTSVVQEESSAGRAAWER.L	2320.08	2	0.78	0.118
Protein transport protein Sec61 beta subunit					
P60468	R.FYTEDSPGLK.V	1156.552	1	0.718	0.257
P60468	R.FYTEDSPGLK.V	1156.552	1	0.645	0.261
P60468	-.PGPTPSGTNVGSSGR.S	1370.666	1	0.665	0.447
P60468	-.PGPTPSGTNVGSSGR.S	1370.666	2	0.372	0.396
P60468	R.FYTEDSPGLK.V	1156.552	2	0.514	9.559
P60468	-.PGPTPSGTNVGSSGR.S	1370.666	2	0.357	0.461
Putative 40-9-1 protein					
Q96QD8	K.TANEGGSLLYEQLGYK.A	1742.86	2	0.634	0.734
Putative Polycomb group protein ASXL1 (Additional sex combs-like protein 1)					
Q8IXJ9	K.QESEQAGVAK.D	1046.511	2	0.35	0.202
Rap guanine nucleotide exchange factor 2 (PDZ domain containing guanine nucleotide exchange factor 1)					
Q9Y4G8	K.INQGLQVPAVSLYPSRKK[.V	2002.157	2	0.781	0.333
Ras GTPase-activating-like protein IQGAP1 (p195)					
P46940	K.EELQSGVDAANSAAQQYQR.R	2064.958	2	0.852	0.435
Ras-related protein Rab-10					
P61026	K.SFENISK.W	824.415	1	0.854	0.613
Ras-related protein Rab-14					
P61106	R.LTSEPQPQR[.E	1059.556	1	0.781	0.454
Ras-related protein Rab-2A					
P61019	K.IQEGVFDINNEANGIK.I	1760.881	2	0.795	0.69
P61019	K.TASNVEEAFINTAK[.E	1498.751	2	0.576	1.238
P61019	K.IQEGVFDINNEANGIK.I	1760.881	2	0.507	0.677
Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah)					
Q9BZG1	R.INSDDSNLYLTASK.K	1540.749	2	0.451	0.527
Ras-related protein Rab-5C (RAB5L) (L1880)					
P51148	K.NEPQNATGAPGR.N	1211.576	2	0.527	1.167

Acc No	Peptide	MH+	z	f	H/L ratio
P51148	R.GVDLQENNPASR.S	1299.629	2	0.314	3.965
Ras-related protein Rab-7					
P51149	R.DEFLIQASPR.D	1175.605	1	0.886	0.433
P51149	R.DPENFPFVVLGNK.I	1475.753	2	0.59	0.732
P51149	R.LVTMQIWDTAGQER.F	1647.816	2	0.306	3.944
P51149	K.ATIGADFLTK.E	1036.567	2	0.842	0.401
P51149	R.FQSLGVAFYR.G	1187.621	2	0.618	0.895
P51149	K.ATIGADFLTK.E	1036.567	1	0.681	0.559
P51149	K.NNIPYFETSAK.E	1283.627	2	0.699	1.631
P51149	K.QETEVELYNEFPEPIK.L	1964.949	2	0.347	2.67
P51149	K.VIILGDSGVGK.T	1057.625	2	0.822	3.896
P51149	R.DEFLIQASPR.D	1175.605	2	0.721	0.805
Ras-related protein Rab-9A (Rab-9)					
P51151	K.EPESFPFVILGNK.I	1476.773	2	0.824	0.237
Retinoic acid-induced protein 3 (G-protein coupled receptor family C group 5 member A) (Retinoic acid-					
Q8NFJ5	R.TNVNVFSELSAPR[.R	1437.746	2	0.6	1.052
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.738	2	0.602	1.077
Q8NFJ5	R.NPMDYPVEDAFC*KPQLVK[.K	2155.033	2	0.641	0.84
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.738	1	0.83	0.597
Q8NFJ5	R.TNVNVFSELSAPR.R	1433.738	2	0.592	1.111
RNA-binding protein with serine-rich domain 1 (SR-related protein LDC2)					
Q15287	K.GYAYVEFENPDEAEK.A	1760.765	2	0.729	0.321
RPS27L protein					
Q49A11	R.DLLHPSLEEEK.K	1309.663	2	0.351	0.42
Ryanodine receptor 3 (Brain-type ryanodine receptor) (RyR3) (RYR-3) (Brain ryanodine receptor-calcium					
Q15413	K.KYDPDLFR.M	1053.536	2	0.87	1.769
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (EC 3.6.3.8) (Calcium pump 2) (SERCA2) (SR					
P16615	R.IGIFGQDEDVTSK.A	1408.696	2	0.927	0.46
P16615	R.DEMVATEQER.T	1207.526	2	0.629	0.629
P16615	R.EEMHLEDSANFIK[.Y	1566.724	2	0.415	1.115
P16615	R.IEVASSVK.L	832.477	1	0.617	0.515
P16615	R.NYLEPGK.E	820.42	1	0.503	0.422
Scavenger receptor class B member 1 (SRB1) (SR-BI) (CD36 antigen-like 1) (CD36 and LIMPII analogous					
Q8WTV0	K.SVAGIGQTGK.I	917.505	1	0.721	0.619

