Table S2: List of all identified and quantified proteins in the quantitative proteome comparision of skin lysates wt and *Ctsb*$^{-/-}$ (replicate 2).

Protein	**Uniprot accession**	**ProteinProphet Prob. Score**	**Unique peptides**	**Total peptides**	**Sequence coverage [%]**	**Fold change (log$_2$) of ASAPratio**	**Fold change standard deviation**	**ASAPratio p-value**
Cathepsin B;	P10605	1	7	9	23.6	-6,644*	-0.001	0.000
Claudin-5;	O54942	0.964	2	2	7.3	-6.644	-0.001	0.000
Chitinase-3-like protein 3;	O35744	1	2	3	8.5	-4.059	-2.03	0.001
Secretory carrier-associated membrane protein 4;	Q9JKV5	0.999	2	2	4.8	-3.837	-0.548	0.000
Parvalbumin alpha;	P32848	1	11	164	45.5	-3.644	-0.456	0.000
Uncharacterized protein;	F6VHB7	0.999	3	3	18	-3.644	-0.456	0.000
Fructose-bisphosphate aldolase B;	Q91Y97	1	2	2	8	-3.474	-1.158	0.001
Major urinary protein 3;	P04939	1	2	2	6.1	-3.322	-0.332	0.000
Troponin C, skeletal muscle;	P20801	1	9	9	35.6	-3.322	-1.661	0.004
Biglycan;	P28653	1	3	3	5.7	-3.322	-0.332	0.000
Myosin-binding protein H;	P70402	1	3	3	13.7	-3.322	-0.997	0.001
Hexokinase-3;	Q3TRM8	0.994	2	2	3.3	-3.322	-0.332	0.000
Glutamate dehydrogenase 1, mitochondrial;	P26443	1	6	6	13.3	-3.184	-0.289	0.000
Betaine--homocysteine S-methyltransferase 1;	O35490	1	4	6	11.3	-2.943	-0.679	0.002
Creatine kinase S-type, mitochondrial;	Q6P8J7	1	14	18	26	-2.837	-2.634	0.076
Cytochrome b-c1 complex subunit 2, mitochondrial;	Q9DB77	1	7	7	15.9	-2.837	-2.634	0.076
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial;	Q91VD9	1	6	8	12.4	-2.737	-1.277	0.014
Coproporphyrinogen-III oxidase, mitochondrial;	P36552	1	2	2	5.4	-2.644	-1.157	0.016
Scavenger receptor cysteine-rich domain-containing protein LOC284297 homolog;	Q8BV57	1	5	5	6	-2.644	-0.992	0.012
ADP/ATP translocase 1;	P48962	1	15	39	25.8	-2.644	-0.496	0.005
ADP/ATP translocase 2;	P51881	1	4	8	22.8	-0.971	-0.076	0.283
Mitochondrial inner membrane protein;	Q8CAQ8	1	2	2	6	-2.556	-0.902	0.013
Cytochrome b-c1 complex subunit 1, mitochondrial;	Q9CZ13	1	9	13	24	-2.474	-0.825	0.017
Ig heavy chain V region 441;	P01806	1	2	2	13.8	-2.322	-0.464	0.014
RIKEN cDNA 8030451F13, isoform CRA_c; Uncharacterized protein;	D3YU50	1	15	19	12.3	-2.322	-0.697	0.018
Collagen triple helix repeat-containing protein 1;	Q9D1D6	1	2	2	9.4	-2.322	-0.581	0.016
Phosphoglucomutase-like protein 5;	Q8BZF8	1	2	2	3.9	-2.184	-0.993	0.052
Collagen alpha-2(I) chain;	Q01149	1	26	40	17.5	-2.12	-0.83	0.046
Mitochondrial carrier homolog 2;	Q791V5	1	4	5	18.5	-2.12	-1.198	0.084
Fatty acid-binding protein, liver;	P12710	1	2	2	16.5	-2.12	-0.184	0.019
Xin actin-binding repeat-containing protein 1;	O70373	1	5	5	5.4	-2.059	-0.172	0.022
Cytochrome c oxidase subunit 2;	P00405	1	4	4	13.2	-2.059	-0.343	0.025
C4b-binding protein;	P08607	1	4	4	8.7	-2.059	-0.601	0.037
Extracellular superoxide dismutase [Cu-Zn];	O09164	1	5	5	24.7	-2	-1.36	0.134
Tetranectin;	P43025	1	9	15	45	-2	-0.4	0.033
Voltage-dependent anion-selective channel protein 3;	Q60931	1	2	2	7.1	-2	-0.32	0.033
Arginase-1;	Q61176	1	9	10	25.4	-2	-0.8	0.065
Myosin light chain 1/3, skeletal muscle isoform;	P05977	1	13	70	45.7	-2	-0.48	0.041
ATP synthase subunit g, mitochondrial;	Q9CPQ8	1	3	8	27.2	-2	-0.16	0.026
Scavenger receptor cysteine-rich type 1 protein M130;	Q2VLH6	1	2	2	1.9	-2	-0.96	0.076
Prelamin-A/C;	P48678	1	4	5	10.2	-1.943	-1.345	0.148

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change (log$_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial;	Q91YT0	1	5	8	19.5	-1.943	-0.673	0.063
Splicing factor U2AF 65 kDa subunit;	P26369	1	5	8	18.6	-1.889	-0.49	0.053
Collagen alpha-1(I) chain;	P11087	1	28	48	17.8	-1.889	-0.91	0.098
ATP synthase subunit O, mitochondrial;	Q9DB20	1	9	11	36.2	-1.889	-0.56	0.057
Uncharacterized protein;	E9Q8E3	1	4	4	4	-1.889	-1.119	0.131
Beta-hexosaminidase subunit beta;	P20060	0.998	2	2	1.7	-1.889	-0.14	0.038
Cytochrome b-c1 complex subunit 7;	Q9D855	1	3	4	18.9	-1.837	-0.328	0.051
Glutamine synthetase;	P15105	1	3	4	12.1	-1.837	-0.918	0.116
Creatine kinase U-type, mitochondrial;	P30275	1	6	9	21.1	-1.837	-0.262	0.046
Nucleobindin-1;	Q02819	1	6	7	9.4	-1.837	-0.59	0.067
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial;	O35459	1	2	2	6.1	-1.786	-0.246	0.051
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	P19783	1	2	5	10.7	-1.786	-0.431	0.063
SPARC;	P07214	1	7	10	23.3	-1.786	-0.677	0.090
Peroxisomal acyl-coenzyme A oxidase 3;	Q9EPL9	1	7	8	8.3	-1.786	-0.308	0.054
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial;	Q921G7	0.999	2	2	5.6	-1.786	-0.246	0.051
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial;	P45952	1	4	4	8.1	-1.737	-0.463	0.073
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial;	Q8K2B3	1	11	15	21.1	-1.737	-0.174	0.055
ATP synthase subunit beta, mitochondrial;	P56480	1	40	91	49.1	-1.69	-0.273	0.073
Uncharacterized protein;	E9Q9T2	1	5	5	13.8	-1.69	-0.654	0.107
Voltage-dependent anion-selective channel protein 1;	Q60932	1	13	17	45.6	-1.69	-0.818	0.139
Xin actin-binding repeat-containing protein 2;	Q4U4S6	0.924	2	2	3.7	-1.69	-0.273	0.067
Transforming growth factor-beta-induced protein ig-h3;	P82198	1	4	4	3.8	-1.644	-0.257	0.079
S-formylglutathione hydrolase;	Q9R0P3	1	11	16	34.8	-1.644	-0.462	0.097
Apoptosis-inducing factor 1, mitochondrial;	Q9Z0X1	1	2	2	5.3	-1.644	-0.822	0.158
Guanine deaminase;	Q9R111	1	15	15	28.4	-1.644	-0.565	0.112
Cathepsin S;	O70370	1	8	11	25.6	-1.599	-0.436	0.107
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial;	Q9CQA3	1	3	4	8.9	-1.599	-0.145	0.079
Septin-5;	Q9Z2Q6	1	2	2	4.6	-1.599	-0.291	0.089
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial;	Q9D6J6	1	9	12	24.2	-1.556	-0.092	0.085
Indolethylamine N-methyltransferase;	P40936	1	2	2	12.1	-1.515	-0.606	0.152
Myomesin 2; Uncharacterized protein;	Q14BI5	1	31	37	21.7	-1.515	-0.996	0.245
Septin-2;	P42208	1	5	5	21.6	-1.515	-0.996	0.245
Myosin-4;	Q5SX39	1	23	31	23.4	-1.515	-0.39	0.121
Myosin-1;	Q5SX40	1	6	7	21.9	-3.059	-2.549	0.045
Myosin-11;	O08638	1	4	4	3.7	-1.69	-0.218	0.062
Myosin-9;	Q8VDD5	1	4	4	4.6	1.422	0.409	0.152
ATP synthase subunit gamma, mitochondrial;	Q91VR2	1	11	12	36.4	-1.515	-0.433	0.126
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial;	Q9CXZ1	0.997	2	2	14.3	-1.515	-1.169	0.292
Ig kappa chain V-III region PC 2880/PC 1229;	P01654	1	3	5	16.2	-1.474	-0.164	0.111
Fatty acid-binding protein, heart;	P11404	1	10	10	42.1	-1.474	-0.614	0.173
Guanine nucleotide-binding protein subunit beta-2-like 1;	P68040	1	17	19	45.7	-1.474	-0.696	0.189
Ribosome-binding protein 1;	Q99PL5	1	6	7	5	-1.474	-0.45	0.147
ATP synthase subunit delta, mitochondrial;	Q9D3D9	1	3	8	13.7	-1.474	-0.328	0.119

