Suppporting Information for

“Quantitative Proteomic Analysis Revealed *N*’-Nitrosonornicotine-induced Down-regulation of Non-muscle Myosin II and Reduced Cell Migration in Cultured Human Skin Fibroblast Cells” by

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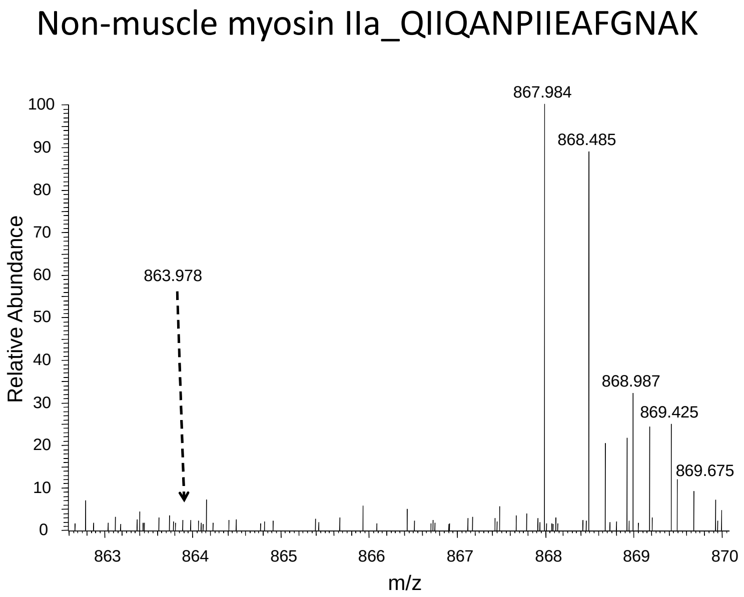
Protein: Non-muscle myosin IIa
Peptide: QIIQANPIIEAFGNAK
Charge: $[M+2H]^{2+}$
Light *m/z*: 863.978
Heavy *m/z*: 867.984



Protein: Glyceraldehyde-3-Phospha
Dehydrogenase
Peptide: IISWYDNEFGYSNR
Charge: $[M+2H]^{2+}$
Light *m/z*: 765.901
Heavy *m/z*: 768.913

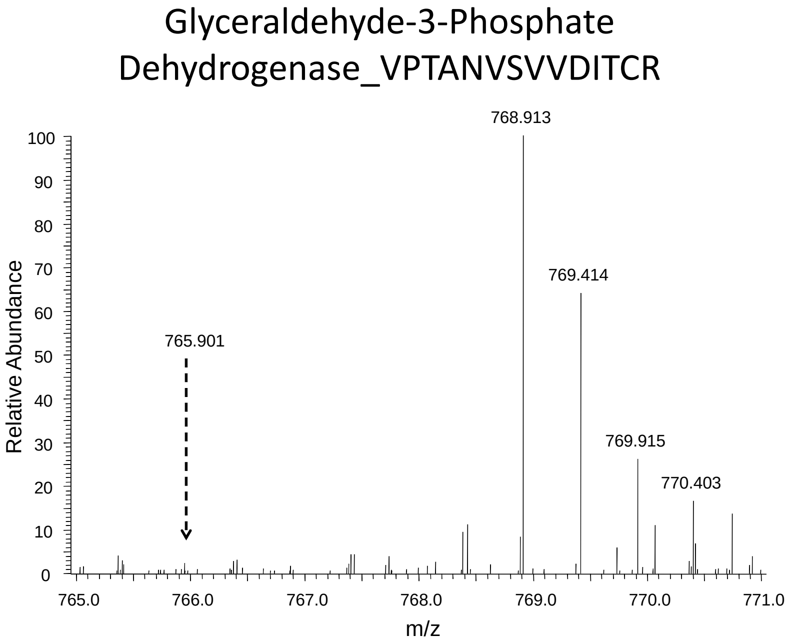


Figure S1. Representative ESI-MS illustrating the nearly complete incorporation of heavy isotope-labeled amino acids ($[^{13}C_6,^{15}N_2]$-L-lysine and $[^{13}C_6]$-L-arginine) in GM00637 cells. Heavy labeled lysate was digested in-gel with trypsin and subjected to LC-MS/MS analysis as described in the text for the mixture of light- and heavy-labeled lysates.

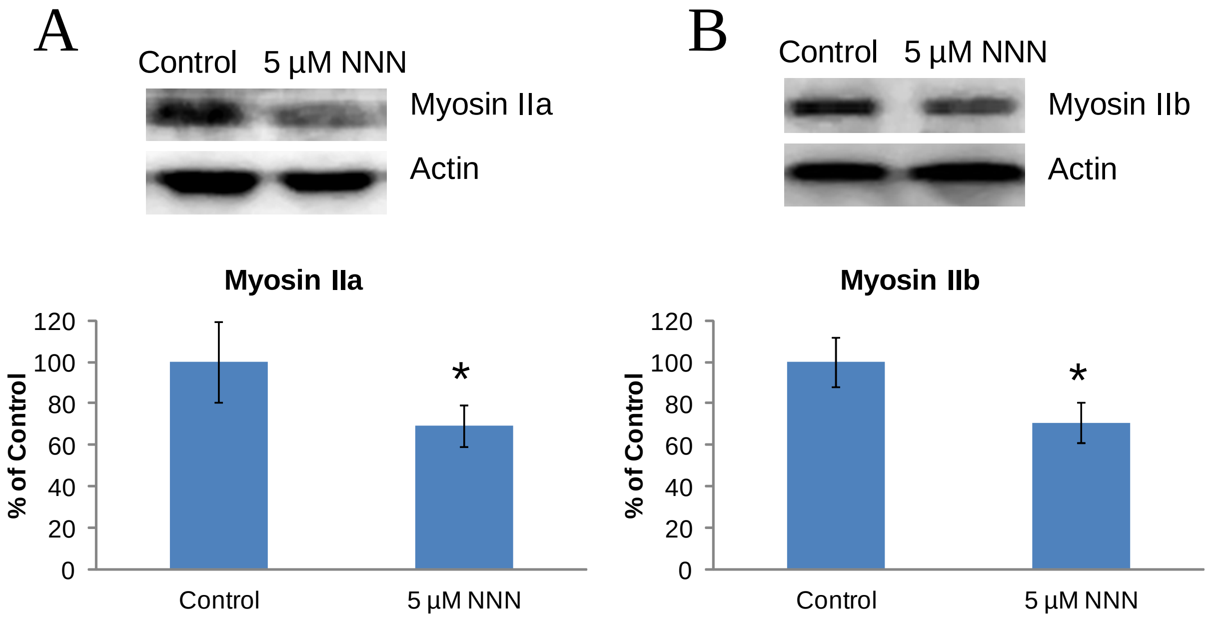


Figure S2: Western Blot analysis for non-muscle Myosin IIa & IIb in human skin fibroblast (GM00637 cells) following 24 hour exposure to 5 µM NNN. (A) Treatment with 5 µM NNN for 24 hrs resulted in a significant decrease in non-muscle myosin IIa (69% of control). (B) Treatment with 5 µM NNN for 24 hrs resulted in a significant decrease in non-muscle myosin IIb (71% of control). Data represent as the mean ± standard deviation. '*', $p < 0.05$, student-t test (n=5).

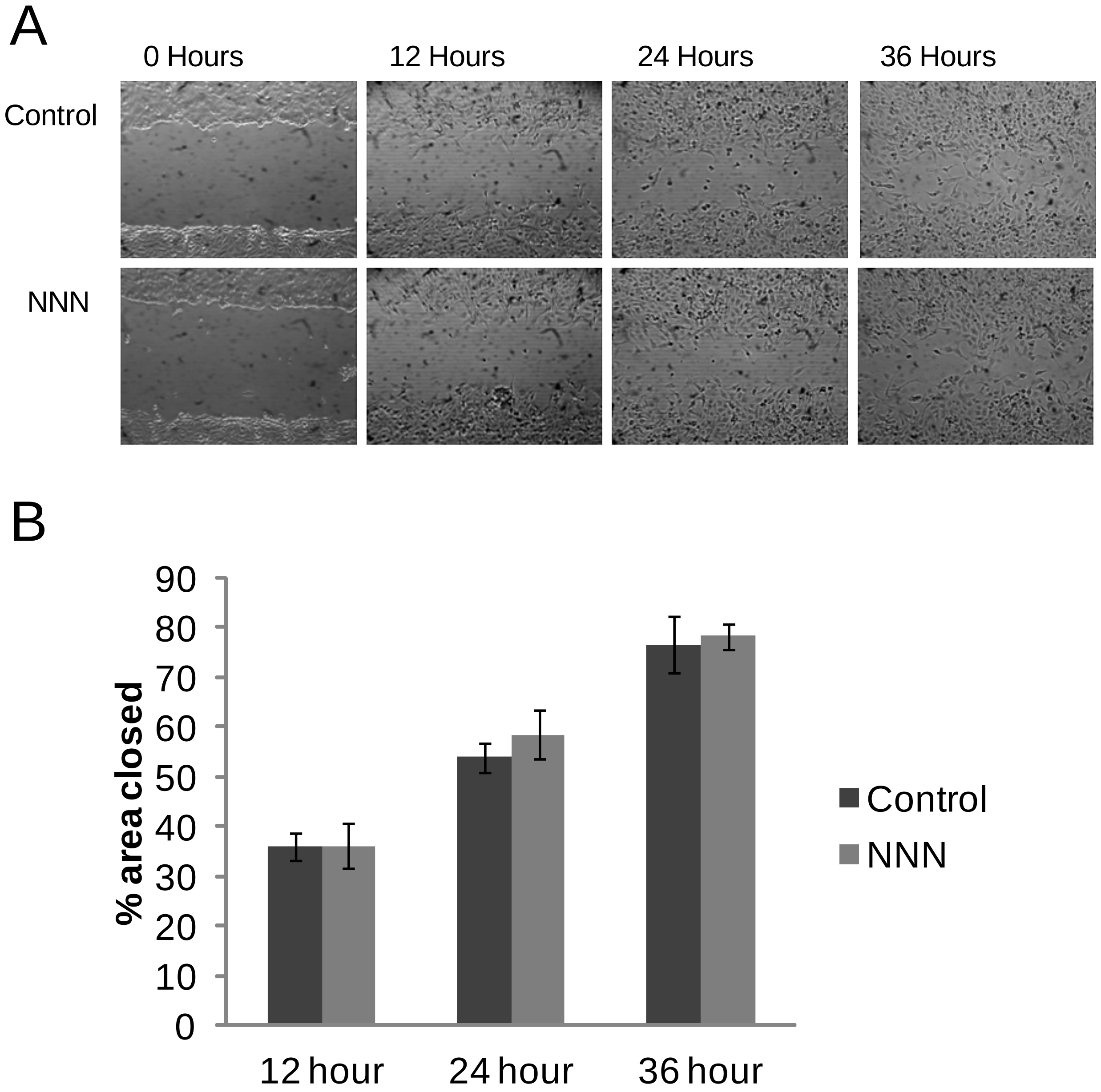


Figure S3. *In vitro* scratch assay for GM00637 cells following a 30 min treatment with 5 µM NNN. (A) Exposure to 5 µM NNN for 30 min failed to alter the ability of GM00637 cells to migrate into scratch area. (B) The percentage of the scratch area closed relative to the 0 hr time point. Data represent as the mean ± standard deviation (n=6).

Table 1. A list of all quantified proteins and their expression ratios in NNN-treated cells versus control untreated cells. Displayed are the Maxquant-derived normalized ratios of light/heavy (“L/H”)-labeled proteins obtained from two forward (labeled as “Forward1” and “Forward2”) and and heavy/light (“H/L”)-labeled proteins from one reverse (labeled as “Reverse”) SILAC labeling experiments. The mean [“Avg”] and standard deviation (“STD”) of protein expression ratios in NNN-treated versus untreated cells derived from at least two sets (including one reverse labeling) of SILAC labeling experiments are also listed. Posterior error probability (PEP) score was calculated using Bayesian statistics as a probability of false hit using the peptide identification score and length of peptide. The PEP score for each protein was determined by multiplying their peptide PEPs, where only peptides with distinct sequences and only highest-scoring identified spectra were used.

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
5.66E-09	0.168	0.161		**0.164**	**0.004**	Autoantigen NOR-90
2.09E-13	0.398	0.131	0.131	**0.220**	**0.154**	Mediator of DNA damage checkpoint protein 1
4.07E-64	0.425	0.144	0.173	**0.247**	**0.154**	Collagen alpha-1(VI) chain
4.5E-145	0.227	0.244	0.280	**0.250**	**0.027**	Alpha-1 type I collagen
2.65E-98	0.128	0.296	0.338	**0.254**	**0.111**	High mobility group protein 2
1.1E-253	0.252	0.329	0.230	**0.271**	**0.052**	Collagen alpha-3(VI) chain
8.26E-97	0.242	0.304		**0.273**	**0.044**	RcDNAJ9
8.59E-11	0.419	0.177	0.227	**0.274**	**0.128**	Zinc finger CCHC domain-containing protein 8
0.000211	0.108		0.447	**0.277**	**0.240**	Adapter-related protein complex 4 subunit epsilon-1
3.23E-18	0.205	0.360		**0.283**	**0.110**	Immunoglobulin superfamily DCC subclass member 2
1.08E-20	0.494	0.127	0.248	**0.290**	**0.187**	Adipophilin
4.52E-33	0.249	0.347		**0.298**	**0.069**	Alpha-2 type I collagen
1.4E-15	0.470	0.177		**0.324**	**0.207**	AAA nuclear coregulator cancer-associated protein
7.7E-107	0.652	0.174	0.188	**0.338**	**0.272**	CALNUC
2.72E-43	0.562	0.123		**0.343**	**0.310**	Embryonal carcinoma differentiation-regulated protein
3.2E-216	0.273		0.449	**0.361**	**0.124**	Short heat shock protein 60 Hsp60s2
1.08E-14	0.334	0.389		**0.361**	**0.039**	MIDAS-containing protein
3.56E-74	0.900	0.103	0.137	**0.380**	**0.451**	68 kDa TATA-binding protein-associated factor
4.58E-58	0.748	0.270	0.131	**0.383**	**0.324**	Down-regulator of transcription 1
1.81E-61	0.850	0.131	0.189	**0.390**	**0.399**	300 kDa nuclear matrix antigen
8.78E-50	0.306	0.466	0.411	**0.394**	**0.081**	dCMP deaminase
7.77E-59	0.822	0.163	0.211	**0.399**	**0.367**	PEST proteolytic signal-containing nuclear protein
2.32E-39	0.831	0.180	0.224	**0.412**	**0.364**	140 kDa Ser/Arg-rich domain protein
1.5E-122	0.915	0.191	0.172	**0.426**	**0.424**	A-kinase anchor protein 12
1.2E-40	0.864	0.217	0.204	**0.428**	**0.378**	Phosphofurin acidic cluster sorting protein 1
0	0.433	0.323	0.532	**0.429**	**0.104**	20 kDa myosin light chain

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.71E-76	0.068	0.771	0.458	**0.432**	**0.352**	High mobility group nucleosome-binding domain-containing protein 2
9.7E-114	0.676	0.196		**0.436**	**0.340**	Monocyte protein 3
2.22E-26	0.769	0.107		**0.438**	**0.468**	Arginine/serine-rich-splicing factor 14
1.97E-86	0.176		0.700	**0.438**	**0.370**	Histone H2A type 2-B
2.9E-08	0.270	0.611		**0.440**	**0.241**	Protein ftsJ homolog 3
2.6E-216	0.394	0.425	0.514	**0.444**	**0.062**	APEX nuclease
4.8E-67	0.503	0.420	0.453	**0.459**	**0.042**	Asparagine synthetase [glutamine-hydrolyzing]
0.001125	0.489		0.429	**0.459**	**0.042**	RNA-binding motif protein 28
1.5E-107	0.566	0.382	0.447	**0.465**	**0.093**	Cardiac myosin light chain 1
3.2E-215	0.991	0.248	0.161	**0.467**	**0.456**	Myosin-Ic
9.1E-56	1.045	0.164	0.195	**0.468**	**0.500**	Rab3 GTPase-activating protein 150 kDa subunit
1.04E-09	0.473	0.503	0.431	**0.469**	**0.036**	Coiled-coil domain-containing protein 72
2.6E-132	0.913	0.314	0.205	**0.477**	**0.381**	Kinesin-like protein 1
1.45E-31	0.348	0.320	0.780	**0.483**	**0.258**	CD49 antigen-like family member F
1.45E-28	0.364	0.572	0.521	**0.486**	**0.108**	Negative elongation factor A
8.96E-11	0.926	0.212	0.322	**0.487**	**0.384**	SAPS domain family member 1
0	0.560	0.484	0.415	**0.487**	**0.073**	Cellular myosin heavy chain, type B
2.39E-61	0.653		0.337	**0.495**	**0.223**	Ribosomal protein S10 variant
3.11E-43	0.532	0.320	0.634	**0.496**	**0.160**	MAPK-interacting and spindle-stabilizing protein-like
8.56E-55	0.638	0.584	0.272	**0.498**	**0.197**	PRP4 homolog
1.4E-101	0.759	0.252	0.485	**0.499**	**0.254**	Golgi integral membrane protein 4
3.99E-19	0.377		0.629	**0.503**	**0.178**	CCNDBP1-interactor
1.45E-43	0.099	0.908		**0.503**	**0.572**	EST1-like protein A
2.1E-83	0.576	0.355	0.583	**0.505**	**0.130**	Membrane-associated protein HEM-2
2.6E-101	0.863	0.305	0.353	**0.507**	**0.309**	E3 ubiquitin-protein ligase BRE1A
1.5E-197	0.415	0.603		**0.509**	**0.133**	Melanoma differentiation-associated protein 9
1.6E-252	0.233	0.444	0.856	**0.511**	**0.317**	High mobility group protein 1
1.58E-15	0.886	0.295	0.352	**0.511**	**0.326**	FYVE-finger protein EIP1
3.31E-92	1.060	0.206	0.280	**0.515**	**0.473**	Nuclear autoantigen of 14 kDa
2.46E-19	0.837	0.198		**0.518**	**0.452**	Syntaxin-10
4.3E-142	0.977	0.213	0.366	**0.519**	**0.404**	30 kDa splicing factor SMNrp
2.3E-240	0.574	0.412	0.573	**0.520**	**0.093**	Laminin B1s chain
6E-05	1.054	0.327	0.189	**0.523**	**0.465**	Protein FAM91A1
6.9E-228	1.109	0.236	0.226	**0.524**	**0.507**	Phospholipase C, gamma 1
5.64E-08	0.594	0.515	0.472	**0.527**	**0.062**	Protein CG-2
0	0.825	0.305	0.456	**0.529**	**0.268**	Tubulin beta-2A chain

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
9.9E-101	0.644	0.510	0.433	**0.529**	**0.107**	UbcH10
1.2E-304	0.478	0.348	0.791	**0.539**	**0.228**	Heterogeneous nuclear ribonucleoprotein M
3.45E-14	0.996	0.248	0.377	**0.540**	**0.400**	HTPHLP
4.37E-52	0.363	0.621	0.637	**0.541**	**0.154**	ATP-dependent DNA helicase Q1
1.8E-128	0.299	0.635	0.700	**0.545**	**0.215**	Histone H1.4
5.2E-107	0.654	0.366	0.617	**0.545**	**0.157**	Myristoylated alanine-rich C-kinase substrate
3.35E-37	1.058	0.216	0.365	**0.546**	**0.449**	CDC2-related protein kinase 5
7.36E-46	1.023	0.336	0.281	**0.547**	**0.413**	NF-kappa-B-activating kinase
5.63E-10	0.466		0.629	**0.547**	**0.116**	UPF0424 protein C1orf128
6.23E-18	0.751	0.628	0.266	**0.548**	**0.252**	Dynamin-2
3.43E-33	0.605	0.494		**0.550**	**0.078**	Exosome complex exonuclease RRP40
0	0.415	0.619	0.620	**0.551**	**0.118**	Cellular myosin heavy chain, type A
4.32E-06	0.444	0.691	0.521	**0.552**	**0.126**	CD99 antigen
3.2E-233	1.327	0.151	0.181	**0.553**	**0.671**	Tumor protein D52-like 2
5.1E-93	1.162	0.342	0.156	**0.553**	**0.535**	cDNA FLJ77693, highly similar to Homo sapiens calpastatin (CAST), transcript variant 3, mRNA
8.51E-29	1.298	0.218	0.144	**0.553**	**0.646**	Prostate antigen recognized and identified by SEREX 1
0	0.638	0.441	0.586	**0.555**	**0.102**	Myosin regulatory light chain MRCL3 variant
1.96E-79	0.831	0.288		**0.560**	**0.384**	cDNA FLJ60565, highly similar to Nuclear pore complex protein Nup153
3.04E-61	0.976	0.284	0.426	**0.562**	**0.366**	CDC46 homolog
1.94E-08	0.688	0.438		**0.563**	**0.176**	Neuroblastoma-amplified gene protein
2.49E-16	0.567	0.797	0.328	**0.564**	**0.234**	DEAH box protein 36
8.06E-73	1.474	0.136	0.084	**0.565**	**0.788**	Adapter-related protein complex 3 subunit beta-1
1.53E-63	0.729	0.511	0.458	**0.566**	**0.143**	Cytoplasmic FMR1-interacting protein 1
2.41E-88	0.348	0.712	0.638	**0.566**	**0.192**	RSU1 protein
2.11E-67	0.813	0.402	0.487	**0.568**	**0.217**	FAS-associated factor 2
2.14E-26	0.788	0.348		**0.568**	**0.311**	RNA polymerase-associated protein CTR9 homolog
7.4E-183	0.742	0.424	0.539	**0.568**	**0.161**	MYH14 variant protein
6.56E-36	0.606		0.532	**0.569**	**0.052**	Hepatocellular carcinoma-associated protein 4
5.64E-56	1.066	0.194	0.447	**0.569**	**0.449**	Coronin-1A
4.96E-45	0.712	0.909	0.097	**0.572**	**0.424**	cDNA FLJ61322, highly similar to RNA-binding motif,single-stranded-interacting protein 1
2.3E-129	0.742	0.368	0.609	**0.573**	**0.190**	Oxysterol-binding protein-related protein 8
1.6E-104	0.905	0.426	0.391	**0.574**	**0.287**	Adapter-related protein complex 3 subunit delta-1
2.14E-17	0.106	1.310	0.308	**0.574**	**0.645**	Ribosomal RNA-processing protein 15
2.2E-204	0.756	0.751	0.225	**0.578**	**0.305**	Activated RNA polymerase II transcriptional coactivator p15

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.68E-36	0.573	0.533	0.633	**0.580**	**0.051**	Mesenchymal stem cell protein DSCD75
5.7E-113	1.160	0.282	0.300	**0.581**	**0.502**	EF-hand calcium-binding protein RLP49
1.8E-291	0.848	0.405	0.493	**0.582**	**0.235**	Pre-mRNA-splicing factor SF3b 155 kDa subunit
6.2E-184	0.470	0.503	0.776	**0.583**	**0.168**	22 kDa actin-binding protein
4.2E-128	0.755	0.405	0.592	**0.584**	**0.176**	Coat protein GPP34
6.59E-22	0.423	1.186	0.143	**0.584**	**0.540**	AXL oncogene
6.6E-135	0.983	0.336	0.434	**0.585**	**0.349**	Protein CDV3 homolog
4.94E-44	1.108	0.245	0.407	**0.587**	**0.459**	C219-reactive peptide
5.03E-26	0.604	0.570		**0.587**	**0.024**	Kinesin-like protein 2
5E-208	0.325	0.805	0.632	**0.587**	**0.243**	Anastellin
2.65E-41	0.949	0.229		**0.589**	**0.509**	Toll interacting protein variant
0	0.572	0.540	0.666	**0.593**	**0.065**	Vimentin
1.5E-07	1.115	0.316	0.352	**0.594**	**0.451**	Oxysterol-binding protein
3.5E-206	0.470	0.603	0.710	**0.594**	**0.120**	Prefoldin subunit 6
2.7E-151	0.658	0.804	0.321	**0.594**	**0.248**	EH domain-containing protein 2
3.73E-13	0.385	0.894	0.509	**0.596**	**0.266**	Monocyte activation antigen Mo3
1.49E-12	0.502	0.763	0.528	**0.598**	**0.144**	40 kDa peptidyl-prolyl cis-trans isomerase
0	0.987	0.515	0.291	**0.598**	**0.356**	130 kDa cis-Golgi matrix protein
9.9E-170	0.665	0.604	0.529	**0.599**	**0.068**	Integrin alpha-V
7.09E-13	0.561	0.593	0.648	**0.601**	**0.044**	Putative uncharacterized protein RIF1
8.35E-74	1.063	0.257	0.489	**0.603**	**0.415**	Erythrocyte 65 kDa protein
0	0.798	0.473	0.539	**0.604**	**0.172**	Chromatin-specific transcription elongation factor 140 kDa subunit
1.4E-146	0.500	0.733	0.579	**0.604**	**0.119**	Melanoma-associated antigen MG50
2.35E-20	0.728	0.475	0.614	**0.606**	**0.127**	Charged multivesicular body protein 2a
5.79E-58	0.390	0.674	0.757	**0.607**	**0.193**	Mitochondrial import inner membrane translocase subunit Tim13
0	0.827	0.744	0.253	**0.608**	**0.310**	GCN1-like protein 1
0	0.785	0.482	0.559	**0.609**	**0.157**	cDNA FLJ55335, highly similar to Tyrosine-protein kinase-like 7
1.6E-35	0.912	0.475	0.443	**0.610**	**0.263**	Protein SDP3
1.2E-191	1.134	0.396	0.306	**0.612**	**0.454**	PAI1 RNA-binding protein 1
0	0.738	0.607	0.493	**0.613**	**0.122**	p180/ribosome receptor
9.54E-12	0.388	0.688	0.773	**0.616**	**0.202**	Endoglin
4E-11	0.726	0.225	0.903	**0.618**	**0.352**	Inhibitor of ASPP protein
1.02E-21	0.814	0.559	0.484	**0.619**	**0.173**	Putative uncharacterized protein QTRTD1
1.07E-16	0.583	0.626	0.657	**0.622**	**0.037**	Twisted gastrulation protein homolog 1
2.18E-42	0.643	0.517	0.709	**0.623**	**0.097**	Cell migration-inducing gene 2 protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.7E-126	0.545	0.813	0.512	**0.623**	**0.165**	Androgen receptor coactivator 55 kDa protein
4.74E-73	1.022	0.348	0.500	**0.623**	**0.354**	Signal transducer and activator of transcription 5B
0	0.748	0.543	0.579	**0.624**	**0.110**	67 kDa calelectrin
1.24E-42	1.550	0.056	0.272	**0.626**	**0.807**	Opa-interacting protein 1
3E-294	0.900	0.541	0.438	**0.626**	**0.242**	Heat shock protein 90-beta b
2.01E-24	1.017	0.503	0.364	**0.628**	**0.344**	Cytosolic Fe-S cluster assembly factor NUBP1
2.3E-10	0.929	0.309	0.649	**0.629**	**0.310**	C-terminal-binding protein 2
1.47E-44	0.474		0.787	**0.630**	**0.222**	Phosphomannomutase 1
3.86E-24	0.638	0.628		**0.633**	**0.007**	Cytoplasmic dynein 2 heavy chain
5.53E-87	0.977	0.529	0.402	**0.636**	**0.302**	Actin-related protein 2/3 complex subunit 5-like protein
4.58E-30	0.922		0.350	**0.636**	**0.405**	cDNA FLJ51089, highly similar to FK506-binding protein 9 (EC 5.2.1.8)
0	0.748	0.452	0.709	**0.636**	**0.161**	Polyadenylate-binding protein 1
7.45E-62	0.873	0.739	0.305	**0.639**	**0.297**	Putative uncharacterized protein MRPS36
3.2E-149	1.391	0.165	0.368	**0.641**	**0.657**	LIM and SH3 domain protein 1
2.04E-11	0.785	0.666	0.480	**0.644**	**0.154**	JV15-2
2.68E-68	1.245	0.311	0.375	**0.644**	**0.522**	Pre-rRNA-processing protein TSR1 homolog
3.24E-75	0.630	0.584	0.718	**0.644**	**0.068**	Deubiquitinating enzyme 11
2.57E-33	0.354	0.935		**0.644**	**0.411**	M-phase phosphoprotein homolog
7.2E-191	1.140	0.456	0.339	**0.645**	**0.433**	Putative uncharacterized protein KIAA0664
1E-103	1.376	0.126	0.437	**0.646**	**0.651**	Phospholipase C-beta-3 neighbouring gene protein
1.5E-176	0.348	0.400	1.192	**0.647**	**0.473**	Putative uncharacterized protein DBN1
1.3E-243	1.151	0.373	0.419	**0.648**	**0.436**	Putative uncharacterized protein DKFZp781N1372
1.61E-37	0.456	0.610	0.877	**0.648**	**0.213**	Follistatin-like protein 1
2.53E-60	0.442	0.803	0.698	**0.648**	**0.186**	Neural cell adhesion molecule L1
4.1E-132	0.593	0.855	0.499	**0.649**	**0.184**	Putative uncharacterized protein CD81
1.23E-98	0.791	0.621	0.542	**0.651**	**0.127**	DNA-directed RNA polymerase II 140 kDa polypeptide
2.5E-48	0.807	0.498	0.651	**0.652**	**0.154**	PP2A B subunit isoform B56-delta
0	0.834	0.521	0.604	**0.653**	**0.162**	Nucleolin
1.01E-06	1.003		0.305	**0.654**	**0.494**	Methionine-R-sulfoxide reductase B3, mitochondrial
0.000899	0.378		0.930	**0.654**	**0.390**	Amino-terminal enhancer of split
1.65E-84	1.031	0.382	0.553	**0.655**	**0.336**	27 kDa Golgi SNARE protein
8.33E-93	1.055	0.526	0.387	**0.656**	**0.352**	Deubiquitinating enzyme FAF-X
6.6E-279	0.666	0.589	0.713	**0.656**	**0.063**	highly similar to Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA
1.3E-252	0.493	0.938	0.544	**0.658**	**0.243**	Alpha-2-macroglobulin receptor

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.91E-59	1.189	0.265	0.521	**0.658**	**0.477**	SAFB protein
9.8E-288	0.986	0.544	0.445	**0.658**	**0.288**	Leucine-rich repeat-containing protein 47
2.8E-34	0.547	0.772		**0.659**	**0.159**	Protein-glutamine gamma-glutamyltransferase 2
1.4E-110	0.631	0.161	1.190	**0.661**	**0.515**	Paxillin
5.04E-12	0.404	1.183	0.395	**0.661**	**0.453**	Dr1-associated corepressor
6.11E-11	1.173	0.452	0.363	**0.663**	**0.444**	Component of gems 3
4.39E-66	0.781	0.641	0.575	**0.666**	**0.105**	Apoptosis-inducing factor 1, mitochondrial
1E-33	0.810	0.574	0.615	**0.666**	**0.126**	c-Myc-responsive protein Rcl
6.69E-43	0.598		0.736	**0.667**	**0.097**	HLA class I histocompatibility antigen, A-10 alpha chain
5.1E-252	1.247	0.373	0.383	**0.668**	**0.501**	100 kDa coated vesicle protein C
1.21E-82	0.733	0.568	0.704	**0.669**	**0.088**	Protein KIAA0196 variant
3.14E-43	0.424		0.914	**0.669**	**0.347**	Dehydrogenase/reductase SDR family member 7
1.27E-07	1.529	0.225	0.254	**0.669**	**0.744**	Death-associated protein 1
3.22E-52	0.829	0.471	0.709	**0.670**	**0.182**	Interleukin-25
3.21E-22	0.702	0.641	0.666	**0.670**	**0.031**	Coiled-coil domain-containing protein 47
1.48E-16	0.467		0.874	**0.670**	**0.288**	Antigen NY-CO-16
0	0.623	0.542	0.846	**0.670**	**0.157**	Plastin-3
3.2E-117	0.070	1.054	0.888	**0.671**	**0.527**	Histone H2A.x
2.3E-67	0.992	0.522	0.498	**0.671**	**0.279**	Endoplasmic oxidoreductin-1-like protein
2.26E-95	1.007	0.335		**0.671**	**0.475**	DEAD box protein 46
3.21E-31	0.413	0.936		**0.674**	**0.370**	Major facilitator superfamily domain-containing protein 10
2.9E-157	0.494	0.773	0.757	**0.675**	**0.157**	Guanine nucleotide-binding protein G(y) subunit alpha
0	1.067	0.358	0.601	**0.675**	**0.360**	Beta-coat protein
4.1E-147	0.806	0.605	0.617	**0.676**	**0.113**	Transaldolase
5.1E-183	0.952	0.662	0.416	**0.677**	**0.268**	Nuclear receptor-binding protein
3.04E-35	0.630	0.817	0.582	**0.677**	**0.124**	Cleavage and polyadenylation specificity factor 160 kDa subunit
8.11E-08	0.511		0.844	**0.678**	**0.236**	Protein FAM83D
1.1E-297	1.032	0.324		**0.678**	**0.500**	Caldesmon
2.6E-146	0.781	0.557	0.697	**0.678**	**0.113**	Chromatin-specific transcription elongation factor 80 kDa subunit
3.6E-236	1.299	0.557	0.180	**0.679**	**0.569**	DNA replication licensing factor MCM6
1.4E-160	0.614	0.820	0.604	**0.679**	**0.122**	Rho-related GTP-binding protein RhoG
1.1E-301	0.798	0.598	0.648	**0.681**	**0.104**	Ribonucleoside-diphosphate reductase large subunit
2.28E-13	1.291	0.430	0.323	**0.681**	**0.531**	Methyltransferase-like protein 1
9.29E-11	0.993	0.129	0.922	**0.682**	**0.480**	Caspase-4

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.04E-12	0.309	1.062		**0.686**	**0.532**	Kinesin-associated protein 3
1.1E-38	0.795	0.569	0.693	**0.686**	**0.113**	Cathepsin P
0	0.828	0.492	0.743	**0.688**	**0.175**	highly similar to Homo sapiens MCM3 minichromosome maintenance deficient 3 (MCM3)
3.48E-90	1.033	0.500	0.531	**0.688**	**0.299**	UV excision repair protein RAD23 homolog A
4.9E-109	1.204	0.362	0.502	**0.690**	**0.451**	cDNA FLJ40132 fis, clone TESTI2012155, highly similar to NUCLEOPORIN-LIKE PROTEIN RIP
7.52E-31	0.794	0.646	0.629	**0.690**	**0.091**	Putative uncharacterized protein NUDT5
6.2E-49	0.933	0.510	0.627	**0.690**	**0.218**	cDNA FLJ78093, highly similar to Homo sapiens ribosomal protein L29 (RPL29), mRNA
5.6E-158	0.265	1.275	0.531	**0.690**	**0.524**	1C9-2
3.39E-86	0.736	0.516	0.820	**0.691**	**0.157**	Fanconi anemia group I protein
1.16E-15	1.287	0.101		**0.694**	**0.839**	Protein transport protein Sec16A
4E-236	0.885	0.482	0.713	**0.694**	**0.202**	Acyl-CoA-binding domain-containing protein 3
3.3E-153	0.663	0.781	0.639	**0.694**	**0.076**	Pre-mRNA-splicing factor ISY1 homolog
6.42E-08	0.576	0.597	0.913	**0.695**	**0.188**	Amphiglycan
1.62E-36	0.578		0.817	**0.697**	**0.169**	Dipeptidyl peptidase 9
6.8E-102	0.939	0.457		**0.698**	**0.341**	Ankyrin repeat and KH domain-containing protein 1
1.35E-59	0.172	0.996	0.929	**0.699**	**0.457**	Histone H2A.Z
2.93E-67	0.448	0.950		**0.699**	**0.356**	Leukocyte common antigen related
4.88E-11	0.631	0.767		**0.699**	**0.097**	SAC2 suppressor of actin mutations 2-like protein
1.52E-93	1.165	0.236		**0.700**	**0.657**	AKAP-KL
1.8E-249	0.662	0.970	0.472	**0.701**	**0.251**	ATP-dependent helicase SKIV2L2
7.59E-06	1.278	0.124		**0.701**	**0.816**	Putative uncharacterized protein CGI-59
0	0.734	0.634	0.739	**0.702**	**0.059**	cDNA FLJ60299, highly similar to Rab GDP dissociation inhibitor beta
0	0.841	0.605	0.662	**0.703**	**0.123**	Elongation factor 2
2.94E-31	0.999	0.529	0.584	**0.704**	**0.257**	ADP-ribosylation factor-like protein 2-binding protein
6.6E-122	1.684	0.201	0.235	**0.707**	**0.846**	Putative uncharacterized protein RAB3GAP1
1.26E-70	0.777	0.718	0.625	**0.707**	**0.076**	Coiled-coil domain-containing protein 53
0	0.838	0.552	0.730	**0.707**	**0.145**	Collapsin response mediator protein 2
0	1.193	0.437	0.491	**0.707**	**0.422**	ATP-dependent RNA helicase p54
2.3E-219	1.111	0.702	0.310	**0.707**	**0.401**	Squamous cell carcinoma antigen recognized by T-cells 3
0	0.953	0.524	0.647	**0.708**	**0.221**	51 kDa FK506-binding protein
1.18E-70	0.759	0.659		**0.709**	**0.071**	cDNA FLJ60533, highly similar to Kinesin-like protein KIF3A
4.8E-225	0.703	0.715		**0.709**	**0.009**	Threonine--tRNA ligase
0.00608	0.479	0.943		**0.711**	**0.328**	CD151 antigen

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.3E-106	0.682	0.730	0.724	**0.712**	**0.026**	CD49 antigen-like family member C
4.51E-30	0.443	0.981		**0.712**	**0.380**	Autocrine motility factor receptor, isoform 2
5.3E-14	0.734	0.691		**0.713**	**0.030**	Enaptin
3.6E-216	0.895	0.756	0.488	**0.713**	**0.207**	61E3.4
2.3E-240	0.782	0.693	0.671	**0.715**	**0.059**	cDNA FLJ55574, highly similar to Calnexin
2.3E-258	0.443	0.533	1.171	**0.716**	**0.397**	Protein slit-like 2
8.1E-207	0.736	0.639	0.773	**0.716**	**0.069**	Putative uncharacterized protein EIF3D
7.7E-112	0.648	0.361	1.143	**0.717**	**0.395**	Ankyrin repeat domain-containing protein 17
1.2E-152	1.377	0.599	0.177	**0.718**	**0.609**	Pre-mRNA-processing factor 6
1.2E-267	0.778	0.753	0.626	**0.719**	**0.082**	BAG family molecular chaperone regulator 2
1.6E-113	1.007	0.394	0.760	**0.720**	**0.309**	Translin-associated factor X
7.1E-72	0.344	1.265	0.553	**0.721**	**0.483**	E2-EPF
1.18E-09	0.360		1.082	**0.721**	**0.511**	highly similar to Solute carrier family 2, facilitated glucosetransporter member 14
1.83E-31	0.944	0.142	1.078	**0.721**	**0.506**	CTTNBP2 N-terminal-like protein
6.9E-156	0.608	0.904	0.654	**0.722**	**0.159**	Baboon M7 virus receptor
5.9E-73	0.590	0.888	0.689	**0.722**	**0.152**	Histone H1x
3.56E-38	0.765	0.717	0.690	**0.724**	**0.038**	Mitochondrial distribution and morphology protein 20
2.79E-84	0.442	1.008		**0.725**	**0.400**	DDRGK domain-containing protein 1
7.7E-125	0.862		0.588	**0.725**	**0.194**	Cadherin-associated Src substrate
2.87E-10	0.209	0.697	1.272	**0.726**	**0.532**	Activating signal cointegrator 1 complex subunit 2
0	1.351	0.460	0.369	**0.727**	**0.542**	600 kDa retinoblastoma protein-associated factor
5.1E-51	0.949	0.804	0.427	**0.727**	**0.269**	Chloride channel CLIC-like protein 1
1.42E-74	0.723	0.758	0.704	**0.728**	**0.027**	ZW10 interactor
4.66E-59	1.144	0.679	0.364	**0.729**	**0.392**	Poly(A) polymerase alpha
2.85E-78	1.014	0.458	0.717	**0.730**	**0.278**	His domain-containing protein tyrosine phosphatase
5.05E-47	0.448	0.849	0.894	**0.730**	**0.246**	28S ribosomal protein S13, mitochondrial
1.64E-41	0.687		0.774	**0.731**	**0.062**	Histone H3-K4 methyltransferase SETD7
1.2E-109	0.769	0.728	0.695	**0.731**	**0.037**	Lysyl hydroxylase 3
2.32E-44	1.037	0.887	0.269	**0.731**	**0.407**	cDNA FLJ54528, highly similar to Serine/threonine-protein kinase MST4 (EC 2.7.11.1)
3.08E-14	0.872	0.591		**0.731**	**0.199**	Platelet Sec1 protein
1.7E-137	0.439	0.990	0.766	**0.732**	**0.277**	5T4 oncofetal antigen
1.39E-88	0.754	0.927	0.514	**0.732**	**0.208**	Ephrin type-A receptor 2
9.1E-119	0.896	0.574	0.726	**0.732**	**0.161**	Aldoketomutase
2.3E-27	0.659	0.780	0.760	**0.733**	**0.065**	Cytokine suppressive anti-inflammatory drug-