Acc No	Peptide	MH+	z	f	H/L ratio
SCO1 protein homolog, mitochondrial precursor					
O75880	R.EEVDQVAR[.A	949.472	1	0.716	0.882
Secretory carrier membrane protein 3					
Q4VX17	R.QYATLDVYNPFETR.E	1716.823	2	0.997	0.406
Sequestosome-1 (Phosphotyrosine-independent ligand for the Lck SH2 domain of 62 kDa) (Ubiquitin-					
Q13501	R.PGPTAESASGPSEDPSVNFLK.N	2086.993	2	0.744	0.928
SH3-binding kinase					
Q52WX2	R.EVSITNSLSSSPFIIK.V	1721.932	2	0.654	0.441
Sideroflexin-1 (Tricarboxylate carrier protein) (TCC)					
Q9H9B4	K.VGIPVTDENGNR.L	1270.639	2	0.832	0.968
Q9H9B4	R.NILLTNEQLESAR[.K	1504.81	2	0.821	1.277
Q9H9B4	K.QAITQVVVSR.I	1100.642	1	0.686	0.394
Signal peptidase complex subunit 2 (EC 3.4.-.-) (Microsomal signal peptidase 25 kDa subunit) (SPase 25					
Q15005	K.NSLDDSAK.K	849.395	1	0.907	0.096
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR[.S	1861.728	2	0.816	0.505
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR.S	1857.72	2	0.769	0.662
Q15005	R.SGGSGGC*SGAGGASNC*GTGSGR[.S	1861.728	2	0.792	0.532
Signal peptidase complex subunit 3 (EC 3.4.-.-) (Microsomal signal peptidase 23 kDa subunit) (SPase 22					
P61009	K.NNALNQVVLWDK.I	1413.749	2	0.593	1.428
Signal recognition particle receptor beta subunit (SR-beta) (Protein APMCF1)					
Q9Y5M8	R.DTQTSITDSC*AVYR.V	1616.722	2	0.392	0.61
Q9Y5M8	R.SAAPSTLDSSSTAPAQLGK.K	1788.897	2	0.808	0.239
Similar to mouse 1500009M05Rik protein					
Q8N5K1	K.DSLINLK.I	802.467	1	0.99	0.5
Sodium/potassium-transporting ATPase alpha-1 chain precursor (EC 3.6.3.9) (Sodium pump 1) (Na+/K+					
P05023	K.IVEIPFNSTNK.Y	1261.679	2	0.606	0.408
P05023	R.AVFQANQENLPILK.R	1584.874	2	0.951	0.285
Solute carrier family 2, facilitated glucose transporter member 1 (Glucose transporter type 1,					
P11166	R.TFDEIASGFR.Q	1142.548	2	0.735	0.338
P11166	R.TFDEIASGFR.Q	1142.548	2	0.984	0.699
Solute carrier family 25 member 24, isoform 1					
Q6NUK1	R.NLGIPLGQDAEEK.I	1383.711	2	0.963	0.07
Sorting and assembly machinery component 50 homolog					
Q9Y512	K.VTGQFPWSSLR.E	1277.664	2	0.73	0.313

Acc No	Peptide	MH+	z	f	H/L ratio
Q9Y512	K.VNQELAGYTGGDVSFIK.E	1797.902	2	0.547	1.234
Q9Y512	K.NLIEVMR.K	874.482	1	0.673	0.608
Q9Y512	R.NSSILPR.R	786.447	1	0.798	0.555
Q9Y512	K.QEILENK.D	873.468	1	0.512	0.712
Q9Y512	R.NSSILPR.R	786.447	1	0.9	0.637
Q9Y512	R.FYLGGPTSVR.G	1096.579	2	0.766	0.333