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change ($\log_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
Uncharacterized protein;	D3YXF5	1	7	7	26.5	-1.474	-0.614	0.166
ATP synthase subunit alpha, mitochondrial;	Q03265	1	31	63	34.4	-1.474	-0.368	0.131
Myosin regulatory light chain 2, skeletal muscle isoform;	P97457	1	12	20	40.2	-1.434	-1.201	0.347
Acyl-CoA synthetase short-chain family member 3, mitochondrial;	Q14DH7	1	6	6	9.8	-1.396	-0.588	0.198
Myomesin-1;	Q62234	1	25	27	10.1	-1.396	-0.771	0.250
Suprabasin;	Q8CIT9	1	9	9	19.5	-1.396	-0.808	0.258
SAM domain and HD domain-containing protein 1;	Q60710	1	9	11	18.5	-1.396	-0.735	0.233
Coagulation factor XII;	Q80YC5	1	5	6	8.9	-1.396	-0.184	0.130
Ig gamma-3 chain C region;	P03987	1	3	3	6.3	-1.396	-0.11	0.124
Hydroxymethylglutaryl-CoA synthase, mitochondrial;	P54869	0.99	2	2	4.1	-1.396	-0.22	0.135
Cytochrome P450 2F2;	P33267	1	2	2	7.9	-1.358	-0.348	0.160
Septin-9;	Q80UG5	1	5	5	10.3	-1.358	-0.522	0.195
Cell cycle control protein 50A;	Q8VEK0	0.999	2	2	7.3	-1.358	-1.254	0.395
Ig gamma-2A chain C region, A allele;	P01863	1	7	13	18.5	-1.322	-0.099	0.144
Annexin A2;	P07356	1	31	116	62.2	-1.322	-0.463	0.197
Gamma-butyrobetaine dioxygenase;	Q924Y0	0.999	2	2	9.7	-1.322	-0.165	0.150
Neural cell adhesion molecule L1-like protein;	P70232	1	3	4	3.6	-1.286	-0.188	0.162
Microfibril-associated glycoprotein 4;	Q9D1H9	1	2	4	7	-1.286	-0.314	0.182
Ferritin heavy chain;	P09528	1	8	10	18.7	-1.252	-0.089	0.173
Thioredoxin-dependent peroxide reductase, mitochondrial;	P20108	1	12	15	28	-1.252	-0.745	0.315
Peroxisomal acyl-coenzyme A oxidase 1;	Q9R0H0	1	4	4	6.2	-1.252	-0.298	0.191
A-kinase anchor protein 12;	Q9WTQ5	1	27	37	13.2	-1.252	-0.507	0.240
Ubiquitin carboxyl-terminal hydrolase isozyme L1;	Q9R0P9	1	3	5	13	-1.252	-0.089	0.171
Uncharacterized protein C9orf102 homolog;	Q6DI94	0.951	2	3	2.1	-1.252	-0.417	0.214
UDP-N-acetylhexosamine pyrophosphorylase;	Q91YN5	1	5	5	9.4	-1.218	-0.227	0.198
Titin;	A2ASS6	1	40	51	1.2	-1.218	-0.567	0.283
Catalase;	P24270	1	22	28	38	-1.218	-0.708	0.322
Lysosome-associated membrane glycoprotein 1;	P11438	1	3	3	5.7	-1.184	-0.135	0.195
Myosin-binding protein C, fast-type;	Q5XKE0	1	35	50	26.1	-1.184	-0.565	0.299
Aflatoxin B1 aldehyde reductase member 2;	Q8CG76	1	10	15	24.3	-1.184	-0.807	0.373
Periplakin;	Q9R269	1	8	8	4.4	-1.184	-0.511	0.279
Ferritin light chain 1;	P29391	1	11	21	38.3	-1.184	-0.161	0.201
Glutathione peroxidase 3;	P46412	1	3	4	15.6	-1.152	-0.102	0.205
Voltage-dependent anion-selective channel protein 2;	Q60930	1	6	8	20.7	-1.152	-0.307	0.239
Extracellular matrix protein 1;	Q61508	1	3	3	11.7	-1.152	-0.538	0.308
Dihydropyrimidinase-related protein 2;	O08553	1	33	53	46	-1.12	-0.682	0.372
Uncharacterized protein;	E9PWE8	1	19	22	29	-0.434	-0.07	0.638
Macrophage colony-stimulating factor 1 receptor;	P09581	0.993	2	3	1.8	-1.12	-0.073	0.214
Complement factor D;	P03953	1	5	6	20.1	-1.089	-0.162	0.235
Decorin;	P28654	1	4	11	5.9	-1.089	-0.139	0.243
Nucleobindin-2;	P81117	1	3	3	4.3	-1.089	-0.209	0.253
Mannose-1-phosphate guanyltransferase beta;	Q8BTZ7	1	3	4	13.9	-1.089	-0.51	0.331
Histidine-rich glycoprotein;	Q9ESB3	1	7	8	13.1	-1.089	-0.649	0.379

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change (log_2) of ASAPratio	Fold change standard deviation	ASAPratio p-value
Serpin B6;	Q60854	1	26	43	42.1	-1.089	-0.162	0.235
Plastin-2;	Q61233	1	30	40	38.1	-1.089	-0.348	0.285
Vacuolar protein sorting-associated protein 29;	Q9QZ88	1	6	7	29	-1.089	-0.348	0.280
Uncharacterized protein;	E9Q2P1	1	9	20	23.4	-1.089	-0.348	0.285
Ig kappa chain V-V region L6;	P01638	0.999	2	2	15.7	-1.089	-0.093	0.226
Long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P51174	1	13	15	22.1	-1.059	-0.64	0.401
Phospholipase B-like 1;	Q8VCI0	1	5	7	11.6	-1.059	-0.066	0.247
Probable C->U-editing enzyme APOBEC-2;	Q9WV35	1	3	3	6.7	-1.059	-0.154	0.257
Glia maturation factor gamma;	Q9ERL7	1	4	4	19.8	-1.059	-0.419	0.323
Collagen alpha-1(III) chain;	P08121	1	6	6	6.5	-1.029	-0.252	0.290
Echinoderm microtubule-associated protein-like 1;	Q05BC3	1	2	2	3.4	-1.029	-0.546	0.382
Beta-galactosidase;	P23780	1	9	10	11	-1.029	-0.252	0.290
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	Q9R0E2	1	5	5	7.4	-1.029	-0.21	0.278
Protein S100-A13;	P97352	1	5	7	31.6	-1	-0.06	0.269
Coatomer subunit delta;	Q5XJY5	1	5	5	7	-1	-0.4	0.354
Sulfated glycoprotein 1;	Q61207	1	16	18	16.7	-1	-0.66	0.450
Aldose 1-epimerase;	Q8K157	1	3	3	9.1	-1	-0.12	0.277
Asporin;	Q99MQ4	1	12	13	26.5	-1	-0.38	0.344
Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase;	Q9DBB8	1	6	6	18.3	-1	-0.16	0.283
Protein RCC2;	Q8BK67	1	8	10	15.6	-1	-0.54	0.397
Uncharacterized protein;	D3Z0Y2	1	27	69	69	-1	-0.14	0.280
NK13; Serine (Or cysteine) peptidase inhibitor, clade B, member 6b; Serine (Or cysteine) peptidase inhibitor, clade B, member 6b, isoform CRA_a; Uncharacterized protein;	O08804	0.996	2	3	6.4	-1	-0.16	0.283
Ig heavy chain V region MOPC 104E;	P01756	1	4	9	16.2	-0.971	-0.076	0.283
Ig kappa chain C region;	P01837	1	8	26	44.3	-0.971	-0.209	0.308
Pleckstrin homology domain-containing family O member 2;	Q8K124	1	2	2	3	-0.971	-0.133	0.291
Four and a half LIM domains protein 1;	P97447	1	16	21	37.5	-0.971	-0.171	0.297
2-oxoglutarate dehydrogenase, mitochondrial;	Q60597	1	33	61	28.3	-0.971	-0.495	0.405
Major vault protein;	Q9EQK5	1	3	3	5	-0.971	-0.209	0.308
ATP synthase subunit d, mitochondrial;	Q9DCX2	0.972	2	2	12.3	-0.971	-0.286	0.326
Myc box-dependent-interacting protein 1;	O08539	1	5	7	11.9	-0.943	-0.417	0.390
Complement factor H;	P06909	1	3	3	2.7	-0.943	-0.417	0.390
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	Q99LD8	1	15	21	37.9	-0.943	-0.236	0.327
Leucine-rich HEV glycoprotein; Leucine-rich alpha-2-glycoprotein; Leucine-rich alpha-2-glycoprotein 1; Uncharacterized protein;	Q91XL1	1	5	8	7.9	-0.943	-0.272	0.336
Carboxymethylenebutenolidase homolog;	Q8R1G2	1	7	8	18	-0.943	-0.109	0.297
Adiponectin;	Q60994	1	2	2	4.9	-0.916	-0.069	0.307
Actin-related protein 2/3 complex subunit 2;	Q9CVB6	1	3	3	11.6	-0.916	-0.328	0.382
ES1 protein homolog, mitochondrial;	Q9D172	1	9	14	24.4	-0.916	-0.363	0.398
Ahnak protein; MCG17833, isoform CRA_b; Uncharacterized protein;	Q8R2L7	1	2	2	43.9	-0.916	-0.104	0.312
Plasma protease C1 inhibitor;	P97290	1	11	12	14.9	-0.916	-0.207	0.345
Collagen alpha-1(VI) chain;	Q04857	1	4	4	4.2	-0.916	-0.467	0.428