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
						binding protein
5.42E-11	0.914	0.240	1.045	**0.733**	**0.432**	Serine/threonine-protein phosphatase
1.72E-08	0.798	0.671	0.734	**0.734**	**0.064**	ADP-ribosylation factor-like protein 6-interacting protein 1
2.63E-98	0.871	0.678	0.656	**0.735**	**0.118**	Natural killer cell-enhancing factor B
0	0.653	0.668	0.886	**0.736**	**0.130**	highly similar to Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA
2.67E-94	0.622	0.760	0.829	**0.737**	**0.105**	highly similar to Homo sapiens cysteinyl-tRNA synthetase (CARS), transcript variant 3, mRNA
2.58E-33	1.070	0.783	0.359	**0.737**	**0.358**	E2-induced gene 5 protein
8.19E-55	1.255	0.518	0.441	**0.738**	**0.449**	5'-AMP-activated protein kinase catalytic subunit alpha-1
0	1.095	0.488	0.637	**0.740**	**0.316**	Myosin phosphatase-targeting subunit 1
1E-122	0.633	0.724	0.863	**0.740**	**0.116**	Phosphoserine aminotransferase
6.02E-20	0.446	1.034		**0.740**	**0.416**	Heat shock 70 kDa protein 14
8.7E-104	0.715	0.763	0.742	**0.740**	**0.024**	Vasodilator-stimulated phosphoprotein
7.5E-148	0.906	0.695	0.621	**0.741**	**0.148**	18 kDa Alu RNA-binding protein
2.6E-274	0.896	0.586		**0.741**	**0.219**	Kinesin light chain 1
0	0.855	0.628	0.741	**0.741**	**0.114**	Conventional kinesin heavy chain
1.19E-10	0.986	0.886	0.352	**0.741**	**0.341**	Charged multivesicular body protein 1a
0	0.876	0.677	0.677	**0.743**	**0.115**	D-3-phosphoglycerate dehydrogenase
0	1.064	0.574	0.591	**0.743**	**0.278**	Alpha-tropomyosin
1.73E-07	1.892	0.212	0.127	**0.743**	**0.995**	CD9 partner 1
1.92E-96	1.317	0.275	0.644	**0.745**	**0.528**	E6AP ubiquitin-protein ligase
9.78E-61	0.948		0.543	**0.746**	**0.287**	Switch-associated protein 70
2.24E-11	1.155	0.249	0.834	**0.746**	**0.459**	Interferon regulatory factor 2-binding protein 1
9.08E-43	1.076	0.735	0.428	**0.746**	**0.324**	Protein SKD2
2.6E-81	0.920	0.276	1.044	**0.746**	**0.413**	E3 ligase for inhibin receptor
2.8E-143	1.379	0.343	0.519	**0.747**	**0.554**	cDNA FLJ51091, highly similar to 65 kDa Yes-associated protein
9.82E-34	0.831	0.740	0.674	**0.748**	**0.079**	ATP synthase subunit delta, mitochondrial
2.04E-91	0.858	0.632	0.757	**0.749**	**0.113**	5-methyltetrahydrofolate--homocysteine methyltransferase
0	0.848	0.740	0.658	**0.749**	**0.095**	Calcium pump 2
1.93E-80	1.030	0.665	0.554	**0.750**	**0.249**	Deoxyhypusine dioxygenase
5.8E-126	1.141	0.362		**0.751**	**0.550**	GTPase-activating protein RAB7
7.9E-102	1.740	0.306	0.209	**0.752**	**0.857**	Epidermal growth factor receptor substrate 15
1.24E-09	0.661	0.844		**0.752**	**0.130**	RNA pseudouridylate synthase domain-containing protein 2

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	0.599	0.475	1.185	**0.753**	**0.379**	DEAD box polypeptide 17 isoform p82 variant
0	1.021	0.626	0.614	**0.754**	**0.231**	Dystrophin-related protein 1
0	0.996	0.805	0.460	**0.754**	**0.272**	UDP-glucose 6-dehydrogenase
1.12E-70	0.857	0.775	0.631	**0.754**	**0.114**	ATP-binding protein associated with cell differentiation
7.73E-21	1.163	0.346		**0.754**	**0.577**	HECT domain and RCC1-like domain-containing protein 2
2.3E-169	0.891	0.605	0.773	**0.756**	**0.144**	EBI3-associated protein of 60 kDa
1.39E-34	1.542	0.351	0.380	**0.757**	**0.679**	Parathymosin
8.31E-09	0.314	1.202		**0.758**	**0.628**	Nestin
0	1.296	0.474	0.505	**0.758**	**0.466**	Beta-hexosaminidase
2.97E-22	0.482		1.037	**0.759**	**0.392**	28S ribosomal protein S30, mitochondrial
0	0.590	0.930		**0.760**	**0.241**	Double-stranded RNA-binding protein 76
1.76E-58	1.105	0.439	0.737	**0.760**	**0.334**	Guanine nucleotide exchange factor VAV2
1.1E-198	0.759	0.180	1.342	**0.760**	**0.581**	Synapse-associated protein 1
0	0.844	0.776	0.663	**0.761**	**0.092**	Placental ribonuclease inhibitor
7.3E-210	0.784	0.777	0.725	**0.762**	**0.032**	Pyrroline-5-carboxylate reductase
4.3E-102	1.265	0.530	0.490	**0.762**	**0.436**	Huntingtin-interacting protein 1
3.94E-12	0.961	0.306	1.019	**0.762**	**0.396**	Probable transcription factor PML
1.06E-87	0.830	0.672	0.787	**0.763**	**0.082**	Protein bicaudal D homolog 2
7.67E-08	0.432	0.824	1.035	**0.763**	**0.306**	N(2),N(2)-dimethylguanosine tRNA methyltransferase
0	1.253	0.700	0.340	**0.765**	**0.460**	highly similar to Homo sapiens phosphoribosylformylglycinamidine synthase (PFAS), mRNA
1.92E-22	0.964	0.566		**0.765**	**0.282**	Ras-related protein Rab-22B
0.002445	0.718	0.546	1.031	**0.765**	**0.246**	Geranylgeranyl transferase type II subunit beta
1.04E-21	1.276	0.412	0.608	**0.765**	**0.453**	Leucine zipper and CTNNBIP1 domain-containing protein
3.77E-86	0.836	0.689	0.771	**0.766**	**0.074**	Long chain base biosynthesis protein 1
4.6E-301	0.902	0.715	0.682	**0.766**	**0.119**	eIF3 p110
1.94E-98	0.535	0.226	1.541	**0.767**	**0.688**	Cdc42-interacting protein 4
1.04E-05	0.482	0.979	0.840	**0.767**	**0.257**	Endopeptidase SP18
2.2E-188	0.674	1.105	0.524	**0.768**	**0.302**	Protein APMCF1
2.4E-51	1.091	0.446		**0.768**	**0.456**	Pentatricopeptide repeat-containing protein 3, mitochondrial
3.97E-05	0.839	0.663	0.805	**0.769**	**0.094**	Beta-G1
5.7E-190	1.228	0.519	0.563	**0.770**	**0.397**	NudC domain-containing protein 2
9.25E-51	1.379	0.409	0.524	**0.770**	**0.530**	Sorting nexin-12
1.6E-161	1.007	0.765	0.540	**0.771**	**0.234**	6-phosphogluconolactonase

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
5.4E-226	0.416		1.126	**0.771**	**0.502**	Nodal modulator 2
0	0.784	0.805	0.728	**0.772**	**0.040**	Radixin isoform b
0	0.868	0.680	0.771	**0.773**	**0.094**	Alpha-soluble NSF attachment protein
5.77E-22	0.421	1.111	0.788	**0.773**	**0.345**	cDNA FLJ52061, highly similar to Translocon-associated protein subunit gamma
6.4E-127	1.055	0.594	0.672	**0.773**	**0.247**	Golgi phosphoprotein 6
8.06E-40	1.141	0.879	0.303	**0.774**	**0.429**	LIM domain-containing preferred translocation partner in lipoma
3.14E-22	0.790	0.716	0.818	**0.775**	**0.052**	Adenosine diphosphoribose pyrophosphatase
2.54E-71	0.996	0.636	0.693	**0.775**	**0.194**	Membrane-associated progesterone receptor component 2
1E-189	0.659	0.842	0.825	**0.775**	**0.101**	Eukaryotic translation initiation factor 2 subunit 1
1.5E-117	1.018	0.199	1.111	**0.776**	**0.502**	Cell proliferation-inducing gene 53 protein
7.41E-46	0.615	0.338	1.373	**0.776**	**0.536**	E3 ubiquitin-protein ligase NEDD4-like
2.72E-21	0.815	0.739		**0.777**	**0.054**	GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
2E-188	0.931	0.786	0.616	**0.778**	**0.157**	Chromosome-associated protein G
3.69E-91	1.048	0.583	0.705	**0.779**	**0.241**	Thymosin beta-10
0	0.804	0.686	0.848	**0.779**	**0.084**	Heat shock 84 kDa
8.3E-249	0.409	1.151		**0.780**	**0.525**	H/ACA ribonucleoprotein complex subunit 2
1.49E-29	0.964	0.652	0.725	**0.780**	**0.163**	Polyposis locus protein 1
2.3E-294	1.064	0.711	0.567	**0.781**	**0.255**	Tyrosyl--tRNA ligase
1.94E-70	0.866	0.737	0.739	**0.781**	**0.074**	Aspartate--tRNA ligase
9.85E-31	0.764		0.800	**0.782**	**0.025**	cDNA FLJ57067, highly similar to Beta-2-microglobulin
3.29E-93	0.733	1.042	0.571	**0.782**	**0.239**	PP2A B subunit isoform B56-epsilon
3.08E-43	0.799	0.706	0.842	**0.782**	**0.070**	Peptidyl-prolyl cis-trans isomerase-like 1
8.6E-38	1.061	0.504		**0.782**	**0.394**	Kinesin-like protein KIF13A
1.96E-10	0.708	0.857		**0.782**	**0.105**	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B
9.63E-58	0.823	0.893	0.634	**0.783**	**0.134**	Endopeptidase Clp
0	0.684	0.811	0.855	**0.783**	**0.088**	Coronin-1C_i2 protein
8E-238	0.954	0.632	0.766	**0.784**	**0.162**	cDNA FLJ50710, highly similar to Phosphoenolpyruvate carboxykinase (GTP), mitochondrial (EC 4.1.1.32)
1.34E-98	1.310	0.388	0.655	**0.784**	**0.474**	Putative uncharacterized protein DKFZp686C1054
3.53E-13	0.617	0.992	0.744	**0.785**	**0.191**	Cytochrome c oxidase polypeptide IV
1.05E-07	0.714	0.857		**0.786**	**0.101**	Protein jagunal homolog 1
6E-102	0.597	0.913	0.848	**0.786**	**0.167**	ATP synthase subunit d, mitochondrial
7.82E-80	0.636	0.835	0.890	**0.787**	**0.133**	Glutathione S-transferase kappa 1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.99E-37	1.643	0.326	0.393	**0.787**	**0.742**	Soluble 29 kDa NSF attachment protein
7.22E-14	0.433	0.271	1.658	**0.787**	**0.758**	JmjC domain-containing histone demethylation protein 2B
9.6E-23	0.815	1.162	0.385	**0.788**	**0.389**	Phosphatidylinositol 4-kinase alpha
5.64E-28	1.100	0.416	0.848	**0.788**	**0.346**	Mitochondrial import inner membrane translocase subunit TIM44
9.9E-115	0.880	0.753	0.732	**0.789**	**0.080**	Nectin-like protein 5
0	0.777	0.459	1.134	**0.790**	**0.338**	cDNA FLJ50617, highly similar to Tubulin beta-7 chain
6.2E-274	0.595	1.039	0.739	**0.791**	**0.226**	DnaJ homolog subfamily A member 1
4.8E-24	0.840	0.744		**0.792**	**0.068**	Guanine insertion enzyme
1.43E-66	1.118	0.692	0.567	**0.792**	**0.289**	MAD1 mitotic arrest deficient-like 1 (Yeast)
9.96E-29	0.923	0.727	0.728	**0.793**	**0.113**	Ethylmalonic encephalopathy protein 1
8.4E-158	0.842	0.290	1.250	**0.794**	**0.482**	Protein NICE-4
0	0.717	0.789	0.884	**0.797**	**0.084**	eIF-4D
1.03E-34	0.709	0.750	0.931	**0.797**	**0.118**	Prefoldin subunit 1
4.1E-15	1.058	0.571	0.763	**0.797**	**0.245**	Alcohol dehydrogenase PAN2
2.5E-108	0.630	0.967		**0.799**	**0.238**	HLA class I histocompatibility antigen, B-15 alpha chain
3.9E-106	1.088	0.442	0.865	**0.799**	**0.328**	38 kDa FK506-binding protein
1.49E-30	0.563	1.258	0.577	**0.799**	**0.397**	Complex I-19kD
5.25E-48	0.298	1.192	0.909	**0.800**	**0.457**	Coiled-coil domain-containing protein 128
5.87E-85	0.760	0.979	0.661	**0.800**	**0.163**	Glycosyltransferase 25 family member 1
2.58E-56	0.989	0.907	0.506	**0.801**	**0.258**	Ribosome maturation protein SBDS
7.63E-24	1.237	0.733	0.432	**0.801**	**0.407**	Apopain
9.2E-21	0.704	0.174	1.525	**0.801**	**0.681**	highly similar to Homo sapiens 2'-5'-oligoadenylate synthetase 3, 100kDa (OAS3), mRNA
0	1.101	0.759	0.544	**0.801**	**0.281**	Glutamine amidotransferase
1.8E-298	0.510	0.930	0.964	**0.801**	**0.253**	40S ribosomal protein S27a
3E-169	0.639	1.026	0.740	**0.801**	**0.201**	Casein kinase I isoform alpha
1.6E-201	0.976	0.602	0.828	**0.802**	**0.189**	Tubulin beta-8 chain
0	1.400	0.295	0.711	**0.802**	**0.558**	ARF-binding protein 1
1.2E-196	0.941	0.781	0.685	**0.802**	**0.130**	ATP synthase subunit O, mitochondrial
3E-109	1.153	0.725	0.534	**0.804**	**0.317**	Schlafen family member 11
5.5E-41	0.763	0.845		**0.804**	**0.058**	Adenylate cyclase-stimulating G alpha protein
4.78E-94	1.404	0.584	0.427	**0.805**	**0.524**	Alanine--tRNA ligase
1.99E-40	0.975	0.703	0.739	**0.806**	**0.148**	High temperature requirement protein A2
5.67E-38	0.982		0.631	**0.807**	**0.249**	cDNA FLJ56558, highly similar to Homo sapiens secernin 2 (SCRN2), mRNA
1.6E-237	0.675	0.896	0.850	**0.807**	**0.117**	Cyclophilin B

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	1.263	0.766	0.392	**0.807**	**0.437**	Cervical mucin-associated protein
1.58E-18	0.696		0.920	**0.808**	**0.159**	PtdIns-4,5-P2 4-Ptase II
5.7E-87	0.842	0.775		**0.809**	**0.048**	C1 factor
2.1E-220	0.567	0.833	1.027	**0.809**	**0.231**	Seryl-tRNA synthetase
1.2E-290	0.706	0.887	0.835	**0.810**	**0.093**	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
2.79E-27	0.918	0.705		**0.811**	**0.151**	Cullin-2
2E-144	0.798	0.761	0.878	**0.812**	**0.060**	SH3 domain-binding glutamic acid-rich-like protein
1.34E-39	0.900	0.700	0.835	**0.812**	**0.102**	eIF-2B GDP-GTP exchange factor subunit alpha
9.4E-102	0.861	0.842	0.733	**0.812**	**0.069**	Importin-8
2.3E-125	0.846	0.833	0.758	**0.812**	**0.047**	Glycoprotein 25L2
3.2E-252	0.729	0.839	0.869	**0.812**	**0.073**	Protein C10
1.1E-162	1.191	0.320	0.927	**0.813**	**0.447**	Adenylyl cyclase-associated protein 2
7.63E-35	0.763	0.863		**0.813**	**0.071**	Protein ariadne-2 homolog
0	0.968	0.739	0.734	**0.813**	**0.134**	Lysyl hydroxylase 2
8.52E-27	0.643		0.984	**0.814**	**0.242**	39S ribosomal protein L39, mitochondrial
9E-269	1.235	0.512	0.695	**0.814**	**0.376**	Cellubrevin
0	1.291	0.582	0.569	**0.814**	**0.413**	Chondroitin sulfate proteoglycan 4
9.7E-157	0.913	0.675	0.855	**0.814**	**0.124**	MIR-interacting saposin-like protein
8.67E-91	0.417	1.212		**0.815**	**0.562**	Histone H1.1
3.6E-112	0.843	0.734	0.868	**0.815**	**0.071**	Cathepsin D
7.99E-45	0.957	0.956	0.534	**0.816**	**0.244**	ATP synthase subunit gamma, mitochondrial
4.08E-15	0.430	1.118	0.900	**0.816**	**0.351**	Solute carrier family 2 (Facilitated glucose transporter), member 1 variant
8.4E-105	0.525	0.955	0.971	**0.817**	**0.253**	Protein S100-A13
2.96E-57	0.515	0.947	0.989	**0.817**	**0.262**	Prosaposin
6.74E-07	0.426	1.119	0.907	**0.817**	**0.355**	Elongation of very long chain fatty acids protein 1
5.09E-42	0.728	1.337	0.388	**0.818**	**0.481**	Cytidine monophosphokinase 2
4.19E-12	0.511		1.125	**0.818**	**0.434**	Cyclin-H
1.17E-35	0.770	0.870	0.815	**0.818**	**0.050**	Golgi transport 1 homolog B
3.7E-120	0.927	0.724	0.805	**0.819**	**0.102**	Actin-related protein 2/3 complex subunit 5
2.48E-20	0.449	1.104	0.902	**0.819**	**0.335**	Uncharacterized protein KIAA0090
9.6E-128	0.728	1.456	0.271	**0.819**	**0.598**	Importin subunit alpha-1
1.82E-15	0.814	0.969	0.673	**0.819**	**0.148**	N-alpha-acetyltransferase 10, NatA catalytic subunit
6.67E-98	0.961	0.802	0.693	**0.819**	**0.135**	Replication factor A protein 2
1.46E-13	0.793		0.845	**0.819**	**0.036**	Cerebroside sulfate activator protein
1.92E-22	0.672	0.904	0.881	**0.819**	**0.128**	Protein disulfide-isomerase TMX3

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
4.6E-261	1.326	0.808	0.325	**0.820**	**0.501**	Cytoskeleton-associated protein 1
5.55E-19	0.867	0.583	1.009	**0.820**	**0.217**	Ubiquitin-associated protein 2
4.8E-91	0.797	0.759	0.905	**0.820**	**0.076**	DTDP-4-keto-6-deoxy-D-glucose 4-reductase
3.1E-224	0.629	0.610	1.222	**0.821**	**0.348**	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3
0	0.636	0.955	0.872	**0.821**	**0.166**	Fibronectin receptor subunit beta
7.72E-08	0.886	0.850	0.728	**0.821**	**0.082**	Vacuolar protein sorting-associated protein 45
4.54E-07	0.695	0.948		**0.821**	**0.179**	Mediator complex subunit 20
6.02E-76	0.737	0.599	1.129	**0.822**	**0.275**	Enigma homolog
6.26E-25	0.707	0.938		**0.823**	**0.163**	RNA 3'-terminal phosphate cyclase
3.62E-90	0.985	0.669	0.814	**0.823**	**0.158**	FKBP1A protein
8.15E-84	0.979	0.658	0.831	**0.823**	**0.161**	Putative uncharacterized protein NAPRT1
2.9E-134	0.624	0.918	0.929	**0.824**	**0.173**	Eukaryotic translation initiation factor 2 subunit 3
1E-143	0.998	0.909	0.565	**0.824**	**0.229**	Chronic myelogenous leukemia tumor antigen 66
1.06E-14	0.640	1.009		**0.824**	**0.261**	Vacuolar protein sorting-associated protein 33A
2.76E-93	0.926	0.766	0.781	**0.825**	**0.088**	ELKS/Rab6-interacting/CAST family member 1
2.5E-108	0.659	1.011	0.807	**0.825**	**0.177**	TGN38 homolog
1.3E-121	1.651	0.348	0.478	**0.825**	**0.718**	51 kDa FK506-binding protein
9.8E-210	1.224	0.797	0.457	**0.826**	**0.384**	Arsenic-transactivated protein
2.4E-82	1.322	0.716	0.441	**0.826**	**0.451**	Brain protein 16
1.66E-40	0.939	0.806	0.733	**0.826**	**0.104**	DNA replication complex GINS protein SLD5
5.97E-84	0.832	0.829	0.819	**0.827**	**0.007**	B-cell receptor-associated protein 31, isoform CRA_b
8E-117	0.830	1.149	0.504	**0.828**	**0.322**	Pyrroline-5-carboxylate reductase 2
0	0.558	0.337	1.590	**0.828**	**0.669**	DEAD box protein 5
9.4E-141	1.170	0.682	0.635	**0.829**	**0.296**	GAP and centrosome-associated protein
0	0.760	0.809	0.919	**0.829**	**0.081**	Actin-interacting protein 1
2.4E-223	0.657	0.875	0.956	**0.829**	**0.155**	Ras-related protein Rab-7a
1.72E-79	1.063	0.791	0.635	**0.830**	**0.217**	Differentiation-related gene 1 protein
2.8E-156	0.887	1.002	0.601	**0.830**	**0.206**	C-2K
1.2E-165	1.193	0.766	0.532	**0.830**	**0.335**	26S proteasome non-ATPase regulatory subunit 9
5E-118	1.004	0.772	0.717	**0.831**	**0.152**	26S proteasome non-ATPase regulatory subunit 11
1.88E-59	0.815	1.005	0.674	**0.831**	**0.166**	Ornithine aminotransferase, hepatic form
9.63E-57	0.672	1.266	0.555	**0.831**	**0.381**	Cleavage and polyadenylation specificity factor 25 kDa subunit
6.3E-106	0.807	0.877	0.812	**0.832**	**0.039**	Steroid receptor RNA activator 1
0	0.904	0.745	0.850	**0.833**	**0.081**	Cytosol aminopeptidase
3.1E-147	0.673	0.796	1.030	**0.833**	**0.181**	C-Myc-binding protein Mm-1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	1.080	0.731	0.689	**0.833**	**0.215**	94 kDa glucose-regulated protein
1.11E-95	1.029	0.740	0.731	**0.833**	**0.169**	cDNA FLJ59210, highly similar to Tubulin-specific chaperone E
2.6E-30	0.835	0.668	0.998	**0.834**	**0.165**	Cbl-interacting protein p70
2.7E-113	1.447	0.524	0.531	**0.834**	**0.531**	Ubiquitin conjugation factor E4 A
0.001432	0.658		1.011	**0.835**	**0.250**	eIF4E-like protein 4E-LP
2.6E-134	1.199	0.446	0.861	**0.835**	**0.377**	Epithelial protein lost in neoplasm
6.73E-49	0.774	0.885	0.847	**0.835**	**0.056**	39S ribosomal protein L15, mitochondrial
1.4E-121	0.939	0.577	0.992	**0.836**	**0.226**	La ribonucleoprotein domain family member 1
3.68E-83	1.136	0.573	0.799	**0.836**	**0.283**	60S ribosomal protein L23a
0	1.142	0.310	1.056	**0.836**	**0.458**	Chromosome condensation-related SMC-associated protein 1
4.5E-199	0.589	0.821	1.101	**0.837**	**0.256**	Cell division control protein 2 homolog
5.85E-10	0.867	0.808		**0.837**	**0.041**	39S ribosomal protein L21, mitochondrial
1.83E-84	0.949	0.752	0.813	**0.838**	**0.101**	COPII-associated small GTPase
9.3E-155	0.888	0.791	0.839	**0.839**	**0.049**	Endoplasmic reticulum resident protein 44
9.72E-38	0.658	1.012	0.850	**0.840**	**0.177**	14-3-3 protein sigma
5.3E-204	1.779	0.460	0.282	**0.840**	**0.818**	Eukaryotic translation initiation factor 4B
1.4E-141	1.078	0.698	0.748	**0.842**	**0.207**	EH domain-containing protein 4
2.75E-66	0.940	0.890	0.699	**0.843**	**0.127**	Pre-mRNA-splicing factor SYF1
0	0.847	0.854	0.832	**0.844**	**0.011**	ATP-dependent RNA helicase #46
7.17E-17	0.598	0.772	1.166	**0.845**	**0.291**	BMP2-induced 3-kb gene protein
3.23E-94	1.004	0.765	0.769	**0.846**	**0.137**	Coiled-coil domain-containing protein 58
2.21E-17	0.915	0.831	0.793	**0.846**	**0.063**	13 kDa FK506-binding protein
6.5E-271	0.727	1.036	0.776	**0.846**	**0.166**	22 kDa neuronal tissue-enriched acidic protein
4.91E-97	0.784	0.795	0.964	**0.848**	**0.101**	60S ribosomal protein L22
3.9E-119	0.891	0.887	0.767	**0.848**	**0.070**	WASH complex subunit 7
0	0.907	0.839	0.799	**0.848**	**0.055**	6-phosphofructokinase type C
0	0.756	0.777	1.013	**0.849**	**0.143**	Chromosome-associated protein E
0	1.153	0.779	0.615	**0.849**	**0.276**	Coatomer subunit gamma
0	1.193	0.659	0.695	**0.849**	**0.298**	TM30p1
5.05E-07	0.675	1.364	0.507	**0.849**	**0.454**	Protein RCC2
6E-155	1.044	0.635	0.869	**0.849**	**0.205**	Programmed cell death protein 5
1.11E-61	0.891	0.857	0.801	**0.850**	**0.046**	DNA replication complex GINS protein PSF1
0	0.931	0.780	0.840	**0.850**	**0.076**	78 kDa glucose-regulated protein
4.2E-271	0.795	0.867	0.888	**0.850**	**0.049**	highly similar to Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (PLOD), mRNA
5.5E-67	0.825	0.899	0.827	**0.850**	**0.042**	CDK5 activator-binding protein C53

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
6.22E-15	0.483		1.217	**0.850**	**0.519**	Adapter-related protein complex 3 mu-1 subunit
1.88E-47	1.108	0.719	0.724	**0.850**	**0.223**	Fumarylacetoacetate hydrolase domain containing 1
5.4E-108	0.498	1.149	0.908	**0.851**	**0.329**	Microsomal signal peptidase 25 kDa subunit
3.8E-191	0.758	0.913	0.883	**0.851**	**0.082**	65 kDa FK506-binding protein
6.9E-103	0.369	1.595	0.590	**0.851**	**0.653**	CML33
1.17E-93	0.895	0.950	0.710	**0.852**	**0.125**	Alpha-SGT
7.1E-103	0.694	0.868	0.993	**0.852**	**0.150**	Endopeptidase 24.15
8.12E-27	0.548	1.155		**0.852**	**0.429**	Adracalin
9.92E-38	1.456	0.461	0.642	**0.853**	**0.530**	1-acylglycerophosphocholine O-acyltransferase
1.53E-44	0.786	0.969	0.806	**0.854**	**0.100**	Protein mago nashi homolog 2
1.68E-79	0.997	0.957	0.608	**0.854**	**0.214**	hSGT2
7.73E-46	0.900	1.024	0.640	**0.855**	**0.196**	Merlin
3.7E-221	1.320	0.564	0.681	**0.855**	**0.407**	Cancer/testis antigen 89
1.41E-67	0.531	0.898	1.140	**0.856**	**0.307**	Glutathione peroxidase 4
5.6E-188	0.813	0.773	0.984	**0.857**	**0.112**	Trafficking protein particle complex subunit 6B
9.07E-66	1.316	0.665	0.590	**0.857**	**0.399**	Abhydrolase domain-containing protein 14B
1.07E-11	0.333	1.382		**0.858**	**0.742**	Cytochrome c oxidase polypeptide Vb
1.9E-185	0.664	0.986	0.925	**0.858**	**0.171**	40S ribosomal protein S28
1.5E-195	0.871	0.919	0.784	**0.858**	**0.068**	Prefoldin subunit 2
0	0.746	0.962	0.868	**0.858**	**0.108**	CD49 antigen-like family member E
2.2E-118	1.541	0.212	0.824	**0.859**	**0.665**	Protein transport protein Sec24B
5.49E-51	0.923	0.715	0.943	**0.860**	**0.126**	DUBA-5
3.9E-13	0.848	0.768	0.966	**0.860**	**0.100**	Toll-like receptor adapter molecule 2 (TICAM-2) (Putative NF-kappa-B- activating protein 502).
1.7E-199	0.786	0.805	0.991	**0.861**	**0.113**	Importin-9
2.63E-27	0.345	0.936	1.302	**0.861**	**0.483**	T-cell activation WD repeat-containing protein
1.68E-18	1.516	0.484	0.586	**0.862**	**0.568**	HH0048
0	0.761	0.850	0.976	**0.862**	**0.108**	58 kDa glucose-regulated protein
5.7E-123	1.192	0.792	0.603	**0.862**	**0.301**	Actin-depolymerizing factor
2.34E-67	0.594	1.200	0.793	**0.862**	**0.309**	Protein FAM96B
1.38E-42	0.948	0.789	0.851	**0.863**	**0.080**	LIM mineralization protein
7.67E-73	0.856	0.936	0.797	**0.863**	**0.070**	BLM-associated protein of 18 kDa
7.3E-177	0.898	0.824	0.869	**0.863**	**0.037**	Dihydropteridine reductase
9.42E-19	0.900	0.687	1.004	**0.864**	**0.162**	Cell division protein kinase 6
1.22E-65	0.374	1.354	0.863	**0.864**	**0.490**	Complex I-B8
0	0.867	0.058	1.667	**0.864**	**0.805**	Heterogeneous nuclear ribonucleoproteins A2/B1
4.23E-74	0.974	0.967	0.652	**0.864**	**0.184**	Cell migration-inducing gene 1 protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.99E-91	0.789	1.033	0.777	**0.866**	**0.145**	Activator 1 37 kDa subunit
5.79E-42	0.924	1.047	0.628	**0.866**	**0.215**	Adenylate kinase isoenzyme 6
6.1E-267	0.695	0.384	1.520	**0.867**	**0.587**	Cold shock domain-containing protein A
1.1E-245	0.913	0.812	0.881	**0.868**	**0.052**	Cytosolic malate dehydrogenase
1.8E-174	0.745	0.961	0.901	**0.869**	**0.111**	ATP synthase subunit b, mitochondrial
1.07E-87	0.701	0.955	0.955	**0.870**	**0.147**	ADP-ribosylation factor-like protein 1
5.03E-21	0.815		0.926	**0.871**	**0.079**	5'(3')-deoxyribonucleotidase, cytosolic type
5.4E-269	1.046	0.614	0.952	**0.871**	**0.227**	cDNA FLJ38560 fis, clone HCHON2003642, highly similar to Astrocytic phosphoprotein PEA-15
2.38E-60	0.686	0.948	0.979	**0.871**	**0.161**	BRO1 domain-containing protein BROX
0	1.232	0.854	0.527	**0.871**	**0.352**	CCT-delta
4.79E-28	0.752	0.609	1.256	**0.872**	**0.340**	Mitochondrial import inner membrane translocase subunit TIM50
2.97E-77	1.337	0.759	0.521	**0.872**	**0.419**	Huntingtin-interacting protein 12
1.02E-96	0.968	0.808	0.843	**0.873**	**0.084**	Putative uncharacterized protein SUMF2
1.7E-175	1.052	0.768	0.800	**0.873**	**0.156**	10 kDa chaperonin
8.6E-07	0.609		1.138	**0.874**	**0.374**	RRP9 homolog
3.39E-39	1.021	0.855	0.746	**0.874**	**0.138**	Vacuolar protein sorting-associated protein 53 homolog
4.33E-27	0.737	0.459	1.427	**0.874**	**0.498**	Uncharacterized protein KIAA0406
4.26E-09	0.584		1.166	**0.875**	**0.412**	DNA-directed RNA polymerase III subunit F
5.7E-138	0.779	0.944	0.903	**0.875**	**0.086**	Protein sel-1 homolog 1
3.03E-14	0.709	1.094	0.823	**0.875**	**0.197**	Neuroendocrine-specific protein-like 2
1.24E-46	0.707	1.044		**0.875**	**0.238**	3'-5' RNA exonuclease OLD35
1.58E-87	0.704	1.069	0.853	**0.876**	**0.184**	cDNA FLJ51909, highly similar to Serine-threonine kinase receptor-associatedprotein
2.23E-11	0.843	0.836	0.948	**0.876**	**0.063**	Transcription factor IIB
3.34E-08	0.850		0.904	**0.877**	**0.038**	Endoplasmic reticulum-Golgi intermediate compartment protein 1
9.6E-209	0.883	0.837	0.911	**0.877**	**0.037**	L-isoaspartyl protein carboxyl methyltransferase
6.02E-12	0.905	0.792	0.934	**0.877**	**0.075**	Kinetochore-associated protein 1
0	1.027	0.867	0.738	**0.877**	**0.145**	Importin-7
0	0.933	0.286	1.414	**0.877**	**0.566**	highly similar to Very-long-chain specific acyl-CoAdehydrogenase, mitochondrial (EC 1.3.99.-)
3.9E-180	0.606	0.980	1.048	**0.878**	**0.238**	Heat shock 70 kDa protein 6
6.58E-09	0.962	0.089	1.582	**0.878**	**0.750**	cDNA FLJ56056
4.7E-41	0.565	1.020	1.048	**0.878**	**0.271**	CAAX prenyl protease 1 homolog
1.84E-35	0.594	1.053	0.988	**0.878**	**0.248**	40S ribosomal protein S16
0	0.902	0.882	0.851	**0.878**	**0.025**	Chloride intracellular channel protein 4
2E-172	0.899	0.822	0.916	**0.879**	**0.050**	Small nuclear ribonucleoprotein Sm D2

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.9E-279	0.863	0.849	0.925	**0.879**	**0.040**	cDNA FLJ59702, highly similar to NADPH--cytochrome P450 reductase (EC 1.6.2.4)
1.5E-76	0.820	1.480	0.338	**0.879**	**0.573**	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
1.09E-72	0.850		0.908	**0.879**	**0.041**	214 kDa nucleoporin
4.84E-46	1.141	0.682	0.817	**0.880**	**0.236**	Adenylate kinase 3-like
6.1E-151	0.847	0.784	1.009	**0.880**	**0.116**	Hydroxymethylbilane synthase
6.62E-46	0.850		0.911	**0.880**	**0.043**	Calpain inhibitor
8.3E-144	1.041	0.770	0.831	**0.881**	**0.142**	Acetylcholinesterase-associated protein
4.6E-121	0.855	0.767	1.022	**0.881**	**0.129**	Exportin(tRNA)
0	1.036	0.856	0.752	**0.882**	**0.144**	Cyclin
0	1.000	0.980	0.666	**0.882**	**0.187**	ATP synthase subunit alpha, mitochondrial
6.61E-11	0.993	0.883	0.771	**0.883**	**0.111**	OMPdecase
1.6E-262	0.882	0.848	0.920	**0.883**	**0.036**	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
6.09E-70	1.655	0.836	0.158	**0.883**	**0.750**	Pyruvate carboxylase, mitochondrial
7.29E-60	1.345	0.650	0.660	**0.885**	**0.398**	cDNA, FLJ96508, Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), mRNA
1.37E-40	0.644	0.950	1.061	**0.885**	**0.216**	Carboxypeptidase A3
1.22E-23	0.635		1.135	**0.885**	**0.353**	Intramembrane protease 1
5.7E-113	0.916	0.963	0.777	**0.885**	**0.097**	F-box-like/WD repeat-containing protein TBL1XR1
9.14E-71	0.859	0.932	0.865	**0.885**	**0.040**	39S ribosomal protein L23, mitochondrial
7.84E-07	0.842	0.932		**0.887**	**0.064**	Choroideraemia protein
6.5E-125	0.981	0.339	1.342	**0.887**	**0.508**	Constitutive coactivator of PPAR-gamma-like protein 1
0	0.726	0.965	0.971	**0.887**	**0.140**	ATP synthase subunit beta, mitochondrial
2E-133	1.436	0.549	0.678	**0.887**	**0.479**	Oxysterol-binding protein 1
3.01E-36	0.832	1.058	0.777	**0.889**	**0.149**	cDNA FLJ53069, highly similar to AP-2 complex subunit mu-1
7.4E-120	1.013	0.830	0.824	**0.889**	**0.107**	Adenylosuccinate synthetase isozyme 2
6.8E-285	0.607	1.162	0.899	**0.889**	**0.277**	Cell cycle protein p38-2G4 homolog
0	0.910	0.315	1.443	**0.889**	**0.565**	Nucleoprotein TPR
3E-136	0.888	0.861	0.919	**0.889**	**0.029**	39S ribosomal protein L49, mitochondrial
4.4E-99	0.662		1.118	**0.890**	**0.323**	cDNA FLJ51188, highly similar to N-acetylglucosamine-6-sulfatase (EC3.1.6.14)
4.01E-69	0.980		0.800	**0.890**	**0.127**	Ras-related protein Rab-6A
2.55E-58	0.322	1.458		**0.890**	**0.803**	Nucleolar protein 56
1.06E-64	0.595		1.187	**0.891**	**0.419**	cDNA FLJ56825, highly similar to WD repeat protein 57
9.2E-126	0.736	0.961	0.975	**0.891**	**0.134**	GrpE protein homolog 1, mitochondrial
1.12E-87	0.819	1.054	0.800	**0.891**	**0.142**	DEAH box protein 30