Source of immunodominant MHC-associated peptides

Q8TCJ2	R.ENPPVEDSSDEDDKR.N	1731.73	2	0.366	3.79
Q8TCJ2	R.ESDYFTPQGEFR[.V	1479.652	2	0.583	0.949

Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain)

Q13813	K.LQTASDESYKDPTNIQSK[.H	2028.985	2	0.922	0.418
Q13813	K.VNSLGETAER.L	1075.538	2	0.622	0.75
Q13813	K.VLETAEDIQER.R	1302.654	2	0.9	0.068
Q13813	K.DLASVNNLLK.K	1086.615	2	0.833	0.857
Q13813	K.LLEAQSHFR[.K	1104.593	2	0.82	1.745
Q13813	K.VLETAEDIQER.R	1302.654	2	0.629	0.119
Q13813	K.AINVQEEK.I	930.489	1	0.925	0.921
Q13813	K.AINVQEEK.I	930.489	1	0.903	1.37
Q13813	R.DLAALGDK.V	802.43	1	0.982	0.339
Q13813	R.SQLLGSAHEVQR.F	1324.697	2	0.764	0.445
Q13813	R.DLSSVQTLLTK.Q	1204.678	2	0.844	0.447
Q13813	K.DLTNVQNLQK.K	1172.627	2	0.655	0.75
Q13813	K.LQIASDENYKDPTNLQGK.L	2034.014	2	0.565	1.083
Q13813	K.DLTNVQNLQK.K	1172.627	1	0.539	0.924

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

Q01082	R.AQTLPTSVVTITSESSPGK.R	1903.002	2	0.474	0.664
Q01082	K.TALPAQSAATLPAR.T	1367.764	1	0.409	1.079

SPFH domain protein 1 precursor (Protein KE04)

O75477	K.EALEPSGENVIQNK.E	1527.765	2	0.557	2.052

SPFH domain protein 2 precursor

O94905	K.LSFGLEDEPLETATK[.E	1653.835	2	0.647	0.502

Splicing coactivator subunit SRm300

Q9UHA8	R.AAFGISDSYVDGSSFDPQR.R	2018.909	2	0.593	0.823
Q9UHA8	R.SPVPSAFSDQSR.C	1277.612	2	0.912	0.368
Q9UHA8	R.SPVPSAFSDQSR.C	1277.612	1	0.752	0.7

Acc No	Peptide	MH+	z	f	H/L ratio
Steroid dehydrogenase homolog (Fragment)					
Q53GQ0	R.TIAVDFASEDIYDK.I	1586.758	2	0.419	0.361
Supervillin (Archvillin) (p205/p250)					
O95425	R.YQTQPVTLGEVEQVQSGK.L	1991.008	2	0.45	0.6
Synaptic glycoprotein SC2					
Q9NZ01	R.LLETLFVHR.F	1127.657	2	0.923	0.244
Tetratricopeptide repeat protein KIAA0103					
Q15006	R.ILQEDPTNTAAR[.K	1332.688	2	0.6	1.144
Q15006	R.ILQEDPTNTAAR.K	1328.681	2	0.668	0.876
THAP domain-containing protein 2					
Q9H0W7	K.ILEQDQQDKTLLSLNLK.Q	1999.107	2	0.76	0.516
Q9H0W7	K.ILEQDQQDKTLLSLNLK.Q	1999.107	2	0.69	0.456
Thioredoxin domain-containing protein 1 precursor (Transmembrane Trx-related protein) (Thioredoxin-					
Q9H3N1	K.VDVTEQPGLSGR.F	1257.643	2	0.853	0.342
Thioredoxin reductase 2 intronic transcript 1					
Q6F5E7	K.VFGQGFPSPLEEIKR[.L	1707.92	2	0.612	0.447
Thyroid receptor-interacting protein 11 (TRIP-11) (Golgi-associated microtubule-binding protein 210)					
Q15643	R.EKEFECHSMKEK.A	1524.682	2	0.56	0.057
TNF receptor-associated factor 5 (RING finger protein 84)					
O00463	R.FVAHSVLENAKNAYIK.D	1803.975	2	0.4	1.03
Transcription factor 20 (Stromelysin 1 PDGF-responsive element-binding protein) (SPRE-binding protein)					
Q9UGU0	R.SASSNSAEAGGDTVTLDDILSLK[.S	2255.102	2	0.763	2.5
Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 antigen) (T9) (p90)					
P02786	R.EEPGEDFPAAR.R	1217.543	2	0.699	0.888
P02786	R.YNSQLLSFVR.D	1226.653	2	0.56	0.135
P02786	K.LAVDEEENADNNTK.A	1561.698	2	0.66	0.449
P02786	K.DSAQNSVIIVDK.N	1288.674	2	0.926	0.862
P02786	K.LAVDEEENADNNTK.A	1561.698	2	0.627	0.542
P02786	K.VSASPLLYTLIEK[.T	1437.833	2	0.776	0.323
Transformation/transcription domain-associated protein (350/400 kDa PCAF-associated factor)					
Q9Y4A5	K.YLQFVAALTDVNTPDETKLK[.M	2270.205	2	0.732	1.161
Translocation protein SEC63 homolog					
Q9UGP8	K.DATSRPTDNILIPQLIR[.E	1927.074	2	0.709	0.908