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change ($\log_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
Secernin-2;	Q8VCA8	1	5	5	13.2	-0.916	-0.501	0.441
MCG21235; Uncharacterized protein;	Q9D1Q5	1	4	4	11.9	-0.916	-0.259	0.352
D-dopachrome decarboxylase;	O35215	1	6	10	42.4	-0.889	-0.412	0.429
Periaxin;	O55103	1	3	3	3.7	-0.889	-0.346	0.405
Cadherin-13;	Q9WTR5	1	4	6	9.2	-0.889	-0.082	0.333
Angiotensin-converting enzyme;	P09470	1	15	21	8.8	-0.889	-0.115	0.327
Major urinary protein 2;	P11589	1	18	35	53.3	-0.889	-0.247	0.373
Calcium/calmodulin-dependent protein kinase type II subunit alpha;	P11798	1	5	5	8.4	-0.889	-0.066	0.331
Echinoderm microtubule-associated protein-like 2;	Q7TNG5	1	7	8	13.2	-0.889	-0.477	0.455
Valacyclovir hydrolase;	Q8R164	1	5	5	18.2	-0.889	-0.247	0.373
Coronin-1C;	Q9WUM4	1	6	6	10.5	-0.889	-0.099	0.336
Septin-7;	O55131	0.994	2	2	8.6	-0.889	-0.329	0.397
Heat shock protein beta-7;	P35385	1	3	4	26	-0.862	-0.125	0.353
Oxidation resistance protein 1;	Q4KMM3	1	2	2	5.5	-0.862	-0.094	0.347
Membrane primary amine oxidase;	O70423	1	7	14	8.5	-0.862	-0.063	0.344
Adseverin;	Q60604	1	4	4	6.3	-0.862	-0.423	0.455
Fructose-1,6-bisphosphatase isozyme 2;	P70695	1	2	2	8.6	-0.837	-0.418	0.469
Copper homeostasis protein cutC homolog;	Q9D8X1	1	4	4	13	-0.837	-0.284	0.413
Integrin beta-4;	A2A863	1	2	2	1.4	-0.837	-0.164	0.377
Hexokinase-2;	O08528	1	24	26	19.9	-0.837	-0.404	0.464
Spermine synthase;	P97355	1	10	10	20.8	-0.837	-0.075	0.357
Enoyl-CoA hydratase, mitochondrial;	Q8BH95	1	5	5	15.5	-0.837	-0.135	0.368
Dci protein; Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase); Uncharacterized protein;	Q8QZV3	1	15	32	26.3	-0.837	-0.12	0.365
40S ribosomal protein SA;	P14206	1	8	13	32.5	-0.811	-0.285	0.429
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1;	Q3TW96	1	13	16	24.1	-0.811	-0.171	0.392
Hemopexin;	Q91X72	1	23	135	26.7	-0.811	-0.043	0.367
Actin, alpha cardiac muscle 1;	P68033	1	6	7	52.3	-0.811	-0.071	0.370
Xanthine dehydrogenase/oxidase;	Q00519	1	33	41	19.6	-0.811	-0.114	0.377
MACRO domain-containing protein 1;	Q922B1	1	5	6	19.5	-0.786	-0.095	0.387
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial;	Q9D2G2	1	4	7	4.6	-0.786	-0.041	0.380
Dihydrolipoyl dehydrogenase, mitochondrial;	O08749	1	17	32	22.8	-0.786	-0.068	0.383
Serpin B8;	O08800	1	7	10	9.9	-0.761	-0.284	0.474
Adenylosuccinate synthetase isozyme 1;	P28650	1	23	33	35.2	-0.761	-0.155	0.427
Procollagen C-endopeptidase enhancer 1;	Q61398	1	5	9	36.3	-0.761	-0.477	0.544
Macrophage mannose receptor 1;	Q61830	1	26	30	14.1	-0.761	-0.181	0.434
Mitotic checkpoint protein BUB3;	Q9WVA3	1	4	4	9.5	-0.761	-0.064	0.395
Coronin-1A;	O89053	1	8	12	9.1	-0.761	-0.052	0.407
Histidine ammonia-lyase;	P35492	1	23	34	29.4	-0.761	-0.206	0.445
Nascent polypeptide-associated complex subunit alpha, muscle-specific form;	P70670	1	33	39	14.9	-0.761	-0.387	0.515
CAP-Gly domain-containing linker protein 1;	Q922J3	1	7	7	5.5	-0.761	-0.077	0.409
S-phase kinase-associated protein 1;	Q9WTX5	1	5	5	20.2	-0.761	-0.619	0.601

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Uncharacterized protein;	F7DBB3	1	17	44	20.3	-0.761	-0.464	0.547
Superoxide dismutase [Cu-Zn];	P08228	1	12	21	32.5	-0.737	-0.295	0.493
Vacuolar protein sorting-associated protein 26B;	Q8C0E2	1	2	2	5.4	-0.737	-0.111	0.429
Nicotinamide phosphoribosyltransferase;	Q99KQ4	1	17	19	32	-0.737	-0.135	0.434
UDP-glucose 6-dehydrogenase;	O70475	1	19	21	32.9	-0.737	-0.27	0.484
L-lactate dehydrogenase A chain;	P06151	1	26	74	52.4	-0.737	-0.16	0.435
L-lactate dehydrogenase B chain;	P16125	1	15	20	32.3	-0.415	-0.039	0.643
Isocitrate dehydrogenase [NADP], mitochondrial;	P54071	1	35	67	39.4	-0.737	-0.111	0.429
Transmembrane protein 43;	Q9DBS1	0.951	2	2	2	-0.737	-0.074	0.422
Complement C4-B;	P01029	1	18	25	9.4	-0.713	-0.129	0.449
Ig gamma-1 chain C region secreted form;	P01868	1	11	36	23.8	-0.713	-0.07	0.435
Carnitine O-acetyltransferase;	P47934	1	2	2	19.7	-0.713	-0.117	0.444
Sorbitol dehydrogenase;	Q64442	1	7	10	11.5	-0.713	-0.456	0.581
Troponin T, fast skeletal muscle;	Q9QZ47	1	3	3	6.7	-0.713	-0.129	0.449
Vimentin;	P20152	1	8	9	14.8	-0.713	-0.257	0.495
Desmin;	P31001	0.999	3	3	5.3	-0.358	-0.055	0.699
Junctophilin-2;	Q9ET78	1	2	2	4.9	-0.713	-0.082	0.436
Peptidyl-prolyl cis-trans isomerase FKBP7;	O54998	1	5	9	13.3	-0.69	-0.234	0.498
Sulfite oxidase, mitochondrial;	Q8R086	1	4	4	9.2	-0.69	-0.067	0.448
Actin-related protein 2/3 complex subunit 1B;	Q9WV32	1	8	9	21	-0.69	-0.145	0.467
Diphthamide biosynthesis protein 2;	Q9CR25	0.993	2	2	4.3	-0.69	-0.601	0.653
Protein S100-A4;	P07091	1	2	2	7.9	-0.667	-0.074	0.463
Serum albumin;	P07724	1	92	3158	66.6	-0.667	-0.106	0.469
Tripartite motif-containing protein 72;	Q1XH17	1	6	6	18.7	-0.667	-0.286	0.535
Spermidine synthase;	Q64674	1	7	7	16.2	-0.667	-0.318	0.560
Cell adhesion molecule 3;	Q99N28	1	2	4	5.5	-0.667	-0.053	0.459
N-acetylneuraminate lyase;	Q9DCJ9	1	11	11	30.3	-0.667	-0.127	0.476
Glyoxylate reductase/hydroxypyruvate reductase;	Q91Z53	1	10	14	29.6	-0.667	-0.191	0.498
Protein DJ-1;	Q99LX0	1	13	22	58.9	-0.667	-0.318	0.553
Peptidyl-prolyl cis-trans isomerase;	A2BGI8	1	3	4	13.3	-0.667	-0.138	0.479
Phosphoglycerate mutase 2;	O70250	1	25	97	47	-0.644	-0.07	0.489
Legumain;	O89017	1	3	3	3.9	-0.644	-0.111	0.499
Porphobilinogen deaminase;	P22907	1	2	4	5.8	-0.644	-0.161	0.512
Lumican;	P51885	1	26	178	38.8	-0.644	-0.07	0.488
Glycerol-3-phosphate dehydrogenase 1-like protein;	Q3ULJ0	1	10	12	16.8	-0.644	-0.252	0.539
Synaptic vesicle membrane protein VAT-1 homolog;	Q62465	1	15	21	32	-0.644	-0.252	0.549
Prenylcysteine oxidase;	Q9CQF9	1	3	3	4	-0.644	-0.091	0.492
Leukocyte elastase inhibitor A;	Q9D154	1	14	27	25.3	-0.644	-0.111	0.499
Dipeptidyl peptidase 2;	Q9ET22	1	8	11	15.6	-0.644	-0.131	0.491
Plasminogen activator inhibitor 2, macrophage;	P12388	1	6	6	11.1	-0.644	-0.151	0.508
Aldehyde dehydrogenase, mitochondrial;	P47738	1	31	81	41.8	-0.644	-0.332	0.578
Retinal dehydrogenase 1;	P24549	1	21	28	24	-1.69	-0.709	0.120
Aldehyde dehydrogenase family 1 member A3;	Q9JHW9	0.994	2	2	6.8	1.428	0.234	0.126