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.72E-28	1.306	0.246	1.123	**0.892**	**0.566**	Mitsugumin-23
1.15E-60	0.635	1.039	1.006	**0.893**	**0.224**	Glutaminase-interacting protein 3
3.1E-224	0.806	1.082	0.796	**0.894**	**0.162**	Aging-associated gene 5 protein
4.33E-29	0.837	0.806	1.041	**0.895**	**0.128**	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 1 protein
3.34E-49	1.084	0.915	0.687	**0.895**	**0.199**	Exosome complex exonuclease RRP44
1.4E-265	0.992	0.571	1.123	**0.896**	**0.288**	cDNA FLJ59211, highly similar to Glucosidase 2 subunit beta
2.28E-47	1.026	0.815	0.846	**0.896**	**0.113**	39S ribosomal protein L43, mitochondrial
5.63E-45	1.223	0.874	0.597	**0.898**	**0.314**	DNA polymerase delta subunit 2
1.7E-106	0.619	0.998	1.078	**0.898**	**0.245**	APP secretase
3.7E-34	0.760	1.037		**0.898**	**0.196**	3-hydroxy-3-methylglutaryl coenzyme A synthase
1.28E-21	0.534	1.337	0.824	**0.898**	**0.407**	Interferon regulatory factor 2-binding protein 2
0	0.870	0.869	0.956	**0.898**	**0.050**	Gene associated with retinoic and interferon-induced mortality 12 protein
8.17E-37	0.765	1.341	0.589	**0.898**	**0.393**	Putative uncharacterized protein UFD1L
0	0.930	0.760	1.007	**0.899**	**0.127**	CCT-theta
0	1.285	0.717	0.697	**0.900**	**0.334**	Heat shock 70 kDa protein 4-like protein
1.86E-98	1.175	0.838	0.687	**0.900**	**0.250**	Non-specific lipid-transfer protein
1.58E-05	1.082	0.839	0.781	**0.901**	**0.159**	NRH dehydrogenase [quinone] 2
2.2E-110	0.924	0.851	0.927	**0.901**	**0.043**	cDNA FLJ60607, highly similar to Acyl-protein thioesterase 1 (EC 3.1.2.-)
4.3E-56	1.339	0.639	0.724	**0.901**	**0.382**	Nucleoplasmin-3
1.5E-102	1.262	0.770	0.671	**0.901**	**0.316**	3-methylcrotonyl-CoA carboxylase 2
0	1.145	0.862	0.697	**0.901**	**0.227**	Adapter-related protein complex 2 beta subunit
7.7E-222	0.910	0.863	0.930	**0.901**	**0.035**	Natural killer cell-enhancing factor A
0	0.924	0.849	0.931	**0.901**	**0.045**	26S proteasome non-ATPase regulatory subunit 1
1.8E-170	1.027	0.598	1.079	**0.902**	**0.264**	ABP125
1.01E-65	0.750	1.679	0.275	**0.902**	**0.714**	Another new gene 2 protein
1.02E-32	0.744	0.883	1.078	**0.902**	**0.168**	4'-phosphopantetheinyl transferase
6.86E-27	0.755		1.050	**0.902**	**0.209**	DNA-directed RNA polymerase II 33 kDa polypeptide
0	1.303	0.502		**0.903**	**0.567**	Golgin B1
1.21E-36	0.823	1.021	0.864	**0.903**	**0.104**	Aldehyde dehydrogenase 10
0	0.917	0.833	0.960	**0.903**	**0.064**	Anchorin CII
2.8E-229	1.013	0.806	0.890	**0.903**	**0.104**	Pyridoxal kinase
9.79E-51	0.777	0.991	0.943	**0.904**	**0.113**	Ras-related protein Rab-32
3.95E-45	0.974	0.883	0.854	**0.904**	**0.063**	CPI-B
4.06E-29	0.784	0.950	0.980	**0.905**	**0.105**	Phosphodeoxyriboaldolase

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
2.33E-06	0.320	1.489		**0.905**	**0.826**	Unhealthy ribosome biogenesis protein 2 homolog
0	0.908	0.861	0.945	**0.905**	**0.042**	14-3-3 protein zeta/delta
2.96E-62	0.958	0.914	0.843	**0.905**	**0.058**	Signal recognition particle 9 kDa protein
1.9E-227	0.867	0.987	0.861	**0.905**	**0.071**	21 kDa transmembrane-trafficking protein
2.06E-35	1.074	0.619	1.024	**0.906**	**0.250**	Nucleoporin 54kDa variant
3.32E-10	0.682	0.972	1.063	**0.906**	**0.199**	Basic fibroblast growth factor
1.22E-89	0.933	0.879		**0.906**	**0.039**	Acid beta-glucosidase
3.54E-05	1.024		0.788	**0.906**	**0.167**	F-box only protein 6
1.2E-99	0.687	1.066	0.966	**0.906**	**0.196**	Aldehyde dehydrogenase, mitochondrial
3.33E-47	0.681	1.123	0.915	**0.906**	**0.221**	Sodium/potassium-dependent ATPase subunit beta-3
5.9E-234	1.435	0.607	0.677	**0.906**	**0.459**	Dual specificity protein phosphatase 3
4.64E-08	0.436	1.137	1.147	**0.907**	**0.407**	Choline phosphatase 3
3.7E-256	1.126	0.762	0.835	**0.908**	**0.193**	Aldehyde dehydrogenase 5
1.1E-124	0.871	0.950	0.903	**0.908**	**0.040**	Methionine adenosyltransferase 2
8E-108	0.465	1.613	0.647	**0.908**	**0.617**	Putative uncharacterized protein RRM2
2.9E-207	0.612	1.267	0.846	**0.908**	**0.332**	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1
3.85E-74	1.412	0.632	0.682	**0.908**	**0.436**	Uncharacterized protein C8orf41
2.57E-33	0.728	1.152	0.845	**0.909**	**0.219**	DnaJ homolog subfamily C member 10
1.3E-158	1.212	0.658	0.856	**0.909**	**0.281**	Granzyme A-activated DNase
1.3E-32	0.368		1.451	**0.909**	**0.766**	Putative uncharacterized protein ABI1
1.1E-41	0.639	0.954	1.135	**0.909**	**0.251**	Putative uncharacterized protein SUMO1
1.12E-70	1.010	0.857	0.861	**0.909**	**0.087**	Prefoldin subunit 4
7.87E-84	1.528	0.776	0.425	**0.909**	**0.563**	Phosphatidylinositol 3-kinase 85 kDa regulatory subunit beta
1.04E-06	0.862	0.957		**0.909**	**0.067**	Putative uncharacterized protein
7.7E-17	0.299	1.520		**0.910**	**0.863**	Phosphatidylserine synthase 1
1.52E-29	0.794	1.145	0.791	**0.910**	**0.203**	Frequenin homolog
1.4E-98	1.029	0.830	0.873	**0.911**	**0.104**	Alcohol dehydrogenase [NADP+]
2.11E-20	0.799	0.990	0.943	**0.911**	**0.100**	Coproporphyrinogen-III oxidase, mitochondrial
1.7E-282	0.637	0.997	1.100	**0.911**	**0.243**	Moloney leukemia virus 10 protein
5.56E-52	0.070	1.753		**0.912**	**1.190**	Glutamate-rich WD repeat-containing protein 1
1.1E-161	0.777	0.847	1.113	**0.912**	**0.178**	Retinoic acid-induced gene B protein
0	0.845	0.869	1.024	**0.913**	**0.097**	Actin, cytoplasmic 2
4.6E-227	0.843	0.968	0.928	**0.913**	**0.064**	Complement component 1 Q subcomponent-binding protein, mitochondrial
0	0.919	1.057	0.766	**0.914**	**0.145**	Ras-related protein Rab-1B
0	0.568	0.983	1.193	**0.915**	**0.318**	Actin-binding protein 280

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.7E-170	1.058	0.773	0.914	**0.915**	**0.143**	Epidermal-type fatty acid-binding protein
7.8E-273	0.926	0.814	1.006	**0.915**	**0.096**	Acidic leucine-rich nuclear phosphoprotein 32 family member A
1.28E-41	0.566	1.286	0.895	**0.916**	**0.360**	Alveolar soft part sarcoma chromosomal region candidate gene 1 protein
1.3E-91	1.055	0.833	0.860	**0.916**	**0.121**	Deoxyhypusine synthase
0	0.976	1.044	0.729	**0.916**	**0.166**	Ras-related protein Rab-1A
0	1.179	0.959	0.611	**0.917**	**0.286**	CCT-eta
3.8E-215	1.067	1.103	0.580	**0.917**	**0.292**	NOL1/NOP2/Sun domain family member 2
3.25E-12	1.097	0.860	0.795	**0.917**	**0.159**	Aspartate--tRNA ligase
1E-120	0.843	0.991	0.920	**0.918**	**0.074**	Adapter protein GRB2
1.78E-47	0.494	1.343		**0.918**	**0.601**	Protein BUD31 homolog
9.83E-20	1.008		0.829	**0.919**	**0.126**	highly similar to Homo sapiens mitochondrial ribosomal protein L10 (MRPL10), mRNA
0	0.583	1.251	0.923	**0.919**	**0.334**	Glycine- and tyrosine-rich RNA-binding protein
5.6E-155	1.015	0.805	0.938	**0.919**	**0.106**	Glycosylation-inhibiting factor
7.88E-23	0.982	0.756	1.019	**0.919**	**0.142**	FK506-binding protein-associated protein
1.38E-77	1.628	0.736	0.395	**0.920**	**0.637**	DCS-1
1.3E-192	0.974	0.911	0.876	**0.920**	**0.049**	Calcyclin-binding protein
3.11E-69	0.953	0.855	0.954	**0.921**	**0.057**	Putative uncharacterized protein TCEB2
5.3E-124	0.819	0.983	0.961	**0.921**	**0.089**	Actin-related protein 2/3 complex subunit 3
1.36E-69	0.856	0.883	1.026	**0.922**	**0.091**	72 kDa ICln-binding protein
2.3E-104	0.463	1.081	1.223	**0.922**	**0.404**	14 kDa phosphohistidine phosphatase
2.3E-159	1.180	1.048	0.540	**0.923**	**0.338**	Glia maturation factor beta
5.2E-70	1.794	0.106	0.872	**0.924**	**0.845**	Cytoplasmic dynein 1 light intermediate chain 2
1.97E-55	0.631	0.321	1.825	**0.926**	**0.794**	Ran-binding protein 3
0	1.400	0.476	0.901	**0.926**	**0.462**	Calponin, acidic isoform
1.22E-24	0.565	1.039	1.173	**0.926**	**0.319**	mRNA turnover protein 4 homolog
0	0.865	0.930	0.984	**0.926**	**0.060**	LDH heart subunit
5.6E-158	0.813	0.946	1.021	**0.927**	**0.105**	Membrane-associated progesterone receptor component 1
1.2E-150	0.976	0.852	0.952	**0.927**	**0.066**	TCP1-chaperonin cofactor A
9.54E-46	1.114	0.816	0.851	**0.927**	**0.163**	Biogenesis of lysosome-related organelles complex 1 subunit 2
6.1E-118	0.702	1.031	1.050	**0.927**	**0.196**	eIF-3 p25
1.6E-103	1.321	0.644	0.817	**0.928**	**0.352**	EF-hand domain-containing protein D2
1.05E-13	0.879	0.159	1.745	**0.928**	**0.794**	RELA protein
3.98E-79	0.738	1.101	0.945	**0.928**	**0.182**	Protein raver-1
1.4E-112	0.729	1.022	1.032	**0.928**	**0.172**	Rho cDNA clone 12

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	0.995	0.881	0.909	**0.928**	**0.059**	Heat shock 70 kDa protein 4
1.9E-107	1.175	0.771	0.841	**0.929**	**0.216**	Prothymosin alpha
0	0.920	0.897	0.972	**0.929**	**0.039**	Glycine hydroxymethyltransferase
0	0.851	0.913	1.024	**0.929**	**0.087**	Chloride channel ABP
2.6E-173	1.169	0.789	0.831	**0.930**	**0.208**	Adenosine 5'-monophosphoramidase
2.24E-31	1.709	0.673	0.407	**0.930**	**0.688**	Pyrroline-5-carboxylate reductase 3
6.09E-14	0.790	1.101	0.899	**0.930**	**0.158**	40S ribosomal protein S30
8.58E-08	0.734		1.127	**0.930**	**0.278**	Major prion protein
8.92E-33	0.938	0.883	0.970	**0.930**	**0.044**	highly similar to Homo sapiens protein phosphatase 1A , magnesium-dependent, alpha isoform (PPM1A), mRNA
2.8E-101	1.210	0.737	0.844	**0.930**	**0.248**	U6 snRNA-associated Sm-like protein LSm5
3.67E-81	0.956	0.865	0.972	**0.931**	**0.058**	Putrescine aminopropyltransferase
3.9E-141	1.020	0.920	0.853	**0.931**	**0.084**	Putative uncharacterized protein ARPC4
4.99E-20	0.633	1.202	0.961	**0.932**	**0.286**	Nicalin
1.08E-82	0.935	1.033	0.828	**0.932**	**0.103**	GTP-binding protein smg p21B
2.09E-85	1.157	0.821	0.819	**0.932**	**0.194**	Acyl-CoA-binding protein
0	0.809	1.243	0.746	**0.933**	**0.271**	CDC21 homolog
3.1E-209	0.784	1.052	0.963	**0.933**	**0.137**	2'-5'-oligoadenylate-binding protein
1.8E-160	0.785	1.132	0.882	**0.933**	**0.179**	B(2)GCN homolog
2.1E-102	1.050	0.866	0.886	**0.934**	**0.101**	GTPase NRas
1.97E-96	0.784	1.145	0.873	**0.934**	**0.188**	Inhibitor of nuclear factor kappa-B kinase-interacting protein
0	0.753	0.994	1.057	**0.934**	**0.161**	Membrane-organizing extension spike protein
0	0.647	1.219	0.939	**0.935**	**0.286**	60S acidic ribosomal protein P2
5.8E-169	1.399	0.847	0.559	**0.935**	**0.427**	Isoleucine--tRNA ligase
2E-260	0.543	0.855	1.407	**0.935**	**0.438**	Protein phosphatase 1C catalytic subunit
2.35E-68	1.080	0.819	0.907	**0.935**	**0.133**	SRA stem-loop-interacting RNA-binding protein, mitochondrial
2E-294	0.851	0.994	0.962	**0.936**	**0.075**	Exportin-5
2.86E-25	0.843	1.365	0.599	**0.936**	**0.391**	Gamma-1-tubulin
0	1.125	0.813	0.869	**0.936**	**0.166**	Superoxide dismutase [Cu-Zn]
5.13E-88	1.104	0.924	0.780	**0.936**	**0.162**	Phosphoglycolate phosphatase
3.38E-63	0.416	1.449	0.945	**0.937**	**0.517**	2,4-dienoyl-CoA reductase [NADPH]
8.09E-78	0.494	1.341	0.975	**0.937**	**0.425**	60S ribosomal protein L13
0	0.519	1.290	1.001	**0.937**	**0.390**	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit
1.67E-48	0.607	1.118	1.086	**0.937**	**0.287**	40S ribosomal protein S6
0	1.057	0.990	0.764	**0.937**	**0.154**	Importin-4

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
8E-110	0.828	0.893	1.091	**0.937**	**0.137**	Vacuolar proton pump subunit D
4.9E-193	1.046	0.826	0.940	**0.937**	**0.110**	highly similar to 26S proteasome non-ATPase regulatory subunit 13
2.9E-155	1.192	0.819	0.801	**0.937**	**0.221**	Calcium-activated neutral proteinase 1
8.86E-74	1.071	0.844	0.897	**0.937**	**0.119**	Isochorismatase domain-containing protein 1
3.1E-171	0.872	0.901	1.039	**0.937**	**0.089**	Cullin-3
0	1.049	0.445	1.319	**0.937**	**0.448**	Bifunctional aminoacyl-tRNA synthetase
1.5E-272	0.736	1.082	0.995	**0.938**	**0.180**	40S ribosomal protein S17
0	0.954	0.915	0.944	**0.938**	**0.020**	Calregulin
4.6E-210	1.166	0.891	0.758	**0.938**	**0.208**	Ferritin light chain
3.13E-10	1.186	0.691		**0.938**	**0.350**	Codanin-1
4.47E-14	0.593	1.284		**0.938**	**0.489**	Uncharacterized protein KIAA2013
1.08E-24	0.739	1.003	1.074	**0.939**	**0.177**	PRPK-binding protein
7.7E-235	1.115	0.817	0.884	**0.939**	**0.156**	LETM1 and EF-hand domain-containing protein 1, mitochondrial
1.7E-40	0.936	0.926	0.956	**0.939**	**0.015**	39S ribosomal protein L17, mitochondrial
1.29E-05	0.993	0.917	0.911	**0.940**	**0.046**	Uncharacterized protein FLJ40176
0	1.239	0.776	0.805	**0.940**	**0.260**	Heat shock protein 75 kDa, mitochondrial
3.98E-18	0.807	0.980	1.035	**0.941**	**0.119**	ADP-ribosylation factor-like protein 6-interacting protein 2
8.7E-242	0.556	1.263	1.003	**0.941**	**0.358**	CD44 antigen
3.6E-181	1.034	0.910	0.879	**0.941**	**0.082**	FSCN1 protein
1.2E-217	1.103	0.767	0.954	**0.941**	**0.168**	Protein Hook homolog 3
4.3E-140	1.705	0.759	0.359	**0.941**	**0.691**	Sorting nexin-6
0.000133	1.004		0.880	**0.942**	**0.087**	Rab-like protein 5
9.05E-38	1.481	0.625	0.722	**0.943**	**0.469**	cDNA FLJ55586, highly similar to MMS19-like protein
3.3E-167	1.081	0.824	0.923	**0.943**	**0.129**	Copine I
4E-216	0.940	0.906	0.985	**0.944**	**0.039**	Protein phosphatase 1 regulatory subunit 22
6.2E-50	0.893	0.891	1.048	**0.944**	**0.090**	Calcium-binding protein BDR-1
2.05E-83	0.770	1.137	0.926	**0.944**	**0.184**	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog
0	1.092	0.821	0.922	**0.945**	**0.137**	ADP-ribosylation factor 4
6.93E-49	0.992	1.073	0.769	**0.945**	**0.158**	Charged multivesicular body protein 6
0	0.946	0.894	0.995	**0.945**	**0.051**	15-hydroxyprostaglandin dehydrogenase [NADP+]
5.76E-36	0.828	0.956	1.051	**0.945**	**0.112**	Macropain delta chain
0	0.959	0.838	1.039	**0.946**	**0.101**	Valyl-tRNA synthetase
0	1.037	0.892	0.909	**0.946**	**0.079**	Cell migration-inducing gene 10 protein
1.87E-93	0.654	1.178	1.005	**0.946**	**0.267**	Calcineurin B homolog

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
5.6E-209	0.351	1.037	1.450	**0.946**	**0.555**	Beta-actin-like protein 2
8.99E-31	0.985	0.887	0.966	**0.946**	**0.052**	Sorting nexin-27
4.16E-95	1.015	0.805	1.019	**0.946**	**0.122**	Cerebral cavernous malformations 3 protein
4.2E-101	0.908	0.895	1.036	**0.946**	**0.078**	Post-proline cleaving enzyme
1.35E-15	0.039	1.854		**0.947**	**1.283**	cDNA FLJ54188, moderately similar to High mobility group protein HMG-I/HMG-Y
4.66E-08	0.975	0.443	1.422	**0.947**	**0.490**	95 kDa retinoblastoma-associated protein
1E-135	0.910	0.918	1.012	**0.947**	**0.057**	CDC42 GTPase-activating protein
6E-48	0.788	0.968	1.086	**0.947**	**0.150**	GTP-binding protein Rheb
1.76E-36	1.072	0.898	0.872	**0.947**	**0.108**	Cytokine receptor-like factor 3
1.8E-185	1.217	0.776	0.848	**0.947**	**0.236**	Anthracycline-associated resistance ARX
1.35E-66	1.045	1.044	0.753	**0.947**	**0.168**	Syntaxin-7
1.76E-50	0.883	1.198	0.762	**0.948**	**0.225**	110 kDa cell membrane glycoprotein
7.82E-12	0.618	1.232	0.994	**0.948**	**0.309**	Adenosine 3'-phospho 5'-phosphosulfate transporter 1
4.88E-53	1.358	0.807	0.679	**0.948**	**0.361**	Cell growth-inhibiting gene 1 protein
7.03E-08	1.335	0.562		**0.949**	**0.546**	Protein LSM12 homolog
9E-274	0.936	0.868	1.045	**0.950**	**0.089**	Catalase
2.4E-177	1.084	0.805	0.963	**0.951**	**0.140**	Esterase D
3.5E-40	0.486	1.116	1.251	**0.951**	**0.408**	39S ribosomal protein L40, mitochondrial
4.7E-197	0.664	1.122	1.066	**0.951**	**0.250**	40S ribosomal protein S18
5.5E-153	0.662	1.066	1.125	**0.951**	**0.252**	Oxidative stress-responsive 1 protein
7.88E-33	1.392	0.694	0.768	**0.951**	**0.383**	Fructosamine-3-kinase-related protein
0	0.824	0.986	1.045	**0.951**	**0.114**	75 kDa glucose-regulated protein
3.31E-28	1.031		0.873	**0.952**	**0.112**	Carbohydrate kinase-like protein
0	0.899	1.009	0.948	**0.952**	**0.055**	Fumarate hydratase, mitochondrial
3.45E-40	0.718	1.212	0.927	**0.953**	**0.248**	Transmembrane and coiled-coil domain-containing protein 1
3.83E-69	1.073	0.841	0.947	**0.953**	**0.116**	Bleomycin hydrolase
0	1.140	0.834	0.889	**0.955**	**0.163**	2-phospho-D-glycerate hydro-lyase
9.68E-57	0.490	1.420		**0.955**	**0.657**	Inhibitor of nuclear factor kappa-B kinase-interacting protein
2.2E-192	1.202	0.717	0.947	**0.956**	**0.243**	Putative uncharacterized protein APEH
4.4E-12	1.918	0.587	0.362	**0.956**	**0.841**	Nuclear ubiquitous casein and cyclin-dependent kinases substrate
2.6E-189	0.858	0.913	1.097	**0.956**	**0.125**	SF3a120
0	1.006	0.901	0.960	**0.956**	**0.053**	cDNA FLJ54957, highly similar to Transketolase (EC 2.2.1.1)
5.3E-228	1.085	0.735	1.049	**0.956**	**0.192**	Brain-type aldolase
0	0.900	1.013		**0.956**	**0.080**	Ran-binding protein 1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.05E-11	0.533	1.039	1.300	**0.957**	**0.390**	DNA-directed RNA polymerase II 23 kDa polypeptide
7.96E-14	0.896	1.220	0.756	**0.957**	**0.238**	Vacuolar proton pump subunit C 1
4.84E-51	0.411	1.365	1.097	**0.958**	**0.492**	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
1.2E-75	0.619	1.329	0.927	**0.958**	**0.356**	Cytochrome c oxidase polypeptide Va
0	0.913	0.982	0.979	**0.958**	**0.039**	Heat shock 70 kDa protein 1/2
6.57E-30	0.848	0.948	1.080	**0.959**	**0.117**	Digestion substraction 1
2.2E-290	0.971	0.974	0.932	**0.959**	**0.024**	Actin-like protein 3
3.55E-30	0.749	1.048	1.082	**0.959**	**0.183**	Ras-related protein Rab-10
1.2E-196	0.913	0.936	1.030	**0.960**	**0.062**	Endoplasmic reticulum resident protein 28
6E-248	1.143	0.728	1.009	**0.960**	**0.212**	Mediator complex subunit 22
1.86E-49	0.421	1.051	1.409	**0.960**	**0.500**	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]
5.1E-182	0.658	1.196	1.028	**0.961**	**0.275**	40S ribosomal protein S19
0	0.461	0.379	2.043	**0.961**	**0.938**	Laminin B2 chain
3.84E-87	1.097	0.972	0.813	**0.961**	**0.142**	Nitrilase homolog 2
8.2E-119	1.207	0.765	0.912	**0.961**	**0.225**	AFB1 aldehyde reductase 1
3.43E-41	0.571	1.174	1.140	**0.961**	**0.339**	Nicastrin
1.8E-121	0.899	0.943	1.047	**0.963**	**0.076**	highly similar to Eukaryotic translation initiation factor 3 subunit 5
0	1.565	1.087	0.237	**0.963**	**0.672**	Proteasome-associated protein ECM29 homolog
4.9E-102	0.904	1.023		**0.963**	**0.084**	26S proteasome non-ATPase regulatory subunit 6
3.6E-125	0.896		1.031	**0.964**	**0.095**	cDNA FLJ51656, highly similar to Actin-like protein 2
1.7E-162	1.139	0.818	0.933	**0.964**	**0.163**	DDVit 1
4.39E-72	1.035	1.267	0.590	**0.964**	**0.344**	Adaptin ear-binding coat-associated protein 2
1.36E-68	0.624	1.219	1.049	**0.964**	**0.307**	60S ribosomal protein L36
1.4E-60	0.920	0.340	1.633	**0.964**	**0.648**	Deubiquitinating enzyme 15
2.33E-25	1.038		0.891	**0.964**	**0.104**	Coiled-coil domain-containing protein 5
0	0.976	0.915	1.004	**0.965**	**0.045**	Aldehyde dehydrogenase family 7 member A1
1.8E-104	0.500	1.431		**0.965**	**0.658**	NADH-ubiquinone oxidoreductase 75 kDa subunit
3.56E-19	0.513	1.419		**0.966**	**0.641**	BRAF35-HDAC complex protein BHC110
5.72E-31	1.680	0.478	0.739	**0.966**	**0.632**	Dyxin
1.1E-110	0.813	1.022	1.063	**0.966**	**0.134**	85 kDa lysosomal membrane sialoglycoprotein
2E-148	1.248	0.678	0.972	**0.966**	**0.285**	C-terminal LIM domain protein 1
2.1E-247	0.922	0.279	1.699	**0.966**	**0.711**	Protein kinase C and casein kinase substrate in neurons protein 2
9.2E-236	0.637	1.261	1.002	**0.967**	**0.313**	40S ribosomal protein S5
7.59E-66	0.950	0.953	0.997	**0.967**	**0.026**	Nori-2

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.1E-145	0.982	0.928	0.991	**0.967**	**0.034**	Adenosylhomocysteinase
8.65E-37	1.539	0.648	0.716	**0.968**	**0.496**	cDNA FLJ53329, highly similar to NADPH:adrenodoxin oxidoreductase, mitochondrial (EC 1.18.1.2)
0	0.953		0.983	**0.968**	**0.021**	14-3-3 protein beta/alpha
5.2E-106	1.003	0.925	0.976	**0.968**	**0.039**	Osteoclast-stimulating factor 1
5.9E-44	1.249	0.689		**0.969**	**0.396**	eIF-2B GDP-GTP exchange factor subunit epsilon
1.06E-87	0.712	1.137	1.058	**0.969**	**0.226**	Hexokinase type II
8.8E-136	0.773	1.210	0.925	**0.969**	**0.221**	Long-chain acyl-CoA synthetase 4
4.68E-11	0.646	1.293		**0.969**	**0.458**	Complex I-51kD
0	0.939	0.901	1.069	**0.970**	**0.088**	Guanosine diphosphate dissociation inhibitor 1
0	0.900	0.908	1.103	**0.970**	**0.115**	Actin, cytoplasmic 1
3.4E-184	1.223	0.897	0.791	**0.971**	**0.225**	SDHA protein
8E-129	1.176	0.779	0.957	**0.971**	**0.198**	DDAHII
1.3E-41	1.178	0.796	0.939	**0.971**	**0.193**	Cullin-5
9.78E-12	0.952	0.959	1.002	**0.971**	**0.027**	39S ribosomal protein L15, mitochondrial
1.2E-111	1.025	1.602	0.287	**0.971**	**0.659**	Charged multivesicular body protein 5
2.5E-112	0.848	1.109	0.956	**0.971**	**0.131**	Gastric cancer antigen Ga19
1.64E-74	0.679	1.084	1.151	**0.971**	**0.255**	Angio-associated, migratory cell protein, isoform CRA_a
2.07E-32	0.957	1.043	0.914	**0.971**	**0.065**	40 kDa erythrocyte membrane protein
1.45E-41	0.686	1.181	1.048	**0.971**	**0.256**	40S ribosomal protein S15a
1.12E-46	0.671	1.097	1.147	**0.972**	**0.261**	1-acylglycerophosphatidylinositol O-acyltransferase
9.3E-166	1.208	0.807	0.900	**0.972**	**0.210**	p120GAP
1.3E-278	1.018	0.900	0.997	**0.972**	**0.063**	1,4-alpha-glucan-branching enzyme
4.5E-58	1.194	0.810	0.912	**0.972**	**0.199**	RNA polymerase II-associated protein 1
2.68E-18	0.954	0.950	1.013	**0.972**	**0.035**	Hcp beta-lactamase-like protein C1orf163
6.2E-115	0.924	0.992	1.003	**0.973**	**0.043**	26S proteasome non-ATPase regulatory subunit 7
4.9E-100	0.941	0.988	0.989	**0.973**	**0.027**	Aldehyde dehydrogenase family 4 member A1
6.32E-66	1.023	1.064	0.834	**0.974**	**0.122**	60 kDa SS-A/Ro ribonucleoprotein
1.9E-151	1.109	0.809	1.003	**0.974**	**0.152**	SNARE-associated protein Snapin
5.7E-202	1.004	1.116	0.801	**0.974**	**0.160**	Ras GTPase-activating-like protein IQGAP3
0	1.011	0.994	0.917	**0.974**	**0.050**	Cullin-associated and neddylation-dissociated protein 1
0	0.897	0.938	1.088	**0.974**	**0.101**	Cellular thyroid hormone-binding protein
1.37E-18	0.863		1.086	**0.974**	**0.158**	Putative uncharacterized protein FNBP1L
7.42E-86	1.317	0.814	0.792	**0.974**	**0.297**	3'-phosphoadenosine-5'-phosphosulfate synthase
3.2E-245	0.870	1.090	0.963	**0.975**	**0.110**	49 kDa TATA box-binding protein-interacting

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
						protein
3.6E-200	1.097	0.867	0.962	**0.975**	**0.116**	Diaphorase-1
3.38E-40	1.103	0.848		**0.976**	**0.181**	GDP-mannose pyrophosphorylase B
1.85E-65	0.774	1.106	1.048	**0.976**	**0.177**	Calcium homeostasis endoplasmic reticulum protein
1.69E-46	0.915	1.011	1.002	**0.976**	**0.053**	Aldehyde dehydrogenase family 16 member A1
0	0.522	1.364	1.042	**0.976**	**0.425**	63 kDa membrane protein
4E-236	1.008	0.768	1.154	**0.977**	**0.195**	Hepatoma-derived growth factor
1.43E-76	1.510	0.583	0.837	**0.977**	**0.479**	Synaptosomal-associated protein 23
0	0.472	1.195	1.264	**0.977**	**0.439**	PWP1-interacting protein 17
2.87E-86	0.758	1.201	0.972	**0.977**	**0.222**	Protein FAM82B
0	0.796	0.715	1.421	**0.977**	**0.387**	Importin subunit alpha-7
6.12E-31	0.843	1.210	0.880	**0.977**	**0.202**	Antigen NY-CO-10
0	0.846	1.020	1.067	**0.977**	**0.116**	Alpha-actinin-4
2.29E-74	0.793	0.881	1.259	**0.977**	**0.247**	Cullin-1
1.15E-28	0.503	1.934	0.495	**0.977**	**0.828**	Tetratricopeptide repeat protein 35
0	0.996	0.934	1.003	**0.978**	**0.038**	Triosephosphate isomerase
1.48E-71	0.796	0.995	1.142	**0.978**	**0.174**	eIF3 p36
2.4E-146	0.995	0.941	0.998	**0.978**	**0.032**	HIBBJ46
3.1E-21	0.892	0.894	1.149	**0.978**	**0.148**	Prenylcysteine lyase
8.5E-109	1.289	0.804	0.843	**0.978**	**0.269**	BolA-like protein 2
1E-108	1.356	0.957	0.622	**0.979**	**0.368**	39S ribosomal protein L12, mitochondrial
2.13E-48	1.351	0.622	0.963	**0.979**	**0.365**	Hepatoma-derived growth factor 2
2.9E-106	0.732	1.139	1.065	**0.979**	**0.216**	40S ribosomal protein S25
5.85E-12	0.844	0.816	1.278	**0.979**	**0.259**	Gem-associated protein 7
1.98E-55	0.869	1.223	0.845	**0.979**	**0.212**	60S ribosomal protein L38
1.8E-121	0.718	1.174	1.047	**0.980**	**0.235**	40S ribosomal protein S21
3.1E-153	0.852	0.825	1.262	**0.980**	**0.245**	Aspartate beta-hydroxylase
5.04E-13	1.122	0.909	0.909	**0.980**	**0.123**	GDP-mannose pyrophosphorylase A
0	1.445	0.393	1.103	**0.980**	**0.537**	Golgi complex-associated protein of 170 kDa
1E-154	0.712	1.107	1.122	**0.981**	**0.232**	TRM112-like protein
7.91E-70	0.904	1.097	0.941	**0.981**	**0.103**	Polypeptide GalNAc transferase 2
0	0.759	1.044	1.139	**0.981**	**0.198**	Alpha E-catenin
3.41E-46	0.813	0.758	1.372	**0.981**	**0.340**	Ankyrin repeat domain-containing protein 13A
3.5E-44	1.211	0.857	0.878	**0.982**	**0.199**	LYR motif-containing protein 7
0	0.975	0.925	1.045	**0.982**	**0.061**	Annexin A4
1.7E-173	1.249	0.611	1.085	**0.982**	**0.331**	Female-lethal(2)D homolog

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.33E-76	0.523	1.418	1.005	**0.982**	**0.448**	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit
3.2E-116	0.938	0.968	1.041	**0.982**	**0.053**	Methyltransferase-like protein 11A
2.2E-128	0.674	1.124	1.150	**0.982**	**0.268**	40S ribosomal protein S2
4E-70	0.872	1.093		**0.983**	**0.156**	3'(2'),5'-bisphosphate nucleotidase 1
6.8E-116	1.095	0.894	0.959	**0.983**	**0.103**	Adenine phosphoribosyltransferase
4.8E-100	0.650	1.246	1.054	**0.983**	**0.304**	40S ribosomal protein S15
4.2E-119	1.022	0.953	0.977	**0.984**	**0.035**	26S proteasome non-ATPase regulatory subunit 12
1.9E-216	0.971	1.025	0.956	**0.984**	**0.036**	Vacuolar proton pump subunit G 1
1.66E-48	0.611	1.343	0.998	**0.984**	**0.366**	cDNA FLJ58953, highly similar to 40S ribosomal protein S20
7.6E-169	1.259	0.882	0.812	**0.984**	**0.240**	Argininosuccinate lyase
4.83E-53	1.076	0.963	0.915	**0.984**	**0.082**	PAF acetylhydrolase 29 kDa subunit
4.32E-79	1.141	1.353	0.459	**0.984**	**0.467**	GSPT1 protein
2.1E-107	0.738	1.146	1.069	**0.985**	**0.217**	Putative uncharacterized protein RAN
8.56E-24	0.989	1.096	0.870	**0.985**	**0.113**	28S ribosomal protein S11, mitochondrial
0	1.076	1.063	0.815	**0.985**	**0.147**	DNA mismatch repair protein Msh2
4.82E-15	1.190		0.780	**0.985**	**0.289**	Protein zwilch homolog
3.1E-279	0.910	0.973	1.072	**0.985**	**0.082**	Cytochrome c
2.7E-280	0.998	1.032	0.925	**0.985**	**0.054**	Elongin 15 kDa subunit
1.96E-37	1.288	0.678	0.990	**0.985**	**0.305**	Ubiquitin-protein ligase E3C
9.06E-79	0.739	1.191	1.026	**0.985**	**0.229**	Cytochrome b5 outer mitochondrial membrane isoform
0	1.453	0.995	0.509	**0.986**	**0.472**	Cofilin, muscle isoform
2.6E-128	0.692	1.115	1.150	**0.986**	**0.255**	Kinetochore protein Spc25
0	1.003	0.937	1.017	**0.986**	**0.043**	CapZ alpha-1
1.9E-207	0.879	1.012	1.067	**0.986**	**0.097**	COP9 signalosome complex subunit 7a
2.52E-94	1.019	0.861	1.079	**0.986**	**0.113**	Protein G7b
1.5E-52	0.871	1.156	0.931	**0.986**	**0.150**	Neuroplastin
9.79E-84	0.549	1.232	1.180	**0.987**	**0.380**	Parvulin-14
4.13E-78	0.963	1.408	0.590	**0.987**	**0.409**	39S ribosomal protein L46, mitochondrial
0	1.068	1.060	0.834	**0.987**	**0.133**	Antigen NY-CO-25
1.2E-213	1.095	0.936	0.935	**0.988**	**0.092**	Nucleoside diphosphate kinase
6.6E-231	1.169	0.877	0.919	**0.989**	**0.158**	HCNPpp
2.4E-107	1.052	0.975	0.940	**0.989**	**0.057**	Dimethylallyltranstransferase
6.07E-72	1.310	0.832	0.826	**0.989**	**0.278**	COMM domain-containing protein 9
1.9E-140	1.209	1.066	0.693	**0.989**	**0.266**	39S ribosomal protein L11, mitochondrial
6.35E-86	0.598	2.003	0.368	**0.989**	**0.885**	DAZ-associated protein 1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
8.6E-123	0.925	0.943	1.101	**0.990**	**0.097**	DnaJ homolog subfamily C member 3
9.2E-253	0.766	1.228	0.977	**0.990**	**0.231**	40S ribosomal protein S7
1.4E-107	1.018	0.983	0.971	**0.991**	**0.025**	Synaptic vesicle membrane protein VAT-1 homolog
2.26E-70	0.920	0.903	1.149	**0.991**	**0.138**	Actin-related protein 2/3 complex subunit 2
1.76E-11	0.991	0.992		**0.991**	**0.001**	Connectin
1.7E-154	0.952	0.979	1.046	**0.992**	**0.048**	Macropain subunit C5
9.28E-05	0.831	1.155		**0.993**	**0.229**	WD repeat-containing protein 65
0	0.508	1.350	1.123	**0.994**	**0.436**	40S ribosomal protein S3
9.3E-178	1.194	0.906	0.882	**0.994**	**0.174**	Apoptosis regulator BAX
1.81E-26	1.163	0.835	0.985	**0.994**	**0.164**	Lumenal domain-like LAP1
0	0.913	1.079	0.992	**0.995**	**0.083**	47 kDa mannose 6-phosphate receptor-binding protein
2.1E-300	1.096	0.869	1.019	**0.995**	**0.115**	Putative uncharacterized protein MATR3
3.7E-281	0.941	0.988	1.056	**0.995**	**0.058**	Myotrophin
1.3E-159	0.938	0.987	1.061	**0.995**	**0.062**	Adenylate kinase 1 variant
4.38E-08	0.722	1.475	0.789	**0.995**	**0.417**	F-box-like/WD repeat-containing protein TBL1X
1.54E-10	1.003	0.988		**0.996**	**0.010**	Uba6-specific E2 conjugating enzyme 1
1E-151	1.353	0.728	0.907	**0.996**	**0.322**	Coiled-coil domain-containing protein 22
2.57E-59	1.131	0.917	0.940	**0.996**	**0.118**	U2 small nuclear ribonucleoprotein B''
3.58E-83	0.916	0.981	1.092	**0.996**	**0.089**	Alpha-galactosidase B
2E-282	0.483	0.690	1.818	**0.997**	**0.718**	54 kDa nuclear RNA- and DNA-binding protein
1.2E-266	0.724	0.793	1.474	**0.997**	**0.415**	Acetolactate synthase-like protein
1.99E-50	0.753	1.028	1.211	**0.997**	**0.231**	Mob1 homolog 1A
7.65E-90	0.810	0.950	1.231	**0.997**	**0.215**	cDNA FLJ30470 fis, clone BRAWH1000040, highly similar to Rap1 GTPase-GDP dissociation stimulator 1
2.84E-15	0.988	1.344	0.660	**0.997**	**0.342**	Tetratricopeptide repeat protein 37
6.9E-235	0.845	1.092	1.056	**0.998**	**0.134**	Aspartate aminotransferase, cytoplasmic
3.58E-92	0.975	0.997	1.024	**0.998**	**0.024**	Protein ZYP
0	1.351	0.981	0.664	**0.999**	**0.343**	18 kDa phosphoprotein
8.8E-106	1.223	0.806	0.970	**0.999**	**0.210**	DNA fragmentation factor 45 kDa subunit
4.2E-254	1.218	0.860	0.922	**1.000**	**0.191**	cDNA FLJ56357, highly similar to Homo sapiens apolipoprotein A-I binding protein (APOA1BP), mRNA
1.73E-40	0.963	1.037		**1.000**	**0.052**	Galectin-related protein
2.02E-74	1.250	0.690	1.062	**1.000**	**0.285**	Golgi coiled-coil protein 1
3.3E-112	1.181	0.954	0.867	**1.001**	**0.162**	CapZ alpha-2
0	0.885	1.069	1.049	**1.001**	**0.101**	70 kDa subunit of Ku antigen