Acc No	Peptide	MH+	z	f	H/L ratio
Translocon-associated protein alpha subunit precursor (TRAP-alpha) (Signal sequence receptor alpha					
P43307	K.GEDFPANNIVK[.F	1207.608	1	0.829	0.64
Translocon-associated protein delta subunit precursor (TRAP-delta) (Signal sequence receptor delta					
P51571	R.FFDEESYSLLR.K	1405.663	2	0.806	0.267
Translocon-associated protein gamma subunit (TRAP-gamma) (Signal sequence receptor gamma subunit)					
Q9UNL2	K.QQSEEDLLLQDFSR.N	1707.818	2	0.438	0.484
Q9UNL2	K.QQSEEDLLLQDFSR.N	1707.818	2	0.649	0.26
Transmembrane 9 superfamily protein member 2 precursor (p76)					
Q99805	R.PSENLGQVLFGER.I	1445.738	2	0.467	0.747
Transmembrane anchor protein 1					
P84157	R.QEEEQDLDGEK.G	1319.56	2	0.634	0.908
P84157	R.QEEEQDLDGEK.G	1319.56	2	0.371	1.141
Transmembrane emp24 domain containing protein 10 precursor (Transmembrane protein Tmp21) (21 kDa					
P49755	K.NYEEIAK.V	866.425	1	0.737	0.527
Transmembrane emp24 domain containing protein 4 precursor					
Q7Z7H5	R.LTSESTNQR.V	1035.506	1	0.675	1.332
Q7Z7H5	R.LTSESTNQR[.V	1039.515	1	0.702	1.171
Transmembrane emp24 domain containing protein 5 precursor					
Q9Y3A6	R.NIQESNFDR.V	1122.517	1	0.316	1.324
Transmembrane emp24 domain containing protein 9 precursor (Glycoprotein 25L2)					
Q9BVK6	R.QLVEQVEQIQK.E	1341.737	2	0.62	1.372
Transmembrane protein 11 (Protein PM1)					
P17152	R.LGPGSSGGSAR.E	945.475	1	0.627	0.311
Transmembrane protein 33 (DB83 protein)					
P57088	R.ALLANALTSALR[.L	1217.734	2	0.796	0.491
P57088	K.LSANQQNILK.F	1128.637	2	0.99	0.395
P57088	R.GSNSLPLLR.S	956.552	2	0.737	0.506
P57088	R.ALLANALTSALR.L	1213.726	2	0.761	0.806
Transmembrane protein 49 (TDC1)					
Q96GC9	K.PFQEYLEAQR.Q	1280.627	2	0.909	0.467
Transmembrane protein PT27 (TPA regulated locus)					
Q9HC07	K.LLNGPGDVETGTSITVPQK[.K	1930.026	2	0.644	0.29
Tricarboxylate transport protein, mitochondrial precursor (Citrate transport protein) (CTP) (Tricarboxylate					