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Aldehyde dehydrogenase, cytosolic 1;	O35945	0.989	2	2	11.6	0.214	0.022	0.813
Saccharopine dehydrogenase-like oxidoreductase;	Q8R127	1	3	3	8.4	-0.644	-0.07	0.475
von Willebrand factor A domain-containing protein 5A;	Q99KC8	1	17	21	15.4	-0.644	-0.211	0.531
Coactosin-like protein;	Q9CQI6	1	2	2	24.6	-0.644	-0.181	0.509
Zinc transporter SLC39A7;	Q31125	1	2	2	2.7	-0.644	-0.07	0.476
Voltage-dependent calcium channel subunit alpha-2/delta-1;	O08532	1	2	2	1.3	-0.621	-0.048	0.498
Creatine kinase M-type;	P07310	1	47	922	60.4	-0.621	-0.086	0.505
Serpin H1;	P19324	1	19	26	30	-0.621	-0.134	0.518
Cytoplasmic aconitate hydratase;	P28271	1	25	37	21.7	-0.621	-0.153	0.524
Platelet glycoprotein 4;	Q08857	1	6	8	11	-0.621	-0.067	0.501
Epoxide hydrolase 1;	Q9D379	1	2	2	7	-0.621	-0.076	0.493
Proliferation-associated protein 2G4;	P50580	1	6	6	12.9	-0.621	-0.401	0.633
C-1-tetrahydrofolate synthase, cytoplasmic;	Q922D8	1	15	17	12.8	-0.621	-0.115	0.513
Dynein light chain 2, cytoplasmic;	Q9D0M5	1	3	3	20.2	-0.621	-0.306	0.593
NHL repeat-containing protein 2;	Q8BZW8	1	2	2	1.8	-0.621	-0.057	0.499
Hematopoietic progenitor cell antigen CD34;	Q64314	1	2	2	7.6	-0.621	-0.086	0.505
Annexin A3;	O35639	1	5	5	11.8	-0.599	-0.127	0.530
Ceruloplasmin;	Q61147	1	39	53	26.8	-0.599	-0.263	0.588
Reticulocalbin-3;	Q8BH97	1	6	12	11.7	-0.599	-0.163	0.544
Glucose-6-phosphate isomerase;	P06745	1	30	63	28	-0.599	-0.091	0.520
Aldose reductase;	P45376	1	18	25	32.9	-0.599	-0.064	0.515
Quinone oxidoreductase;	P47199	1	5	7	16.9	-0.599	-0.1	0.521
Ras suppressor protein 1;	Q01730	1	6	8	22.4	-0.599	-0.073	0.516
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial;	Q9EQ20	1	9	15	14.6	-0.599	-0.29	0.599
Methionine aminopeptidase 2;	O08663	1	2	2	4.4	-0.599	-0.054	0.512
Leukotriene A-4 hydrolase;	P24527	1	30	48	33.2	-0.578	-0.224	0.584
Peptidyl-prolyl cis-trans isomerase C;	P30412	1	6	8	20.8	-0.578	-0.06	0.526
Heparin cofactor 2;	P49182	1	8	10	7.9	-0.578	-0.155	0.556
Thiosulfate sulfurtransferase;	P52196	1	7	9	14.2	-0.578	-0.138	0.548
Carbonyl reductase [NADPH] 2;	P08074	1	14	20	38.9	-0.578	-0.078	0.531
Vacuolar protein sorting-associated protein 26A;	P40336	1	4	4	9.2	-0.578	-0.112	0.540
Actin-related protein 2/3 complex subunit 3;	Q9JM76	1	6	8	23.6	-0.578	-0.069	0.528
Alpha-adducin;	Q9QYC0	1	6	7	11.5	-0.578	-0.259	0.602
GDH/6PGL endoplasmic bifunctional protein;	Q8CFX1	0.947	2	2	1	-0.578	-0.052	0.525
F-actin-capping protein subunit alpha-2;	P47754	1	3	4	10.8	-0.556	-0.213	0.598
Creatine kinase B-type;	Q04447	1	21	35	36.7	-0.556	-0.131	0.562
Beta-lactamase-like protein 2;	Q99KR3	1	2	2	6.2	-0.556	-0.025	0.536
Serrate RNA effector molecule homolog;	Q99MR6	1	8	8	3.4	-0.556	-0.482	0.716
Fetuin-B;	Q9QXC1	1	8	20	24.7	-0.556	-0.049	0.538
Uncharacterized protein;	F8WIT2	1	43	70	39.1	-0.556	-0.311	0.645
Glutathione S-transferase Mu 2;	P15626	1	12	15	48.6	-0.556	-0.131	0.560
Glutathione S-transferase Mu 1;	P10649	1	9	14	29.8	-0.862	-0.11	0.351
Abhydrolase domain-containing protein 14B;	Q8VCR7	1	3	3	15.7	-0.556	-0.041	0.537

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Flavin reductase (NADPH);	Q923D2	1	8	11	38.8	-0.556	-0.049	0.538
Lambda-crystallin homolog;	Q99KP3	1	6	6	15.7	-0.556	-0.041	0.537
Band 4.1-like protein 3;	Q9WV92	1	8	8	11.3	-0.556	-0.074	0.543
Fumarylacetoacetase;	P35505	1	6	6	13.4	-0.535	-0.093	0.561
Annexin A5;	P48036	1	28	47	45.1	-0.535	-0.078	0.558
Endoplasmic reticulum resident protein 29;	P57759	1	6	7	13.7	-0.535	-0.124	0.572
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2;	P62880	1	5	7	23.8	-0.535	-0.349	0.678
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1;	P62874	1	4	4	10.3	0.227	0.023	0.803
Myosin light polypeptide 6;	Q60605	1	10	19	30.5	-0.535	-0.085	0.559
Nebulin; Uncharacterized protein;	A2AQA9	1	7	11	1.4	-0.535	-0.357	0.681
Nucleoside diphosphate kinase;	E9PZF0	1	12	35	67	-0.535	-0.186	0.600
N-alpha-acetyltransferase 50;	Q6PGB6	1	3	3	19.6	-0.535	-0.163	0.591
Acylphosphatase-1;	P56376	1	5	7	36.4	-0.515	-0.059	0.580
Reticulocalbin-1;	Q05186	1	3	3	7.1	-0.515	-0.419	0.724
Complement factor I;	Q61129	1	9	13	9.6	-0.515	-0.037	0.577
NEDD8-activating enzyme E1 regulatory subunit;	Q8VBW6	1	2	2	5.1	-0.515	-0.309	0.675
Fibrinogen gamma chain;	Q8VCM7	1	16	24	29.4	-0.515	-0.162	0.605
Filamin-C;	Q8VHX6	1	14	14	5.5	-0.515	-0.103	0.592
Oxysterol-binding protein-related protein 1;	Q91XL9	1	2	2	5.4	-0.515	-0.11	0.582
Aconitate hydratase, mitochondrial;	Q99KI0	1	62	102	44.4	-0.515	-0.052	0.578
Plasma glutamate carboxypeptidase;	Q9WVJ3	1	6	6	11.9	-0.515	-0.103	0.592
Epididymal secretory protein E1;	Q9Z0J0	1	5	9	18.8	-0.515	-0.037	0.563
Myelin protein P0;	P27573	1	4	6	14.1	-0.515	-0.037	0.563
Pyruvate kinase isozymes M1/M2;	P52480	1	61	299	57.8	-0.515	-0.125	0.601
Actin-related protein 3;	Q99JY9	1	15	18	36.1	-0.515	-0.081	0.572
Phosphoglucomutase-1;	Q9D0F9	1	33	45	41.8	-0.515	-0.081	0.579
Cytosolic non-specific dipeptidase;	Q9D1A2	1	27	44	34.3	-0.515	-0.074	0.570
Alpha-aminoadipic semialdehyde dehydrogenase;	Q9DBF1	1	13	20	15.2	-0.515	-0.029	0.562
Proteasome subunit beta type-8;	P28063	1	2	3	4.3	-0.515	-0.044	0.564
Quinone oxidoreductase-like protein 1;	Q921W4	0.994	2	2	6	-0.515	-0.088	0.576
Clathrin light chain B;	Q6IRU5	0.979	2	2	7.4	-0.515	-0.059	0.579
C-terminal-binding protein 1;	O88712	1	4	5	11.1	-0.494	-0.049	0.591
SWI/SNF complex subunit SMARCC2;	Q6PDG5	1	2	2	1.9	-0.494	-0.097	0.604
Protein NDRG2;	Q9QYG0	1	14	21	37.2	-0.494	-0.077	0.597
Serotransferrin;	Q921I1	1	76	467	52.5	-0.494	-0.077	0.597
Uncharacterized protein;	E9Q0S6	1	5	5	3.6	-0.494	-0.285	0.689
Lysosomal alpha-mannosidase;	O09159	1	4	4	4.8	-0.474	-0.191	0.660
Plasminogen;	P20918	1	9	12	8.5	-0.474	-0.151	0.641
Alpha-2-HS-glycoprotein;	P29699	1	17	70	35.1	-0.474	-0.079	0.612
Cytochrome b5;	P56395	1	3	3	30	-0.474	-0.053	0.606
Proteasome activator complex subunit 1;	P97371	1	3	3	8	-0.474	-0.362	0.740
Fumarate hydratase, mitochondrial;	P97807	1	27	40	38.3	-0.474	-0.204	0.665
Calcium-regulated heat stable protein 1;	Q9CR86	1	2	6	10.8	-0.474	-0.053	0.605

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4-trimethylaminobutyraldehyde dehydrogenase;	Q9JLJ2	1	22	32	30.4	-0.474	-0.125	0.629
Paralemmin-1;	Q9Z0P4	1	3	4	6.8	-0.474	-0.066	0.609
Gelsolin;	P13020	1	28	66	22.1	-0.474	-0.086	0.620
Beta-enolase;	P21550	1	31	168	57.1	-0.474	-0.033	0.603
Alpha-enolase;	P17182	1	16	50	63.6	-0.029	-0.009	0.971
Enolase;	B0QZL1	1	4	4	66.5	-1.089	-0.093	0.237
Purine nucleoside phosphorylase;	P23492	1	8	9	24.6	-0.474	-0.053	0.605
Copine-1;	Q8C166	1	8	9	17.5	-0.474	-0.039	0.603
3-hydroxyisobutyrate dehydrogenase, mitochondrial;	Q99L13	1	14	25	25.4	-0.474	-0.125	0.629
Aspartate aminotransferase, mitochondrial;	P05202	1	34	69	40	-0.454	-0.093	0.631
Cysteine and glycine-rich protein 1;	P97315	1	6	10	17.6	-0.454	-0.149	0.655
Fibulin-1;	Q08879	1	10	12	9.4	-0.454	-0.131	0.647
Triosephosphate isomerase;	P17751	1	35	321	64.7	-0.454	-0.056	0.620
Adenylosuccinate lyase;	P54822	1	8	11	17.1	-0.454	-0.037	0.616
Disabled homolog 2;	P98078	1	6	7	12.1	-0.454	-0.267	0.712
Secernin-3;	Q3TMH2	1	4	5	9.6	-0.454	-0.093	0.631
Septin-11;	Q8C1B7	1	6	6	17.3	-0.454	-0.056	0.620
Pyridoxal kinase;	Q8K183	1	11	11	19.6	-0.454	-0.112	0.639
Scavenger mRNA-decapping enzyme DcpS;	Q9DAR7	1	12	20	29.9	-0.454	-0.199	0.680
V-type proton ATPase subunit E 1;	P50518	1	2	2	4	-0.454	-0.05	0.618
SH3 and PX domain-containing protein 2B;	A2AAY5	1	4	4	3.9	-0.434	-0.076	0.640
Xaa-Pro dipeptidase;	Q11136	1	3	3	6.1	-0.434	-0.047	0.632
Ribonuclease inhibitor;	Q91VI7	1	52	77	68.4	-0.434	-0.07	0.637
Protein phosphatase 1 regulatory subunit 3A;	Q99MR9	1	8	8	9	-0.434	-0.123	0.659
Actin-related protein 2/3 complex subunit 5;	Q9CPW4	1	2	2	12.6	-0.434	-0.047	0.632
Serine protease inhibitor A3K;	P07759	1	39	731	50.7	-0.434	-0.07	0.638
Serine protease inhibitor A3N;	Q91WP6	1	4	4	19.4	-0.34	-0.073	0.720
Uncharacterized protein;	D3Z450	1	3	3	10.2	-0.494	-0.035	0.589
Propionyl-CoA carboxylase alpha chain, mitochondrial;	Q91ZA3	1	7	8	6.6	-0.434	-0.129	0.661
Afamin;	O89020	1	16	16	15.8	-0.415	-0.105	0.676
Ig gamma-2B chain C region;	P01867	1	7	8	15.6	-0.415	-0.144	0.692
Microtubule-associated protein 1B;	P14873	1	5	6	1.7	-0.415	-0.044	0.656
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial;	Q61425	1	6	7	17.8	-0.415	-0.066	0.651
Alanine aminotransferase 1;	Q8QZR5	1	7	8	12.3	-0.415	-0.066	0.663
UPF0366 protein C11orf67 homolog;	Q8R0P4	1	2	4	13.1	-0.415	-0.039	0.656
GDP-fucose protein O-fucosyltransferase 1;	Q91ZW2	1	2	2	4.5	-0.415	-0.05	0.646
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	Q9CWS0	1	3	3	17.6	-0.415	-0.072	0.664
Ribosome-recycling factor, mitochondrial;	Q9D6S7	1	2	2	6.5	-0.415	-0.055	0.659
Phosphoglycerate mutase 1;	Q9DBJ1	1	22	66	50.8	-0.415	-0.177	0.710
Apoptosis-associated speck-like protein containing a CARD;	Q9EPB4	1	8	9	35.2	-0.415	-0.122	0.684
Ribonuclease 4;	Q9JJH1	1	6	7	27.7	-0.415	-0.133	0.688
Adenylate kinase isoenzyme 1;	Q9R0Y5	1	18	45	57.7	-0.415	-0.061	0.648
Beta-glucuronidase;	P12265	1	7	9	6.5	-0.415	-0.066	0.662