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.2E-204	1.728	0.243	1.032	**1.001**	**0.743**	Leukemia-associated phosphoprotein p18
1.66E-14	0.883	0.850	1.272	**1.002**	**0.235**	Phosphoribisomerase
1.69E-38	1.053	1.006	0.947	**1.002**	**0.053**	C-Src kinase
0	1.089	0.994	0.923	**1.002**	**0.083**	Glucose phosphomutase 2
3E-118	1.202	0.781	1.024	**1.002**	**0.212**	Cofactor of BRCA1
3.85E-19	0.235	1.312	1.460	**1.002**	**0.669**	DSH homolog 2
0	0.536	1.085	1.387	**1.002**	**0.431**	High density lipoprotein-binding protein
1E-235	1.004	0.500	1.504	**1.003**	**0.502**	cDNA FLJ59571, highly similar to Eukaryotic translation initiation factor 4gamma 2
2.1E-136	0.654	1.255	1.099	**1.003**	**0.312**	60S ribosomal protein L35
5.86E-59	0.923	1.010	1.079	**1.004**	**0.078**	Synaptobrevin homolog YKT6
1.49E-27	0.926	1.025	1.064	**1.005**	**0.071**	Alcohol dehydrogenase 5
2.4E-120	0.917	1.106	0.993	**1.005**	**0.095**	Carrier family 6, member 8 variant
0	0.955	0.950	1.114	**1.006**	**0.093**	Diadenosine tetraphosphate synthetase
3E-258	1.049	1.052	0.919	**1.006**	**0.076**	Nuclear protein localization protein 4 homolog
2.6E-240	0.998	0.292	1.731	**1.007**	**0.719**	cAMP-dependent protein kinase type II-alpha regulatory subunit
8.83E-96	0.681	1.182	1.161	**1.008**	**0.284**	40S ribosomal protein S14
9.4E-171	0.475	1.291	1.257	**1.008**	**0.461**	60S ribosomal protein L19
1.27E-31	1.321	0.806	0.898	**1.008**	**0.274**	Abhydrolase domain-containing protein 11
2.72E-84	1.530	0.698	0.797	**1.008**	**0.454**	Heme-binding protein 2
2.35E-72	0.833	1.184		**1.008**	**0.248**	Branched-chain-amino-acid aminotransferase
3.86E-95	0.653	1.379	0.994	**1.009**	**0.363**	Protein LUMA
1.42E-35	1.108	1.015	0.904	**1.009**	**0.102**	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial
0	0.954	1.013	1.060	**1.009**	**0.053**	Malate dehydrogenase, mitochondrial
6E-122	0.966	0.997	1.065	**1.009**	**0.051**	Replication factor A protein 3
9.3E-106	0.971	0.925	1.133	**1.010**	**0.109**	cDNA FLJ56307, highly similar to Ubiquitin thioesterase protein OTUB1 (EC 3.4.-.-)
0	1.038	1.058	0.934	**1.010**	**0.067**	Cellular apoptosis susceptibility protein
3.32E-44	0.674	1.317	1.038	**1.010**	**0.323**	Signal sequence receptor subunit delta
7.85E-18	1.142	0.849	1.039	**1.010**	**0.148**	Protein transport protein Sec61 subunit beta
2.26E-80	1.046	1.002	0.985	**1.011**	**0.032**	39S ribosomal protein L47, mitochondrial
2.27E-69	0.387	1.672	0.974	**1.011**	**0.643**	Complex I subunit B13
3.7E-143	1.255	0.802	0.976	**1.011**	**0.229**	Growth suppressor 1
0	0.998	0.977	1.059	**1.011**	**0.043**	Alpha-glucosidase 2
0	0.701	1.179	1.153	**1.011**	**0.269**	Elongation factor 1-alpha 1
8E-233	0.956	0.962	1.117	**1.012**	**0.091**	Endoplasmic reticulum resident protein 46
9.96E-10	0.984	1.116	0.936	**1.012**	**0.093**	L-3-phosphoserine phosphatase

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.5E-151	0.817	1.125	1.094	**1.012**	**0.170**	FAS-associated death domain protein
8.12E-69	1.141	0.898	1.000	**1.013**	**0.122**	UPF0587 protein C1orf123
8.35E-15	0.911	0.545	1.583	**1.013**	**0.526**	Adipocyte-derived leucine aminopeptidase
3.3E-262	1.511	0.712	0.816	**1.013**	**0.434**	Nicotinamide N-methyltransferase
1.32E-05	0.794	1.219	1.028	**1.013**	**0.213**	E3 ubiquitin-protein ligase LRSAM1
1.09E-18	0.996	1.069	0.976	**1.014**	**0.049**	ESCRT-I complex subunit TSG101
2.62E-24	0.591	1.580	0.871	**1.014**	**0.510**	Uncharacterized protein KIAA1797
7.8E-194	0.978		1.050	**1.014**	**0.051**	Putative uncharacterized protein TOR1AIP1
2.8E-219	0.940	1.020	1.083	**1.015**	**0.072**	COP9 signalosome complex subunit 3
1.63E-44	0.519	1.582	0.944	**1.015**	**0.535**	Complex III subunit 4
0	0.942	0.977	1.126	**1.015**	**0.098**	14-3-3 protein epsilon
6.36E-97	1.266	0.846	0.933	**1.015**	**0.221**	SF3a66
8.2E-120	0.784	1.312	0.949	**1.015**	**0.270**	56 kDa U2AF65-associated protein
0	1.017	1.003	1.024	**1.015**	**0.011**	Autocrine motility factor
0	1.247	1.073	0.725	**1.015**	**0.265**	PP2A subunit A isoform PR65-beta
1.1E-124	0.901	1.051	1.093	**1.015**	**0.101**	Citrate synthase, mitochondrial
2.6E-123	1.169	0.831	1.045	**1.015**	**0.171**	Cancerous inhibitor of PP2A
3.2E-228	0.992	0.945	1.108	**1.015**	**0.084**	Macropain subunit C9
2.01E-29	0.847	1.000	1.199	**1.015**	**0.177**	cDNA FLJ56327, highly similar to 26S proteasome non-ATPase regulatory subunit 8
2.6E-07	1.198		0.833	**1.015**	**0.258**	Secernin-2
2.9E-196	1.023	1.004	1.019	**1.015**	**0.010**	Glutamate dehydrogenase 1, mitochondrial
6.3E-261	0.960	1.151	0.937	**1.016**	**0.118**	U2 small nuclear ribonucleoprotein A'
0	0.883	1.121	1.044	**1.016**	**0.121**	155 kDa nucleoporin
1.37E-10	0.866	1.008	1.176	**1.017**	**0.155**	E217K
0	0.900	1.003	1.148	**1.017**	**0.125**	2-phospho-D-glycerate hydro-lyase
2.8E-125	0.789	1.303	0.959	**1.017**	**0.262**	Phenylalanine--tRNA ligase beta chain
3.9E-197	1.138	0.966	0.947	**1.017**	**0.105**	30 kDa prosomal protein
1.88E-45	0.727	0.973	1.352	**1.018**	**0.315**	Cell division protein kinase 2
8.2E-144	0.924	1.112		**1.018**	**0.133**	Pannexin-1
1.06E-76	1.240	1.060	0.754	**1.018**	**0.246**	ATP-binding cassette sub-family C member 1
1.44E-86	0.734	1.111	1.210	**1.018**	**0.251**	Intersex-like protein
1.85E-33	1.053	0.918	1.085	**1.019**	**0.088**	Cancer-associated Sm-like
1.75E-85	1.065	0.936	1.055	**1.019**	**0.072**	Macropain subunit C8
1.33E-22	1.214	0.990	0.852	**1.019**	**0.183**	Cartilage-associated protein
8.06E-13	0.914	1.160	0.982	**1.019**	**0.127**	Eukaryotic translation initiation factor 1A domain-containing protein
1E-102	0.862	1.066	1.128	**1.019**	**0.139**	Histidine--tRNA ligase

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.2E-227	0.852	1.212	0.992	**1.019**	**0.181**	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform
2.7E-302	1.051	0.967	1.039	**1.019**	**0.046**	Adenylate kinase 2, mitochondrial
0	0.901	1.026	1.132	**1.019**	**0.116**	AGX-1
2.23E-13	0.555	1.038	1.465	**1.019**	**0.455**	General transcription factor IIA subunit 1
2.2E-163	1.165		0.874	**1.020**	**0.205**	DNA polymerase
0	0.999	1.023	1.037	**1.020**	**0.019**	14-3-3 protein beta/alpha
2E-244	0.983		1.057	**1.020**	**0.052**	cDNA FLJ76436
9.6E-112	0.768	1.034	1.258	**1.020**	**0.245**	Cell immortalization-related protein 2
0	0.892	1.027	1.144	**1.021**	**0.126**	Importin subunit beta-1
0	1.009	1.109	0.944	**1.021**	**0.083**	26S proteasome non-ATPase regulatory subunit 2
1.55E-32	0.792	1.185	1.086	**1.021**	**0.204**	39S ribosomal protein L13, mitochondrial
5.6E-197	1.029	0.921	1.115	**1.021**	**0.097**	Heme-binding protein 1
0	0.975	1.033	1.056	**1.022**	**0.042**	cDNA FLJ75174, highly similar to Homo sapiens calmodulin 1 (phosphorylase kinase, delta), mRNA
1.3E-144	0.916	0.989	1.162	**1.022**	**0.126**	Protein transport protein Sec24A
6.8E-157	0.614	1.445	1.008	**1.022**	**0.415**	G protein subunit beta-2
8.36E-66	1.054	0.940	1.073	**1.022**	**0.072**	Proteasome chain 13
6.2E-147	1.209	1.158	0.701	**1.023**	**0.280**	Cytosolic NADP-isocitrate dehydrogenase
8.75E-13	0.764	0.932	1.374	**1.023**	**0.315**	Proteasome activator complex subunit 4
1.7E-166	0.840	1.012	1.218	**1.023**	**0.189**	Enhancer of rudimentary homolog
0	0.972	1.045	1.053	**1.023**	**0.044**	[Acyl-carrier-protein] S-acetyltransferase
1.7E-59	1.139	0.950	0.984	**1.024**	**0.101**	Profilin
1.7E-184	1.020	1.442	0.612	**1.025**	**0.415**	cDNA FLJ53276, moderately similar to DNA replication licensing factor MCM2
1.5E-169	1.052	1.015	1.008	**1.025**	**0.024**	Palmitoyl-protein thioesterase 1
7.9E-105	1.075	1.032	0.969	**1.025**	**0.053**	ATL-derived factor
6.79E-47	0.941	1.304	0.831	**1.025**	**0.248**	Guanine nucleotide-binding protein subunit alpha-13
2.83E-27	1.018	1.235	0.822	**1.025**	**0.207**	COP9 signalosome complex subunit 5
8.33E-64	0.680	1.161	1.235	**1.026**	**0.301**	Carnitine O-palmitoyltransferase 1, liver isoform
0	0.697	1.553	0.827	**1.026**	**0.461**	Fer-1-like protein 3
1.1E-196	1.001	0.989	1.089	**1.026**	**0.055**	Rho GDP-dissociation inhibitor 1
7.36E-11	1.294	0.759		**1.027**	**0.378**	Nitrilase homolog 1
3.8E-171	1.457	0.891	0.732	**1.027**	**0.381**	cDNA FLJ56840, highly similar to Galactokinase (EC 2.7.1.6)
0	1.006	0.972	1.104	**1.027**	**0.069**	14-3-3 protein tau
0	1.238	1.004	0.840	**1.027**	**0.200**	ABP-278
1.25E-19	0.605	1.232	1.249	**1.029**	**0.367**	Smu-1 suppressor of mec-8 and unc-52 protein homolog

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
4.16E-20	0.754	1.045	1.287	**1.029**	**0.267**	Calcium-binding protein 39
0	1.036	0.901	1.150	**1.029**	**0.125**	cDNA FLJ75085, highly similar to Homo sapiens glutaminyl-tRNA synthetase (QARS), mRNA
7.9E-38	0.876	0.927	1.284	**1.029**	**0.222**	Elongator complex protein 1
3.92E-77	1.299	1.013	0.777	**1.030**	**0.261**	COMM domain-containing protein 1
3.01E-29	0.859	1.023	1.207	**1.030**	**0.174**	28S ribosomal protein S7, mitochondrial
1.1E-157	1.103	1.001	0.988	**1.030**	**0.063**	DDAHI
7.6E-125	0.999	1.007	1.086	**1.031**	**0.048**	Inorganic pyrophosphatase
3.27E-63	1.359	0.703		**1.031**	**0.464**	Cat eye syndrome critical region protein 5
0	0.818	1.117	1.158	**1.031**	**0.186**	Heat shock 70 kDa protein 8
1.8E-167	1.012	0.992	1.090	**1.031**	**0.052**	tRNA (adenine-N(1)-)-methyltransferase catalytic subunit TRMT61A
2E-163	0.805	1.024	1.266	**1.031**	**0.231**	Regulator of G-protein signaling 10
6.71E-36	1.055	1.079	0.961	**1.032**	**0.063**	Activator 1 36 kDa subunit
1.2E-149	1.029	0.976	1.089	**1.032**	**0.057**	cDNA FLJ76855, highly similar to Homo sapiens exportin 7 (XPO7), mRNA
8.12E-28	0.921	0.979	1.195	**1.032**	**0.144**	Glycolipid transfer protein
2.05E-69	1.782	0.791	0.522	**1.032**	**0.663**	Serine racemase
5.38E-59	0.707	1.210	1.179	**1.032**	**0.282**	40S ribosomal protein S24
5.15E-32	0.937	1.128		**1.032**	**0.135**	ATPase family protein 2 homolog
0	1.193	0.874	1.031	**1.033**	**0.160**	Gamma-tropomyosin
2.4E-117	0.765	1.300		**1.033**	**0.378**	4-alpha-glucanotransferase
1.42E-27	0.393	1.995	0.711	**1.033**	**0.848**	Chromosome 20 open reading frame 43
3.4E-277	1.055	0.934	1.110	**1.033**	**0.090**	Acidic leucine-rich nuclear phosphoprotein 32 family member B
1E-141	0.475	1.559	1.066	**1.033**	**0.543**	Sb1.8
0	1.100	0.966		**1.033**	**0.095**	Procollagen-proline,2-oxoglutarate-4-dioxygenase subunit alpha-1
0	0.914	0.999	1.187	**1.033**	**0.140**	230 kDa bullous pemphigoid antigen
8.29E-57	0.685	0.335	2.083	**1.034**	**0.925**	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 1
5.04E-24	0.844	1.011	1.249	**1.035**	**0.203**	28S ribosomal protein S6, mitochondrial
0	1.103	0.912	1.089	**1.035**	**0.106**	Proteasome subunit alpha type-7
4.23E-23	0.633	1.128	1.344	**1.035**	**0.364**	40S ribosomal protein S23
1.04E-15	0.570	1.386	1.148	**1.035**	**0.420**	60S ribosomal protein L35a
6.64E-94	0.874	1.002	1.231	**1.035**	**0.181**	CROC-1
1.09E-33	0.421	1.650		**1.036**	**0.869**	Ribosome biogenesis regulatory protein homolog
1.2E-129	1.409	0.956	0.743	**1.036**	**0.340**	Flavoprotein subunit of complex II
3.1E-163	1.144	1.064	0.900	**1.036**	**0.124**	22 kDa protein
5.8E-242	0.827	1.322	0.962	**1.037**	**0.256**	Kinesin heavy chain isoform 5A

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
2.2E-167	0.756	1.230	1.125	**1.037**	**0.249**	GPI transamidase component PIG-S
6.73E-51	0.939	1.147	1.030	**1.039**	**0.104**	ADP-ribosylation factor-like protein 3
7.67E-79	0.751	1.300	1.066	**1.039**	**0.276**	Foocen
3.6E-101	0.907	0.116	2.094	**1.039**	**0.996**	cDNA FLJ54538, highly similar to Transportin-2
4.2E-100	0.959	0.888	1.271	**1.039**	**0.204**	Protein transport protein Sec24D
1.47E-11	0.942	1.181	0.995	**1.039**	**0.126**	Protein SCO1 homolog, mitochondrial
0.000539	0.636	1.246	1.238	**1.040**	**0.350**	Histidine-rich membrane protein Ke4
1.4E-179	1.060	1.027	1.033	**1.040**	**0.017**	Probable fructose-2,6-bisphosphatase TIGAR
0	0.963	1.010	1.148	**1.040**	**0.096**	Putative uncharacterized protein RNPEP
2.97E-57	1.697	0.447	0.977	**1.040**	**0.627**	Stathmin-2
8.6E-125	0.981	1.048	1.092	**1.041**	**0.056**	Biliverdin reductase A
1.59E-72	0.913	1.119	1.091	**1.041**	**0.112**	SET domain-containing protein 3
1.08E-09	1.365	0.232	1.526	**1.041**	**0.705**	Mitochondrial ribosomal protein S28 variant
0	1.106	1.129	0.890	**1.041**	**0.132**	Endomembrane proton pump 58 kDa subunit
1.8E-109	0.490	1.557	1.077	**1.041**	**0.534**	60S ribosomal protein L7
2.3E-190	1.138	1.015	0.971	**1.041**	**0.087**	Pyridoxal phosphate phosphatase
1.51E-66	0.954	0.962	1.209	**1.042**	**0.145**	Protein C20orf11
1.4E-298	1.159	0.988	0.979	**1.042**	**0.102**	26S protease regulatory subunit 8
2.2E-200	0.978	0.992	1.157	**1.042**	**0.100**	GTP-binding protein 9
5.2E-185	1.106	0.999	1.024	**1.043**	**0.056**	Asparagine--tRNA ligase
0	0.917	1.077	1.135	**1.043**	**0.113**	UPF0568 protein C14orf166
6E-240	1.024	1.045	1.061	**1.043**	**0.019**	UV excision repair protein RAD23 homolog B
1.23E-63	1.113	0.972	1.044	**1.043**	**0.070**	14 kDa thioredoxin-related protein
1.43E-48	0.849	1.208	1.074	**1.043**	**0.181**	Coactivator-associated arginine methyltransferase 1, isoform CRA_b
6.77E-83	0.895	1.104	1.131	**1.043**	**0.129**	Glucosamine 6-phosphate N-acetyltransferase
1.8E-201	0.490	1.545	1.098	**1.044**	**0.530**	60S ribosomal protein L5
1.1E-208	0.807	1.160	1.166	**1.044**	**0.205**	Oncogene c-mel
5.89E-14	1.887	0.984	0.261	**1.044**	**0.815**	Dihydrolipoamide dehydrogenase-binding protein of pyruvate dehydrogenase complex
2.8E-279	0.938	1.153	1.042	**1.044**	**0.107**	Beta'-coat protein
2.5E-261	1.066	1.047	1.020	**1.044**	**0.023**	Macropain zeta chain
5.77E-20	1.011	1.300	0.822	**1.045**	**0.241**	28S ribosomal protein S23, mitochondrial
1.1E-163	1.062	0.905	1.167	**1.045**	**0.132**	Putative uncharacterized protein
2E-302	0.917	1.169	1.049	**1.045**	**0.126**	Coatomer subunit epsilon
0	1.071	1.001	1.064	**1.045**	**0.038**	Carbonyl reductase [NADPH] 3
4.3E-154	0.560	1.456	1.120	**1.045**	**0.453**	40S ribosomal protein S4, X isoform
1.76E-28	1.545	1.464	0.128	**1.045**	**0.796**	Hrs-binding protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
9.7E-103	0.962	0.990	1.187	**1.047**	**0.123**	cDNA FLJ56285, highly similar to ADP-ribosylation factor-like protein 8B
1.8E-141	0.801	1.526	0.813	**1.047**	**0.415**	39S ribosomal protein L1, mitochondrial
7.69E-24	1.082	1.155	0.905	**1.047**	**0.128**	cDNA FLJ55157, highly similar to Eukaryotic translation initiation factor 4E
4.98E-85	1.379	0.849	0.915	**1.048**	**0.289**	Cytochrome b5
9.7E-246	0.664	1.299	1.180	**1.048**	**0.338**	60S ribosomal protein L14
1.5E-65	1.084	0.991	1.072	**1.049**	**0.051**	dTMP kinase
3.78E-25	0.996	1.174	0.978	**1.049**	**0.108**	Ser/Arg-related nuclear matrix protein
2.77E-32	0.757	1.341		**1.049**	**0.413**	Glycogen [starch] synthase, muscle
2.85E-16	0.774	1.076	1.297	**1.049**	**0.262**	Lysosomal-associated membrane protein 2, isoform CRA_b
9.13E-37	1.354	0.811	0.983	**1.049**	**0.277**	Chromosome 21 leucine-rich protein
1.8E-59	1.091	0.909	1.147	**1.049**	**0.124**	Casein kinase 2 beta polypeptide
0	1.010	0.398	1.742	**1.050**	**0.673**	Deleted in breast cancer gene 1 protein
0	1.038	1.154	0.959	**1.050**	**0.098**	Nucleolar phosphoprotein B23
8.91E-15	0.935	1.165		**1.050**	**0.163**	Phosphatidylinositol 3-kinase 85 kDa regulatory subunit alpha
7.43E-71	1.005	1.028	1.119	**1.050**	**0.061**	NADPH:quinone reductase
7.1E-37	0.941	0.198	2.013	**1.051**	**0.912**	Hepatocyte growth factor-regulated tyrosine kinase substrate
6.77E-69	0.602	1.322	1.230	**1.051**	**0.392**	Alpha-mannosidase 2
2.42E-88	0.854	1.108	1.192	**1.051**	**0.176**	Huntingtin-interacting protein 2
0	1.003	0.933	1.218	**1.051**	**0.149**	Amyloid beta precursor protein-binding protein 1, 59 kDa
0	1.163	0.986	1.005	**1.051**	**0.097**	26S protease regulatory subunit 6B
5.69E-86	0.589	1.083	1.483	**1.052**	**0.448**	Protein FAM3C
8.8E-205	1.136	0.988	1.032	**1.052**	**0.076**	Glucose-6-phosphate 1-dehydrogenase
4.7E-155	0.937	1.194	1.026	**1.052**	**0.131**	Macropain subunit C7-I
1.06E-34	0.980	1.074	1.106	**1.053**	**0.065**	Acid DNase
2.2E-141	1.183	0.903	1.074	**1.053**	**0.141**	U1 small nuclear ribonucleoprotein A
2.79E-17	0.615	1.492		**1.054**	**0.620**	Serine/threonine-protein phosphatase 4 regulatory subunit 3B
5.1E-38	1.130	0.658	1.380	**1.056**	**0.367**	CD2 antigen cytoplasmic tail-binding protein 2
0	0.932	0.993	1.243	**1.056**	**0.165**	Replication protein C
3.1E-93	0.691	1.199	1.278	**1.056**	**0.318**	Activator-recruited cofactor 32 kDa component
0	1.330	0.971	0.869	**1.057**	**0.242**	Glycogen phosphorylase, liver form
0	1.138	1.084	0.949	**1.057**	**0.097**	130 kDa leucine-rich protein
0	1.022	1.154	0.996	**1.057**	**0.085**	RNA polymerase B transcription factor 3
0	0.817	1.215	1.142	**1.058**	**0.212**	APC-binding protein EB1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
5.49E-13	0.774	1.289	1.112	**1.058**	**0.262**	60S ribosomal protein L36a-like
1.21E-12	1.112		1.005	**1.058**	**0.076**	Inosine-5'-monophosphate dehydrogenase
1.66E-36	1.468	0.868	0.840	**1.058**	**0.355**	highly similar to Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial
4.2E-104	1.020	0.965	1.192	**1.059**	**0.118**	Azoreductase
0	1.078	1.029	1.070	**1.059**	**0.026**	Acetoacetyl-CoA thiolase
0	0.524	1.454	1.200	**1.059**	**0.481**	Chromosome-associated polypeptide C
4.12E-17	0.919	0.986	1.273	**1.059**	**0.188**	2-hydroxyacyl-CoA lyase 1
3.75E-15	0.783	1.337		**1.060**	**0.392**	Torsin family 1 member B
0	1.068	1.073	1.039	**1.060**	**0.018**	26S protease regulatory subunit 6A
0	1.093	1.003	1.084	**1.060**	**0.049**	Profilin I
1.56E-86	1.188	1.089	0.907	**1.061**	**0.143**	Mannose-6-phosphate isomerase
3.39E-69	0.961	1.097	1.129	**1.062**	**0.089**	Elongation factor Ts, mitochondrial
7.5E-70	0.891	1.052	1.244	**1.062**	**0.177**	Serine--tRNA ligase
5.1E-246	1.181	1.029	0.977	**1.062**	**0.106**	26S protease regulatory subunit 10B
2.2E-22	1.117	0.421	1.650	**1.063**	**0.616**	Uncharacterized protein C9orf142
2.3E-113	0.784	1.401	1.004	**1.063**	**0.312**	Vacuolar proton pump subunit E 1
2E-244	1.249	0.929	1.011	**1.063**	**0.166**	3,2-trans-enoyl-CoA isomerase, mitochondrial
0	1.163	0.952	1.074	**1.063**	**0.106**	Early endosome antigen 1
6.07E-48	0.958	1.381	0.853	**1.064**	**0.279**	19 kDa FK506-binding protein
0	0.944	1.307	0.943	**1.065**	**0.210**	AIR carboxylase
0.000134	0.964	1.923	0.307	**1.065**	**0.812**	ATP-dependent helicase GTF2F2
0	0.735	1.304	1.156	**1.065**	**0.295**	116 kDa U5 small nuclear ribonucleoprotein component
1E-233	1.097	1.216	0.883	**1.065**	**0.169**	Long-chain acyl-CoA synthetase 3
9.7E-143	1.206	0.990	1.004	**1.066**	**0.121**	70 kDa lysosomal alpha-glucosidase
0	0.768	0.243	2.188	**1.066**	**1.006**	PABPC4 protein
7.5E-203	1.241	0.854	1.106	**1.067**	**0.197**	cDNA FLJ40895 fis, clone UTERU2002294, highly similar to Prostaglandin E synthase 3 (EC 5.3.99.3)
0	1.397	0.856	0.948	**1.067**	**0.290**	General vesicular transport factor p115
1.54E-41	1.205	1.029	0.968	**1.067**	**0.123**	PRA1 family protein 2
1.48E-52	1.079	1.132	0.991	**1.068**	**0.071**	Phosphatidylinositide phosphatase SAC1
4.63E-76	1.093	1.205	0.906	**1.068**	**0.151**	Probable O-sialoglycoprotein endopeptidase
6.4E-208	1.578	0.964	0.663	**1.068**	**0.466**	N-ethylmaleimide-sensitive fusion protein
3.7E-99	0.649	1.275	1.280	**1.068**	**0.363**	Putative uncharacterized protein RPL32
1.94E-48	0.942	1.147	1.117	**1.069**	**0.111**	Carnitine O-palmitoyltransferase 2, mitochondrial
1.92E-26	0.466	1.671		**1.069**	**0.852**	Testes-specific vespid and pathogenesis protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
						1b
2.3E-117	0.819	1.408	0.980	**1.069**	**0.304**	Cell division protein kinase 4
0	1.110	1.185	0.913	**1.069**	**0.140**	Medium tumor antigen-associated 61 kDa protein
1.4E-132	0.859	1.137	1.212	**1.069**	**0.186**	39S ribosomal protein L28, mitochondrial
1.87E-83	0.564	1.516	1.129	**1.070**	**0.478**	60S ribosomal protein L10a
0	0.879	1.100	1.231	**1.070**	**0.178**	Annexin A1
4.61E-11	0.606	2.379	0.226	**1.070**	**1.149**	CDK7/cyclin-H assembly factor
6.04E-20	0.455	1.643	1.115	**1.071**	**0.595**	Pescadillo homolog
2.7E-186	1.178	0.673	1.362	**1.071**	**0.357**	Oligoribonuclease, mitochondrial
5.4E-260	0.973	1.020	1.221	**1.071**	**0.132**	PAF acetylhydrolase 30 kDa subunit
2.46E-11	0.737	1.586	0.892	**1.072**	**0.452**	60S ribosomal protein L18a
2.71E-35	0.257	0.774	2.187	**1.073**	**0.999**	Bruton tyrosine kinase-associated protein 135
2.01E-94	1.091	1.059	1.070	**1.073**	**0.016**	Catechol O-methyltransferase
1.5E-135	0.756	1.287	1.176	**1.073**	**0.280**	CD107 antigen-like family member A
6.8E-139	1.061	1.069	1.089	**1.073**	**0.014**	26S proteasome non-ATPase regulatory subunit 10
1.8E-109	0.749	1.477	0.995	**1.074**	**0.370**	60S ribosomal protein L17
0	1.267	0.952	1.002	**1.074**	**0.169**	Arginine--tRNA ligase
3.8E-115	1.462	1.094	0.665	**1.074**	**0.399**	Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase, isoform CRA_a
5.11E-51	0.708	1.368	1.145	**1.074**	**0.336**	ADP-ribosylation factor-like protein 2
1.65E-40	0.956	1.076	1.189	**1.074**	**0.116**	Cell division cycle-associated protein 1
1.8E-189	0.992	1.038	1.192	**1.074**	**0.105**	Glyoxylate reductase/hydroxypyruvate reductase
6.98E-09	1.093	1.196	0.933	**1.074**	**0.133**	Dimethylallyltranstransferase
1.22E-47	1.306	1.146	0.771	**1.074**	**0.274**	Importin alpha Q2
2.9E-90	0.971	1.139	1.113	**1.074**	**0.090**	28S ribosomal protein S18-2, mitochondrial
4.47E-27	1.245	0.891	1.088	**1.075**	**0.177**	Putative MAPK-activating protein PM10
0	1.435	0.818	0.972	**1.075**	**0.321**	GTP-binding protein 1
2.88E-20	0.807		1.343	**1.075**	**0.379**	Glutathione peroxidase
0	1.102	0.987	1.138	**1.075**	**0.079**	Actin, alpha skeletal muscle
6.32E-18	0.709	1.432	1.087	**1.076**	**0.362**	Putative uncharacterized protein RPS27
2.4E-295	0.550	1.484	1.195	**1.076**	**0.478**	37 kDa laminin receptor precursor
5.13E-89	0.758	1.423	1.048	**1.076**	**0.333**	60S ribosomal protein L26
3.2E-226	1.027	0.976	1.227	**1.076**	**0.133**	26S proteasome non-ATPase regulatory subunit 3
4.48E-68	1.532	0.510	1.188	**1.076**	**0.520**	B17.2-like
1.3E-142	0.997	1.251	0.982	**1.077**	**0.151**	Nef-binding protein 1
1.6E-111	0.899	1.131	1.200	**1.077**	**0.158**	Activator 1 38 kDa subunit
0	1.512	0.642		**1.077**	**0.615**	highly similar to Rattus norvegicus tropomyosin 1,

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
						alpha (Tpm1), transcript variant 8, mRNA
8.7E-106	0.821	1.335	1.075	**1.077**	**0.257**	Niemann-Pick C1 protein
0	1.155	1.072	1.004	**1.077**	**0.076**	26S protease subunit S5 basic
2.1E-56	0.839	1.236	1.158	**1.078**	**0.210**	COP9 signalosome complex subunit 6
3.43E-23	1.188	0.967		**1.078**	**0.156**	Putative GTP-binding protein RAY-like
0.00024	0.718	1.438		**1.078**	**0.509**	Alpha mannosidase 6A8B
1.02E-86	0.875	1.565	0.798	**1.079**	**0.422**	ATP-dependent RNA helicase DDX48
1.5E-113	0.889	1.120	1.228	**1.079**	**0.173**	Phosphatidylinositol transfer protein beta isoform
7.46E-77	1.204	1.057	0.976	**1.079**	**0.116**	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 3
7.8E-219	0.896	1.324	1.017	**1.079**	**0.221**	Methionine--tRNA ligase
3.14E-13	0.890	1.251	1.096	**1.079**	**0.181**	Phosphatidylinositol transfer protein alpha isoform
0	1.065	0.978	1.196	**1.079**	**0.110**	14-3-3 protein gamma
0	1.105	1.149	0.985	**1.080**	**0.085**	26S protease regulatory subunit 4
1.46E-25	1.190	1.005	1.045	**1.080**	**0.097**	Diablo homolog, mitochondrial
2.31E-69	1.238	1.122	0.881	**1.080**	**0.182**	cDNA FLJ51518, highly similar to Annexin A11
0	0.523	1.693	1.026	**1.080**	**0.587**	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit
3.3E-240	0.928	1.117	1.196	**1.080**	**0.137**	DnaJ homolog subfamily C member 7
0	1.121	1.054	1.066	**1.081**	**0.036**	BPG-dependent PGAM 1
4.55E-14	0.935	1.155	1.154	**1.082**	**0.127**	28S ribosomal protein S2, mitochondrial
6.9E-205	1.231	1.161	0.854	**1.082**	**0.200**	highly similar to Eukaryotic translation initiation factor 3 subunit 3
9.3E-113	1.082	1.154	1.011	**1.082**	**0.071**	Adipocyte plasma membrane-associated protein
6.28E-54	1.195	0.985	1.067	**1.082**	**0.106**	Amidophosphoribosyltransferase
1.17E-35	0.933	1.179	1.136	**1.083**	**0.132**	highly similar to Adaptor-related protein complex 1 mu-1 subunit
0	1.001	1.133	1.115	**1.083**	**0.072**	Deubiquitinating enzyme 5
8.16E-35	0.601	1.415	1.233	**1.083**	**0.427**	60S ribosomal protein L15
1.9E-204	0.933	1.159	1.158	**1.083**	**0.130**	SF3a60
4.1E-137	0.766	1.191	1.293	**1.084**	**0.280**	Tumor protein, translationally-controlled 1
1.8E-17	0.998		1.170	**1.084**	**0.122**	Coiled-coil domain-containing protein 44
8.6E-126	1.314	0.884	1.054	**1.084**	**0.217**	ES1 protein homolog, mitochondrial
2.4E-252	0.749	1.375	1.128	**1.084**	**0.315**	O-GlcNAc transferase subunit p110
0	1.008	1.131	1.114	**1.084**	**0.066**	14-3-3 protein eta
6.08E-57	1.141	0.824	1.288	**1.084**	**0.237**	Protein phosphatase 1B
9.82E-55	0.865	1.122	1.269	**1.085**	**0.204**	Malic enzyme 1
8.45E-62	0.807	1.222	1.229	**1.086**	**0.242**	Chronic myelogenous leukemia tumor antigen 28
2.12E-61	1.476	1.525	0.259	**1.087**	**0.717**	LisH domain and HEAT repeat-containing protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
						KIAA1468
2.56E-47	1.107	1.192	0.964	**1.087**	**0.115**	cDNA, FLJ93510, highly similar to Homo sapiens JTV1 gene (JTV1), mRNA
0	0.909	1.216	1.138	**1.088**	**0.159**	15S Mg(2+)-ATPase p97 subunit
1.32E-13	1.080	1.047	1.137	**1.088**	**0.045**	Mitochondrial ribosomal protein S18A
3.52E-62	0.897	1.279		**1.088**	**0.270**	28S ribosomal protein S29, mitochondrial
1.9E-226	0.662	1.434	1.169	**1.088**	**0.392**	40S ribosomal protein S8
2.96E-85	1.034	1.025	1.208	**1.089**	**0.103**	HSMT3
2.89E-82	0.943	1.236		**1.090**	**0.207**	Arylsulfatase A
0.000146	0.497	1.682		**1.090**	**0.838**	Transmembrane protein 126A
9.61E-88	1.183	1.000	1.086	**1.090**	**0.092**	Ribulose-5-phosphate-3-epimerase
2.12E-93	0.964	1.199	1.109	**1.091**	**0.119**	Acyl-CoA thioesterase 7
3.7E-99	0.983	1.128	1.161	**1.091**	**0.095**	5'-nucleotidase domain-containing protein 1
1.49E-38	1.002	1.065	1.206	**1.091**	**0.104**	Glutathione S-transferase Mu 2
4.44E-78	0.700	1.434	1.140	**1.091**	**0.369**	N-acetyltransferase 13
0	1.113	1.023	1.139	**1.092**	**0.061**	1-Cys peroxiredoxin
7.16E-95	0.622	1.548	1.106	**1.092**	**0.463**	60S ribosomal protein L30
0	0.994	1.117	1.165	**1.092**	**0.088**	Fructose-bisphosphate aldolase A
2.3E-242	1.152	1.251	0.875	**1.092**	**0.195**	Ras-related protein Rab-14
0	0.958	1.084	1.236	**1.093**	**0.139**	Metavinculin
0	1.033	1.153		**1.093**	**0.085**	Leukotriene A(4) hydrolase
0	1.338	0.867	1.076	**1.094**	**0.236**	150 kDa oxygen-regulated protein
0.001599	0.881	1.086	1.314	**1.094**	**0.217**	Katanin p60 ATPase-containing subunit A-like 2
2.87E-38	1.090	1.087	1.107	**1.094**	**0.011**	APOBEC1-binding protein 2
0	1.233	0.868	1.183	**1.095**	**0.198**	5'-methylthioadenosine phosphorylase
0	1.332	0.972	0.982	**1.095**	**0.205**	Leucine--tRNA ligase
0	0.773	0.524	1.989	**1.095**	**0.784**	Matrix-remodeling-associated protein 1
2.17E-08	0.552	1.641		**1.097**	**0.770**	Myb-binding protein 1A
0	1.014	1.156	1.120	**1.097**	**0.074**	Glutathione synthase
1.13E-75	0.887	0.918	1.487	**1.097**	**0.338**	Aromatic esterase 2
3.99E-49	1.218	0.967	1.111	**1.099**	**0.126**	Glioblastoma-amplified sequence
4.26E-59	1.360	1.106	0.831	**1.099**	**0.264**	Putative uncharacterized protein DKFZp686M24262
5.6E-198	1.126	1.130	1.041	**1.099**	**0.050**	ER-Golgi intermediate compartment 53 kDa protein
7.1E-220	0.975	1.368	0.957	**1.100**	**0.232**	L1
1.16E-53	0.952	1.419	0.930	**1.100**	**0.276**	Cell migration-inducing gene 5 protein
0	1.103	1.017	1.181	**1.100**	**0.082**	Glyceraldehyde-3-phosphate dehydrogenase