Acc No	Peptide	MH+	z	f	H/L ratio
P53007	K.TQLQLDER.S	1002.521	1	0.825	0.513
P53007	K.FIHDQTSPNPK[.Y	1287.646	2	0.623	0.179
Tumor necrosis factor ligand superfamily member 4 (OX40 ligand) (OX40L) (Glycoprotein GP34) (TAX					
P23510	R.VQPLEENVGNAARPRFER[.N	2086.092	2	0.908	1.029
TXNDC14 protein					
Q561W0	K.AGDNIPEEQPVASTPTTVSDGENK.K	2456.142	2	0.395	0.979
Type-1 angiotensin II receptor-associated protein (AT1 receptor-associated protein)					
Q6RW13	R.SAYQTIDSAEAPADPFAVPEGR.S	2292.078	2	0.542	1.019
Ubiquinol-cytochrome c reductase complex 7.2 kDa protein (EC 1.10.2.2) (Cytochrome C1, nonheme 7 kDa					
Q9UDW1	R.AFDQGADAIYDHINEGK[.L	1867.859	2	0.847	3.456
Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor (EC 1.10.2.2) (Complex					
P22695	K.TIAQGNLSNTDVQAAK.N	1630.839	2	0.706	0.645
P22695	R.GGLGLSGAK[.A	763.444	1	0.854	0.961
P22695	K.TIAQGNLSNTDVQAAK.N	1630.839	2	0.826	0.469
P22695	K.TIAQGNLSNTDVQAAK.N	1630.839	2	0.715	0.774
Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (EC 1.10.2.2)					
P31930	R.IAEVDASVVR.E	1058.584	1	0.53	0.841
P31930	R.NALVSHLDGTTPVC*EDIGR.S	2053.997	2	0.827	0.97
P31930	R.IAEVDASVVR.E	1058.584	2	0.935	0.242
UPF0198 protein CGI-141					
Q9Y3E0	R.VPVLGSLLNLPGIR.S	1447.9	2	0.622	0.939
Vacuolar ATP synthase subunit d (EC 3.6.3.14) (V-ATPase d subunit) (Vacuolar proton pump d subunit)					
P61421	R.LYPEGLAQLAR.A	1230.684	2	0.853	0.348
Vesicle trafficking protein SEC22b (SEC22 vesicle trafficking protein-like 1)					
O75396	R.NLGSINTELQDVQR.I	1586.813	2	0.935	0.323
O75396	K.LNEQSPTR.C	944.48	1	0.449	0.685
O75396	R.DLQQYQSQAK.Q	1208.591	1	0.751	0.543
O75396	R.DLQQYQSQAK.Q	1208.591	2	0.708	0.709
Vesicle-associated membrane protein-associated protein A (VAMP-associated protein A) (VAMP-A) (VAP-A)					
Q9P0L0	K.FKGPFTDVVTTNLK.L	1566.853	2	0.648	0.303
Q9P0L0	K.PHSVSLNDTETR[.K	1359.663	2	0.601	0.823
Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane					
P21796	K.LTFDSSFSPNTGK.K	1400.669	2	0.331	1.288
P21796	R.VTQSNFAVGYK.T	1213.621	1	0.78	0.541

Acc No	Peptide	MH+	z	f	H/L ratio
P21796	K.LTFDSSFSPNTGK.K	1400.669	2	0.3	1.217
P21796	R.VTQSNFAVGYK[.T	1217.629	1	0.748	0.511
P21796	R.VTQSNFAVGYK.T	1213.621	1	0.874	0.26
P21796	R.VTQSNFAVGYK[.T	1217.629	2	0.663	1.029
P21796	K.LTFDSSFSPNTGKK.N	1528.764	2	0.647	0.901
P21796	R.VTQSNFAVGYK[.T	1217.629	2	0.67	0.917
P21796	R.VTQSNFAVGYK.T	1213.621	2	0.751	0.942
P21796	K.SENGLEFTSSGSANTETTK.V	1959.878	2	0.362	3.418
P21796	K.LTFDSSFSPNTGK.K	1400.669	1	0.462	0.699
P21796	K.LTFDSSFSPNTGK.K	1400.669	1	0.454	1.098
P21796	K.LTFDSSFSPNTGK.K	1400.669	1	0.553	1.449
P21796	K.WNTDNTLGTEITVEDQLAR.G	2176.052	2	0.393	1.097

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

Q9Y277	K.LTLDTIFVPNTGK.K	1418.789	2	0.713	0.241
Q9Y277	K.VC*NYGLTFTQK.W	1330.646	2	0.696	0.204
Q9Y277	K.LTLDTIFVPNTGK.K	1418.789	2	0.551	0.549
Q9Y277	K.LSQNNFALGYK.A	1254.648	2	0.979	0.206
Q9Y277	K.VNNASLIGLGYTQTLR.P	1719.939	2	0.58	2.046
Q9Y277	K.LSQNNFALGYK.A	1254.648	2	0.802	0.141
Q9Y277	K.LTLDTIFVPNTGK.K	1418.789	2	0.402	0.582

WD-repeat protein 67

Q96DN5	R.NKCYQEVAKLLR.E	1464.799	2	0.939	0.073

Zinc finger protein 512

Q96ME7	R.QQPGIELPETELSLR.V	1709.907	2	0.725	0.44