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Prolow-density lipoprotein receptor-related protein 1;	Q91ZX7	1	28	32	5.1	-0.415	-0.216	0.729
Secernin-1;	Q9CZC8	1	4	5	7.7	-0.415	-0.039	0.656
Glyceraldehyde-3-phosphate dehydrogenase;	E9QAC7	1	9	59	64	-0.415	-0.055	0.647
Glyceraldehyde-3-phosphate dehydrogenase;	E9Q0E3	1	2	5	56.8	-6.644	-0.001	0.000
Uncharacterized protein;	F8VPN4	1	40	49	23.7	-0.415	-0.061	0.648
Ig mu chain C region secreted form;	P01872	1	7	9	9.9	-0.396	-0.026	0.667
Histone H4;	P62806	1	6	6	21.4	-0.396	-0.047	0.671
Tetratricopeptide repeat protein 38;	A3KMP2	1	10	10	17.4	-0.396	-0.12	0.687
Inorganic pyrophosphatase 2, mitochondrial;	Q91VM9	1	4	4	12.2	-0.396	-0.208	0.740
Propionyl-CoA carboxylase beta chain, mitochondrial;	Q99MN9	1	14	17	15.5	-0.396	-0.115	0.688
Uncharacterized protein;	E9Q6D8	1	10	12	15.5	-0.396	-0.219	0.745
Capping protein (Actin filament), gelsolin-like; Capping protein (Actin filament), gelsolin-like, isoform CRA_a; Uncharacterized protein;	Q99LB4	1	22	51	43.3	-0.396	-0.083	0.681
Carboxypeptidase B2;	Q9JHH6	1	2	2	9	-0.396	-0.115	0.695
Platelet-activating factor acetylhydrolase IB subunit alpha;	P63005	1	7	8	9	-0.377	-0.044	0.684
Beta-2-glycoprotein 1;	Q01339	1	9	12	22.6	-0.377	-0.176	0.739
Synemin;	Q70IV5	1	5	7	4.7	-0.377	-0.039	0.683
NADH-cytochrome b5 reductase 3;	Q9DCN2	1	2	3	4	-0.377	-0.118	0.710
Arachidonate 5-lipoxygenase;	P48999	0.999	2	2	1.3	-0.377	-0.054	0.685
Proteasome subunit beta type-10;	O35955	0.971	2	2	4	-0.377	-0.02	0.679
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial;	P35486	1	10	13	19.7	-0.358	-0.041	0.696
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Q8BMF4	1	22	31	25.4	-0.358	-0.096	0.714
L-asparaginase;	Q8C0M9	1	4	4	12.9	-0.358	-0.05	0.697
Retinoid-inducible serine carboxypeptidase;	Q920A5	1	5	7	11	-0.358	-0.142	0.741
N-acetylneuraminic acid synthase (Sialic acid synthase); Uncharacterized protein;	Q99J77	1	5	6	14.8	-0.358	-0.028	0.693
Caveolin-1;	P49817	1	5	5	24.7	-0.358	-0.078	0.708
Citrate lyase subunit beta-like protein, mitochondrial;	Q8R4N0	1	3	3	9.8	-0.358	-0.147	0.741
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial;	Q9WUM5	1	8	14	12.1	-0.34	-0.043	0.709
Aspartyl aminopeptidase;	Q9Z2W0	1	12	12	31.9	-0.34	-0.073	0.727
Kelch repeat and BTB (POZ) domain containing 10; MCG12931; Uncharacterized protein;	A2AUC9	1	3	3	3.3	-0.34	-0.034	0.707
Annexin A8;	O35640	1	21	30	41	-0.34	-0.043	0.709
60S ribosomal protein L12;	P35979	1	6	6	39.4	-0.34	-0.116	0.740
MCG142264, isoform CRA_a; Uncharacterized protein;	D3Z494	1	5	5	14.2	-0.34	-0.039	0.709
Uncharacterized protein;	E9PYJ9	1	25	32	24.2	-0.34	-0.211	0.788
Phosphoenolpyruvate carboxykinase, cytosolic [GTP];	Q9Z2V4	0.994	3	3	5.5	-0.34	-0.039	0.709
Histamine N-methyltransferase;	Q91VF2	0.974	2	2	6.1	-0.34	-0.052	0.712
Alcohol dehydrogenase class-3;	P28474	1	10	20	16.6	-0.322	-0.064	0.729
Isochorismatase domain-containing protein 2A, mitochondrial;	P85094	1	6	6	13.1	-0.322	-0.024	0.718
Protein phosphatase 1F;	Q8CGA0	1	3	4	6.2	-0.322	-0.125	0.757
Spectrin alpha chain, brain;	P16546	1	19	21	7.2	-0.322	-0.097	0.744
Glutathione S-transferase P 1;	P19157	1	12	16	31.1	-0.322	-0.06	0.728

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Liver carboxylesterase N;	P23953	1	17	41	17.3	-0.322	-0.036	0.721
Carboxylesterase 3;	Q8VCT4	1	17	25	20.2	-1.184	-0.404	0.252
Uncharacterized protein;	D3Z5G7	1	11	24	15.2	-0.415	-0.044	0.644
Microtubule-associated protein 4;	P27546	1	24	30	17.9	-0.322	-0.081	0.736
Peroxiredoxin-1;	P35700	1	19	42	67.8	-0.322	-0.048	0.724
Peroxiredoxin-4;	O08807	1	5	6	21.9	-0.434	-0.041	0.630
Actin-related protein 2/3 complex subunit 4;	P59999	1	4	5	16.1	-0.322	-0.024	0.730
Phosphatidylethanolamine-binding protein 1;	P70296	1	9	20	52.4	-0.322	-0.028	0.719
Copine-3;	Q8BT60	1	12	12	22	-0.322	-0.097	0.744
Putative hydroxypyruvate isomerase;	Q8R1F5	1	5	5	20.6	-0.322	-0.036	0.720
Mannose-6-phosphate isomerase;	Q924M7	1	7	7	17.3	-0.322	-0.113	0.752
Glycogen phosphorylase, muscle form;	Q9WUB3	1	57	87	45.6	-0.322	-0.064	0.729
Glycogen phosphorylase, brain form;	Q8CI94	1	13	13	21.7	0.111	0.016	0.908
Glycogen phosphorylase, liver form;	Q9ET01	1	4	4	9.4	-0.644	-0.07	0.488
Uncharacterized protein;	E9PWQ3	1	11	11	4.6	-0.322	-0.153	0.774
SPRY domain-containing protein 4;	Q91WK1	1	2	2	4.3	-0.322	-0.028	0.719
Vitamin D-binding protein;	P21614	1	35	56	52.7	-0.304	-0.165	0.795
Phosphoglycolate phosphatase;	Q8CHP8	1	6	7	16.2	-0.304	-0.086	0.753
Probable proline racemase;	Q9CXA2	1	9	11	20.1	-0.304	-0.026	0.744
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial;	Q9D051	1	19	32	32.3	-0.304	-0.03	0.732
Endoplasmic reticulum resident protein 44;	Q9D1Q6	1	13	16	19.5	-0.304	-0.165	0.804
BAG family molecular chaperone regulator 3;	Q9JLV1	1	6	8	6.4	-0.304	-0.09	0.766
Kinesin light chain 1;	O88447	1	5	5	8.3	-0.304	-0.195	0.810
Phosphoglycerate kinase 1;	P09411	1	34	121	46.5	-0.304	-0.034	0.734
Epidermal growth factor receptor;	Q01279	1	12	16	9.3	-0.304	-0.176	0.809
Aldo-keto reductase family 1 member C18;	Q8K023	1	4	7	7.1	-0.304	-0.034	0.734
Enoyl-CoA delta isomerase 2, mitochondrial;	Q9WUR2	0.999	2	2	5.9	-0.304	-0.038	0.734
Dehydrogenase/reductase SDR family member 7;	Q9CXR1	0.956	2	3	5.9	-0.304	-0.026	0.732
Biotinidase;	Q8CIF4	0.942	2	2	1.7	-0.304	-0.03	0.732
Complement C3;	P01027	1	104	175	34.2	-0.286	-0.087	0.778
Malate dehydrogenase, mitochondrial;	P08249	1	49	133	63.6	-0.286	-0.028	0.757
Glutathione reductase, mitochondrial;	P47791	1	9	10	15.1	-0.286	-0.038	0.760
Leukocyte surface antigen CD47;	Q61735	1	3	5	4.6	-0.286	-0.045	0.762
Sepiapterin reductase;	Q64105	1	19	23	37.2	-0.286	-0.021	0.756
Sulfhydryl oxidase 1;	Q8BND5	1	6	7	5.9	-0.286	-0.031	0.749
Murinoglobulin-1;	P28665	1	77	130	30.5	-0.286	-0.063	0.768
Serine/threonine-protein phosphatase 2A activator;	P58389	1	6	13	16.7	-0.286	-0.052	0.764
Annexin A11;	P97384	1	10	10	14.9	-0.286	-0.07	0.771
Nitrilase homolog 1;	Q8VDK1	1	4	4	9	-0.286	-0.028	0.757
Aminopeptidase N;	P97449	1	11	11	11.7	-0.269	-0.049	0.776
Inter-alpha-trypsin inhibitor heavy chain H3;	Q61704	1	8	8	9.6	-0.269	-0.042	0.774
Alcohol dehydrogenase class 4 mu/sigma chain;	Q64437	1	6	7	18.2	-0.269	-0.029	0.770
Mitochondrial-processing peptidase subunit beta;	Q9CXT8	1	3	3	3.7	-0.269	-0.029	0.769