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.05E-50	0.766	1.210	1.326	**1.101**	**0.296**	Pre-mRNA branch site protein p14
5.78E-71	1.090	1.153	1.058	**1.101**	**0.049**	Antioxidant enzyme AOE372
1.45E-94	1.240	1.103	0.959	**1.101**	**0.140**	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial
1.5E-102	0.952	1.271	1.080	**1.101**	**0.161**	Lissencephaly-1 protein
3.27E-20	1.151	1.052		**1.102**	**0.069**	Dynactin subunit 6
9.45E-13	1.486	0.880	0.940	**1.102**	**0.334**	28S ribosomal protein S5, mitochondrial
0	0.636	1.268	1.403	**1.102**	**0.410**	Damage-specific DNA-binding protein 1
6.86E-94	0.649	1.351	1.306	**1.102**	**0.393**	Chromatin assembly factor 1 subunit C
5.6E-129	1.157	1.015	1.136	**1.103**	**0.076**	[Protein ADP-ribosylarginine] hydrolase-like protein 2
0	0.966	1.444	0.898	**1.103**	**0.298**	Beta-catenin
3.91E-16	1.300	0.981	1.028	**1.103**	**0.172**	UPF0553 protein C9orf64
1.2E-189	1.016	1.080	1.215	**1.104**	**0.102**	Biliverdin reductase B
1.71E-12	0.693	1.210	1.407	**1.104**	**0.369**	Lysosomal acid phosphatase
1.29E-19	0.801	0.538	1.973	**1.104**	**0.764**	DEAD box protein 47
6.25E-20	2.006	0.335	0.971	**1.104**	**0.843**	DNA-binding factor KBF1
7.4E-122	1.395	0.974	0.943	**1.104**	**0.253**	Nucleolar protein 17 homolog
2.1E-164	0.792	1.341	1.180	**1.104**	**0.282**	Cell proliferation-inducing gene 15 protein
7.8E-303	1.076	1.128	1.111	**1.105**	**0.027**	ADP-ribosylation factor 1
6.86E-75	0.977	0.882	1.456	**1.105**	**0.308**	NEDD8 carrier protein
0	1.321	0.952	1.044	**1.105**	**0.192**	Electron transfer flavoprotein subunit alpha, mitochondrial
2.3E-76	1.082	1.285	0.950	**1.106**	**0.168**	Cell proliferation-inducing gene 46 protein
0	1.218	1.030	1.070	**1.106**	**0.099**	Actin-depolymerizing factor
1.5E-97	1.149	0.964	1.206	**1.106**	**0.127**	Protein kinase C alpha type
7.9E-111	1.314	1.287	0.719	**1.107**	**0.336**	Coiled-coil domain-containing protein 6
0	1.264	0.113	1.943	**1.107**	**0.925**	Cervical mucin-associated protein
2.6E-115	0.912	1.244	1.164	**1.107**	**0.173**	Rho cDNA clone 9
2.43E-16	1.691	1.010	0.620	**1.107**	**0.542**	eIF-2B GDP-GTP exchange factor subunit gamma
2.2E-171	1.161	1.412	0.752	**1.108**	**0.334**	COP9 signalosome complex subunit 7b
0	1.192	1.100	1.036	**1.109**	**0.078**	26S protease regulatory subunit 7
4.91E-36	0.921	1.491	0.918	**1.110**	**0.330**	Leucine-rich repeat-containing protein 57
0	0.861	1.015	1.454	**1.110**	**0.307**	p164 ROCK-2
1.1E-134	0.664	1.110	1.556	**1.110**	**0.446**	Malignant T cell-amplified sequence 1
3.59E-92	0.399	1.434	1.498	**1.111**	**0.617**	G2/mitotic-specific cyclin-B1
0	1.058	1.060	1.213	**1.111**	**0.089**	Hsc70/Hsp90-organizing protein
1.04E-19	1.048	1.038	1.247	**1.111**	**0.118**	Aicardi-Goutieres syndrome 3 protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.15E-15	0.999	1.223		**1.111**	**0.158**	NmrA-like family domain-containing protein 1
2.21E-28	1.241	0.835	1.257	**1.111**	**0.239**	Cysteine desulfurase, mitochondrial
7.8E-297	1.522	0.849	0.963	**1.111**	**0.360**	28 kDa heat shock protein
1E-294	1.011	0.985	1.338	**1.111**	**0.197**	COP9 signalosome complex subunit 4
0	0.726	1.351	1.259	**1.112**	**0.337**	cDNA FLJ55427, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9)
5.46E-93	1.077	1.105	1.156	**1.113**	**0.040**	27 kDa prosomal protein
7.6E-197	1.190	1.181	0.974	**1.115**	**0.122**	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
2.3E-173	0.155	2.070	1.120	**1.115**	**0.958**	Histone H1.2
1.8E-261	0.503	2.325	0.517	**1.115**	**1.048**	Complex III subunit 2
1.6E-87	1.606	0.995	0.744	**1.115**	**0.443**	Dynamin-1
5.55E-64	0.362	1.869		**1.115**	**1.065**	CSN12-like protein
1.7E-155	1.184	1.089	1.075	**1.116**	**0.059**	Fumarylacetoacetate hydrolase domain-containing protein 2A
3E-275	1.145	1.244	0.963	**1.117**	**0.143**	Arsenite-resistance protein 2
0	1.055	1.078	1.219	**1.117**	**0.089**	Monocyte protein 4
4E-126	1.264	1.183	0.906	**1.118**	**0.188**	Deoxycytidine kinase
3.95E-75	0.806	1.431	1.117	**1.118**	**0.313**	60S ribosomal protein L26-like 1
2.43E-34	1.126	0.963	1.271	**1.120**	**0.154**	GTP-binding protein HSR1
0	1.083	1.226	1.053	**1.120**	**0.093**	Glycogen phosphorylase, brain form
1.22E-70	1.023	0.858	1.481	**1.121**	**0.323**	Tetratricopeptide repeat protein 9C
1.52E-94	1.301	0.996	1.067	**1.121**	**0.160**	26 kDa prosomal protein
3.13E-34	1.153	1.017	1.193	**1.121**	**0.092**	Glutathione reductase, mitochondrial
2.2E-99	0.997	1.161	1.206	**1.121**	**0.110**	28 kDa heat- and acid-stable phosphoprotein
3.8E-232	1.146	1.084	1.136	**1.122**	**0.033**	Acidic nucleoplasmic DNA-binding protein 1
5.66E-76	0.626	1.520	1.224	**1.123**	**0.455**	60S ribosomal protein L11
1.1E-149	0.997	1.123	1.249	**1.123**	**0.126**	L-iditol 2-dehydrogenase
3.5E-111	0.985	1.241	1.143	**1.123**	**0.129**	U6 snRNA-associated Sm-like protein LSm3
5.6E-117	1.055	1.091	1.225	**1.124**	**0.090**	Cytoplasmic dynein 1 light intermediate chain 1
1.2E-105	0.789	1.523	1.059	**1.124**	**0.371**	5F7
2.59E-14	1.131	1.145	1.097	**1.124**	**0.025**	Iron-sulfur subunit of complex II
6.63E-06	0.620	1.629		**1.125**	**0.714**	Complex I-ASHI
3.2E-288	0.636	1.697	1.041	**1.125**	**0.535**	p90
4.8E-272	1.118	1.120	1.137	**1.125**	**0.010**	Macropain subunit C3
3.6E-151	1.223	1.157	0.995	**1.125**	**0.117**	COP9 homolog
6.47E-16	1.104	1.578	0.695	**1.125**	**0.442**	Band 4.1-like protein 2

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
2.3E-28	0.420	1.831		**1.126**	**0.998**	Mitochondrial 2-oxoglutarate/malate carrier protein
0	0.999	1.172	1.208	**1.126**	**0.112**	Isoleucine--tRNA ligase
7.63E-43	0.768	1.728	0.883	**1.126**	**0.524**	1F5 antigen
2.5E-103	1.015	1.211	1.154	**1.127**	**0.101**	Mammalian lin-seven protein 3
2.34E-83	0.931	1.151	1.299	**1.127**	**0.186**	Mitochondrial tRNA nucleotidyl transferase, CCA-adding
0	1.006	1.137	1.239	**1.127**	**0.117**	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase
5.2E-136	1.239	0.423	1.722	**1.128**	**0.656**	DNA mismatch repair protein Msh6
0	0.882	1.104	1.399	**1.128**	**0.259**	Cavin-1
2.63E-50	0.658	1.689	1.039	**1.129**	**0.521**	39 kDa phosphoribosypyrophosphate synthase-associated protein
5.2E-228	0.604	1.544	1.241	**1.130**	**0.480**	60S ribosomal protein L12
0	1.422	0.896	1.072	**1.130**	**0.267**	cDNA FLJ51602, highly similar to Interferon-induced guanylate-binding protein 1
0	0.974	1.153	1.263	**1.130**	**0.146**	14 kDa laminin-binding protein
0	0.772	1.377	1.244	**1.131**	**0.318**	4F2 cell-surface antigen heavy chain
1.3E-276	1.666	0.283	1.449	**1.132**	**0.744**	133 kDa FK506-binding protein
1.5E-295	1.187	1.080	1.132	**1.133**	**0.054**	Calgizzarin
7.72E-65	1.078	1.136	1.184	**1.133**	**0.053**	Aspartyl aminopeptidase
3.78E-53	1.122	1.254	1.024	**1.134**	**0.115**	Putative uncharacterized protein CUL4A
9.7E-155	0.861	1.119	1.421	**1.134**	**0.280**	Ran-binding protein 6
4.59E-79	1.342	0.921	1.139	**1.134**	**0.211**	CAP-Gly domain-containing linker protein 2
1.3E-169	1.115	1.078	1.211	**1.135**	**0.069**	Conjugase
5.49E-40	0.458	1.254	1.693	**1.135**	**0.626**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54, isoform CRA_a
2.57E-34	1.035	0.780	1.591	**1.135**	**0.415**	Inversely correlated with estrogen receptor expression 1
8.7E-122	0.941		1.330	**1.135**	**0.275**	Calmodulin-dependent calcineurin A subunit alpha isoform
3.5E-117	1.125	1.154	1.128	**1.136**	**0.016**	3-ketoacyl-CoA thiolase
4.6E-25	0.924		1.348	**1.136**	**0.300**	Syntaxin-3
2.3E-296	1.046	1.075	1.287	**1.136**	**0.132**	UPF0027 protein C22orf28
2.19E-19	0.592	2.613	0.204	**1.136**	**1.294**	Ubiquitin carrier protein R2
0	0.792	1.394	1.225	**1.137**	**0.311**	40S ribosomal protein S3a
1.19E-85	1.079	1.230	1.101	**1.137**	**0.082**	ERT1
1.27E-26	1.087	1.076	1.249	**1.137**	**0.097**	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1
1.1E-32	1.178	1.037	1.198	**1.138**	**0.088**	14.5 kDa translational inhibitor protein
3.18E-51	0.439	1.837		**1.138**	**0.988**	c-Ki-ras
1E-172	0.994	1.053	1.369	**1.139**	**0.202**	Inosine phosphorylase

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.9E-180	0.964	1.262	1.193	**1.139**	**0.156**	Cyclophilin F
3.7E-113	1.019	0.810	1.590	**1.140**	**0.404**	AKAP 120-like protein
1.16E-07	0.806	1.596	1.020	**1.141**	**0.409**	Protein NN8-4AG
0	0.871	0.767	1.783	**1.141**	**0.559**	Alpha-tubulin ubiquitous
0	1.078	1.150	1.195	**1.141**	**0.059**	Aspartate aminotransferase, mitochondrial
2.6E-119	1.327	0.977	1.120	**1.141**	**0.176**	Endoplasmic reticulum resident protein 18
4.1E-131	0.707	1.328	1.391	**1.142**	**0.378**	Nuclear distribution protein C homolog
6.66E-09	0.729		1.558	**1.143**	**0.586**	Uncharacterized protein C3orf59
2.8E-173	1.772	0.569	1.091	**1.144**	**0.603**	cDNA FLJ60624, highly similar to Epidermal growth factor receptor substrate 15-like 1
1.6E-122	0.639	1.573	1.221	**1.144**	**0.472**	60S acidic ribosomal protein P0
0	1.206	0.381	1.848	**1.145**	**0.735**	Desmoyokin
3.93E-91	0.923	1.535	0.977	**1.145**	**0.339**	26S proteasome non-ATPase regulatory subunit 14
2.5E-192	1.223	0.831	1.382	**1.146**	**0.284**	BAG family molecular chaperone regulator 5
9E-152	0.709	1.370	1.360	**1.146**	**0.379**	Histone acetyltransferase type B subunit 2
3.53E-17	1.083	1.259	1.098	**1.147**	**0.098**	Endoplasmic reticulum-Golgi intermediate compartment protein 3
3.99E-74	0.765	1.327	1.347	**1.147**	**0.330**	Eukaryotic peptide chain release factor subunit 1
0	1.063	1.108	1.270	**1.147**	**0.109**	p160 ROCK-1
5.7E-124	0.262	2.032		**1.147**	**1.252**	Alanyl aminopeptidase
7.21E-37	1.493	0.866	1.085	**1.148**	**0.318**	Cytochrome c-releasing factor 21
3.89E-11	0.976	1.320		**1.148**	**0.244**	cDNA FLJ53353, highly similar to ATP-binding cassette sub-family D member 3
8.13E-50	0.892	0.728	1.825	**1.148**	**0.592**	ElaC homolog protein 2
7E-216	1.142	1.097	1.207	**1.149**	**0.055**	Antioxidant protein 1
2.2E-207	0.522	0.866	2.060	**1.149**	**0.807**	Lamina-associated polypeptide 2, isoforms beta/gamma
0	1.211	1.322	0.917	**1.150**	**0.209**	5'-phosphoribosylglycinamide transformylase
6.4E-224	0.682	1.346	1.421	**1.150**	**0.407**	60S acidic ribosomal protein P1
3.42E-91	0.866	1.451	1.133	**1.150**	**0.293**	60S ribosomal protein L21
0	1.188	0.665	1.598	**1.150**	**0.467**	MYH-1c
0	1.278	0.682	1.491	**1.150**	**0.419**	Calcium-activated neutral proteinase small subunit
5.8E-113	1.039	1.089	1.324	**1.150**	**0.152**	7,8-dihydro-8-oxoguanine triphosphatase
1.24E-70	0.807	1.358	1.287	**1.151**	**0.300**	40S ribosomal protein S13
3E-283	1.151	1.151		**1.151**	**0.000**	Adapter-related protein complex 1 subunit beta-1
0	0.933	1.196	1.324	**1.151**	**0.199**	Filamin B
4.33E-61	0.787	1.516		**1.151**	**0.515**	PAT1-like protein 1
0	1.227	1.109	1.118	**1.151**	**0.066**	Centromere/kinetochore protein zw10 homolog

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	0.873	1.195	1.387	**1.152**	**0.260**	Clathrin heavy chain 1
8.6E-112	1.084	1.098	1.276	**1.153**	**0.107**	Bendless-like ubiquitin-conjugating enzyme
3.32E-21	0.943	2.126	0.389	**1.153**	**0.887**	C-terminal-binding protein 1
3.67E-76	0.924	2.193	0.343	**1.153**	**0.946**	Deubiquitinating enzyme 13
0.010498	0.772		1.535	**1.153**	**0.540**	Protein RER1
1.66E-75	1.070	1.090	1.300	**1.153**	**0.128**	ERT2
0	1.203	1.105	1.153	**1.153**	**0.049**	Glutathione S-transferase P
4.9E-119	0.575	1.638	1.248	**1.154**	**0.538**	60S ribosomal protein L8
8.9E-240	1.102	1.221	1.140	**1.154**	**0.061**	Deubiquitinating enzyme 14
6.98E-60	0.813	1.221	1.431	**1.155**	**0.314**	Dermal papilla-derived protein 9
1.33E-19	1.465		0.845	**1.155**	**0.438**	cDNA FLJ54713, highly similar to Gephyrin
1.29E-81	0.914	1.381	1.171	**1.155**	**0.234**	76 kDa protein
7.09E-43	1.116	1.163	1.188	**1.156**	**0.037**	Acyl-protein thioesterase 2
4.36E-07	1.065		1.247	**1.156**	**0.129**	Protein FAM61B
4.3E-132	0.488	1.901	1.080	**1.156**	**0.710**	Complex III subunit 1
2.8E-121	0.831	1.515	1.123	**1.156**	**0.343**	ATP-dependent RNA helicase DDX42
2.85E-53	0.809	1.287	1.374	**1.156**	**0.304**	HIRA-interacting protein 5
4.99E-61	0.804	1.171	1.497	**1.157**	**0.347**	Mitochondrial outer membrane protein 25
1E-178	0.834	1.145	1.494	**1.158**	**0.330**	Alpha-MPP
6.8E-167	1.111	1.449	0.914	**1.158**	**0.271**	Calcium-binding and coiled-coil domain-containing protein 1
2.12E-32	0.874	1.300	1.299	**1.158**	**0.246**	RalBP1-associated Eps domain-containing protein 1
5.1E-138	1.220	1.180	1.074	**1.158**	**0.075**	70 kDa mitochondrial autoantigen of primary biliary cirrhosis
4.5E-116	1.210	1.014	1.252	**1.159**	**0.127**	Signal recognition particle 19 kDa protein
6.76E-15	1.437	0.980	1.060	**1.159**	**0.244**	Dynactin complex subunit 22 kDa subunit
8.2E-108	1.276	1.017	1.186	**1.159**	**0.132**	SUMO-activating enzyme subunit 1
1.23E-11	1.333	1.165	0.982	**1.160**	**0.175**	Protein FAM96A
4.23E-05	0.784	1.439	1.259	**1.160**	**0.338**	HBeAg-binding protein 2 binding protein A
9.29E-93	0.714	1.449	1.318	**1.160**	**0.393**	40S ribosomal protein S11
4.1E-104	0.929	0.270	2.283	**1.161**	**1.027**	HBEBP2-binding protein C
2.12E-26	0.759	1.447	1.278	**1.161**	**0.359**	60S ribosomal protein L36a
0	0.919	0.838	1.727	**1.161**	**0.491**	Chromobox protein homolog 3
6.4E-208	0.765	1.394	1.325	**1.161**	**0.345**	Cleavage and polyadenylation specificity factor 68 kDa subunit
1E-177	1.070	1.230	1.188	**1.162**	**0.083**	Haloacid dehalogenase-like hydrolase domain-containing protein 2
4.74E-38	0.832	1.493		**1.162**	**0.467**	UPF0493 protein KIAA1632

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
2.5E-172	0.950	1.146	1.393	**1.163**	**0.222**	Imidodipeptidase
1.18E-57	0.442	1.361	1.687	**1.163**	**0.646**	60S ribosomal protein L18
3.26E-33	0.920	1.243	1.329	**1.164**	**0.215**	Exosome complex exonuclease MTR3
1.77E-82	0.385	2.112	0.997	**1.165**	**0.876**	DNA-directed RNA polymerase II subunit D
3E-111	0.604	1.457	1.435	**1.165**	**0.486**	PDZ domain-containing protein 11
3.75E-89	0.968	1.464	1.066	**1.166**	**0.262**	Endoplasmic reticulum lipid raft-associated protein 2
7.51E-58	1.217	1.165	1.116	**1.166**	**0.050**	eIF-3 p48
1.4E-177	0.589	1.648	1.262	**1.166**	**0.536**	60S ribosomal protein L3
1.8E-300	1.122	1.167	1.212	**1.167**	**0.045**	Neuron cytoplasmic protein 9.5
3.2E-211	1.103	0.719	1.678	**1.167**	**0.482**	Binder of OVCA1-1
5.11E-16	1.142		1.192	**1.167**	**0.035**	MRPS17 protein
0	1.085		1.251	**1.168**	**0.117**	Procollagen-proline,2-oxoglutarate-4-dioxygenase subunit alpha-2
1.9E-108	1.359	1.016	1.128	**1.168**	**0.175**	ATP-dependent RNA helicase DDX19A
1.52E-81	0.718	1.536	1.250	**1.168**	**0.415**	Auberger B antigen
0	0.811	1.527		**1.169**	**0.506**	cDNA FLJ38698 fis, clone KIDNE2002015, highly similar to HEAT SHOCK 70 kDa PROTEIN 1
0	0.836	0.292	2.382	**1.170**	**1.085**	Protein linking IAP with cytoskeleton 1
1.53E-38	1.053	1.165	1.293	**1.170**	**0.120**	Phosphotyrosyl phosphatase activator
7.62E-62	1.495	0.846		**1.171**	**0.459**	Sterile alpha and Armadillo repeat protein
1.67E-77	1.118	1.282	1.111	**1.171**	**0.097**	Echinoderm microtubule-associated protein-like 4
3.45E-27	0.832	2.024	0.657	**1.171**	**0.744**	PTPRF-interacting protein
4.6E-239	1.068	1.111	1.334	**1.171**	**0.143**	Glycerol-3-phosphate dehydrogenase, mitochondrial
1.8E-188	1.032	1.401	1.087	**1.173**	**0.199**	highly similar to Homo sapiens pleckstrin homology domain containing, family C member 1 (PLEKHC1)
0	0.736	1.441	1.346	**1.174**	**0.383**	220 kDa U5 snRNP-specific protein
3.5E-265	1.077	1.072	1.374	**1.174**	**0.173**	KRAB-associated protein 1
1.68E-94	1.018	2.032	0.474	**1.175**	**0.791**	Dopamine-responsive gene 1 protein
1.1E-115	1.096	0.903	1.527	**1.175**	**0.319**	cDNA, FLJ96656, highly similar to Homo sapiens SPFH domain family, member 1 (SPFH1), mRNA
0	1.041	1.068	1.417	**1.175**	**0.210**	Cyclophilin A
1.1E-272	1.137	1.292	1.098	**1.176**	**0.103**	6-phosphogluconate dehydrogenase, decarboxylating
1.59E-64	1.736	0.951	0.841	**1.176**	**0.488**	CTP synthase 2
2.18E-80	1.110	1.126	1.293	**1.176**	**0.101**	2-oxoglutarate dehydrogenase complex component E2
3.6E-126	1.077	1.013	1.440	**1.177**	**0.230**	Peptidyl-prolyl cis-trans isomerase H
1.77E-13	0.988	1.237	1.307	**1.177**	**0.168**	Gem-associated protein 6

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
8.3E-256	1.214	1.139	1.179	**1.177**	**0.038**	CHORD domain-containing protein 1
1.07E-05	1.122		1.233	**1.178**	**0.078**	Lysophospholipase-like protein 1
0	0.619	1.712	1.203	**1.178**	**0.547**	100 kDa coactivator
7.59E-88	1.335		1.021	**1.178**	**0.222**	BRCA1-A complex subunit MERIT40
5.9E-146	1.087	1.228	1.222	**1.179**	**0.080**	Macropain chain Z
7.78E-78	0.926	1.543	1.070	**1.180**	**0.323**	Beta-SGT
0	1.295	1.110	1.135	**1.180**	**0.100**	IMPDH-II
7.84E-39	0.789	1.796	0.962	**1.182**	**0.538**	Small nuclear ribonucleoprotein Sm D1
2.06E-54	0.708	1.781	1.058	**1.182**	**0.547**	Neuroblastoma-derived sulfhydryl oxidase
3.5E-119	1.125	1.100	1.322	**1.182**	**0.121**	Beta-hexosaminidase subunit beta
7.8E-204	0.969	1.083	1.495	**1.182**	**0.276**	Uroporphyrinogen decarboxylase
1.03E-64	1.107	1.180	1.262	**1.183**	**0.078**	Androgen-regulated short-chain dehydrogenase/reductase 1
3.3E-136	1.026	1.330	1.194	**1.183**	**0.152**	Lysosomal acid alpha-mannosidase
1E-288	1.338	1.113	1.101	**1.184**	**0.133**	11S regulator complex subunit alpha
3.02E-71	1.925	0.830	0.799	**1.185**	**0.641**	100 kDa U5 snRNP-specific protein
2E-242	0.964	1.095	1.495	**1.185**	**0.277**	Calcium-activated neutral proteinase 2
0	0.907	1.246	1.403	**1.185**	**0.253**	Cytosolic thyroid hormone-binding protein
5.7E-122	0.451	2.149	0.956	**1.185**	**0.872**	60S ribosomal protein L6
0	1.046	1.049	1.460	**1.185**	**0.238**	Collapsin response mediator protein 4 long variant
1.5E-15	0.922		1.449	**1.185**	**0.373**	Pre-mRNA-splicing factor 3
2.34E-43	2.374	0.510	0.672	**1.185**	**1.032**	p125
5.96E-21	1.193	1.050	1.313	**1.185**	**0.132**	Phosphomannomutase 2
0	1.044	1.247	1.266	**1.185**	**0.123**	Chromosome region maintenance 1 protein homolog
1.3E-119	0.933	0.894	1.729	**1.185**	**0.471**	Basic leucine zipper and W2 domain-containing protein 2
1.2E-178	0.517	2.118	0.922	**1.185**	**0.832**	Adenine nucleotide translocator 2
2.78E-14	1.704	1.091	0.762	**1.186**	**0.478**	Dehydrogenase/reductase SDR family member 4
0	0.988	1.207	1.364	**1.186**	**0.189**	Heat shock 86 kDa
0	1.104	1.190	1.267	**1.187**	**0.082**	Glucose phosphomutase 1
4E-161	1.209	1.170	1.184	**1.188**	**0.020**	Lysine--tRNA ligase
0	0.739	1.478	1.347	**1.188**	**0.395**	Activated leukocyte cell adhesion molecule
3E-149	1.061		1.316	**1.188**	**0.181**	ESCRT-I complex subunit VPS28
4.2E-245	1.166	1.172	1.231	**1.189**	**0.036**	15-oxoprostaglandin 13-reductase
0	1.115	1.294	1.161	**1.190**	**0.093**	Importin subunit beta-3
5.2E-285	0.487	2.404	0.679	**1.190**	**1.056**	APOBEC1-binding protein 1
1.7E-236	1.296	1.171	1.106	**1.191**	**0.097**	93 kDa nucleoporin

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	1.235		1.147	**1.191**	**0.063**	Myosin I beta
5E-87	0.719	1.763	1.090	**1.191**	**0.529**	40S ribosomal protein S9
0	1.049	1.365	1.159	**1.191**	**0.160**	78 kDa gastrin-binding protein
3.85E-05	0.670	1.480	1.424	**1.191**	**0.452**	mRNA export factor
6.4E-32	1.411	0.974	1.189	**1.191**	**0.219**	Phosphomevalonate kinase
5.5E-110	1.209	1.211	1.156	**1.192**	**0.031**	APG7-like
8.46E-72	1.184	1.193	1.200	**1.193**	**0.008**	Endoplasmic reticulum stress-response protein 25
8.5E-165	1.094	1.157	1.327	**1.193**	**0.120**	Casein kinase II subunit alpha'
5.71E-14	0.615	1.770		**1.193**	**0.817**	Exocyst complex component 7
8.48E-23	0.721	1.513	1.346	**1.193**	**0.418**	Sodium/potassium-dependent ATPase subunit beta-1
8.98E-17	1.487	0.953	1.140	**1.193**	**0.271**	Protein NipSnap homolog 3A
2.04E-21	0.973	1.415		**1.194**	**0.312**	Inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase
2.2E-197	0.681	0.745	2.157	**1.195**	**0.835**	MM1
0	1.004	1.309	1.272	**1.195**	**0.167**	Maternal-embryonic 3
4.64E-59	0.292	1.351	1.942	**1.195**	**0.836**	Kinesin-like protein 6
0	0.743	1.365	1.478	**1.195**	**0.396**	Activating signal cointegrator 1 complex subunit 3-like 1
1.09E-41	0.907	1.293	1.388	**1.196**	**0.255**	TLD domain-containing protein KIAA1609
4.34E-41	0.628	1.466	1.499	**1.198**	**0.494**	60S ribosomal protein L27
1.4E-240	0.617	1.562	1.414	**1.198**	**0.508**	Cell proliferation-inducing gene 21 protein
2.64E-97	0.658	1.243	1.692	**1.198**	**0.519**	Syntaxin-8
2.82E-87	0.961	1.211	1.423	**1.198**	**0.232**	Glutathione S-transferase omega-1
0	1.623	0.819	1.154	**1.199**	**0.404**	17-beta-hydroxysteroid dehydrogenase 10
3.43E-27	0.707	0.753	2.137	**1.199**	**0.813**	Proteasome inhibitor PI31 subunit
2.93E-12	0.434		1.964	**1.199**	**1.082**	EIF4E-binding protein
1.95E-91	1.077	1.173	1.349	**1.200**	**0.138**	Alien homolog
1.99E-13	1.066		1.334	**1.200**	**0.189**	Ester hydrolase C11orf54
2.49E-22	1.032	1.178	1.392	**1.201**	**0.181**	Palmitoyl-CoA oxidase
3.33E-96	0.797	1.761	1.045	**1.201**	**0.501**	cDNA FLJ55177, highly similar to Ras-related protein Ral-B
5.6E-191	0.978	0.298	2.327	**1.201**	**1.033**	Adenovirus early region 1B-associated protein 5
1.8E-114	0.690	1.453	1.462	**1.201**	**0.443**	Splicing factor U2AF 35 kDa subunit
2.75E-24	0.971	1.433		**1.202**	**0.327**	Glutathione S-transferase Mu 1
0	1.183	1.125	1.297	**1.202**	**0.087**	Endoplasmic reticulum resident protein 70
1.8E-193	0.985	1.357	1.264	**1.202**	**0.194**	Zinc finger protein 259
2.4E-100	0.918	1.230	1.458	**1.202**	**0.271**	BET3 homolog
2.67E-46	1.055	1.349		**1.202**	**0.208**	Elongator complex protein 3

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
7.8E-124	0.972		1.433	**1.202**	**0.326**	ADP-ribosylation factor-binding protein GGA1
5.22E-58	1.335	1.070		**1.202**	**0.187**	DNA-directed RNA polymerase III largest subunit
4.6E-263	0.781	1.548	1.280	**1.203**	**0.389**	40S ribosomal protein S12
1.67E-26	1.019	1.277	1.312	**1.203**	**0.160**	GDP-fucose protein O-fucosyltransferase 1
0	1.163	1.082	1.366	**1.204**	**0.147**	6-phosphofructokinase, liver type
1.5E-101	1.295	1.113		**1.204**	**0.129**	Beta-tubulin cofactor D
4.5E-138	1.206	1.582	0.825	**1.204**	**0.379**	Pre-mRNA-splicing factor SRP20
1.05E-06	0.656	1.895	1.062	**1.204**	**0.631**	SFT2 domain-containing protein 2
9.44E-68	1.108	1.194	1.311	**1.204**	**0.102**	Proline synthase co-transcribed bacterial homolog protein
5.82E-10	1.233	1.054	1.326	**1.204**	**0.139**	Putative uncharacterized protein IVD
2E-219	1.329	1.022	1.263	**1.205**	**0.161**	Pyridoxal-dependent decarboxylase domain-containing protein 1
0	0.994	1.233	1.387	**1.205**	**0.198**	Cullin-4B
0	1.206	1.236	1.173	**1.205**	**0.032**	Talin-2
1.67E-41	1.208	1.204		**1.206**	**0.003**	B3GAT3 protein
8.25E-05	1.450		0.962	**1.206**	**0.345**	Coiled-coil domain-containing protein 93
0	0.522	1.803	1.296	**1.207**	**0.645**	Carboxypeptidase D
0	1.077	0.720	1.825	**1.207**	**0.564**	SM22-alpha homolog
4.21E-50	1.143	1.627	0.855	**1.208**	**0.390**	cDNA FLJ54837, highly similar to Inositol monophosphatase (EC 3.1.3.25)
4.3E-139	1.568	0.945	1.115	**1.209**	**0.322**	Reticulocalbin-1
1.16E-17	0.605	0.834	2.190	**1.210**	**0.857**	GTP-binding protein RAY
7.45E-17	0.944	1.230	1.457	**1.210**	**0.257**	Angiotensin-binding protein
6E-172	0.821	1.332	1.478	**1.210**	**0.345**	Eukaryotic translation initiation factor 3, subunit E interacting protein
9.53E-13	0.566	1.855		**1.211**	**0.911**	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial
5.8E-274	1.079	1.311	1.242	**1.211**	**0.119**	6-phosphogluconolactonase
1.8E-168	1.035	1.249	1.350	**1.212**	**0.161**	N-acetylneuraminate synthase
0	0.869	1.335	1.431	**1.212**	**0.300**	Heterogeneous nuclear ribonucleoprotein U
1.34E-16	1.180	1.345	1.111	**1.212**	**0.120**	Protein kinase B
1.66E-09	0.862	1.563		**1.213**	**0.496**	WD repeat-containing protein 18
0	1.181	1.076	1.384	**1.214**	**0.157**	Glutaminase kidney isoform, mitochondrial
1.35E-11	1.254	1.109	1.279	**1.214**	**0.092**	Chromosome 20 open reading frame 27
1.8E-84	0.722	1.411	1.509	**1.214**	**0.429**	N-acetyltransferase 10
1.1E-157	0.978	1.322	1.344	**1.215**	**0.205**	Bifunctional coenzyme A synthase
1.07E-13	0.687	2.242	0.718	**1.216**	**0.889**	Translocation protein 1
4.9E-32	0.933	1.106	1.608	**1.216**	**0.351**	Associate of Myc 1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.3E-12	0.830	1.492	1.326	**1.216**	**0.344**	40S ribosomal protein S29
6.1E-300	1.000	1.284	1.370	**1.218**	**0.194**	Nucleosome assembly protein 1-like 4
0	0.799	1.250	1.605	**1.218**	**0.404**	17-beta-hydroxysteroid dehydrogenase 4
7.6E-220	0.974	1.348	1.333	**1.218**	**0.211**	Breast carcinoma-amplified sequence 2
3.2E-103	1.758	1.043	0.856	**1.219**	**0.476**	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial
2.4E-105	1.427	1.089	1.141	**1.219**	**0.182**	cDNA FLJ31171 fis, clone KIDNE2000046, highly similar to 3-mercaptopyruvate sulfurtransferase
8.1E-285	1.401	1.055	1.201	**1.219**	**0.174**	HINT-3
6.1E-41	1.130	1.120	1.408	**1.219**	**0.164**	Aldehyde reductase
4.9E-229	0.754	1.688		**1.221**	**0.660**	Antiapoptosis clone 11 protein
4.24E-38	0.896	1.568	1.200	**1.221**	**0.336**	40S ribosomal protein S26
3.37E-60	0.929	1.383	1.353	**1.221**	**0.254**	RNA polymerase II subunit A C-terminal domain phosphatase SSU72
0	1.089	1.264	1.313	**1.222**	**0.118**	Interferon-induced protein 53
2.03E-37	1.013	1.249	1.403	**1.222**	**0.197**	28S ribosomal protein S22, mitochondrial
2.82E-07	0.801	0.969	1.898	**1.223**	**0.591**	HECT domain and RCC1-like domain-containing protein 4
0	1.259	1.112	1.300	**1.224**	**0.099**	Oncogene DJ1
3.79E-67	0.927	1.305	1.442	**1.225**	**0.267**	cDNA FLJ59791, highly similar to Importin-11
7.38E-77	0.503	1.368	1.805	**1.225**	**0.663**	cDNA FLJ57190, highly similar to Actin-binding protein anillin
8.4E-60	1.129	1.154	1.392	**1.225**	**0.145**	Aminoacylproline aminopeptidase
7.1E-164	0.598	1.406	1.672	**1.225**	**0.559**	Thymidylate synthase
8E-206	1.168		1.284	**1.226**	**0.083**	Ankyrin repeat and FYVE domain-containing protein 1
1.4E-45	0.556	1.805	1.318	**1.226**	**0.630**	23 kDa highly basic protein
5.56E-11	1.806	0.903	0.971	**1.226**	**0.503**	SLAIN motif-containing protein 2
3.7E-163	0.696	0.946	2.040	**1.227**	**0.715**	11B6
1.4E-243	2.119	1.039	0.523	**1.227**	**0.814**	Dynamin-like 120 kDa protein, form S1
1.07E-56	0.998	1.095	1.589	**1.227**	**0.317**	cDNA FLJ56394, highly similar to N-acetylglucosamine kinase (EC 2.7.1.59)
1.32E-10	0.989	1.211	1.484	**1.228**	**0.247**	Aminoacylase-1-like protein 2
7.01E-64	1.043	1.289	1.354	**1.228**	**0.164**	Antigen NY-CO-7
1.69E-52	1.227	1.231		**1.229**	**0.003**	cDNA FLJ51495, highly similar to ADP-ribosylation factor 5
1.53E-32	0.952		1.505	**1.229**	**0.391**	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial
6.85E-40	0.527	1.630	1.529	**1.229**	**0.610**	Solute carrier family 35 member E1
2.4E-225	0.850	1.469	1.369	**1.229**	**0.332**	Protein A6
1.4E-131	1.058	1.619	1.014	**1.230**	**0.337**	Melanoma-associated antigen p97

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.11E-47	0.748	1.805	1.139	**1.230**	**0.534**	60S ribosomal protein L27a
9.5E-155	1.039	1.345	1.309	**1.231**	**0.167**	Beta-MPP
7.59E-42	1.039	1.283	1.373	**1.231**	**0.173**	cDNA FLJ53927, highly similar to Beta-hexosaminidase alpha chain (EC 3.2.1.52)
1.66E-19	1.095	1.369		**1.232**	**0.193**	Polyamine-modulated factor 1
3.72E-30	0.786	1.470	1.440	**1.232**	**0.387**	Carnitine acetyltransferase
1.3E-109	0.974	1.228	1.495	**1.232**	**0.261**	Beta-galactosidase
1.83E-45	1.219	1.185	1.293	**1.232**	**0.055**	UPF0368 protein Cxorf26
0	1.423	1.488	0.788	**1.233**	**0.387**	Nicotinamide phosphoribosyltransferase
3.4E-164	0.748	1.060	1.892	**1.233**	**0.591**	Intron-binding protein aquarius
2.6E-207	1.193	1.282	1.230	**1.235**	**0.045**	Aldehyde dehydrogenase family 6 member A1
1.5E-197	1.012	0.373	2.323	**1.236**	**0.994**	Androgen receptor coactivator 160 kDa protein
4E-50	0.975		1.498	**1.236**	**0.370**	140 kDa nucleolar phosphoprotein
1.9E-100	0.724	0.797	2.189	**1.236**	**0.826**	Coiled-coil and C2 domain-containing protein 1A
1.6E-156	1.030	1.749	0.931	**1.237**	**0.446**	Isochorismatase domain-containing protein 2, mitochondrial
6.56E-89	1.047	1.317	1.348	**1.237**	**0.166**	Beta-diketonase
1.9E-134	0.486	1.989		**1.237**	**1.063**	Putative uncharacterized protein DENR
0	0.873	0.824	2.017	**1.238**	**0.675**	ATP-dependent helicase RENT1
6.48E-47	1.433	0.960	1.322	**1.238**	**0.247**	Protein NipSnap homolog 1
6.4E-102	0.918	1.344	1.453	**1.238**	**0.283**	cDNA FLJ56334, highly similar to SEC13-related protein
7.83E-85	1.031	1.278	1.408	**1.239**	**0.192**	COP9 signalosome complex subunit 1
0	1.261	1.302	1.156	**1.239**	**0.075**	Adenylosuccinase
1.56E-10	0.997		1.482	**1.240**	**0.343**	Cysteine-S-conjugate beta-lyase 2
0	1.152	1.398	1.170	**1.240**	**0.137**	Vacuolar ATPase isoform VA68
9.8E-102	1.086	1.288	1.350	**1.241**	**0.138**	DCN1-like protein 1
3.1E-99	1.664	1.127	0.933	**1.241**	**0.378**	Calcium-binding protein ERC-55
4.9E-135	1.053	1.283	1.392	**1.243**	**0.173**	Calregulin
5.3E-114	1.065	0.622	2.042	**1.243**	**0.727**	DNA replication complex GINS protein PSF3
5.29E-33	1.273	1.214		**1.243**	**0.042**	Cyclophilin-33B
3.3E-300	1.482	1.066	1.188	**1.246**	**0.214**	3-hydroxyisobutyrate dehydrogenase, mitochondrial
2.94E-74	1.014	0.942	1.781	**1.246**	**0.465**	Copper chaperone for superoxide dismutase
2.46E-14	1.253		1.240	**1.247**	**0.009**	Low molecular mass protein 2
1.53E-58	0.460	1.837	1.446	**1.248**	**0.710**	Putative uncharacterized protein EIF2A
9.6E-176	1.299	1.246	1.201	**1.249**	**0.049**	cDNA FLJ30560 fis, clone BRAWH2004217, highly similar to AP-1 complex subunit gamma-1
4.83E-13	0.757	1.278	1.714	**1.250**	**0.479**	Putative uncharacterized protein TRPT1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.4E-169	1.254	1.120	1.377	**1.250**	**0.128**	Adenylate kinase 3
1.2E-213	1.283	1.230	1.238	**1.251**	**0.029**	Actin-RPV
9E-147	0.708	1.368	1.676	**1.251**	**0.494**	Surfeit locus protein 4
4.57E-47	0.672	1.390	1.690	**1.251**	**0.523**	Mitotic checkpoint protein BUB3
1.38E-67	0.541	1.765	1.447	**1.251**	**0.635**	Butyrate-induced protein 1
4.62E-78	0.089	1.918	1.748	**1.252**	**1.011**	Histone H4
5.43E-42	0.729	0.729	2.297	**1.252**	**0.905**	Activator-recruited cofactor 105 kDa component
0	0.865	1.016	1.877	**1.252**	**0.546**	Alpha-actinin cytoskeletal isoform
2.63E-11	0.433	1.052	2.273	**1.253**	**0.936**	Charged multivesicular body protein 3
9.31E-39	0.967	1.177	1.618	**1.254**	**0.332**	Probable saccharopine dehydrogenase
6.7E-173	1.478	1.007	1.278	**1.254**	**0.237**	Coatomer subunit gamma-2
1.7E-159	0.604	1.806	1.354	**1.254**	**0.607**	Ribosomal protein L10
6.2E-102	0.934	1.508	1.322	**1.255**	**0.293**	CNDP dipeptidase 2
0	0.720	2.032	1.014	**1.255**	**0.688**	CCAAT-binding transcription factor I subunit A
1.74E-65	0.737	1.798	1.232	**1.255**	**0.531**	highly similar to Peptidyl-tRNA hydrolase 2, mitochondrial (EC 3.1.1.29)
1.2E-113	1.060	1.319	1.388	**1.256**	**0.173**	Barrier-to-autointegration factor
0	1.195	1.325	1.249	**1.256**	**0.065**	ATP-dependent RNA helicase DDX1
8.91E-05	0.794		1.719	**1.257**	**0.654**	CFTR-associated ligand
1.28E-47	0.570	1.866	1.335	**1.257**	**0.651**	193 kDa vault protein
1.4E-121	0.945	1.910	0.915	**1.257**	**0.566**	Sideroflexin-1
1.39E-19	0.856	1.425	1.490	**1.257**	**0.348**	Immunity-related GTPase family Q protein
1.45E-21	1.259	1.307	1.205	**1.257**	**0.051**	Mammalian ependymin-related protein 1
9.3E-282	1.392	0.756	1.624	**1.257**	**0.449**	3-oxoacid-CoA transferase 1
1.9E-155	1.276	1.240		**1.258**	**0.026**	Hypoxanthine-guanine phosphoribosyltransferase
0	1.190	1.137	1.447	**1.258**	**0.166**	Kinesin heavy chain isoform 5C
7.81E-33	1.125	0.904	1.748	**1.259**	**0.438**	Neural Wiskott-Aldrich syndrome protein
0	0.988	1.327	1.462	**1.259**	**0.244**	p195
1.6E-201	1.167	0.724	1.888	**1.260**	**0.587**	Signal recognition particle 54 kDa protein
0	1.004	1.201	1.580	**1.262**	**0.293**	Adenylyl cyclase-associated protein 1
4.1E-181	0.875	1.371	1.542	**1.263**	**0.347**	Nervous system over-expressed protein 20
3.5E-220	1.485	1.138	1.167	**1.263**	**0.192**	Cytidine monophosphate kinase
1.5E-11	1.149		1.379	**1.264**	**0.162**	CAAT box DNA-binding protein subunit C
0	0.907	1.397	1.489	**1.265**	**0.313**	Cytoplasmic dynein 1 heavy chain 1
2.5E-145	0.581	1.721	1.493	**1.265**	**0.603**	Interleukin enhancer-binding factor 2
2.31E-69	0.893	0.532	2.371	**1.265**	**0.975**	Human cervical cancer suppressor gene 4 protein
0	1.420	1.176	1.201	**1.265**	**0.134**	Signal transducer and activator of transcription 1-alpha/beta

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.86E-97	1.092	1.450	1.254	**1.265**	**0.179**	Protein phosphatase T
1.9E-99	0.887	1.303	1.609	**1.266**	**0.362**	KIF1-binding protein
4.14E-94	0.523	2.010		**1.266**	**1.052**	Phosphate carrier protein, mitochondrial
1.21E-06	1.157	1.119	1.524	**1.267**	**0.224**	Thiopurine methyltransferase
5.48E-24	1.087	1.448		**1.267**	**0.255**	Choline transporter-like protein 2
2.97E-11	1.226	1.372	1.204	**1.267**	**0.091**	Adenosine 5'-phosphotransferase
1.3E-113	0.748	1.838	1.217	**1.268**	**0.547**	Endothelin-converting enzyme 1
2.6E-249	1.535	1.391	0.878	**1.268**	**0.345**	Alpha-aminoadipic semialdehyde synthase, mitochondrial
5.8E-149	1.176	1.158	1.470	**1.268**	**0.175**	NEDD8-activating enzyme E1 catalytic subunit
5.12E-16	1.192	1.425	1.190	**1.269**	**0.135**	Glutathione S-transferase theta-1
2.4E-204	0.896	1.198	1.712	**1.269**	**0.413**	Cyclin-A/CDK2-associated protein p19
5.7E-170	1.168	1.264	1.376	**1.269**	**0.104**	Spermidine aminopropyltransferase
1.6E-26	1.025	1.614	1.172	**1.270**	**0.307**	MACRO domain-containing protein 1
9.53E-63	1.116	1.034	1.664	**1.271**	**0.342**	Exportin-4
8.2E-191	1.129	1.446	1.240	**1.272**	**0.161**	Galactowaldenase
1.3E-136	1.243	1.324	1.251	**1.272**	**0.045**	Phosphoribosyl pyrophosphate synthase I
2.59E-41	0.479	2.723	0.619	**1.274**	**1.257**	Uncharacterized protein C7orf50
6.2E-25	0.809	1.424	1.589	**1.274**	**0.411**	A34.5
0	1.060	0.638	2.125	**1.274**	**0.766**	Acute-phase response factor
2E-131	1.090	0.513	2.219	**1.274**	**0.868**	D-fructose-6-phosphate amidotransferase 1
1.6E-164	1.863	0.890	1.069	**1.274**	**0.518**	Ally of AML-1 and LEF-1
3.66E-28	0.798	1.756	1.271	**1.275**	**0.479**	DnaJ homolog subfamily C member 17
5.95E-80	0.623	0.859	2.344	**1.275**	**0.933**	Protein transport protein Sec23B
2.1E-107	1.285	0.714	1.826	**1.275**	**0.556**	Activator of 90 kDa heat shock protein ATPase homolog 1
1.9E-128	1.063	1.401	1.368	**1.277**	**0.186**	Glutaredoxin-3
2.22E-69	0.934	1.452	1.447	**1.277**	**0.297**	Importin-12
0	0.454	0.924	2.455	**1.278**	**1.046**	100 kDa DNA-pairing protein
7.8E-99	0.730	0.330	2.774	**1.278**	**1.311**	HLA-B associated transcript 3
1.75E-45	0.697	1.723	1.415	**1.278**	**0.526**	Zinc finger protein 185 variant 721
5.5E-206	1.210	1.346		**1.278**	**0.096**	6-phosphofructokinase, muscle type
0	1.046	1.346	1.444	**1.278**	**0.208**	NAP-1-related protein
0	0.852	1.012	1.974	**1.279**	**0.607**	L-lactate dehydrogenase
1.34E-30	1.038	1.458	1.343	**1.280**	**0.217**	GAPex-5
5.14E-97	0.710	1.494	1.635	**1.280**	**0.498**	Prolylcarboxypeptidase (Angiotensinase C), isoform CRA_b
9.04E-58	0.815	0.470	2.557	**1.280**	**1.119**	tRNA (adenine-N(1)-)-methyltransferase non-catalytic subunit TRM6

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.4E-188	1.126	1.362	1.354	**1.281**	**0.134**	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
1.12E-25	1.199	1.871	0.772	**1.281**	**0.554**	Protein phosphatase inhibitor 2
0	1.062	1.277	1.503	**1.281**	**0.221**	Deubiquitinating enzyme 7
1.5E-137	0.876	1.923	1.044	**1.281**	**0.562**	Densin-180-like protein
0	0.766	1.837	1.241	**1.281**	**0.537**	Putative uncharacterized protein CIT
6.2E-127	1.064	1.273	1.507	**1.282**	**0.222**	Glycine hydroxymethyltransferase
1.8E-213	1.774	0.964	1.107	**1.282**	**0.433**	Alu corepressor 1
1.4E-125	1.137	1.311	1.399	**1.282**	**0.133**	cDNA FLJ59687, highly similar to Secernin-1
2.04E-46	0.600	1.966		**1.283**	**0.966**	ATPase family homolog up-regulated in senescence cells 1
6.73E-73	0.974	1.147	1.731	**1.284**	**0.396**	Antigen NY-CO-13
4.1E-295	1.309	0.559	1.985	**1.284**	**0.713**	GCUNC-45
3.95E-58	0.993	1.365	1.496	**1.284**	**0.261**	UPF0160 protein MYG1, mitochondrial
4.17E-62	0.873	1.187	1.796	**1.285**	**0.470**	41 kDa phosphoribosypyrophosphate synthetase-associated protein
0	1.081	1.369	1.406	**1.285**	**0.178**	620 kDa actin-binding protein
0	0.081		2.493	**1.287**	**1.705**	Histone H2B
0	1.137	1.359	1.368	**1.288**	**0.131**	Dipeptidyl aminopeptidase III
1.12E-11	1.252	1.325		**1.288**	**0.052**	ATP-specific succinyl-CoA synthetase subunit beta
8E-165	0.736	2.997	0.139	**1.291**	**1.508**	General transcription factor 3C polypeptide 3
2.66E-69	0.995	1.588		**1.291**	**0.419**	Branched-chain-amino-acid aminotransferase, cytosolic
1.7E-107	1.318		1.267	**1.293**	**0.036**	Ankyrin repeat domain-containing protein 28
1.69E-12	1.148	1.773	0.958	**1.293**	**0.426**	HD domain-containing protein 2
4.8E-166	0.874	1.551	1.457	**1.294**	**0.367**	Mannosyl-oligosaccharide glucosidase
1.59E-54	0.691	1.898	1.294	**1.295**	**0.603**	2',5'-phosphodiesterase 12
2.09E-86	1.202	0.936	1.746	**1.295**	**0.413**	Gamma-soluble NSF attachment protein
0.000399	0.695		1.896	**1.295**	**0.849**	Nucleoporin SEH1
7.7E-61	1.158	1.407	1.321	**1.295**	**0.127**	Ubiquitin carboxyl-terminal hydrolase isozyme L3
2.22E-64	1.875	1.258	0.752	**1.295**	**0.562**	Integrator complex subunit 7
5.7E-198	0.912	1.679		**1.296**	**0.542**	Cytoplasmic dynein 1 intermediate chain 2
1.5E-200	0.948	1.818	1.123	**1.296**	**0.461**	Hsp90 chaperone protein kinase-targeting subunit
1.5E-102	0.426	1.560	1.903	**1.297**	**0.773**	LIV-1 subfamily of ZIP zinc transporter 4
0	0.811	1.251	1.829	**1.297**	**0.510**	Kinetochore protein Spc24
0	0.859	1.402	1.631	**1.297**	**0.396**	Talin-1
0	0.757	1.526	1.609	**1.298**	**0.470**	Pre-mRNA-splicing factor SF3b 130 kDa subunit
6.8E-158	1.176	1.275	1.442	**1.298**	**0.134**	Protein flightless-1 homolog
2.21E-23	1.434	1.162		**1.298**	**0.193**	Leucine-rich repeat-containing protein 40

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
8.33E-95	0.967	1.821	1.109	**1.299**	**0.458**	highly similar to Homo sapiens RCD1 required for cell differentiation 1 homolog (RQCD1), mRNA
3.28E-44	1.031	1.310	1.556	**1.299**	**0.263**	Selenoprotein Z
1.7E-103	0.730	1.525	1.645	**1.300**	**0.497**	Nardilysin (N-arginine dibasic convertase)
5.55E-41	0.841	0.998	2.060	**1.300**	**0.663**	DNA primase 58 kDa subunit
1.18E-27	1.093	1.511		**1.302**	**0.296**	Docking protein alpha
3.5E-245	1.675	1.379	0.852	**1.302**	**0.417**	3'-phosphoadenosine-5'-phosphosulfate synthase
0	0.737	1.597	1.573	**1.302**	**0.490**	Putative uncharacterized protein DKFZp779B0247
1.7E-179	1.335	1.286	1.296	**1.306**	**0.026**	Carbonyl reductase II
6.8E-177	1.266	1.192	1.459	**1.306**	**0.138**	Dendritic cell-derived IFNG-induced protein
2.03E-53	0.992	1.730	1.198	**1.306**	**0.381**	Ras-related protein Rab-5B
2.3E-134	0.835	1.330	1.757	**1.307**	**0.461**	CF-1 77 kDa subunit
9.77E-07	0.649	1.970		**1.310**	**0.934**	DNA excision repair protein ERCC-4
0	1.113	1.256	1.563	**1.310**	**0.230**	Beta-II spectrin
8.66E-63	0.958	1.256	1.721	**1.311**	**0.385**	Beta-lactamase-like protein 2
8.52E-27	1.000	1.328	1.607	**1.312**	**0.303**	NHL repeat-containing protein 2
1.78E-73	1.219	1.687	1.029	**1.312**	**0.339**	p53-induced gene 3 protein
5.3E-166	1.089	1.161	1.690	**1.313**	**0.328**	Apoptosis-linked gene 2 protein
1.7E-113	1.257	1.388	1.299	**1.314**	**0.067**	cDNA FLJ59142, highly similar to Epididymal secretory protein E1
1.21E-24	1.026	0.453	2.465	**1.315**	**1.037**	cDNA FLJ58590, highly similar to YLP motif-containing protein 1
3E-109	1.346	1.728	0.870	**1.315**	**0.430**	Interferon-induced 35 kDa protein
9.52E-29	0.591	1.853	1.501	**1.315**	**0.651**	Complex I-PDSW
3.4E-102	0.802	1.293	1.851	**1.315**	**0.525**	Pyridoxamine-phosphate oxidase
9.78E-29	0.784	0.283	2.882	**1.316**	**1.379**	Putative uncharacterized protein DKFZp667H197
2.69E-78	0.689	2.265	0.998	**1.317**	**0.835**	39S ribosomal protein L4, mitochondrial
7.3E-112	0.789	1.717	1.446	**1.317**	**0.477**	ADP-ribosylation factor-like protein 6-interacting protein 5
6.7E-210	1.327	1.259	1.370	**1.319**	**0.056**	Dihydrolipoamide dehydrogenase
0	0.948	1.510	1.499	**1.319**	**0.321**	cDNA FLJ55458, highly similar to Programmed cell death 6-interacting protein
3.25E-44	0.885		1.753	**1.319**	**0.614**	Putative uncharacterized protein TFG
2E-109	0.968	1.100	1.893	**1.320**	**0.500**	Importin alpha Q1
9.98E-86	1.467	1.159	1.335	**1.321**	**0.155**	Tubulin--tyrosine ligase-like protein 12
6.99E-89	1.315	1.795	0.853	**1.321**	**0.471**	Hydroxysteroid dehydrogenase-like protein 2
1E-73	1.084	2.106	0.776	**1.322**	**0.696**	Syntaxin 12
2.05E-62	1.123		1.527	**1.325**	**0.286**	Putative uncharacterized protein SCFD1
4.33E-15	1.917	0.734		**1.325**	**0.836**	Elongation factor G 2, mitochondrial

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
2.2E-288	1.125	0.739	2.113	**1.326**	**0.709**	Heterogeneous nuclear ribonucleoprotein U-like protein 2
0	0.959	1.551	1.468	**1.326**	**0.320**	Lamina-associated polypeptide 2, isoform alpha
5.55E-59	0.744	1.588	1.646	**1.326**	**0.505**	Abeta-degrading protease
1.8E-193	0.960	0.855	2.164	**1.327**	**0.727**	11S regulator complex subunit gamma
2.12E-15	1.742	0.914		**1.328**	**0.585**	Selenoprotein O
0	0.945	1.210	1.830	**1.328**	**0.454**	cDNA FLJ52765, highly similar to Calponin-2
0	1.196	1.357	1.433	**1.329**	**0.121**	Aconitase 2, mitochondrial
1.12E-07	1.970	0.277	1.741	**1.329**	**0.918**	Deubiquitinating enzyme 24
2.6E-103	1.089	1.025	1.877	**1.330**	**0.474**	FIS1 homolog
6.6E-39	0.985	1.676		**1.331**	**0.489**	Ankyrin repeat domain-containing protein 40
4.6E-168	0.713	1.419	1.860	**1.331**	**0.579**	60 kDa poly(U)-binding-splicing factor
1.66E-36	0.904		1.760	**1.332**	**0.605**	Heat shock protein-binding protein 1
2.4E-114	1.092	1.363	1.548	**1.334**	**0.229**	Glucosamine-6-phosphate deaminase 1
6.77E-18	1.562	1.587	0.856	**1.335**	**0.415**	Arginine/proline-rich coiled-coil domain-containing protein 1
6.98E-09	0.807	0.615	2.582	**1.335**	**1.084**	Putative uncharacterized protein CWC22
2.1E-41	1.411	1.261		**1.336**	**0.106**	Brain and reproductive organ-expressed protein
1.6E-134	1.000	1.438	1.571	**1.337**	**0.299**	3D3/LYRIC
4.1E-149	0.971	1.402	1.647	**1.340**	**0.342**	Mitochondrial Rho GTPase 2
6E-213	1.597		1.084	**1.341**	**0.363**	highly similar to Homo sapiens capping protein (actin filament), gelsolin-like(CAPG), mRNA
4.66E-39	0.693	1.046	2.285	**1.341**	**0.836**	U1 small nuclear ribonucleoprotein 70 kDa
1.66E-07	0.772	1.539	1.712	**1.341**	**0.501**	GAA1 protein homolog
0	0.971	1.597	1.459	**1.342**	**0.329**	Protein A1S9
5.91E-55	0.457	3.314	0.259	**1.343**	**1.710**	Modulator of non-genomic activity of estrogen receptor
2.1E-242	1.717	1.091	1.227	**1.345**	**0.329**	3-ketoacyl-CoA thiolase, mitochondrial
4.3E-108	1.102	2.481	0.456	**1.346**	**1.035**	LIM protein RIL
9E-232	1.145		1.549	**1.347**	**0.285**	CapZ beta
3.06E-19	0.638	2.060		**1.349**	**1.005**	FCH domain only protein 2
1.42E-69	0.869	0.626	2.556	**1.350**	**1.051**	88 kDa nucleoporin
4.21E-55	1.387	1.324	1.342	**1.351**	**0.032**	Pre-mRNA-splicing factor SRP55
1.3E-269	1.026	1.694	1.334	**1.351**	**0.334**	cDNA FLJ61202, highly similar to Multisynthetase complex auxiliary component p43
7.87E-31	0.721	1.982		**1.352**	**0.892**	Contactin-associated protein 1
1.49E-49	0.772	1.385	1.898	**1.352**	**0.564**	Autosomal dominant polycystic kidney disease type II protein
2.49E-45	1.075	1.658	1.331	**1.355**	**0.292**	cDNA FLJ54536, highly similar to Mitochondrial 28S ribosomal protein S27

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
5.3E-150	0.801	1.207	2.057	**1.355**	**0.641**	Coatomer subunit zeta-1
1.69E-63	0.925	2.304	0.838	**1.355**	**0.822**	Mammalian guanine nucleotide exchange factor mSec12
9.5E-122	1.095	1.808	1.165	**1.356**	**0.393**	Protein transport protein Sec24C
3.9E-110	1.422	1.214	1.433	**1.356**	**0.123**	highly similar to Homo sapiens glutathione transferase zeta 1 (GSTZ1), transcript variant 3, mRNA
1.8E-120	0.709	2.128	1.233	**1.357**	**0.718**	cDNA FLJ53381, highly similar to Monocarboxylate transporter 1
8.58E-16	1.102		1.612	**1.357**	**0.361**	UPF0760 protein C2orf29
4.2E-236	1.404	1.242	1.424	**1.357**	**0.100**	Coactosin-like protein
1.4E-278	1.453	1.256	1.364	**1.358**	**0.099**	Putative uncharacterized protein PSME2
0	1.439	1.277		**1.358**	**0.115**	Extended synaptotagmin-1
0	1.056	1.247	1.776	**1.360**	**0.373**	NSFL1 cofactor p47
2.89E-19	1.349	1.288	1.445	**1.361**	**0.079**	Glyoxalase II
4.43E-84	0.797	2.640	0.648	**1.362**	**1.109**	Ezrin-radixin-moesin-binding phosphoprotein 50
2.9E-159	1.303	1.381	1.400	**1.362**	**0.051**	Acetyl-CoA acetyltransferase, cytosolic
1.9E-122	1.344	1.301	1.440	**1.362**	**0.071**	Adipocyte acid phosphatase
6.83E-21	1.056	1.464	1.567	**1.362**	**0.270**	Cytoplasmic antiproteinase 2
2.36E-09	1.426	1.138	1.524	**1.363**	**0.201**	DnaJ homolog subfamily C member 20
4.51E-95	1.353	1.383	1.354	**1.363**	**0.017**	Inosine triphosphate pyrophosphatase
3.94E-31	1.132	1.250	1.708	**1.363**	**0.305**	Bax antagonist selected in saccharomyces 1
8.85E-09	1.406	1.322		**1.364**	**0.059**	Exocyst complex component 3
3.8E-176	1.452	1.338	1.306	**1.365**	**0.077**	Heme oxygenase 2
9.83E-11	0.609	2.121		**1.365**	**1.069**	Ecotropic retroviral leukemia receptor homolog
0	0.889	0.965	2.248	**1.367**	**0.764**	Tubulin beta-2 chain
8.9E-188	1.557	1.269	1.276	**1.367**	**0.164**	Superoxide dismutase [Mn], mitochondrial
5.9E-195	1.933	0.507	1.665	**1.368**	**0.758**	Protein-tyrosine phosphatase 1D
6.33E-84	0.929	1.948	1.230	**1.369**	**0.524**	Calcineurin-like phosphoesterase domain-containing protein 1
2.68E-89	1.143	1.595	1.370	**1.369**	**0.226**	4-trimethylaminobutyraldehyde dehydrogenase
3.65E-17	1.473	1.358	1.280	**1.370**	**0.097**	Acyl-CoA thioester hydrolase 9
4.29E-40	0.591	1.237	2.284	**1.371**	**0.855**	Alpha-(1,6)-fucosyltransferase
0	0.592	2.092	1.436	**1.373**	**0.752**	DNA-dependent protein kinase catalytic subunit
0	1.069	1.609	1.447	**1.375**	**0.277**	Puromycin-sensitive aminopeptidase
1.14E-27	0.993	1.142	1.991	**1.375**	**0.538**	BTG1-binding factor 1
2.86E-22	0.674	2.469	0.985	**1.376**	**0.959**	Alba-like protein C9orf23
4.69E-36	0.791	0.879	2.460	**1.377**	**0.939**	Glycogen synthase kinase-3 beta
0	1.001	1.352	1.785	**1.379**	**0.393**	Hepatocellular carcinoma autoantigen p62

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	1.543	1.005	1.590	**1.379**	**0.325**	eIF3 p167
0	1.422	1.206	1.511	**1.380**	**0.157**	ABP-278
5.2E-295	0.565	1.207	2.370	**1.381**	**0.915**	CFR-1
3.5E-106	0.840	1.569	1.734	**1.381**	**0.476**	Ras-related protein Rab-5A
3.18E-21	1.242		1.521	**1.381**	**0.197**	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase
1.1E-236	0.833	2.327	0.984	**1.381**	**0.823**	Erythrocyte band 7 integral membrane protein
1.08E-15	0.383	1.404	2.366	**1.385**	**0.992**	Cleavage and polyadenylation specificity factor 73 kDa subunit
4.6E-238	0.718	1.085	2.353	**1.386**	**0.858**	ATP-dependent RNA helicase eIF4A-1
0	1.194	1.179	1.787	**1.386**	**0.347**	Alpha-glucosidase 2
7.39E-67	0.983	1.978	1.206	**1.389**	**0.522**	APC-binding protein EB2
2.48E-26	0.478	2.355	1.339	**1.391**	**0.940**	Fragile X mental retardation 1 protein
7.06E-16	0.550	2.233		**1.391**	**1.190**	Hyaluronan mediated motility receptor
3.38E-89	0.443	1.744	1.988	**1.392**	**0.830**	Collagen alpha-1(V) chain
1.33E-30	1.196	1.346	1.634	**1.392**	**0.222**	Chorea-acanthocytosis protein
3E-233	1.337	1.344	1.499	**1.393**	**0.091**	Glutaredoxin-related protein 5, mitochondrial
8.6E-227	1.421	0.501	2.264	**1.396**	**0.882**	Lon protease homolog, mitochondrial
1.43E-10	0.932	2.528	0.728	**1.396**	**0.985**	17-beta-hydroxysteroid dehydrogenase 12
4.25E-28	0.787	1.233	2.170	**1.396**	**0.706**	Inactive ubiquitin-specific peptidase 39
6.84E-31	1.033	2.138	1.019	**1.397**	**0.643**	3-hydroxy-3-methylglutarate-CoA lyase
2.39E-06	1.206		1.589	**1.398**	**0.271**	Leucine-rich repeat-containing protein 20
4.13E-30	0.897	1.669	1.633	**1.400**	**0.436**	EPM2A-interacting protein 1
2.6E-131	0.766	2.375	1.058	**1.400**	**0.857**	Ras-related protein Ral-A
0	1.001		1.804	**1.402**	**0.568**	Nuclear autoantigenic sperm protein
0	1.015	1.792		**1.403**	**0.550**	Hemidesmosomal protein 1
1.9E-127	0.629	1.835	1.748	**1.404**	**0.672**	53 kDa BRG1-associated factor A
2E-99	0.675		2.133	**1.404**	**1.031**	Putative uncharacterized protein NOP2
9.7E-215	0.985	2.181	1.056	**1.407**	**0.671**	Intersectin-2
2.2E-252	1.061	0.809	2.352	**1.407**	**0.827**	100 kDa coated vesicle protein A
0	1.003	1.259	1.962	**1.408**	**0.497**	48 kDa TATA box-binding protein-interacting protein
5.53E-98	1.349	1.640	1.235	**1.408**	**0.209**	Abraxas brother protein 1
5.31E-37	0.526	0.642	3.067	**1.412**	**1.435**	cAMP regulatory element-associated protein 1
9.1E-195	0.854	1.571	1.811	**1.412**	**0.498**	Archain 1, isoform CRA_a
7.3E-147	1.281	1.612	1.345	**1.413**	**0.176**	2,3-diketo-5-methylthio-1-phosphopentane phosphatase
4.91E-49	0.650	2.541	1.050	**1.414**	**0.997**	Protease-activated kinase 1
4.59E-58	0.873	0.929	2.440	**1.414**	**0.889**	Cadherin-2

PEP	**Ratio H/L Reverse**	**Ratio L/H Forward1**	**Ratio L/H Forward2**	**Avg**	**STD**	**Protein Names**
1.1E-259	1.238	1.591		**1.414**	**0.250**	Putative uncharacterized protein EIF3CL
8.5E-287	0.931	0.188	3.124	**1.414**	**1.527**	Acidic leucine-rich nuclear phosphoprotein 32 family member E
2.42E-43	1.234	1.569	1.440	**1.415**	**0.169**	CB1 cannabinoid receptor-interacting protein 1
5.1E-151	1.052	1.555	1.639	**1.415**	**0.317**	KDEL motif-containing protein 2
9.9E-163	0.731	1.401	2.114	**1.415**	**0.691**	Elongation factor 1-beta
2.6E-104	0.729	1.402	2.117	**1.416**	**0.694**	Small nuclear ribonucleoprotein Sm D3
4.1E-110	1.071	1.337	1.849	**1.419**	**0.395**	Cytokine-induced protein of 29 kDa
2.8E-113	0.892	1.549	1.821	**1.420**	**0.478**	Nucleoporin NUP188 homolog
1.7E-119	0.874	1.745	1.649	**1.423**	**0.477**	DnaJ homolog subfamily B member 1
1.1E-219	1.164	1.507	1.602	**1.424**	**0.231**	Sepiapterin reductase
0	1.106	0.964	2.204	**1.425**	**0.679**	CCT-gamma
2.63E-31	0.814	1.197	2.263	**1.425**	**0.751**	ANO6 protein
0	0.956	0.940	2.384	**1.426**	**0.829**	Alpha-tubulin 6
0	0.335	2.016	1.930	**1.427**	**0.947**	Basement membrane-associated chondroitin proteoglycan
1.55E-61	1.204	1.814	1.268	**1.429**	**0.335**	Phosphopantothenate--cysteine ligase
8.2E-244	1.385	1.561	1.343	**1.430**	**0.116**	Actin regulatory protein CAP-G
2.6E-107	1.160	0.872	2.264	**1.432**	**0.735**	CCR4-associated factor 1
5.5E-112	1.542	1.264	1.496	**1.434**	**0.149**	Cellular glutathione peroxidase
1.24E-20	1.144	0.826	2.335	**1.435**	**0.795**	WASH complex subunit FAM21A
3.7E-171	1.331	1.274	1.713	**1.439**	**0.239**	ATP-dependent RNA helicase eIF4A-2
1.07E-38	1.005	1.535	1.778	**1.439**	**0.395**	DNA primase 49 kDa subunit
3.6E-301	0.900	1.046	2.376	**1.441**	**0.813**	Protein transport protein Sec23A
6.22E-89	0.818	1.825	1.684	**1.442**	**0.545**	CLIP-associating protein 1
4.4E-267	1.157	1.715	1.457	**1.443**	**0.279**	OGDH protein
1.54E-67	1.014		1.874	**1.444**	**0.608**	DEAD box protein 46
2E-210	0.663	2.607	1.065	**1.445**	**1.026**	Alpha-NAC
1.28E-90	1.211	1.985	1.140	**1.446**	**0.469**	cDNA FLJ61560, highly similar to Tight junction protein ZO-2
6.6E-166	1.008	1.113	2.216	**1.446**	**0.669**	Akt phosphorylation enhancer
3E-118	0.492	2.547	1.300	**1.446**	**1.035**	NAD(P) transhydrogenase, mitochondrial
3.7E-115	0.976	1.685	1.679	**1.446**	**0.408**	CF-1 64 kDa subunit
1.91E-52	0.790	0.192	3.358	**1.447**	**1.682**	Guanine nucleotide exchange factor H1
4.06E-21	0.517	2.946	0.877	**1.447**	**1.311**	Complex I-30kD
1.59E-94	1.307	1.445	1.589	**1.447**	**0.141**	DnaJ homolog subfamily B member 4
6.1E-267	0.385	2.914	1.047	**1.449**	**1.311**	Prohibitin
5.57E-28	0.592	2.182	1.574	**1.450**	**0.802**	Protein tyrosine phosphatase, receptor type, K

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.8E-112	1.015	1.341	2.001	**1.452**	**0.502**	cDNA FLJ31747 fis, clone NT2RI2007377, highly similar to RNA-BINDING PROTEIN EWS
9E-110	0.880	1.104	2.375	**1.453**	**0.807**	cDNA FLJ54710, highly similar to Target of Myb protein 1
1.3E-226	1.445	1.770	1.159	**1.458**	**0.306**	Calumenin, isoform CRA_c
6.68E-30	0.771	0.829	2.775	**1.458**	**1.141**	18 kDa Sin3-associated polypeptide
2.67E-17	0.879	0.988	2.516	**1.461**	**0.915**	Ras GTPase-activating-like protein IQGAP2
2.5E-201	0.935	2.686	0.764	**1.462**	**1.064**	25 kDa FK506-binding protein
3.05E-52	0.757	3.106	0.531	**1.465**	**1.426**	Secretory carrier-associated membrane protein 1
1.65E-63	0.437	0.344	3.617	**1.466**	**1.864**	ATP-dependent RNA helicase DDX24
4.64E-18	0.472	2.276	1.668	**1.472**	**0.918**	B5
0	0.743	1.873	1.802	**1.473**	**0.633**	Annexin A2
1.3E-173	1.243	1.485	1.697	**1.475**	**0.227**	Calpactin I light chain
3.07E-24	0.940	2.446	1.040	**1.475**	**0.842**	Extracellular signal-regulated kinase 6
0	0.633	2.259	1.536	**1.476**	**0.815**	Helix-destabilizing protein
2.11E-43	0.654	2.146	1.629	**1.476**	**0.758**	Synaptic glycoprotein SC2
0	1.274	1.487	1.679	**1.480**	**0.203**	ER-Golgi SNARE of 24 kDa
8.05E-52	0.922	1.512	2.007	**1.480**	**0.543**	UbcH2
5.07E-54	1.015	1.992	1.434	**1.480**	**0.490**	Mammalian STE20-like protein kinase 1
2.11E-59	0.841	1.409	2.191	**1.480**	**0.678**	Pre-mRNA-splicing factor SRP75
5.72E-40	0.967	1.503	1.973	**1.481**	**0.503**	Activator 1 40 kDa subunit
4.3E-154	0.726	1.989	1.729	**1.481**	**0.667**	Highly expressed in cancer protein
0	1.094	1.209	2.141	**1.481**	**0.574**	Aspartate carbamoyltransferase
5.36E-26	1.353	1.116	1.978	**1.482**	**0.445**	107 kDa nucleoporin
7.6E-41	0.703	2.262		**1.482**	**1.102**	Kinetochore-associated protein NSL1 homolog
4.72E-29	0.754	2.210		**1.482**	**1.030**	Pumilio homolog 2
1.7E-97	1.517	1.451		**1.484**	**0.047**	Acetoacetyl-CoA synthetase
1.23E-38	0.770	0.259	3.423	**1.484**	**1.698**	Neurogenic locus notch homolog protein 2
2.72E-21	0.394	2.140	1.921	**1.485**	**0.951**	Cell division cycle protein 73 homolog
5.41E-72	1.106	2.881	0.473	**1.487**	**1.249**	Protein DDI1 homolog 2
5.1E-169	0.880	1.762	1.820	**1.487**	**0.527**	Nuclear matrix protein 200
1.73E-65	1.053	1.688	1.726	**1.489**	**0.378**	Augmenter of liver regeneration
0	0.839	2.183	1.449	**1.491**	**0.673**	Adenylyl cyclase-associated protein 1
7.35E-96	0.070		2.911	**1.491**	**2.009**	Histone H3.2
6.88E-39	0.605	1.897	1.971	**1.491**	**0.768**	Nucleoporin NDC1
0	1.752	1.250	1.488	**1.496**	**0.251**	Enoyl-CoA hydratase 1
9E-08	1.018		1.975	**1.496**	**0.677**	Four and a half LIM-domain protein 2
3.9E-155	1.101	1.315	2.075	**1.497**	**0.512**	Treacher Collins syndrome protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
3.8E-71	0.895	2.759	0.837	**1.497**	**1.093**	DNA-binding protein NEFA
1.92E-55	1.527	0.653	2.316	**1.499**	**0.832**	Cytosolic Fe-S cluster assembly factor NUBP2
2.9E-112	0.156	2.422	1.925	**1.501**	**1.191**	Histone H1.5
1.6E-184	1.778	1.363	1.368	**1.503**	**0.238**	Clathrin light chain A
4.43E-21	0.713	3.119	0.682	**1.504**	**1.398**	Zinc finger CCCH-type antiviral protein 1-like
0	1.031	1.636	1.847	**1.505**	**0.424**	Alanine--tRNA ligase
4.28E-12	0.807	2.202		**1.505**	**0.986**	Carboxypeptidase M
7.71E-53	1.236	1.927	1.352	**1.505**	**0.370**	Glucosamine-6-phosphate deaminase 2
3E-24	0.639	2.373		**1.506**	**1.226**	Neural polypyrimidine tract-binding protein
1.5E-248	1.164	1.059	2.295	**1.506**	**0.685**	ATP-binding cassette 50
4.18E-91	1.111	0.965	2.445	**1.507**	**0.816**	E3 ubiquitin/ISG15 ligase TRIM25
3.21E-61	0.783	1.618	2.120	**1.507**	**0.675**	UPF0557 protein C10orf119
5.6E-114	0.907	1.833	1.781	**1.507**	**0.521**	N-recognin-7
1.64E-64	0.969	2.753	0.801	**1.507**	**1.082**	Glycine-rich protein
3.17E-80	0.891	2.007	1.627	**1.508**	**0.567**	Ras-related protein Rab-8B
8.56E-89	1.115	0.844	2.570	**1.510**	**0.928**	Leucine zipper transcription factor-like protein 1
1.5E-186	1.283	1.436	1.811	**1.510**	**0.271**	EEF1D protein
2.66E-14	0.308	2.207	2.015	**1.510**	**1.045**	RNA-binding motif protein 42
0.000237	1.256		1.765	**1.511**	**0.360**	GDP-D-mannose dehydratase
1.04E-87	0.850	0.848	2.838	**1.512**	**1.148**	Eukaryotic translation initiation factor 3 subunit M
2.14E-95	0.537	1.782	2.219	**1.513**	**0.873**	Caltractin isoform 1
2.6E-189	1.119	1.685	1.737	**1.514**	**0.343**	Adapter molecule crk
1E-120	0.921	2.680	0.943	**1.514**	**1.010**	DnaJ homolog subfamily C member 8
1.04E-21	0.453	2.575		**1.514**	**1.500**	eNOS-interacting protein
6E-192	1.041	3.050	0.458	**1.516**	**1.360**	Hsc70-interacting protein
2.1E-16	1.088	0.779	2.684	**1.517**	**1.023**	Caseinolytic peptidase B protein homolog
2.6E-196	0.643	0.710	3.201	**1.518**	**1.458**	Tight junction protein 1
1.2E-232	1.032	2.029	1.496	**1.519**	**0.499**	La autoantigen
7.19E-37	1.355	1.544	1.658	**1.519**	**0.153**	Leucine--tRNA ligase
1.87E-50	0.991	2.531	1.044	**1.522**	**0.874**	Homozygously deleted in neuroblastoma 1
1.8E-108	1.219	0.815	2.533	**1.523**	**0.898**	FAS-associated factor 1
7.09E-50	0.755	1.758	2.055	**1.523**	**0.681**	ARF GTPase-activating protein GIT2
2.3E-211	0.558	1.890	2.127	**1.525**	**0.846**	Heme oxygenase 1
2.33E-33	1.090	1.866	1.629	**1.528**	**0.398**	CAAX farnesyltransferase subunit alpha
7.61E-98	0.352	3.411	0.826	**1.530**	**1.646**	Adenine nucleotide translocator 3
0	0.918	1.559	2.113	**1.530**	**0.598**	ABP-280-like protein
6.06E-72	0.969	1.001	2.625	**1.532**	**0.947**	28S ribosomal protein S28, mitochondrial

PEP	**Ratio H/L Reverse**	**Ratio L/H Forward1**	**Ratio L/H Forward2**	**Avg**	**STD**	**Protein Names**
0.00579	0.518	2.962	1.117	**1.532**	**1.274**	Antigenic surface determinant protein OA3
2.01E-47	1.250	1.537	1.813	**1.533**	**0.281**	ACC-alpha
9.09E-43	1.582	1.340	1.684	**1.535**	**0.176**	PRKC apoptosis WT1 regulator protein
1.28E-54	0.691	2.734	1.181	**1.535**	**1.067**	CDw90
8E-100	1.042	1.773	1.797	**1.537**	**0.429**	Serine/threonine-protein phosphatase 4 regulatory subunit 3A
1.05E-26	0.409	2.265	1.939	**1.538**	**0.991**	Cell growth-regulating nucleolar protein
0	0.657	1.803	2.154	**1.538**	**0.783**	DNA repair protein RAD50
9.39E-07	0.952		2.130	**1.541**	**0.833**	Kinesin-like protein KIF7
2.31E-60	0.821	2.000	1.807	**1.543**	**0.632**	Transmembrane protein 214
2.71E-06	0.856	2.230		**1.543**	**0.971**	highly similar to Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, gamma isoform
2.87E-06	0.433	1.919	2.279	**1.543**	**0.979**	cDNA FLJ42859 fis, clone BRHIP2009414, highly similar to Bax inhibitor 1
7.49E-08	0.981	2.108		**1.544**	**0.797**	Erythroid alpha-spectrin
7.07E-12	0.551	1.040	3.047	**1.546**	**1.323**	Cell proliferation-inducing gene 50 protein
0	0.728	0.726	3.186	**1.547**	**1.419**	Tubulin 5 beta
7.57E-50	1.391	1.510	1.741	**1.547**	**0.178**	Profilin II
1.82E-46	1.029	1.972	1.641	**1.547**	**0.479**	35 kDa lectin
1.8E-247	1.407	0.717	2.520	**1.548**	**0.910**	EH domain-containing protein 1
7.77E-62	0.912	1.462	2.272	**1.549**	**0.684**	Nuclear distribution protein nudE homolog 1
7.89E-13	1.012	1.533	2.101	**1.549**	**0.544**	Thyroid hormone receptor-associated protein 3
0	0.659	1.927	2.060	**1.549**	**0.774**	Tubulin beta-6 chain
0	0.546	1.606	2.495	**1.549**	**0.976**	47 kDa heat shock protein
6.74E-86	0.446	2.034	2.170	**1.550**	**0.959**	Endothelial differentiation-related factor 1
0	0.617	2.406	1.631	**1.552**	**0.898**	300 kDa mannose 6-phosphate receptor
7.25E-18	0.478	2.411	1.766	**1.552**	**0.984**	Methylmalonic aciduria and homocystinuria type C protein
1.15E-09	0.730	2.374		**1.552**	**1.162**	Decay-accelerating factor splicing variant 5
1.5E-202	0.036	3.742	0.880	**1.553**	**1.942**	Histone H2A type 1-B/E
7.88E-47	1.892	1.688	1.080	**1.553**	**0.423**	B-cell signal transduction molecule alpha 4
4.12E-69	1.370	1.739		**1.554**	**0.260**	EEF1A protein
8.48E-41	0.829	1.825	2.014	**1.556**	**0.637**	Cell cycle progression restoration gene 3 protein
1.99E-69	0.963	2.025	1.680	**1.556**	**0.542**	Cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa
2.81E-76	1.408		1.710	**1.559**	**0.213**	Bax-interacting factor 1
1.37E-85	1.459	0.712	2.507	**1.560**	**0.902**	highly similar to Phosphoacetylglucosamine mutase (EC 5.4.2.3)
3E-158	0.808	2.107	1.768	**1.561**	**0.674**	Epidermal growth factor receptor