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Cysteine-rich with EGF-like domain protein 2;	Q9CYA0	1	3	3	6.6	-0.269	-0.023	0.769
Carbohydrate kinase domain-containing protein;	Q9CZ42	1	2	2	13.4	-0.269	-0.042	0.774
Fructose-bisphosphate aldolase A;	P05064	1	28	338	79.1	-0.269	-0.029	0.770
Lysosomal protective protein;	P16675	1	10	13	14.6	-0.269	-0.058	0.780
Coagulation factor XIII A chain;	Q8BH61	1	6	6	9.6	-0.269	-0.039	0.778
C-type lectin domain family 11 member A;	O88200	1	2	2	3.4	-0.252	-0.033	0.784
Fatty acid-binding protein, adipocyte;	P04117	1	14	68	59.1	-0.252	-0.03	0.777
Glutathione peroxidase 1;	P11352	1	13	21	50.2	-0.252	-0.03	0.783
Basigin;	P18572	1	4	4	9.5	-0.252	-0.066	0.797
78 kDa glucose-regulated protein;	P20029	1	33	56	35	-0.252	-0.042	0.787
Protein-glutamine gamma-glutamyltransferase 2;	P21981	1	3	3	3.9	-0.252	-0.024	0.780
Actin-related protein 2;	P61161	1	4	4	5.8	-0.252	-0.018	0.781
Cathepsin D;	P18242	1	20	33	26.3	-0.252	-0.027	0.783
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1;	Q91YQ5	1	2	2	5.6	-0.252	-0.036	0.785
Thy-1 membrane glycoprotein;	P01831	1	2	3	7.4	-0.234	-0.03	0.796
Receptor-type tyrosine-protein phosphatase C;	P06800	1	3	3	3.5	-0.234	-0.047	0.802
Adenosine kinase;	P55264	1	13	13	23.3	-0.234	-0.052	0.804
Caspase-3;	P70677	1	3	3	14.1	-0.234	-0.118	0.837
Zinc-alpha-2-glycoprotein;	Q64726	1	9	12	23.5	-0.234	-0.011	0.793
Iron-sulfur cluster assembly 2 homolog, mitochondrial;	Q9DCB8	1	2	2	15.6	-0.234	-0.028	0.795
Coronin-1B;	Q9WUM3	1	3	3	11.6	-0.234	-0.047	0.802
Branched-chain-amino-acid aminotransferase, mitochondrial;	O35855	1	10	13	17	-0.234	-0.033	0.799
Annexin A4;	P97429	1	25	31	42.9	-0.234	-0.132	0.844
3-mercaptopyruvate sulfurtransferase;	Q99J99	1	15	18	34.7	-0.234	-0.063	0.809
Uncharacterized protein;	E9PV38	1	11	14	14.5	-0.234	-0.033	0.797
Uncharacterized protein;	E9Q616	1	180	233	37.3	-0.234	-0.105	0.829
Eukaryotic translation initiation factor 5A-1;	P63242	1	4	4	19	-0.218	-0.023	0.807
Laminin subunit alpha-4;	P97927	1	3	3	1.6	-0.218	-0.096	0.840
Haloacid dehalogenase-like hydrolase domain-containing protein 2;	Q3UGR5	1	8	11	16.2	-0.218	-0.033	0.809
Fibrinogen beta chain;	Q8K0E8	1	23	53	30.6	-0.218	-0.023	0.807
NADP-dependent malic enzyme;	P06801	1	12	16	20.1	-0.218	-0.028	0.808
Epidermal growth factor receptor substrate 15;	P42567	1	6	8	5.2	-0.218	-0.16	0.872
Perilipin-2;	P43883	1	4	4	12	-0.218	-0.109	0.847
Protein transport protein Sec23A;	Q01405	1	4	5	7.2	-0.218	-0.018	0.806
Alcohol dehydrogenase [NADP+];	Q9JII6	1	14	20	32.6	-0.218	-0.035	0.810
Uncharacterized protein;	F6TL02	1	6	9	19.6	-0.218	-0.048	0.815
Ig alpha chain C region;	P01878	1	5	10	7	-0.201	-0.065	0.837
Acylphosphatase-2;	P56375	1	5	9	20.6	-0.201	-0.097	0.854
Vacuolar protein sorting-associated protein 45;	P97390	1	2	2	2.5	-0.201	-0.021	0.831
Platelet-activating factor acetylhydrolase IB subunit beta;	Q61206	1	6	7	18.9	-0.201	-0.016	0.830
Apolipoprotein A-I-binding protein;	Q8K4Z3	1	9	12	24.8	-0.201	-0.025	0.829
N-acetylmuramoyl-L-alanine amidase;	Q8VCS0	1	5	8	6.4	-0.201	-0.035	0.823
Ester hydrolase C11orf54 homolog;	Q91V76	1	7	7	23.8	-0.201	-0.021	0.831

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Lactoylglutathione lyase;	Q9CPU0	1	8	14	22.3	-0.201	-0.021	0.819
Torsin-1B;	Q9ER41	1	6	6	6.2	-0.201	-0.016	0.830
Omega-amidase NIT2;	Q9JHW2	1	8	8	23.2	-0.201	-0.051	0.840
Destrin;	Q9R0P5	1	11	16	34.5	-0.201	-0.055	0.843
Kininogen-1;	O08677	1	29	80	36	-0.201	-0.021	0.819
Malate dehydrogenase, cytoplasmic;	P14152	1	16	43	26.6	-0.201	-0.035	0.835
Peroxiredoxin-5, mitochondrial;	P99029	1	18	34	41	-0.201	-0.021	0.819
Puromycin-sensitive aminopeptidase;	Q11011	1	28	32	22.3	-0.201	-0.055	0.843
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial;	Q8BH04	1	6	7	7.7	-0.201	-0.095	0.862
UPF0587 protein C1orf123 homolog;	Q8BHG2	1	4	6	20.3	-0.201	-0.085	0.848
Endoplasmic reticulum aminopeptidase 1;	Q9EQH2	1	6	6	4.9	-0.201	-0.025	0.832
Transforming protein RhoA;	Q9QUI0	1	10	16	32.6	-0.201	-0.046	0.839
Uncharacterized protein;	E9Q8T1	1	11	11	4.9	-0.201	-0.065	0.847
Cysteine sulfinic acid decarboxylase;	Q9DBE0	1	3	3	3.2	-0.201	-0.037	0.835
Serine/threonine-protein kinase OSR1;	Q6P9R2	1	3	3	8.3	-0.184	-0.065	0.861
Complement component C8 beta chain;	Q8BH35	1	6	7	11.9	-0.184	-0.027	0.845
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial;	Q8CHT0	1	5	5	7.5	-0.184	-0.019	0.842
Phosphoacetylglucosamine mutase;	Q9CYR6	1	3	3	5.6	-0.184	-0.019	0.843
Threonyl-tRNA synthetase, cytoplasmic;	Q9D0R2	1	3	4	4.2	-0.184	-0.027	0.843
Mitochondrial-processing peptidase subunit alpha;	Q9DC61	1	5	5	6.8	-0.184	-0.096	0.877
Isovaleryl-CoA dehydrogenase, mitochondrial;	Q9JHI5	1	10	10	13.2	-0.184	-0.033	0.840
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial;	Q9Z2I9	1	16	20	22.5	-0.184	-0.086	0.872
Sec24 related gene family, member D (S. cerevisiae); Uncharacterized protein;	Q6NXL1	1	7	8	6.2	-0.184	-0.027	0.845
Protein disulfide-isomerase A3;	P27773	1	47	127	47.1	-0.184	-0.077	0.867
Pantothenate kinase 1;	Q8K4K6	1	2	2	4	-0.168	-0.028	0.858
Glutathione peroxidase 7;	Q99LJ6	1	4	4	16.1	-0.168	-0.019	0.855
Protein S100-A11;	P50543	1	8	10	34.7	-0.168	-0.019	0.855
Myoferlin;	Q69ZN7	1	10	10	3.3	-0.168	-0.051	0.868
MCG21506; Macrophage galactose N-acetyl-galactosamine specific lectin 2 isoform i; Uncharacterized protein;	A9XX86	1	3	3	11.7	-0.168	-0.042	0.862
CD 81 antigen, isoform CRA_c; CD81 antigen; Tapa-1 protein; Uncharacterized protein;	Q91V78	1	4	5	19.1	-0.168	-0.013	0.854
Lysosomal alpha-glucosidase;	P70699	0.999	2	2	1.9	-0.168	-0.015	0.854
Pre-B-cell leukemia transcription factor-interacting protein 1;	Q3TVI8	0.999	2	2	7.5	-0.168	-0.025	0.856
Dynein light chain roadblock-type 1;	P62627	1	5	5	51	-0.152	-0.022	0.868
UPF0586 protein C9orf41 homolog;	Q80UY1	1	4	4	5.8	-0.152	-0.044	0.877
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial;	Q9D0K2	1	30	48	34.8	-0.152	-0.014	0.866
Carbonic anhydrase 13;	Q9D6N1	1	3	3	10.7	-0.152	-0.044	0.877
EGF-containing fibulin-like extracellular matrix protein 1;	Q8BPB5	1	8	12	16.8	-0.152	-0.022	0.868
Vitronectin;	P29788	1	2	2	3.8	-0.152	-0.012	0.865
Leucine carboxyl methyltransferase 1; Leucine carboxyl methyltransferase 1, isoform CRA_b; Uncharacterized protein;	A2RTH5	0.999	2	2	2.4	-0.152	-0.056	0.886
Cytochrome c, somatic;	P62897	1	2	3	10.5	-0.136	-0.007	0.877