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
2.2E-186	0.859	2.350	1.476	**1.562**	**0.749**	EPB72-like protein 2
1.25E-23	0.497		2.631	**1.564**	**1.509**	cDNA, FLJ95791, highly similar to Homo sapiens aurora kinase B (AURKB), mRNA
1.3E-252	1.279	2.097	1.316	**1.564**	**0.462**	C-t-PAK2
5.09E-28	1.062	1.638	1.997	**1.566**	**0.472**	Thioredoxin domain-containing protein 1
7.65E-44	1.088	2.044		**1.566**	**0.676**	General transcription factor IIF 74 kDa subunit
2.1E-106	0.926	2.843	0.937	**1.569**	**1.104**	cAMP-dependent protein kinase type I-alpha regulatory subunit
7.97E-51	1.380	1.731	1.599	**1.570**	**0.177**	cDNA FLJ51819, weakly similar to Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
3.01E-18	0.689	3.290	0.736	**1.572**	**1.488**	Sperm-associated antigen 7
4.08E-39	1.785	0.863	2.068	**1.572**	**0.630**	eIF-2B GDP-GTP exchange factor subunit delta
5.45E-63	0.467	2.680		**1.573**	**1.564**	Myeloid-associated differentiation marker
3.51E-21	0.813	2.308	1.603	**1.574**	**0.748**	60S ribosomal protein L34
4.55E-32	0.801	1.925	2.001	**1.576**	**0.672**	Sm protein B/B'
5.44E-60	0.967	0.877	2.886	**1.577**	**1.135**	Intestine-specific plastin
2.3E-186	1.179	1.749	1.803	**1.577**	**0.346**	Malic enzyme 2
1.61E-57	0.589	2.044	2.099	**1.577**	**0.856**	Cell division cycle 5-like protein
5.81E-51	1.362	1.895	1.478	**1.578**	**0.281**	5H9 antigen
5.6E-130	1.237	1.852	1.647	**1.579**	**0.313**	Intercellular adhesion molecule 1
2.92E-50	1.482	1.740	1.513	**1.579**	**0.141**	ADP-dependent glucokinase
1.6E-68	0.842	2.043	1.865	**1.583**	**0.648**	Ovarian/Breast septin epsilon
7.23E-70	0.684		2.492	**1.588**	**1.279**	Protein quaking
3.26E-69	1.012	1.815	1.938	**1.588**	**0.503**	Transmembrane protein 165
4.4E-172	0.287	2.239	2.244	**1.590**	**1.129**	Drug-sensitive protein 1
1.9E-152	0.922	1.742	2.110	**1.592**	**0.608**	Delta(3),delta(2)-enoyl-CoA isomerase
4.1E-108	1.316	2.429	1.034	**1.593**	**0.738**	Axin interaction partner and dorsalization antagonist
2.55E-70	1.115	2.465	1.208	**1.596**	**0.754**	cDNA FLJ46245 fis, clone TESTI4020596, highly similar to Homo sapiens calpain 5 (CAPN5)
5E-202	0.878	1.875	2.043	**1.599**	**0.630**	C9orf88 variant protein
1.27E-42	1.333	1.524	1.947	**1.601**	**0.314**	Rhodanese
1.3E-239	0.553	2.688	1.564	**1.602**	**1.068**	Atriopeptidase
1.18E-31	0.544	1.849	2.421	**1.605**	**0.962**	CLL-associated antigen KW-14
9.8E-203	0.828	1.909	2.079	**1.605**	**0.679**	Heterogeneous nuclear ribonucleoprotein F
3.6E-160	1.220	1.836	1.761	**1.606**	**0.336**	Golgin subfamily A member 1
1.08E-28	1.471	2.385	0.961	**1.606**	**0.721**	Cytochrome c-type heme lyase
3.4E-265	1.064	2.134	1.631	**1.610**	**0.536**	Diaphanous-related formin-1
0	0.889	2.081	1.868	**1.613**	**0.636**	Clonal evolution-related gene on chromosome 14 protein

PEP	**Ratio H/L Reverse**	**Ratio L/H Forward1**	**Ratio L/H Forward2**	**Avg**	**STD**	**Protein Names**
1.1E-101	0.578	1.860	2.411	**1.616**	**0.940**	ATP-dependent RNA helicase #3
3.7E-135	0.735	1.934	2.201	**1.623**	**0.781**	SNU66 homolog
1.1E-179	0.732	1.022	3.120	**1.624**	**1.303**	highly similar to Rattus norvegicus basic leucine zipper and W2 domains 1 (Bzw1), mRNA
2.2E-45	0.766	2.486		**1.626**	**1.216**	Fzo homolog
7.03E-44	0.888	1.928	2.070	**1.629**	**0.646**	Proteasome maturation protein
5.49E-36	0.701	2.704	1.483	**1.629**	**1.009**	weakly similar to Mus musculus spermatogenesis associated, serine-rich 2 (Spats2), mRNA
1.5E-131	1.019	2.911	0.960	**1.630**	**1.110**	Amplaxin
1.15E-48	0.964	0.161	3.771	**1.632**	**1.896**	Nucleoporin p58/p45
1.6E-139	2.784	0.924	1.196	**1.634**	**1.005**	ATP-dependent RNA helicase DDX19B
4.98E-46	1.233	1.564	2.110	**1.636**	**0.443**	Splicing factor 9G8
7E-101	1.012	2.260		**1.636**	**0.883**	Non-functional aryl hydrocarbon receptor interacting protein
1.19E-60	0.797	3.726	0.387	**1.637**	**1.821**	Purine-rich element-binding protein B
2.08E-60	2.329	1.202	1.381	**1.637**	**0.606**	D-dopachrome decarboxylase
0	1.330	2.546	1.050	**1.642**	**0.795**	FYVE and coiled-coil domain-containing protein 1
1.92E-83	1.083	1.894	1.949	**1.642**	**0.485**	Ly-GDI
5.08E-12	0.818	2.056	2.057	**1.644**	**0.715**	Serine/threonine-protein phosphatase 4 regulatory subunit 2
1.88E-70	0.776	1.816	2.340	**1.644**	**0.796**	eIF3 p42
5.31E-13	0.285	1.526	3.121	**1.644**	**1.422**	Novel nuclear protein 1
9E-185	0.310	3.792	0.832	**1.645**	**1.878**	Flotillin-1
1.06E-93	0.570	1.937	2.429	**1.645**	**0.963**	Histone deacetylase 2
3.78E-44	0.882	1.973	2.082	**1.646**	**0.664**	Actin-related protein 2/3 complex subunit 1A
4.4E-225	0.683	1.709	2.552	**1.648**	**0.936**	Splicing factor U2AF 65 kDa subunit
3.4E-137	1.445	0.218	3.282	**1.648**	**1.542**	Nercc1 kinase
3.32E-67	0.286	3.010		**1.648**	**1.926**	Met-induced mitochondrial protein
0	0.750	0.861	3.337	**1.649**	**1.462**	highly similar to Homo sapiens poly(rC) binding protein 2 (PCBP2), transcript variant 2, mRNA
0	1.031	0.749	3.169	**1.650**	**1.323**	CCT-epsilon
8.01E-67	1.441	1.057	2.452	**1.650**	**0.721**	Arsenical pump-driving ATPase
5.4E-230	0.876	2.732	1.342	**1.650**	**0.966**	Cell proliferation-inducing gene 54 protein
0	0.842	1.899	2.211	**1.651**	**0.718**	Replication factor A protein 1
2.4E-99	0.554	3.006	1.399	**1.653**	**1.246**	Putative RNA-binding protein 3
2.8E-119	0.739	1.780	2.443	**1.654**	**0.859**	Metastasis-associated 1-like 1
3.5E-153	0.632	2.875	1.471	**1.659**	**1.133**	Antigen NY-CO-4
4.5E-291	0.952	1.915	2.114	**1.660**	**0.621**	Lung resistance-related protein
2.02E-44	0.657		2.666	**1.662**	**1.420**	Neural polypyrimidine tract-binding protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.32E-95	0.931	2.395		**1.663**	**1.036**	Dysferlin
4E-116	0.829	1.839	2.321	**1.663**	**0.761**	80 kDa nuclear cap-binding protein
3.38E-07	0.400	2.926		**1.663**	**1.787**	highly similar to Breast cancer anti-estrogen resistance protein 1
1.02E-25	0.353	3.400	1.239	**1.664**	**1.568**	Cellular disintegrin-related protein
1.91E-21	0.913	1.915	2.165	**1.664**	**0.663**	Zinedin variant
8.47E-56	0.849	3.084	1.063	**1.665**	**1.234**	Guanine nucleotide-binding protein alpha-q
2.1E-174	1.625	0.951	2.422	**1.666**	**0.736**	CTP synthase 1
2.9E-198	0.490	3.061	1.449	**1.667**	**1.299**	60S ribosomal protein L1
2E-36	1.037	2.646	1.324	**1.669**	**0.858**	Alpha-2-macroglobulin receptor-associated protein
5.4E-191	0.338	3.720	0.949	**1.669**	**1.802**	B-cell receptor-associated protein BAP37
0	0.826		2.516	**1.671**	**1.195**	EIF4G1 protein
3.32E-21	0.643	4.260	0.111	**1.672**	**2.258**	60 kDa chaperonin
6.35E-83	1.781	2.485	0.751	**1.672**	**0.872**	Elongation factor Tu GTP-binding domain-containing protein 1
7.3E-110	0.707	2.127	2.184	**1.673**	**0.837**	Ras-related protein Rab-21
2.21E-55	0.648	2.038	2.334	**1.673**	**0.900**	Eukaryotic translation initiation factor 2-alpha kinase 2
3.73E-08	0.900	2.567	1.556	**1.674**	**0.840**	Bone marrow stromal cell ubiquitin-like protein
2.2E-78	0.779	2.487	1.760	**1.675**	**0.857**	Eukaryotic translation initiation factor 5
1E-28	1.689	1.560	1.779	**1.676**	**0.110**	MacGAP
3.51E-36	0.706	1.221	3.102	**1.676**	**1.261**	Histone deacetylase 1
1.11E-09	0.692	2.645	1.702	**1.679**	**0.977**	CARD adapter inducing interferon beta
5.7E-244	1.327	1.933	1.799	**1.686**	**0.319**	Cell growth-inhibiting gene 39 protein
1.3E-141	1.829	1.686	1.549	**1.688**	**0.140**	Cathepsin C
3.15E-58	0.347	1.567	3.150	**1.688**	**1.405**	U3 small nucleolar RNA-associated protein 18 homolog
3.2E-192	1.376	1.831	1.859	**1.689**	**0.271**	Cell proliferation-inducing gene 31 protein
5.33E-56	0.685	0.467	3.919	**1.690**	**1.933**	Pre-mRNA-splicing factor SF3b 49 kDa subunit
4.28E-26	0.615	0.416	4.046	**1.692**	**2.041**	Putative uncharacterized protein TAX1BP1
0	0.317	2.648	2.115	**1.693**	**1.221**	Collagen alpha-1(XII) chain
5.51E-05	0.015	3.382		**1.698**	**2.381**	Triadin
1.7E-250	1.313	1.284	2.502	**1.699**	**0.695**	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
3.55E-40	1.254	2.358	1.494	**1.702**	**0.580**	90 kDa ribosomal protein S6 kinase 3
5E-221	1.125	1.860	2.122	**1.702**	**0.517**	Eukaryotic translation initiation factor 5B
3.2E-119	0.529	2.727	1.853	**1.703**	**1.106**	Transcription elongation factor A protein 1
8E-135	1.046	1.930	2.134	**1.703**	**0.578**	Integral nuclear envelope inner membrane protein
3.2E-127	0.802	1.841	2.468	**1.704**	**0.841**	Glycylpeptide N-tetradecanoyltransferase 1

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
7.2E-216	0.832	1.336	2.949	**1.706**	**1.106**	358 kDa nucleoporin
2.17E-95	2.668	0.875	1.586	**1.710**	**0.903**	cDNA FLJ56946, highly similar to Cysteine-rich protein 2
1.17E-16	1.404	0.667	3.060	**1.710**	**1.226**	Protein kinase C-like 2
3.38E-76	1.109	2.100	1.923	**1.711**	**0.528**	Beta-catenin-like protein 1
1.51E-09	0.953	2.895	1.299	**1.715**	**1.036**	ADP-ribosylation factor-interacting protein 1
2.1E-201	0.905	1.979	2.281	**1.721**	**0.723**	5'-3' exoribonuclease 2
5.4E-208	0.664	2.277	2.230	**1.724**	**0.918**	Mammalian branch point-binding protein
5.8E-151	1.006	1.723	2.445	**1.725**	**0.719**	Coronin-1B
2.71E-28	0.380	1.748	3.048	**1.725**	**1.335**	Cell death protein RIP
1.11E-45	1.008	2.474	1.696	**1.726**	**0.734**	Papillary renal cell carcinoma translocation-associated gene protein
4.18E-44	0.528	0.934	3.717	**1.726**	**1.736**	ATPase family AAA domain-containing protein 3A
8.82E-64	3.340	1.782	0.064	**1.729**	**1.638**	Beta-III spectrin
1.16E-22	1.407	0.902	2.888	**1.732**	**1.032**	Mediator of RhoA-dependent invasion
1.84E-98	0.906	1.479	2.813	**1.732**	**0.978**	Actin-related protein 2/3 complex subunit 1B
1.38E-19	0.050	0.936	4.212	**1.733**	**2.192**	39S ribosomal protein L44, mitochondrial
0	0.807	4.072	0.327	**1.736**	**2.038**	Adenylyl cyclase-associated protein
1.16E-13	1.526	1.949		**1.737**	**0.299**	28S ribosomal protein S25, mitochondrial
1.96E-86	0.739	3.422	1.055	**1.739**	**1.466**	cDNA FLJ57527, highly similar to 60S ribosomal protein L31
3.8E-93	1.126	0.914	3.181	**1.740**	**1.252**	cDNA FLJ54030, highly similar to Polymerase delta-interacting protein 3
1E-80	0.865		2.617	**1.741**	**1.239**	cDNA FLJ58199, highly similar to Fragile X mental retardation syndrome-related protein 1
2.8E-35	0.835		2.648	**1.741**	**1.282**	ABI gene family member 3
3.49E-45	0.756	1.627	2.843	**1.742**	**1.048**	Glutamine-rich protein 1
2.7E-266	0.993	1.352	2.894	**1.746**	**1.010**	Sorting nexin-2
2.19E-30	0.714	2.179	2.346	**1.746**	**0.898**	cDNA FLJ61553, highly similar to Focal adhesion kinase 1 (EC 2.7.10.2)
4.27E-31	1.224		2.270	**1.747**	**0.739**	Rab GTPase-binding effector protein 1
8.91E-07	0.557	0.378	4.309	**1.748**	**2.219**	MAGE tumor antigen CCF
0	1.198	1.916	2.131	**1.748**	**0.488**	Citrate hydro-lyase
6.9E-84	1.276	1.690	2.285	**1.750**	**0.507**	Adapter protein containing PH domain, PTB domain and leucine zipper motif 1
0	0.892	1.978	2.383	**1.751**	**0.771**	Alpha-CP1
1.7E-217	1.072	2.216	1.978	**1.755**	**0.603**	Arylacetamide deacetylase-like 1
1.48E-79	1.708	1.803		**1.755**	**0.067**	Actin-related protein 1B
5.33E-53	0.557	2.239	2.471	**1.756**	**1.045**	62 kDa nucleoporin
0	1.327	1.031	2.914	**1.757**	**1.013**	C-1-tetrahydrofolate synthase, cytoplasmic

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	0.805	1.132	3.338	**1.758**	**1.378**	60 kDa chaperonin
0	1.369	2.022	1.885	**1.759**	**0.345**	CAP-Gly domain-containing linker protein 1
9.67E-11	0.143	3.377		**1.760**	**2.287**	Demethylase
5.89E-25	0.914		2.611	**1.762**	**1.199**	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
4.06E-21	0.433	3.101		**1.767**	**1.887**	ATP-dependent RNA helicase DDX18
0.000661	0.462	1.875	2.970	**1.769**	**1.258**	Leucine-rich repeat and WD repeat-containing protein 1
0	0.980	1.923	2.404	**1.769**	**0.724**	Alpha-II spectrin
7.43E-87	1.264	3.017	1.030	**1.770**	**1.086**	Methyl-CpG-binding domain protein 3
0	1.078	0.787	3.450	**1.772**	**1.461**	Acute morphine dependence-related protein 2
6.97E-26	0.783	0.675	3.861	**1.773**	**1.809**	Protein phosphatase X
2.08E-56	0.652	2.369	2.298	**1.773**	**0.971**	Putative uncharacterized protein FAM98B
2.08E-20	1.228	1.506	2.594	**1.776**	**0.722**	PHD finger-like domain-containing protein 5A
1E-92	1.124	1.773	2.433	**1.776**	**0.655**	Cysteine and glycine-rich protein 2
1.07E-56	0.845	3.499	0.986	**1.777**	**1.494**	BAT2 domain-containing protein 1
1.3E-182	1.825	1.018	2.490	**1.778**	**0.737**	Symplekin
1.17E-54	0.697	1.882	2.766	**1.781**	**1.038**	Developmentally-regulated GTP-binding protein 1
3.4E-220	0.982	2.423	1.947	**1.784**	**0.734**	cDNA, FLJ94230, highly similar to Homo sapiens thioredoxin-like 1 (TXNL1), mRNA
3.4E-31	1.440	0.687	3.243	**1.790**	**1.314**	Sulfide:quinone oxidoreductase, mitochondrial
5.39E-42	0.536	1.414	3.420	**1.790**	**1.478**	Cation-chloride cotransporter 6
1.1E-304	1.047	1.080	3.248	**1.792**	**1.261**	cDNA, FLJ92904, highly similar to Homo sapiens casein kinase 2, alpha 1 polypeptide (CSNK2A1), mRNA
3.3E-213	1.068	1.109	3.199	**1.792**	**1.219**	Cellular nucleic acid-binding protein
4.61E-24	0.526	1.375	3.482	**1.794**	**1.522**	CXXC-type zinc finger protein 9
2.7E-214	0.838	1.449	3.095	**1.794**	**1.168**	50 kDa nucleoporin
1.3E-105	0.946	2.570	1.868	**1.795**	**0.815**	GAP SH3 domain-binding protein 2
1.77E-94	0.371	1.690	3.325	**1.795**	**1.480**	highly similar to Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 1 (UHRF1), mRNA
1E-66	0.958	2.079	2.356	**1.797**	**0.740**	Homer protein homolog 3
7.62E-95	2.243	1.640	1.514	**1.799**	**0.389**	Calcium-regulated heat stable protein 1
0	1.415	2.125	1.860	**1.800**	**0.359**	cDNA FLJ56465, highly similar to Dynactin-1
0	0.369	3.233		**1.801**	**2.025**	70 kDa lamin
4.59E-16	1.788	0.762	2.855	**1.802**	**1.047**	3-ketoacyl-CoA thiolase, peroxisomal
6.05E-72	2.084	0.881	2.445	**1.803**	**0.819**	Ca(2+)/calmodulin-dependent protein kinase phosphatase
4.19E-08	0.914	2.276	2.230	**1.807**	**0.773**	Basophilic leukemia-expressed protein Bles03

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
5.02E-21	0.866	3.056	1.499	**1.807**	**1.127**	96 kDa nucleoporin
7.8E-131	1.207	2.443	1.776	**1.809**	**0.619**	Monocyte Arg-serpin
0	1.382	0.945	3.101	**1.809**	**1.140**	ATP-dependent dihydroxyacetone kinase
0	1.043	0.927	3.463	**1.811**	**1.432**	CCT-alpha
6E-111	0.738		2.887	**1.812**	**1.519**	Arg/Glu/Asp-rich protein of 120 kDa
7.4E-103	1.530	1.252	2.658	**1.813**	**0.744**	Core-binding factor subunit beta
0	1.227	2.484	1.737	**1.816**	**0.632**	NUMA1 variant protein
1.9E-221	1.536	1.251	2.663	**1.817**	**0.746**	GRIP1-associated protein 1
0	0.641	2.208	2.606	**1.818**	**1.039**	Septin-11
6.46E-52	0.895	1.157	3.415	**1.822**	**1.385**	Coiled-coil domain-containing protein 131
2.1E-138	1.207	1.297	2.967	**1.824**	**0.991**	Signal recognition particle 68 kDa protein
3.2E-103	0.906	2.428	2.142	**1.826**	**0.809**	Inorganic pyrophosphatase 2, mitochondrial
0	1.142	0.382	3.961	**1.828**	**1.886**	Kinesin-like protein 2
0	0.834	2.796	1.859	**1.829**	**0.981**	ATP-dependent RNA helicase DDX3X
0	0.950	1.710	2.842	**1.834**	**0.952**	Importin beta-2
1.32E-44	0.734	3.327	1.441	**1.834**	**1.340**	60S ribosomal protein L17
1.13E-25	0.687	3.882	0.937	**1.835**	**1.777**	Protein ITFG3
3.31E-07	1.361	1.774	2.380	**1.838**	**0.513**	cDNA FLJ61231, highly similar to Apoptosis-stimulating of p53 protein 2
7.37E-57	1.289	1.969	2.260	**1.839**	**0.498**	Dual specificity mitogen-activated protein kinase kinase 3
0	0.716	1.733	3.080	**1.843**	**1.186**	Coding region determinant-binding protein
3.75E-16	1.371	1.180	2.979	**1.843**	**0.988**	CDC42-binding protein kinase beta
6.3E-259	1.121	1.329	3.086	**1.845**	**1.080**	Ran GTPase-activating protein 1
1.9E-36	0.222	3.469		**1.845**	**2.296**	Nucleolar protein 6
8.85E-64	1.442	2.548	1.548	**1.846**	**0.610**	cDNA FLJ55764, highly similar to Apolipoprotein-L2
2.57E-61	0.768	2.819	1.961	**1.849**	**1.030**	GATA zinc finger domain-containing protein 2B
1.85E-35	0.710	3.146	1.691	**1.849**	**1.226**	Coated vesicle-associated kinase of 90 kDa
6.44E-32	0.534	2.190	2.824	**1.849**	**1.183**	140 kDa nuclear and cell adhesion-related phosphoprotein
7.86E-20	0.620	0.651	4.280	**1.850**	**2.104**	59 kDa serine/threonine-protein kinase
7.55E-60	0.775	1.475	3.308	**1.852**	**1.309**	Putative uncharacterized protein MPP6
0	1.759	1.589	2.211	**1.853**	**0.321**	256 kDa golgin
2.17E-86	3.125	0.584		**1.854**	**1.797**	RING finger protein 104
3.97E-84	1.503	1.235	2.825	**1.854**	**0.851**	Cell cycle and apoptosis regulatory protein 1
1.83E-98	0.557	3.164		**1.860**	**1.843**	ATPase, H+ transporting, lysosomal V0 subunit a1, isoform CRA_a
0	0.682	2.135	2.783	**1.867**	**1.076**	Heterogeneous nuclear ribonucleoprotein H

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
6.53E-09	1.014	2.725		**1.870**	**1.210**	Antigen NY-CO-1
0	1.070	1.565	2.975	**1.870**	**0.989**	Melanocortin receptor 1
1.01E-33	2.234	0.295	3.086	**1.872**	**1.430**	Exocyst complex component 5
2.35E-08	0.754	2.779	2.084	**1.872**	**1.029**	Phosphorylation regulatory protein HP-10
5.8E-84	1.257	1.364	3.001	**1.874**	**0.977**	Chr2Syt
1.82E-35	0.728		3.030	**1.879**	**1.628**	60S ribosomal protein L24
0	1.146	2.277	2.246	**1.889**	**0.644**	HLA-DR-associated protein II
1.8E-113	0.597	3.395	1.677	**1.889**	**1.411**	Sorting nexin-1
5.31E-95	0.987	1.498	3.188	**1.891**	**1.152**	205 kDa nucleoporin
1.69E-68	2.013	1.901	1.764	**1.893**	**0.124**	RING finger protein 109
1.57E-96	1.525	1.611	2.576	**1.904**	**0.583**	Uncharacterized protein C1orf77
1.3E-57	0.322	3.608	1.806	**1.912**	**1.645**	cDNA FLJ46359 fis, clone TESTI4049786, highly similar to Hexokinase-1 (EC 2.7.1.1)
7.7E-216	0.820	2.588	2.337	**1.915**	**0.956**	Protein A6
9.2E-110	0.465	4.436	0.846	**1.916**	**2.191**	Transducin beta-like protein 2
2.28E-09	1.673	2.165		**1.919**	**0.348**	Inositol monophosphatase 3
8.64E-12	0.846	2.216	2.729	**1.930**	**0.973**	Hepatocyte odd protein shuttling protein
8.3E-92	1.764	1.313	2.733	**1.937**	**0.726**	Cysteine and glycine-rich protein 1
0	0.658	2.030	3.131	**1.940**	**1.239**	Importin subunit alpha-2
5.29E-48	0.896	2.626	2.302	**1.942**	**0.920**	Septin-8
0	0.903	2.543	2.380	**1.942**	**0.903**	CCT-beta
1.5E-123	0.671	3.034	2.126	**1.944**	**1.192**	75 kDa DNA-pairing protein
4.3E-107	1.122	2.712	2.010	**1.948**	**0.797**	Alternative-splicing factor 1
2.73E-35	1.743	2.047	2.059	**1.949**	**0.179**	Autoantigen Ge-1
0	0.970	1.092	3.787	**1.950**	**1.593**	UDP--Glc:glycoprotein glucosyltransferase
2.1E-293	1.078	2.044	2.736	**1.953**	**0.833**	Phospholipase A-2-activating protein
3.53E-71	1.491	2.274	2.110	**1.958**	**0.413**	GTP-binding protein 1
1.9E-154	1.020	3.427	1.442	**1.963**	**1.286**	Vesicle-associated membrane protein-associated protein B/C
1.62E-10	0.391	1.313	4.200	**1.968**	**1.987**	Bucentaur
3.4E-114	1.656	3.752	0.505	**1.971**	**1.646**	cDNA FLJ54775, highly similar to Syntaxin-binding protein 2
1.73E-86	0.805	2.362	2.759	**1.975**	**1.032**	Protein-tyrosine phosphatase 1B
7.9E-232	1.406	0.902	3.631	**1.980**	**1.452**	Elongation factor Tu, mitochondrial
0	0.896	2.716	2.335	**1.982**	**0.960**	ATP-dependent DNA helicase VIII
9.6E-169	0.860	1.864	3.224	**1.982**	**1.186**	highly similar to Homo sapiens, neural cell expressed,developmentally down-regulated gene 1
2.25E-59	1.141	2.520	2.289	**1.983**	**0.739**	Cardiac lineage protein 1
2.85E-07	0.667	0.638	4.658	**1.988**	**2.313**	Oxysterol-binding protein-related protein 11

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.1E-240	1.413	2.571		**1.992**	**0.819**	Phosphoribosyl pyrophosphate synthase II
0	0.812	2.323	2.851	**1.995**	**1.058**	Mitochondrial import receptor subunit TOM70
0	0.339	3.340	2.309	**1.996**	**1.525**	Leucine-rich repeat-containing protein 59
5.33E-27	0.730	2.287	2.986	**2.001**	**1.155**	DNA repair protein XRCC1
3.9E-62	1.081	3.471	1.464	**2.005**	**1.283**	Putative uncharacterized protein GTPBP3
3.5E-244	0.866	2.098	3.066	**2.010**	**1.103**	Chap1
3.76E-73	0.824	2.118	3.094	**2.012**	**1.138**	NudC domain-containing protein 3
5.8E-291	1.155	2.870		**2.012**	**1.212**	Calcium/calmodulin-dependent protein kinase type II subunit delta
3.1E-223	0.574	3.635	1.831	**2.013**	**1.538**	eEF-1B gamma
3.4E-96	1.316	3.133	1.615	**2.021**	**0.974**	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial
0	1.061	1.235	3.784	**2.026**	**1.524**	Protein disulfide isomerase P5
2.82E-08	0.308	2.834	2.943	**2.028**	**1.491**	28 kDa cis-Golgi SNARE p28
0	1.525	2.221	2.340	**2.029**	**0.440**	Aldehyde dehydrogenase family 18 member A1
3.6E-177	0.567	4.602	0.935	**2.035**	**2.231**	Epidermal surface antigen
1E-215	1.163	2.299	2.646	**2.036**	**0.775**	Protein phosphatase 1C
3E-42	1.265	2.260	2.593	**2.040**	**0.691**	Crk-like protein
1.97E-09	1.194	1.585	3.344	**2.041**	**1.145**	ADP-ribosylation factor GTPase-activating protein 3
0	0.430	2.937	2.770	**2.045**	**1.402**	NAD(+) ADP-ribosyltransferase 1
1.32E-57	0.948	3.145		**2.046**	**1.553**	Activated protein C receptor
6.7E-276	0.336	3.276	2.543	**2.051**	**1.530**	Lamin-B2
0	0.728	2.968	2.475	**2.057**	**1.177**	ATP-dependent RNA helicase A
6.77E-07	0.712	1.996	3.481	**2.063**	**1.386**	Ovarian cancer-related protein
3.5E-191	1.407	0.780	4.021	**2.070**	**1.719**	ICD-M
4.57E-14	0.741	2.331	3.142	**2.071**	**1.221**	Ataxin-3
2E-14	0.848	1.772	3.595	**2.071**	**1.398**	60 kDa BRG-1/Brm-associated factor subunit A
2.3E-137	0.659	2.835	2.755	**2.083**	**1.234**	Antigen p25
9.07E-31	1.045	2.069	3.148	**2.087**	**1.051**	APG16-like 1
9.53E-75	0.826	2.211	3.225	**2.088**	**1.204**	TBC1 domain family, member 13
3.9E-118	0.413	3.719	2.132	**2.088**	**1.653**	Cell proliferation-inducing gene 4/52 protein
3.29E-70	1.769	2.602	1.897	**2.089**	**0.448**	Rab GTPase-binding effector protein 2
2.97E-06	0.375	3.156	2.738	**2.090**	**1.499**	Putative uncharacterized protein PPAN
1.2E-226	0.733	2.992	2.545	**2.090**	**1.196**	DnaJ homolog subfamily C member 9
9.2E-212	1.125	1.211	3.944	**2.093**	**1.604**	DNase IV
2.8E-147	0.677	2.867	2.765	**2.103**	**1.236**	60S ribosomal protein L7a
1.57E-54	1.371	1.325	3.615	**2.104**	**1.309**	Carbamoylphosphate synthetase I

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
7.5E-228	0.599	2.840	2.882	**2.107**	**1.306**	Pre-mRNA-splicing factor SF3b 145 kDa subunit
2.18E-89	0.955	4.164	1.214	**2.111**	**1.783**	Asparaginyl endopeptidase
1.34E-40	0.655	1.705	3.983	**2.114**	**1.701**	TATA box-binding protein-associated factor 2S
4E-25	0.189	3.241	2.913	**2.114**	**1.675**	Telomeric repeat-binding factor 2-interacting protein 1
1.2E-108	0.829	2.772	2.758	**2.120**	**1.118**	Anamorsin
9E-99	1.007	3.013	2.365	**2.128**	**1.024**	Protein 40-6-3
6.95E-45	0.908	3.324	2.154	**2.129**	**1.208**	Chloride channel, nucleotide sensitive 1A
3.2E-104	1.840	1.908	2.639	**2.129**	**0.443**	BH3-interacting domain death agonist
3.53E-48	1.028	1.787	3.581	**2.132**	**1.311**	Adrenodoxin-like protein, mitochondrial
0	4.133	0.131		**2.132**	**2.830**	Heterogeneous nuclear ribonucleoprotein U
1.41E-16	0.594	3.287	2.553	**2.145**	**1.392**	DNA-directed RNA polymerase I subunit E
4.26E-71	0.779	3.149	2.513	**2.147**	**1.227**	Chromatin accessibility complex 15 kDa protein
6.73E-29	0.716	3.128	2.608	**2.151**	**1.270**	Adapter protein CMS
0	2.170	2.898	1.425	**2.165**	**0.737**	Putative uncharacterized protein FLNA
1.2E-157	0.326	3.507	2.662	**2.165**	**1.648**	Colonic and hepatic tumor over-expressed gene protein
5.56E-37	0.737	3.445	2.331	**2.171**	**1.361**	Coilin
1.8E-157	1.405	0.849	4.263	**2.172**	**1.832**	Microsomal prostaglandin E synthase 2
2.6E-112	0.764	2.117	3.649	**2.177**	**1.443**	Endonuclease domain-containing 1 protein
4.26E-91	0.616	2.806	3.119	**2.180**	**1.364**	Tat-cotransactivator 2 protein
3.1E-121	0.826	1.747	3.971	**2.181**	**1.617**	CLL-associated antigen KW-11
2.1E-214	0.887	3.622	2.047	**2.185**	**1.373**	BRG1-associated factor 170
9.5E-99	0.592	1.938	4.033	**2.188**	**1.734**	SHC-transforming protein 1
0	0.647	2.677	3.240	**2.188**	**1.364**	Far upstream element-binding protein 2
1.12E-50	1.154	2.838	2.575	**2.189**	**0.906**	One-twenty two protein 1
1.14E-49	0.425	1.962	4.184	**2.190**	**1.890**	highly similar to Homo sapiens smoothelin (SMTN), transcript variant 2, mRNA
1.15E-05	0.651	1.564	4.357	**2.191**	**1.931**	Chromosome-associated protein H2
3.53E-72	1.192	2.751	2.642	**2.195**	**0.871**	Rho GTPase-activating protein 17
2.28E-64	0.744	3.799	2.056	**2.200**	**1.532**	Putative uncharacterized protein ZC3H14
7.45E-37	0.717	3.869	2.024	**2.203**	**1.583**	Bcl-2-associated transcription factor 1
1.6E-254	0.629	4.746	1.240	**2.205**	**2.221**	Fas ligand-associated factor 1
8.47E-19	1.265	3.580	1.773	**2.206**	**1.217**	Uridine phosphorylase 1
1.33E-94	0.198	5.086	1.335	**2.206**	**2.558**	Outer mitochondrial membrane protein porin 1
1.94E-05	0.051	4.366		**2.209**	**3.051**	Stoned B
2.26E-28	0.699	3.399	2.534	**2.211**	**1.379**	Putative RNA-binding protein Luc7-like 2
1.15E-34	0.529	2.466	3.645	**2.213**	**1.573**	Muscleblind-like protein 1

PEP	**Ratio H/L Reverse**	**Ratio L/H Forward1**	**Ratio L/H Forward2**	**Avg**	**STD**	**Protein Names**
3.95E-50	0.671	3.347	2.629	**2.216**	**1.385**	Kinesin-like protein 5
8.6E-141	0.966	0.922	4.762	**2.217**	**2.204**	Amphiphysin II
1.13E-24	0.591	3.461	2.599	**2.217**	**1.472**	Tetratricopeptide repeat protein 1
1.55E-69	1.379	2.978	2.295	**2.217**	**0.802**	eIF3 p35
0	0.927	3.681	2.050	**2.219**	**1.384**	50 kDa dynein-associated polypeptide
8.2E-137	1.322	2.562	2.779	**2.221**	**0.786**	Protein phosphatase methylesterase 1
6E-234	1.237	3.391	2.035	**2.221**	**1.089**	Heterogeneous nuclear ribonucleoprotein A0
1.45E-56	1.986		2.463	**2.225**	**0.338**	Neuroendocrine-specific protein
1.8E-286	0.773	3.092	2.821	**2.229**	**1.268**	CDC10 protein homolog
2.21E-18	1.152	3.321		**2.236**	**1.533**	Delayed-early protein HRS
7E-45	0.566	2.796	3.353	**2.238**	**1.475**	ERIC-1
2.96E-11	0.636	0.765	5.328	**2.243**	**2.672**	Kinesin-2
8.5E-176	0.337	3.772	2.627	**2.246**	**1.749**	CLL-associated antigen KW-7
1.86E-19	0.763	1.454	4.539	**2.252**	**2.011**	Activity-dependent neuroprotective protein
2.78E-66	1.619	2.395	2.744	**2.253**	**0.576**	Collagen alpha-1(VII) chain
6.5E-41	1.643	1.964	3.158	**2.255**	**0.798**	L-serine deaminase
9.77E-26	0.593	2.737	3.448	**2.259**	**1.486**	Zinc finger protein 207 variant
2.07E-27	0.944	1.450	4.391	**2.262**	**1.861**	Leucine zipper protein 1
2.66E-06	1.183		3.351	**2.267**	**1.533**	Janus kinase and microtubule-interacting protein 3
8.18E-13	0.816	2.007	3.992	**2.272**	**1.605**	Pleckstrin homology-like domain family B member 1
4.41E-08	2.219	2.142	2.484	**2.282**	**0.179**	Iboctadekin
1.6E-152	1.078	3.048	2.736	**2.288**	**1.059**	Annexin A7
1.9E-207	1.186	2.748	2.936	**2.290**	**0.961**	Heterogeneous nuclear ribonucleoprotein 2H9
4.1E-136	0.804	2.281	3.799	**2.295**	**1.497**	N-glycanase 1
1.05E-22	0.804	2.218	3.871	**2.298**	**1.535**	G-rich sequence factor 1
2.28E-09	0.733	3.003	3.162	**2.299**	**1.359**	Programmed cell death protein 2-like
1.28E-59	0.923	2.212	3.794	**2.310**	**1.438**	Chromokinesin-A
3.08E-15	1.458	3.251	2.229	**2.313**	**0.900**	Metallothionein-0
5.32E-86	1.359	3.314	2.266	**2.313**	**0.979**	Amisyn
2.11E-43	0.296	4.332		**2.314**	**2.853**	Heterochromatin protein 1-binding protein 3
1.78E-06	0.281	4.359		**2.320**	**2.883**	RCC1-I
8.6E-133	1.303	3.038	2.634	**2.325**	**0.908**	Protein PR264
2.38E-29	1.239	4.119	1.626	**2.328**	**1.563**	Renal carcinoma antigen NY-REN-31
3.1E-14	0.797	4.000	2.193	**2.330**	**1.605**	cDNA, FLJ92684, highly similar to Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA
7.2E-220	0.597	2.845	3.571	**2.338**	**1.550**	TAR DNA-binding protein 43
1.9E-104	0.399	3.583	3.051	**2.344**	**1.706**	cDNA FLJ55508, highly similar to Sad1/unc-84-like