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SUMO-conjugating enzyme UBC9;	P63280	1	2	4	5.7	-0.136	-0.006	0.877
Corticosteroid-binding globulin;	Q06770	1	8	12	6.5	-0.136	-0.01	0.877
ATP-dependent RNA helicase DDX1;	Q91VR5	1	2	2	1.8	-0.136	-0.013	0.878
Prostaglandin reductase 1;	Q91YR9	1	7	7	18.2	-0.136	-0.018	0.879
Complement factor B;	P04186	1	19	26	15.1	-0.136	-0.037	0.887
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	Q8QZS1	1	3	3	8.8	-0.136	-0.033	0.884
Argininosuccinate lyase;	Q91YI0	1	6	6	8.4	-0.136	-0.019	0.879
Uncharacterized protein;	Q9DBD0	1	13	16	13.9	-0.136	-0.012	0.878
Uncharacterized protein;	E9Q7L0	1	2	2	4.6	-0.136	-0.021	0.880
Epididymis-specific alpha-mannosidase;	O54782	1	2	2	2.8	-0.12	-0.013	0.901
Myoglobin;	P04247	1	13	28	41.6	-0.12	-0.023	0.904
Plasma kallikrein;	P26262	1	11	13	13.5	-0.12	-0.018	0.903
Ras-related protein Rab-23;	P35288	1	3	3	13.5	-0.12	-0.056	0.910
Transketolase;	P40142	1	35	75	36.1	-0.12	-0.03	0.899
Cofilin-2;	P45591	1	10	29	36.7	-0.12	-0.018	0.903
Electron transfer flavoprotein subunit alpha, mitochondrial;	Q99LC5	1	29	50	46.2	-0.12	-0.01	0.901
Protein SEC13 homolog;	Q9D1M0	1	6	9	11.8	-0.12	-0.034	0.908
GMP reductase 1;	Q9DCZ1	1	3	3	10.7	-0.12	-0.012	0.889
SH3 domain-binding glutamic acid-rich-like protein;	Q9JJU8	1	3	3	44.7	-0.12	-0.013	0.901
Inositol monophosphatase 1;	O55023	1	7	10	22.4	-0.12	-0.016	0.890
Isocitrate dehydrogenase [NADP] cytoplasmic;	O88844	1	34	56	44.7	-0.12	-0.037	0.909
V-type proton ATPase catalytic subunit A;	P50516	1	15	18	21.9	-0.12	-0.046	0.904
3-ketoacyl-CoA thiolase A, peroxisomal;	Q921H8	1	19	24	38	-0.12	-0.018	0.891
Phosphotriesterase-related protein;	Q60866	1	2	3	7.1	-0.12	-0.064	0.923
Serine/threonine-protein kinase PAK 1;	O88643	1	3	3	5.7	-0.105	-0.021	0.916
Integrin beta-2;	P11835	1	3	3	4.3	-0.105	-0.08	0.943
Arylsulfatase B;	P50429	1	4	5	3.4	-0.105	-0.037	0.923
Neutral alpha-glucosidase AB;	Q8BHN3	1	22	31	16.2	-0.105	-0.079	0.942
Thioredoxin domain-containing protein 5;	Q91W90	1	18	26	28.8	-0.105	-0.012	0.913
Guanine nucleotide-binding protein G(i) subunit alpha-2;	P08752	1	11	12	20.3	-0.105	-0.051	0.930
Galectin-3-binding protein;	Q07797	1	4	4	4.3	-0.105	-0.06	0.934
Choline transporter-like protein 2;	Q8BY89	1	2	2	2.4	-0.105	-0.011	0.913
Pyridoxine-5'-phosphate oxidase;	Q91XF0	0.997	2	4	3.1	-0.105	-0.011	0.913
Alpha-parvin;	Q9EPC1	1	4	4	4.2	-0.089	-0.007	0.923
Maleylacetoacetate isomerase;	Q9WVL0	1	15	17	45.8	-0.089	-0.019	0.927
Uncharacterized protein;	F8VQL5	1	4	10	31.2	-0.089	-0.009	0.924
Filamin-A;	Q8BTM8	1	79	114	26.1	-0.089	-0.039	0.937
Protein kinase, cAMP dependent regulatory, type II alpha; Protein kinase, cAMP dependent regulatory, type II alpha, isoform CRA_b; Uncharacterized protein; cAMP-dependent protein kinase type II-alpha regulatory chain;	Q8K1M3	1	8	8	23.4	-0.089	-0.009	0.924
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2;	O88428	1	3	3	7.6	-0.074	-0.022	0.940
Laminin subunit gamma-1;	P02468	1	7	7	4.2	-0.074	-0.02	0.940
Peroxisomal multifunctional enzyme type 2;	P51660	1	4	4	5	-0.074	-0.045	0.953

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change (log_2) of ASAPratio	Fold change standard deviation	ASAPratio p-value
UDP-glucose:glycoprotein glucosyltransferase 1;	Q6P5E4	1	5	7	3.7	-0.074	-0.009	0.935
UTP--glucose-1-phosphate uridylyltransferase;	Q91ZJ5	1	25	41	25.4	-0.074	-0.022	0.940
Alpha-mannosidase 2C1;	Q91W89	1	2	2	3.3	-0.074	-0.032	0.946
Hydroxysteroid (17-beta) dehydrogenase 10; Uncharacterized protein;	A2AFQ2	1	6	7	16.5	-0.074	-0.023	0.941
Isoamyl acetate-hydrolyzing esterase 1 homolog;	Q9DB29	1	2	2	6.8	-0.074	-0.01	0.936
Glutathione S-transferase A4;	P24472	0.969	2	2	9.9	-0.074	-0.009	0.936
WD repeat-containing protein 1;	O88342	1	21	36	33.3	-0.059	-0.01	0.947
Cellular retinoic acid-binding protein 1;	P62965	1	4	4	27	-0.059	-0.01	0.948
Far upstream element-binding protein 2;	Q3U0V1	1	19	29	21.9	-0.059	-0.013	0.955
Protein disulfide-isomerase;	P09103	1	37	61	40.7	-0.059	-0.01	0.947
Peptidyl-prolyl cis-trans isomerase FKBP10;	Q61576	1	10	12	12.2	-0.059	-0.009	0.947
Niemann-Pick C1 protein;	O35604	1	2	4	0.9	-0.059	-0.005	0.945
Twinfilin-2;	Q9Z0P5	1	2	2	7.4	-0.059	-0.037	0.962
Actin-like protein 6A;	Q9Z2N8	0.999	2	2	15.7	-0.059	-0.012	0.948
Complement component C9;	P06683	1	14	18	17.9	-0.044	-0.009	0.959
Galectin-1;	P16045	1	13	24	37.8	-0.044	-0.012	0.960
182 kDa tankyrase-1-binding protein;	P58871	1	9	9	5.1	-0.044	-0.007	0.958
Probable fructose-2,6-bisphosphatase TIGAR;	Q8BZA9	1	6	6	25.7	-0.044	-0.008	0.959
Carbonyl reductase 3; Uncharacterized protein;	Q8K354	1	9	13	31.8	-0.044	-0.008	0.958
UPF0160 protein MYG1, mitochondrial;	Q9JK81	1	5	5	20.9	-0.044	-0.013	0.961
Sodium/potassium-transporting ATPase subunit beta-1;	P14094	0.995	2	2	7.6	-0.044	-0.005	0.957
Superoxide dismutase [Mn], mitochondrial;	P09671	1	9	17	23.4	-0.029	-0.009	0.971
Antithrombin-III;	P32261	1	20	28	28	-0.029	-0.012	0.973
Leukemia inhibitory factor receptor;	P42703	1	6	6	6.5	-0.029	-0.002	0.968
Interleukin-1 receptor accessory protein;	Q61730	1	8	9	10.7	-0.029	-0.006	0.980
Osteoclast-stimulating factor 1;	Q62422	1	12	18	42.3	-0.029	-0.004	0.969
Xaa-Pro aminopeptidase 1;	Q6P1B1	1	12	12	13.7	-0.029	-0.018	0.977
Neudesin;	Q9CQ45	1	4	4	17	-0.029	-0.002	0.979
Protein ETHE1, mitochondrial;	Q9DCM0	1	7	8	29.5	-0.029	-0.014	0.985
Electron transfer flavoprotein subunit beta;	Q9DCW4	1	15	25	37.3	-0.029	-0.002	0.979
Proline synthase co-transcribed bacterial homolog protein;	Q9Z2Y8	1	4	4	8	-0.029	-0.003	0.979
Integrin beta-1;	P09055	1	9	9	9.1	-0.029	-0.005	0.980
Profilin-1;	P62962	1	25	91	64.3	-0.029	-0.002	0.968
Acyl-protein thioesterase 1;	P97823	1	4	4	23	-0.029	-0.004	0.979
Isoleucyl-tRNA synthetase, mitochondrial;	Q8BIJ6	1	8	8	6.7	-0.029	-0.017	0.977
NEDD8-activating enzyme E1 catalytic subunit;	Q8C878	1	6	8	17.4	-0.029	-0.004	0.969
Tetraspanin-13;	Q9D8C2	0.985	2	2	6	-0.029	-0.004	0.980
6-phosphofructokinase, muscle type;	P47857	1	21	28	16.3	-0.014	-0.001	0.990
Hydroxyacid-oxoacid transhydrogenase, mitochondrial;	Q8R0N6	1	2	2	4.9	-0.014	-0.002	0.990
Cell surface glycoprotein MUC18;	Q8R2Y2	1	5	7	6.8	-0.014	-0.003	0.991
CD109 antigen;	Q8R422	1	4	4	1.5	-0.014	-0.001	0.990
Epidermal growth factor receptor kinase substrate 8-like protein 1;	Q8R5F8	1	3	3	3.8	-0.014	-0.005	0.991
Transmembrane emp24 domain-containing protein 10;	Q9D1D4	1	3	3	9.6	-0.014	-0.004	0.988