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
						protein 2
1.62E-66	0.773	3.092	3.197	**2.354**	**1.370**	Paraspeckle component 1
1.64E-79	0.724	3.316	3.022	**2.354**	**1.419**	Npw38-binding protein
4.56E-10	0.903		3.817	**2.360**	**2.060**	Uncharacterized protein C11orf84
5.49E-39	1.892	1.699	3.530	**2.373**	**1.006**	APG3-like
1.77E-75	1.468	0.497	5.161	**2.375**	**2.461**	Gem-associated protein 5
0	1.207	2.982	3.000	**2.396**	**1.030**	Cell cycle-related and expression-elevated protein in tumor
6.23E-60	1.749	2.198	3.267	**2.405**	**0.780**	Adapter protein containing PH domain, PTB domain and leucine zipper motif 2
3.43E-42	0.275	3.398	3.542	**2.405**	**1.846**	Autoantigen PM/Scl 2
1.22E-83	0.852	4.756	1.610	**2.406**	**2.070**	85 kDa nucleoporin
8.27E-11	0.518	3.005	3.696	**2.406**	**1.671**	Lark homolog
8.48E-12	0.801	4.773	1.653	**2.409**	**2.091**	35 kDa nucleoporin
2.11E-54	0.257	4.565		**2.411**	**3.046**	DEAD box protein 21
0	1.068	4.627	1.547	**2.414**	**1.932**	DNA helicase V
1.64E-34	1.290	2.327	3.648	**2.422**	**1.182**	ATP-dependent RNA helicase DDX50
1.53E-18	0.825	4.545	1.905	**2.425**	**1.914**	CWF19-like protein 1
1E-233	0.577	1.024	5.697	**2.433**	**2.836**	RRP12-like protein
3.75E-69	0.969	3.048	3.284	**2.434**	**1.274**	Cavin-3
1.52E-24	0.300	4.070	2.956	**2.442**	**1.937**	Hornerin
6.99E-37	0.863	3.249	3.218	**2.444**	**1.369**	Protein SH(2)A
1.82E-11	0.371	4.566		**2.469**	**2.967**	Sucrose nonfermenting protein 2 homolog
1.04E-05	1.393		3.562	**2.477**	**1.533**	Condensin-2 complex subunit D3
6.97E-69	1.116	2.980	3.394	**2.496**	**1.214**	RNA polymerase II-associated protein 3
0	1.418	1.858	4.229	**2.502**	**1.512**	Signal recognition particle 72 kDa protein
1.23E-48	0.600	2.577	4.377	**2.518**	**1.889**	Lysp100b
2.85E-25	1.442	2.713	3.428	**2.528**	**1.006**	Dynactin subunit 4
1.44E-45	0.711	3.882	3.004	**2.532**	**1.637**	mRNA export factor TAP
1.56E-24	1.355	0.375	5.872	**2.534**	**2.932**	La ribonucleoprotein domain family member 4
1.05E-08	0.770	4.331		**2.551**	**2.518**	ATP-dependent RNA helicase DHX8
5.46E-11	0.919		4.185	**2.552**	**2.309**	Pre-mRNA-splicing factor 38A
0	0.793	3.442	3.428	**2.554**	**1.526**	Dual specificity mitogen-activated protein kinase kinase 1
2.98E-35	1.028	3.174	3.478	**2.560**	**1.336**	Striatin
0	0.838	2.116	4.727	**2.561**	**1.982**	cDNA FLJ52712, highly similar to Tubulin beta-6 chain
1.29E-13	0.360	3.321	4.025	**2.569**	**1.945**	Nesprin-3
2.74E-35	1.130	0.436	6.151	**2.572**	**3.119**	13S Golgi transport complex 90 kDa subunit

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
0	1.218	2.994	3.507	**2.573**	**1.201**	IGF-II mRNA-binding protein 3
1.4E-288	0.470	3.072	4.197	**2.580**	**1.912**	DNA-directed RNA polymerase II subunit A
3.3E-132	0.765	3.670	3.309	**2.581**	**1.583**	136 kDa double-stranded RNA-binding protein
6.2E-181	1.050	2.700	4.035	**2.595**	**1.495**	L1880
7.99E-50	0.899	4.052	2.874	**2.608**	**1.593**	Target of Myb-like protein 2
1.85E-13	1.053	2.483	4.295	**2.611**	**1.625**	Uncharacterized protein C20orf72
2E-184	1.352	3.233	3.250	**2.612**	**1.091**	SH3-domain GRB2-like endophilin B2
7E-48	1.398	3.746	2.692	**2.612**	**1.176**	Leukocyte elastase inhibitor
6.4E-229	1.218	3.992	2.642	**2.617**	**1.387**	133 kDa nucleoporin
1.4E-17	0.891	5.042	1.922	**2.618**	**2.161**	Uncharacterized protein KIAA0819
2.45E-24	0.468	0.754	6.674	**2.632**	**3.503**	Nucleolar protein 5
1.89E-48	0.313	6.769	0.815	**2.632**	**3.591**	EBNA1-binding protein 2
8.81E-44	0.561	4.110	3.254	**2.642**	**1.852**	46 kDa mannose 6-phosphate receptor
4.2E-112	1.906	2.539	3.486	**2.644**	**0.795**	dCTP pyrophosphatase 1
4.28E-89	0.592	4.445	2.921	**2.653**	**1.941**	Structural maintenance of chromosomes protein 6
6.1E-108	1.959	2.774	3.242	**2.658**	**0.649**	35-alpha calcimedin
1.7E-138	0.744	3.281	3.963	**2.663**	**1.696**	Serine/arginine-rich-splicing regulatory protein 86
1.13E-42	0.756	4.079	3.159	**2.665**	**1.716**	Arginine-rich 54 kDa nuclear protein
2.69E-28	1.332		4.006	**2.669**	**1.891**	Ubiquitin domain-containing protein UBFD1
1.5E-267	0.954	3.290	3.767	**2.670**	**1.505**	Mitochondrial import receptor subunit TOM34
1.42E-33	0.945	3.503	3.595	**2.681**	**1.504**	Protein Tara
5.9E-138	1.173	3.564	3.330	**2.689**	**1.318**	Copine III
1.63E-23	0.779	2.518	4.777	**2.691**	**2.005**	Nucleolysin TIA-1 isoform p15
1.53E-33	1.150	1.686	5.263	**2.699**	**2.236**	Zinc finger protein MCG4
4.68E-69	1.075	1.352	5.705	**2.710**	**2.597**	Acyl-CoA thioesterase 7
2.9E-184	0.846	6.039	1.252	**2.712**	**2.888**	Charged multivesicular body protein 4b
2.61E-45	1.321	2.456	4.374	**2.717**	**1.543**	Clathrin light chain B
5E-154	0.600	5.117	2.481	**2.733**	**2.269**	cDNA FLJ60076, highly similar to ELAV-like protein 1
4.1E-124	0.372	4.102	3.744	**2.739**	**2.058**	MAP1 light chain LC1
0	1.082	3.805	3.347	**2.744**	**1.458**	CG-1 antigen
0	0.633	4.024	3.623	**2.760**	**1.853**	Polypyrimidine tract binding protein 1
8.8E-135	1.135	4.398		**2.766**	**2.307**	TRIP12 protein
2.73E-22	2.169	1.729	4.406	**2.768**	**1.435**	SMARCA4 protein
0	0.788		4.748	**2.768**	**2.800**	DNA helicase V
3.2E-184	0.833	4.165	3.310	**2.769**	**1.731**	Cyclin-dependent kinase inhibitor 2B-related protein
6E-265	1.130	4.992	2.228	**2.784**	**1.990**	DnaJ homolog subfamily C member 13

PEP	**Ratio H/L Reverse**	**Ratio L/H Forward1**	**Ratio L/H Forward2**	**Avg**	**STD**	**Protein Names**
0	0.595	4.486	3.283	**2.788**	**1.992**	Heterogeneous nuclear ribonucleoproteins C1/C2
1.41E-31	0.653	3.097	4.669	**2.806**	**2.023**	Deubiquitinating enzyme 10
2.12E-20	0.296	4.504	3.627	**2.809**	**2.220**	Bromodomain-containing protein 2
2.2E-276	0.715	3.770	3.947	**2.810**	**1.817**	Caprin-1
5.1E-217	0.832	3.927	3.672	**2.811**	**1.718**	Far upstream element-binding protein 3
3.99E-11	1.956	2.606	3.874	**2.812**	**0.976**	Cavin-2
0	0.861	3.552	4.023	**2.812**	**1.706**	Tropomodulin-3
1.58E-79	0.971	2.720	4.771	**2.821**	**1.902**	Component of oligomeric Golgi complex 3
6.4E-134	1.059	4.003	3.412	**2.825**	**1.557**	Metastasis-associated protein MTA1
1.1E-128	1.131	1.996	5.350	**2.826**	**2.228**	Uveal autoantigen with coiled-coil domains and ankyrin repeats
4.36E-51	0.801	3.791	3.891	**2.828**	**1.756**	MICAL-like protein 1
1.2E-130	1.316	0.983	6.195	**2.831**	**2.918**	GTP-specific succinyl-CoA synthetase subunit beta
2.57E-32	0.845	4.139	3.513	**2.832**	**1.750**	cDNA FLJ61157, highly similar to XPA-binding protein 1
1.6E-23	0.220	5.465		**2.843**	**3.709**	Outer mitochondrial membrane protein porin 2
2.26E-61	1.069	2.790	4.694	**2.851**	**1.813**	CLASP2 protein
2.3E-261	0.477	6.294	1.807	**2.859**	**3.048**	5'-nucleotidase
9.99E-30	0.241	1.763	6.625	**2.876**	**3.334**	RNA-binding protein with serine-rich domain 1
6.5E-159	1.073	3.180	4.420	**2.891**	**1.692**	A6-related protein
2.07E-31	0.829	5.390	2.456	**2.892**	**2.311**	Cancer/testis antigen 84
0	0.448	4.956	3.310	**2.905**	**2.281**	Lamin-B1
8.52E-10	1.507	0.891	6.346	**2.914**	**2.987**	HEAT repeat-containing protein 3
1.11E-38	0.375	4.190	4.180	**2.915**	**2.200**	Gamma-interferon-inducible protein 16
1E-200	0.621	4.444	3.704	**2.923**	**2.027**	Double-stranded RNA-binding protein Staufen homolog 1
1.5E-297	0.565	4.128	4.076	**2.923**	**2.042**	Heterogeneous nuclear ribonucleoprotein R
1.85E-13	0.627	5.062	3.089	**2.926**	**2.222**	Pericentriolar material 1 protein
7.73E-54	1.139	2.713	4.948	**2.933**	**1.914**	Inositol 1,4,5-trisphosphate receptor type 3
6.5E-126	1.080	2.167	5.577	**2.941**	**2.347**	Sorting nexin-5
0	0.733	2.608	5.490	**2.943**	**2.396**	Cytovillin
7.75E-47	1.151	3.884	3.827	**2.954**	**1.562**	p59scr
0	0.850	4.001	4.016	**2.956**	**1.824**	86 kDa subunit of Ku antigen
4.93E-26	0.736	2.289	5.886	**2.970**	**2.642**	BRG1-associated factor 155
4E-81	0.737	5.108	3.070	**2.971**	**2.187**	AH antigen
2.64E-39	0.736	3.884	4.302	**2.974**	**1.949**	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
3.9E-111	1.213	3.927	3.816	**2.985**	**1.536**	PEF protein with a long N-terminal hydrophobic domain

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.2E-77	0.765	3.520	4.685	**2.990**	**2.013**	ATP-dependent RNA helicase DHX29
8E-226	1.069	4.545	3.382	**2.999**	**1.769**	Autoantigen p542
2.35E-23	0.629		5.400	**3.015**	**3.374**	highly similar to CALCIUM/CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE 1C
7.28E-24	0.630	4.773	3.648	**3.017**	**2.142**	18S rRNA dimethylase
1.57E-74	0.800	4.728	3.558	**3.029**	**2.017**	Erasin
1.57E-08	0.577	5.488		**3.033**	**3.473**	Ciliary rootlet coiled-coil protein
1.94E-16	0.629	4.805	3.691	**3.042**	**2.163**	Heterogeneous nuclear ribonucleoprotein L-like
1.04E-36	0.532	4.091	4.549	**3.057**	**2.199**	Double-stranded RNA-binding protein Staufen homolog 2
5.19E-37	0.915	2.168	6.178	**3.087**	**2.749**	Enhancer of mRNA-decapping protein 3
7.35E-26	0.948	2.527	5.797	**3.091**	**2.473**	Interferon-inducible double stranded RNA-dependent protein kinase activator A
0.004041	2.756		3.464	**3.110**	**0.501**	Proto-oncogene c-Ski
5E-142	1.504	4.153	3.692	**3.116**	**1.415**	Metallothionein-2
4.82E-69	1.133		5.106	**3.119**	**2.810**	Tumor suppressor p53-binding protein 1
7.91E-07	0.490	5.789		**3.139**	**3.747**	DEAD box protein 27
6.85E-96	0.462	3.495	5.566	**3.174**	**2.567**	GAP-associated tyrosine phosphoprotein p62
3E-165	0.704	3.975	4.849	**3.176**	**2.185**	Hepatocellular carcinoma protein 1
2E-32	0.508	3.625	5.399	**3.177**	**2.476**	MHC class I region proline-rich protein CAT53
0	1.355	4.120	4.108	**3.194**	**1.593**	Nesprin-2
1.02E-14	1.047	3.971	4.608	**3.209**	**1.899**	Nuclear poly(A)-binding protein 1
2.42E-12	0.808	6.319	2.632	**3.253**	**2.807**	hTREX120
3.7E-160	0.850	3.794	5.168	**3.271**	**2.206**	Glycoprotein p43
3.97E-06	1.035	3.731	5.119	**3.295**	**2.077**	cDNA FLJ32696 fis, clone TESTI2000358
1.44E-06	0.369		6.246	**3.307**	**4.156**	Bystin
1.2E-59	1.100	4.710	4.152	**3.320**	**1.943**	Apoptotic chromatin condensation inducer in the nucleus
6.27E-63	0.804	5.870		**3.337**	**3.582**	MP70 protein family member
2.9E-09	0.943		5.739	**3.341**	**3.391**	Septin-10
1.3E-28	0.838	2.136	7.051	**3.342**	**3.277**	G patch domain-containing protein 9
1.41E-56	0.489	5.365	4.188	**3.347**	**2.544**	Protein DEK
7.65E-09	0.159	3.819	6.136	**3.371**	**3.014**	Histone H1'
1.7E-180	0.978	5.583	3.623	**3.394**	**2.311**	Epidermal growth factor receptor kinase substrate 8
1.18E-05	0.915	6.220	3.646	**3.594**	**2.653**	Dual specificity protein kinase TTK
9.82E-28	0.583	8.689	1.683	**3.652**	**4.397**	Ribosomal RNA processing protein 1 homolog B
2.41E-62	0.591	3.294	7.123	**3.669**	**3.282**	MBNL protein

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.7E-32	0.260	4.137	6.671	**3.690**	**3.229**	BRG1-associated factor 57
9.32E-81	0.788	5.060	5.284	**3.711**	**2.534**	highly similar to Homo sapiens phosphate cytidylyltransferase 1, choline, alpha isoform (PCYT1A), mRNA
1.25E-10	1.390	0.557	9.317	**3.755**	**4.835**	Cyclin-G-associated kinase
0	0.848	3.725	6.912	**3.828**	**3.033**	Neural precursor cell expressed developmentally down-regulated protein 5
1.06E-19	0.939	6.729		**3.834**	**4.094**	Protein FAM45A
9.1E-126	1.020	1.058	9.456	**3.844**	**4.860**	Leprecan-like protein 2
3.1E-09	0.230	5.867	5.541	**3.879**	**3.165**	Activator 1 140 kDa subunit
5.55E-60	1.194	7.359	3.153	**3.902**	**3.150**	Cleavage and polyadenylation specificity factor 59 kDa subunit
3.23E-70	0.987	3.532	7.484	**4.001**	**3.274**	Paraspeckle protein 2
1.2E-164	0.607	7.492		**4.050**	**4.869**	MHC class I antigen
0	0.670	8.201	3.394	**4.088**	**3.813**	Heterogeneous nuclear ribonucleoprotein L
3.3E-117	0.269	6.700	5.390	**4.120**	**3.399**	Core histone macro-H2A.1
2.34E-08	0.118	7.522	4.819	**4.153**	**3.747**	Alpha-trypsin chain 1
1.02E-31	0.913	6.948	4.758	**4.206**	**3.055**	Pre-mRNA-splicing factor SRp30C
5.5E-11	0.868	7.544	4.214	**4.209**	**3.338**	CMP-N-acetylneuraminic acid synthase
9.31E-52	0.440	4.838	7.392	**4.223**	**3.517**	Male germ cell RacGap
8.16E-07	0.561	5.750	6.375	**4.229**	**3.191**	40 kDa SR-repressor protein
6.77E-11	1.580	1.847	9.441	**4.289**	**4.464**	ATP-binding cassette sub-family F member 3
1.4E-215	0.618	7.508	4.770	**4.298**	**3.469**	FTP-3
3.34E-68	0.474	7.262	5.241	**4.326**	**3.485**	Heterogeneous nuclear ribonucleoprotein A3
1.57E-38	0.439	3.671	8.931	**4.347**	**4.286**	DNA ligase 3
8.42E-47	0.667	7.847	4.590	**4.368**	**3.595**	Zinc finger protein 326
3.13E-58	1.075	1.685	10.760	**4.507**	**5.424**	Malic enzyme 3
1.19E-07	0.626	5.124	8.134	**4.628**	**3.779**	Protein FAM98A
9.87E-79	0.735	9.970	3.535	**4.747**	**4.735**	Putative RNA-binding protein Luc7-like 1
5.3E-117	0.771	1.538	13.330	**5.213**	**7.040**	IWS1-like protein
1.19E-06	0.955		9.889	**5.422**	**6.318**	Cofactor required for Sp1 transcriptional activation subunit 8
0	0.113	8.642	8.089	**5.615**	**4.773**	Cytokeratin-9
3.73E-07	0.069	11.459		**5.764**	**8.054**	Dystrophin
2.29E-59	1.075	10.654		**5.865**	**6.774**	Diphthamide biosynthesis methyltransferase
1.2E-17	0.801	11.316		**6.059**	**7.435**	DNA polymerase
6.92E-11	5.162	11.689	1.539	**6.130**	**5.144**	Autoantigen PM/Scl 1
2.45E-40	0.640	12.215		**6.428**	**8.185**	C-alpha-formylglycine-generating enzyme 1
7.6E-16	1.609	10.907	6.841	**6.452**	**4.661**	Cancer/testis antigen 1.10

PEP	Ratio H/L Reverse	Ratio L/H Forward1	Ratio L/H Forward2	Avg	STD	Protein Names
1.8E-13	0.853	12.629	6.437	**6.640**	**5.891**	3-hydroxyisobutyrate dehydrogenase-like protein
6.99E-48	0.527	19.814	0.785	**7.042**	**11.062**	Protein DB83
8.76E-06	13.906	2.107		**8.007**	**8.343**	Alpha-1,3-mannosyltransferase ALG2
6.76E-13	0.682	11.231	16.271	**9.395**	**7.955**	50 kDa nuclear polyadenylated RNA-binding protein
2.15E-20	0.251	29.771	13.363	**14.462**	**14.790**	Putative uncharacterized protein ALB
0.000276	0.478		218.050	**109.264**	**153.846**	Cyclin-A2

Table S2. Summary of all proteins signifcantly altered in this study (IPI HUMAN V.3.6 was used as database for Maxquant searching and FDR was set less than 1%).

International Protein Index	Protein Name	Average Ratio (Treated/Untreated)		
IPI00014533	Autoantigen NOR-90	**0.16**	±	**0.04**
IPI00552897	Mediator of DNA damage checkpoint protein 1	**0.22**	±	**0.15**
IPI00291136	Collagen alpha-1(VI) chain	**0.25**	±	**0.15**
IPI00297646	Alpha-1 type I collagen	**0.25**	±	**0.03**
IPI00219097	High mobility group protein 2	**0.25**	±	**0.11**
IPI00022200	Collagen alpha-3(VI) chain	**0.27**	±	**0.05**
IPI00014718	RcDNAJ9	**0.27**	±	**0.04**
IPI00556594	Zinc finger CCHC domain-containing protein 8	**0.27**	±	**0.13**
IPI00010213	Adapter-related protein complex 4 subunit epsilon-1	**0.28**	±	**0.24**
IPI00023814	Immunoglobulin superfamily DCC subclass member 2 (NEO1)	**0.28**	±	**0.11**
IPI00293307	Adipophilin	**0.29**	±	**0.19**
IPI00304962	Alpha-2 type I collagen	**0.30**	±	**0.07**
IPI00170548	AAA nuclear coregulator cancer-associated protein	**0.32**	±	**0.21**
IPI00295542	CALNUC	**0.34**	±	**0.27**
IPI00022095	Myelin expression factor 3-like protein 1	**0.34**	±	**0.31**
IPI00076042	Short heat shock protein 60 Hsp60s2	**0.36**	±	**0.12**
IPI00167941	MIDAS-containing protein	**0.36**	±	**0.04**
IPI00008991	TATA-binding protein-associated phosphoprotein	**0.38**	±	**0.32**
IPI00782992	300 kDa nuclear matrix antigen	**0.39**	±	**0.40**
IPI00554705	Deoxycytidylate deaminase	**0.39**	±	**0.08**
IPI00291608	PEST proteolytic signal-containing nuclear protein	**0.40**	±	**0.37**
IPI00143753	U2-associated protein SR140	**0.41**	±	**0.36**
IPI00220278	Myosin regulatory light chain 9 (20 kDa)	**0.43**	±	**0.10**
IPI00217950	High mobility group nucleosome-binding domain-containing protein 2	**0.43**	±	**0.35**
IPI00023649	Monocyte protein 3	**0.44**	±	**0.34**
IPI00554436	Arginine/serine-rich-splicing factor 14	**0.44**	±	**0.47**
IPI00216730	Histone H2A type 2-B	**0.44**	±	**0.37**
IPI00217686	Protein ftsJ homolog 3	**0.44**	±	**0.24**
IPI00215911	APEX nuclease	**0.44**	±	**0.06**
IPI00554777	Asparagine synthetase [glutamine-hydrolyzing]	**0.46**	±	**0.04**
IPI00304187	RNA-binding motif protein 28	**0.46**	±	**0.04**

International Protein Index	**Protein Name**	**Average Ratio (Treated/Untreated)**		
IPI00243742	Cardiac myosin light chain 1	**0.46**	**±**	**0.09**
IPI00006378	PP2A B subunit isoform B'-alpha	**0.47**	**±**	**0.04**
IPI00010697	Integrin alpha-6	**0.48**	**±**	**0.26**
IPI00394679	Negative elongation factor A	**0.49**	**±**	**0.11**
IPI00790503	Myosin heavy chain, non-muscle IIb	**0.49**	**±**	**0.07**
IPI00749512	Ribosomal protein S10 variant	**0.50**	**±**	**0.22**
IPI00150269	PRP4 homolog	**0.50**	**±**	**0.20**
IPI00004962	Golgi integral membrane protein 4	**0.50**	**±**	**0.25**
IPI00022963	CCNDBP1-interactor	**0.50**	**±**	**0.18**
IPI00409684	Membrane-associated protein HEM-2	**0.50**	**±**	**0.13**
IPI00251559	E3 ubiquitin-protein ligase BRE1A	**0.51**	**±**	**0.31**
IPI00299086	Melanoma differentiation-associated protein 9	**0.51**	**±**	**0.13**
IPI00419258	High mobility group protein 1	**0.51**	**±**	**0.32**
IPI00296922	Laminin B1s chain	**0.52**	**±**	**0.09**
IPI00607576	Protein CG-2	**0.53**	**±**	**0.06**
IPI00013475	Tubulin beta-2A chain	**0.53**	**±**	**0.27**
IPI00013002	UbcH10	**0.53**	**±**	**0.11**
IPI00171903	Heterogeneous nuclear ribonucleoprotein M	**0.54**	**±**	**0.23**
IPI00178431	ATP-dependent DNA helicase Q1	**0.54**	**±**	**0.15**
IPI00217467	Histone H1.4	**0.54**	**±**	**0.22**
IPI00219301	Myristoylated alanine-rich C-kinase substrate	**0.55**	**±**	**0.16**
IPI00015351	UPF0424 protein C1orf128	**0.55**	**±**	**0.12**
IPI00033022	Dynamin-2	**0.55**	**±**	**0.25**
IPI00015956	Exosome complex exonuclease RRP40	**0.55**	**±**	**0.08**
IPI00019502	Myosin heavy chain, non-muscle IIa	**0.55**	**±**	**0.12**
IPI00253036	CD99 molecule	**0.55**	**±**	**0.13**
IPI00604523	Myosin regulatory light chain MRCL3 variant	**0.56**	**±**	**0.10**
IPI00910194	Nucleoporin 153kDa	**0.56**	**±**	**0.38**
IPI00333913	Neuroblastoma-amplified gene protein	**0.56**	**±**	**0.18**
IPI00027415	DEAH box protein 36	**0.56**	**±**	**0.23**
IPI00644231	Cytoplasmic FMR1-interacting protein 1	**0.57**	**±**	**0.14**
IPI00847168	RSU1 protein	**0.57**	**±**	**0.19**
IPI00172656	FAS-associated factor 2	**0.57**	**±**	**0.22**
IPI00477468	SH2 domain-binding protein 1	**0.57**	**±**	**0.31**
IPI00926581	Myosin heavy chain, non-muscle IIc	**0.57**	**±**	**0.16**

International Protein Index	**Protein Name**	**Average Ratio (Treated/Untreated)**		
IPI00217104	Hepatocellular carcinoma-associated protein 4	**0.57**	±	**0.05**
IPI00102991	RNA-binding motif, single-stranded-interacting protein 1	**0.57**	±	**0.42**
IPI00163644	Oxysterol-binding protein-related protein 8	**0.57**	±	**0.19**
IPI00007004	Ribosomal RNA-processing protein 15	**0.57**	±	**0.64**
IPI00221222	Activated RNA polymerase II transcriptional coactivator p15	**0.58**	±	**0.31**
IPI00171421	Mesenchymal stem cell protein DSCD75	**0.58**	±	**0.05**
IPI00026089	Spliceosome-associated protein 155	**0.58**	±	**0.23**
IPI00216138	22 kDa actin-binding protein	**0.58**	±	**0.17**
IPI00005490	Coat protein GPP34	**0.58**	±	**0.18**
IPI00296992	Tyrosine-protein kinase receptor UFO	**0.58**	±	**0.54**
IPI00306400	Kinesin-like protein 2	**0.59**	±	**0.02**
IPI00855785	Fibronectin	**0.59**	±	**0.24**
IPI00418471	Vimentin	**0.59**	±	**0.07**
IPI00005657	Prefoldin subunit 6	**0.59**	±	**0.12**
IPI00100980	EH domain-containing protein 2	**0.59**	±	**0.25**
IPI00010676	Monocyte activation antigen Mo3	**0.60**	±	**0.27**
IPI00003927	40 kDa peptidyl-prolyl cis-trans isomerase	**0.60**	±	**0.14**
IPI00027505	Integrin alpha-V	**0.60**	±	**0.07**
IPI00924510	Rap1-interacting factor 1 homolog	**0.60**	±	**0.04**
IPI00026970	Chromatin-specific transcription elongation factor 140 kDa subunit	**0.60**	±	**0.17**
IPI00016112	Melanoma-associated antigen MG50	**0.60**	±	**0.12**
IPI00004416	Chromatin-modifying protein 2a	**0.61**	±	**0.13**
IPI00001589	Mitochondrial import inner membrane translocase subunit Tim13	**0.61**	±	**0.19**
IPI00001159	GCN1-like protein 1	**0.61**	±	**0.31**
IPI00946792	Protein-tyrosine kinase 7	**0.61**	±	**0.16**
IPI00856098	p180/ribosome receptor	**0.61**	±	**0.12**
IPI00017567	Endoglin	**0.62**	±	**0.20**
IPI00439948	Inhibitor of ASPP protein	**0.62**	±	**0.35**
IPI00074010	Queuine tRNA-ribosyltransferase domain-containing protein 1	**0.62**	±	**0.17**
IPI00749454	Cell migration-inducing gene 2 protein	**0.62**	±	**0.10**
IPI00761017	Androgen receptor coactivator 55 kDa protein	**0.62**	±	**0.17**
IPI00221226	Annexin A6	**0.62**	±	**0.11**

International Protein Index	**Protein Name**	**Average Ratio (Treated/Untreated)**		
IPI00294903	Phosphomannomutase 1	**0.63**	±	**0.22**
IPI00171494	Dynein cytoplasmic heavy chain 2	**0.63**	±	**0.01**
IPI00008524	Polyadenylate-binding protein 1	**0.64**	±	**0.16**
IPI00024305	Mothers against decapentaplegic homolog 3	**0.64**	±	**0.15**
IPI00184533	Deubiquitinating enzyme 11	**0.64**	±	**0.07**
IPI00794221	Developmentally-regulated brain protein	**0.65**	±	**0.47**
IPI00029723	Follistatin-like protein 1	**0.65**	±	**0.21**
IPI00871467	Neural cell adhesion molecule L1 (L1CAM)	**0.65**	±	**0.19**
IPI00657752	Putative uncharacterized protein CD81	**0.65**	±	**0.18**
IPI00027808	RNA polymerase II subunit 2	**0.65**	±	**0.13**
IPI00000030	PP2A B subunit isoform B'-delta	**0.65**	±	**0.15**
IPI00604620	Nucleolin	**0.65**	±	**0.16**
IPI00328748	arginine-rich, mutated in early stage tumors (ARMET), mRNA	**0.66**	±	**0.06**
IPI00020557	Alpha-2-macroglobulin receptor	**0.66**	±	**0.24**
IPI00294578	Protein-glutamine gamma-glutamyltransferase 2	**0.66**	±	**0.16**
IPI00220031	Paxillin	**0.66**	±	**0.52**
IPI00477494	Dr1-associated corepressor	**0.66**	±	**0.45**
IPI00000690	Apoptosis-inducing factor 1, mitochondrial	**0.67**	±	**0.11**
IPI00007926	c-Myc-responsive protein Rcl	**0.67**	±	**0.13**
IPI00785070	HLA class I histocompatibility antigen, A-10 alpha chain	**0.67**	±	**0.10**
IPI00748472	WASH complex subunit strumpellin	**0.67**	±	**0.09**
IPI00006957	Dehydrogenase/reductase SDR family member 7	**0.67**	±	**0.35**
IPI00024642	Coiled-coil domain-containing protein 47	**0.67**	±	**0.03**
IPI00216694	Plastin-3	**0.67**	±	**0.16**
IPI00219037	Histone H2A.x	**0.67**	±	**0.53**
IPI00305551	Guanine nucleotide-binding protein G(y) subunit alpha	**0.67**	±	**0.16**
IPI00024993	Enoyl-CoA hydratase 1	**1.50**	±	**0.25**
IPI00014587	Clathrin light chain A	**1.50**	±	**0.24**
IPI00550894	Glucosamine-6-phosphate deaminase 2	**1.50**	±	**0.37**
IPI00064086	EEF1D protein	**1.51**	±	**0.27**
IPI00014213	Leucine--tRNA ligase	**1.52**	±	**0.15**
IPI00396015	ACC-alpha	**1.53**	±	**0.28**
IPI00001871	PRKC apoptosis WT1 regulator protein	**1.54**	±	**0.18**

International Protein Index	**Protein Name**	**Average Ratio (Treated/Untreated)**		
IPI00219468	Profilin II	**1.55**	**±**	**0.18**
IPI00019148	B-cell signal transduction molecule alpha 4	**1.55**	**±**	**0.42**
IPI00382804	EEF1A protein	**1.55**	**±**	**0.26**
IPI00006558	Bax-interacting factor 1	**1.56**	**±**	**0.21**
IPI00419979	C-t-PAK2	**1.56**	**±**	**0.46**
IPI00909579	Acyl-CoA synthetase family member 2, mitochondrial	**1.57**	**±**	**0.18**
IPI00220232	eIF-2B GDP-GTP exchange factor subunit delta	**1.57**	**±**	**0.63**
IPI00011201	Malic enzyme 2	**1.58**	**±**	**0.35**
IPI00215997	CD9 molecule	**1.58**	**±**	**0.28**
IPI00008494	Intercellular adhesion molecule 1	**1.58**	**±**	**0.31**
IPI00556385	ADP-dependent glucokinase	**1.58**	**±**	**0.14**
IPI00216293	Rhodanese	**1.60**	**±**	**0.31**
IPI00031115	Golgin subfamily A member 1	**1.61**	**±**	**0.34**
IPI00023406	Cytochrome c-type heme lyase	**1.61**	**±**	**0.72**
IPI00003377	Arginine/serine-rich splicing factor 7 type B	**1.64**	**±**	**0.44**
IPI00013466	Arsenite-stimulated ATPase	**1.65**	**±**	**0.72**
IPI00290142	CTP synthase 1	**1.67**	**±**	**0.74**
IPI00296353	Rho GTPase-activating protein 18	**1.68**	**±**	**0.11**
IPI00328350	Cell growth-inhibiting gene 39 protein	**1.69**	**±**	**0.32**
IPI00022810	Cathepsin C	**1.69**	**±**	**0.14**
IPI00294065	Cell proliferation-inducing gene 31 protein	**1.69**	**±**	**0.27**
IPI00013723	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	**1.70**	**±**	**0.69**
IPI00013167	28S ribosomal protein S25, mitochondrial	**1.74**	**±**	**0.30**
IPI00015836	Adapter protein containing PH domain, PTB domain and leucine zipper motif 1	**1.75**	**±**	**0.51**
IPI00029469	Actin-related protein 1B	**1.76**	**±**	**0.07**
IPI00013455	CAP-Gly domain-containing linker protein 1	**1.76**	**±**	**0.34**
IPI00005511	PHD finger-like domain-containing protein 5A	**1.78**	**±**	**0.72**
IPI00023344	Symplekin	**1.78**	**±**	**0.74**
IPI00304409	Calcium-regulated heat stable protein 1	**1.80**	**±**	**0.39**
IPI00935906	cDNA FLJ56465, highly similar to Dynactin-1	**1.80**	**±**	**0.36**
IPI00007117	Monocyte Arg-serpin	**1.81**	**±**	**0.62**
IPI00024871	Core-binding factor subunit beta	**1.81**	**±**	**0.74**
IPI00872028	NUMA1 variant protein	**1.82**	**±**	**0.63**
IPI00873904	GRIP1-associated protein 1	**1.82**	**±**	**0.75**

International Protein Index	**Protein Name**	**Average Ratio (Treated/Untreated)**		
IPI00939154	Apoptosis-stimulating of p53 protein 2	**1.84**	**±**	**0.51**
IPI00218858	Mitogen-activated protein kinase kinase 3 isoform B variant	**1.84**	**±**	**0.50**
IPI00220007	Apolipoprotein L2	**1.85**	**±**	**0.61**
IPI00927614	Golgin subfamily A member 4	**1.85**	**±**	**0.32**
IPI00301311	Phosphatase 2A inhibitor I2PP2A	**1.89**	**±**	**0.64**
IPI00514832	RING finger protein 109	**1.89**	**±**	**0.12**
IPI00719040	Uncharacterized protein C1orf77	**1.90**	**±**	**0.58**
IPI00787853	Inositol monophosphatase 3	**1.92**	**±**	**0.35**
IPI00442073	Cysteine and glycine-rich protein 1	**1.94**	**±**	**0.73**
IPI00376317	Autoantigen Ge-1	**1.95**	**±**	**0.18**
IPI00010463	GTP-binding protein 1	**1.96**	**±**	**0.41**
IPI00008982	Aldehyde dehydrogenase family 18 member A1	**2.03**	**±**	**0.44**
IPI00004839	Crk-like protein	**2.04**	**±**	**0.69**
IPI00412499	Rab GTPase-binding effector protein 2	**2.09**	**±**	**0.45**
IPI00420084	BH3-interacting domain death agonist	**2.13**	**±**	**0.44**
IPI00553169	Filamin A	**2.16**	**±**	**0.74**
IPI00064767	Rho GTPase-activating protein 17	**2.20**	**±**	**0.87**
IPI00003971	Neuroendocrine-specific protein	**2.22**	**±**	**0.34**
IPI00025418	Collagen alpha-1(VII) chain	**2.25**	**±**	**0.58**
IPI00290198	Iboctadekin	**2.28**	**±**	**0.18**
IPI00008750	Metallothionein-0	**2.31**	**±**	**0.90**
IPI00005978	Splicing factor SC35	**2.33**	**±**	**0.91**
IPI00172513	Adapter protein containing PH domain, PTB domain and leucine zipper motif 2	**2.40**	**±**	**0.78**
IPI00012197	Deoxycytidine-triphosphatase 1	**2.64**	**±**	**0.80**
IPI00024095	Annexin A3	**2.66**	**±**	**0.65**
IPI00005809	Cavin-2	**2.81**	**±**	**0.98**
IPI00022498	Metallothionein-2	**3.12**	**±**	**1.42**

Table S3: Summary of cellular pathways perturbed in GM00637 cells following exposure to 5 µM NNN for 24 hours (Gene Ontology Results from GenMAPP/MAPPFinder 2.1)**.**

Myosin (GO, z-score = 5.42)
Myosin regulatory light chain MRCL3 variant (fold change = 0.56)
Myosin heavy chain, non-muscle IIa (fold change = 0.55)
Myosin heavy chain, non-muscle IIb (fold change = 0.49)
Myosin heavy chain, non-muscle IIc (fold change = 0.57)
Cardiac myosin light chain 1 (fold change = 0.46)
Myosin regulatory light chain 9 (20 kDa) (fold change = 0.43)

Extracellular matrix (GO, z-score = 5.33)
Collagen alpha-3(VI) chain (fold change = 0.27)
Fibronectin (fold change = 0.59)
Protein-glutamine gamma-glutamyltransferase 2 (fold change = 0.66)
Collagen alpha-1(VII) chain (fold change = 2.25)
Laminin B1s chain (fold change = 0.52)
Collagen alpha-1(VI) chain (fold change = 0.25)
Alpha-2 type I collagen (fold change = 0.30)
Alpha-1 type I collagen (fold change = 0.25)

Collagen (GO, z-score = 5.18)
Collagen alpha-3(VI) chain (fold change = 0.27)
Collagen alpha-1(VII) chain (fold change = 2.25)
Collagen alpha-1(VI) chain (fold change = 0.25)
Alpha-2 type I collagen (fold change = 0.30)
Alpha-1 type I collagen (fold change = 0.25)

Cell adhesion (GO, z-score = 5.12).
Collagen alpha-3(VI) chain (fold change = 0.27)
Collagen alpha-1(VII) chain (fold change = 2.25)
Collagen alpha-1(VI) chain (fold change = 0.25)
CD9 molecule (fold change = 1.58)
CD99 molecule (fold change = 0.55)
Fibronectin (fold change = 0.59)
Endoglin (fold change = 0.62)
Neural cell adhesion molecule L1 (L1CAM) (fold change = 0.65)
Laminin B1s chain (fold change = 0.52)
Symplekin (fold change = 1.78)
Protein-tyrosine kinase 7 (fold change = 0.61)
Immunoglobulin superfamily DCC subclass member 2 (Neo1) (fold change = 0.28)

Phosphate Transport (GO, z-score = 4.34)
Collagen alpha-3(VI) chain (fold change = 0.27)
Collagen alpha-1(VII) chain (fold change = 2.25)
Collagen alpha-1(VI) chain (fold change = 0.25)
Alpha-2 type I collagen (fold change = 0.30)
Alpha-1 type I collagen (fold change = 0.25)

Anion Transport (GO, z-score = 4.24)
Collagen alpha-3(VI) chain (fold change = 0.27)
Collagen alpha-1(VII) chain (fold change = 2.25)
Collagen alpha-1(VI) chain (fold change = 0.25)
Alpha-2 type I collagen (fold change = 0.30)
Alpha-1 type I collagen (fold change = 0.25)
Arsenite-stimulated ATPase (fold change = 1.65)
cDNA FLJ56465, highly similar to Dynactin-1 (fold change = 1.8)
Rhodanese (fold change = 1.60)

Base-excision repair (GO, z-score = 4.15)
APEX nuclease (fold change = 0.44)
High mobility group protein 1 (fold change = 0.51)
High mobility group protein 2 (fold change = 0.25)

Lymphocyte activation (GO, z-score = 4.15)
B-cell signal transduction molecule alpha 4 (fold change = 1.55)
Putative uncharacterized protein CD81 (fold change = 0.64)
Iboctadekin (fold change = 2.28)

Vascular endothelial growth factor receptor activity (GO, z-score 4.10)
Immunoglobulin superfamily DCC subclass member 2 (NEO1) (fold change = 0.28)
Protein-tyrosine kinase 7 (fold change = 0.61)

Calcium and Calmodulin Dependent protein kinase activity (GO, z-score = 4.1)
Calcium/calmodulin-dependent protein kinase type II delta chain (fold change = 2.01)
CaM Kinase II (fold change = 2.50)