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Phosphoserine aminotransferase;	Q99K85	1	16	16	35.9	-0.014	-0.005	0.991
Selenoprotein O;	Q9DBC0	1	3	3	7.2	-0.014	-0.003	0.990
Dystrophin;	P11531	1	3	3	3.3	0	0	0.999
Nuclear factor NF-kappa-B p105 subunit;	P25799	1	2	2	2.3	0	0	0.999
5'-nucleotidase;	Q61503	1	4	4	3.8	0	0	0.999
Alpha-1-antitrypsin 1-1;	P07758	1	11	31	34.4	0	0	0.999
Alpha-1-antitrypsin 1-2;	P22599	1	10	18	35.6	-0.201	-0.021	0.831
Alpha-1-antitrypsin 1-4;	Q00897	1	7	11	30	-0.234	-0.025	0.794
Annexin A1;	P10107	1	37	78	55.5	0	0	0.999
PEST proteolytic signal-containing nuclear protein;	Q6P8I4	1	2	3	21.1	0	0	0.999
Proteasome subunit alpha type-3;	O70435	1	4	4	14.1	0.014	0.006	0.990
Pyruvate dehydrogenase protein X component, mitochondrial;	Q8BKZ9	1	7	7	16.4	0.014	0.004	0.990
5'(3')-deoxyribonucleotidase, cytosolic type;	Q9JM14	1	5	8	20	0.014	0.001	0.988
Peptidyl-prolyl cis-trans isomerase FKBP2;	P45878	0.953	2	2	8.6	0.014	0.001	0.988
Dipeptidyl peptidase 3;	Q99KK7	1	8	10	11	0.029	0.005	0.979
Carboxypeptidase N subunit 2;	Q9DBB9	1	6	8	9.5	0.029	0.01	0.980
Obscurin;	A2AAJ9	1	4	4	0.5	0.029	0.005	0.979
H-2 class I histocompatibility antigen, L-D alpha chain;	P01897	1	6	7	13.3	0.029	0.006	0.979
H-2 class I histocompatibility antigen, Q10 alpha chain;	P01898	1	3	3	15.1	0.696	0.541	0.632
H-2 class I histocompatibility antigen, K-B alpha chain;	P01901	1	3	3	13.4	0.176	0.02	0.850
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;	P62137	1	12	13	31.6	0.029	0.007	0.979
Histidine triad nucleotide-binding protein 1;	P70349	1	7	28	51.6	0.029	0.013	0.982
Rho GDP-dissociation inhibitor 2;	Q61599	1	9	20	22	0.029	0.004	0.978
Toll-interacting protein;	Q9QZ06	1	3	5	12.3	0.029	0.006	0.979
Zinc-binding alcohol dehydrogenase domain-containing protein 2;	Q8BGC4	1	6	6	14.1	0.043	0.009	0.959
Thimet oligopeptidase;	Q8C1A5	1	18	23	20.4	0.043	0.01	0.959
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1;	Q8R3B1	1	3	3	3	0.043	0.018	0.964
Myosin light chain kinase 2, skeletal/cardiac muscle;	Q8VCR8	1	11	16	13.5	0.043	0.008	0.958
Transaldolase;	Q93092	1	12	26	22	0.043	0.007	0.958
Band 4.1-like protein 2;	O70318	1	10	14	10	0.043	0.011	0.960
Hydroxyacylglutathione hydrolase, mitochondrial;	Q99KB8	1	8	11	23.6	0.043	0.008	0.968
Low molecular weight phosphotyrosine protein phosphatase;	Q9D358	1	5	6	18.4	0.043	0.003	0.957
Hypoxia up-regulated protein 1;	Q9JKR6	1	21	25	16	0.043	0.015	0.962
Plectin;	Q9QXS1	1	24	27	6.1	0.043	0.019	0.973
D-2-hydroxyglutarate dehydrogenase, mitochondrial;	Q8CIM3	1	2	2	3.6	0.057	0.004	0.947
Sorting nexin-5;	Q9D8U8	1	8	11	11.9	0.057	0.019	0.953
Keratin, type II cytoskeletal 1b;	Q6IFZ6	1	9	9	14.3	0.057	0.012	0.949
Keratin, type II cytoskeletal 71;	Q9R0H5	1	2	2	6.3	5.232	2.217	0.000
Glyoxalase domain-containing protein 4;	Q9CPV4	1	13	16	29	0.057	0.014	0.950
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;	P13707	1	25	37	45.4	0.07	0.015	0.939
Lysophosphatidic acid phosphatase type 6;	Q8BP40	1	5	7	12.4	0.07	0.011	0.938
Sulfatase-modifying factor 2;	Q8BPG6	1	3	5	8.6	0.07	0.006	0.936
Complement component C8 alpha chain;	Q8K182	1	11	11	16.9	0.07	0.015	0.939

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U6 snRNA-associated Sm-like protein LSm2;	O35900	1	2	2	27.4	0.07	0.016	0.940
Baculoviral IAP repeat-containing protein 4;	Q60989	1	3	3	4.2	0.07	0.013	0.938
Heterogeneous nuclear ribonucleoprotein A1;	P49312	1	11	14	27.2	0.084	0.039	0.940
Myosin light chain kinase, smooth muscle;	Q6PDN3	1	11	15	5.6	0.084	0.029	0.935
Deoxyribonucleoside 5'-monophosphate N-glycosidase;	Q80VJ3	1	2	2	8.1	0.084	0.006	0.926
Protein canopy homolog 2;	Q9QXT0	1	5	7	20.9	0.084	0.009	0.927
Peptidyl-prolyl cis-trans isomerase FKBP9;	Q9Z247	1	6	8	7.9	0.084	0.035	0.938
Selenium-binding protein 1;	P17563	1	32	50	48.5	0.084	0.036	0.938
BTB/POZ domain-containing protein KCTD12;	Q6WVG3	1	7	7	26	0.084	0.01	0.928
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial;	P53395	1	4	4	2.3	0.084	0.006	0.926
Crk-like protein;	P47941	1	4	4	5.9	0.098	0.006	0.916
Isochorismatase domain-containing protein 1;	Q91V64	1	7	10	13.5	0.098	0.011	0.917
COP9 signalosome complex subunit 1;	Q99LD4	1	3	3	5.5	0.098	0.019	0.919
Calumenin;	O35887	1	3	4	7.6	0.098	0.03	0.924
Voltage-dependent L-type calcium channel subunit beta-1;	Q8R3Z5	1	3	3	7.2	0.098	0.021	0.920
Rab11 family-interacting protein 5;	Q8R361	0.972	2	2	1.4	0.098	0.012	0.917
Protein disulfide-isomerase A4;	P08003	1	16	20	18.5	0.111	0.043	0.920
Epidermal growth factor receptor substrate 15-like 1;	Q60902	1	3	3	5.4	0.111	0.016	0.908
Elongation factor Tu, mitochondrial;	Q8BFR5	1	6	8	8.8	0.111	0.035	0.916
TIP41-like protein;	Q8BH58	1	4	4	10	0.111	0.017	0.908
EH domain-containing protein 4;	Q9EQP2	1	7	9	9.1	0.111	0.01	0.906
Inositol polyphosphate 1-phosphatase;	P49442	1	3	4	7.6	0.111	0.053	0.925
Eukaryotic translation initiation factor 2A;	Q8BJW6	1	5	5	8.3	0.111	0.04	0.918
Plastin-3;	Q99K51	1	22	38	25.9	0.111	0.031	0.907
40S ribosomal protein S12;	Q6ZWZ6	1	10	15	46.2	0.111	0.034	0.915
Tyrosine-protein kinase CSK;	P41241	1	2	2	5.1	0.111	0.037	0.917
Serine/threonine-protein kinase WNK1;	P83741	1	2	2	3.2	0.111	0.009	0.906
AMP deaminase 1;	Q3V1D3	0.997	2	3	1.2	0.111	0.007	0.906
Platelet-activating factor acetylhydrolase IB subunit gamma;	Q61205	0.96	2	2	11.9	0.111	0.011	0.898
Transthyretin;	P07309	1	11	34	46.3	0.124	0.016	0.888
Phosphoglucomutase-2;	Q7TSV4	1	14	20	17.1	0.124	0.058	0.916
Selenide, water dikinase 1;	Q8BH69	1	5	7	7.7	0.124	0.007	0.886
Early endosome antigen 1;	Q8BL66	1	2	2	3.5	0.124	0.026	0.901
Complement component C8 gamma chain;	Q8VCG4	1	2	2	20.8	0.124	0.014	0.887
L-xylulose reductase;	Q91X52	1	3	3	9.3	0.124	0.011	0.888
Inorganic pyrophosphatase;	Q9D819	1	19	33	44.4	0.124	0.019	0.889
Prolargin;	Q9JK53	1	10	15	15.6	0.124	0.04	0.907
Heme-binding protein 1;	Q9R257	1	4	4	14.7	0.124	0.015	0.888
ADP-ribosylation factor-like protein 3;	Q9WUL7	1	8	9	34.1	0.124	0.011	0.897
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial;	Q9Z2I8	1	8	11	22.7	0.124	0.026	0.895
Uncharacterized protein;	D3Z6I7	1	2	2	10.7	0.124	0.017	0.888
Mitogen-activated protein kinase 12;	O08911	1	6	6	9.5	0.124	0.028	0.902

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Elongation factor 1-alpha 1;	P10126	1	15	79	34.6	0.124	0.058	0.908
Elongation factor 1-alpha 2;	P62631	1	9	17	22.5	-1	-0.3	0.315
Ezrin;	P26040	1	7	7	10.4	0.124	0.015	0.888
Moesin;	P26041	1	6	6	9	-0.837	-0.299	0.418
Radixin;	P26043	1	4	4	5.5	0.043	0.005	0.968
NEDD9-interacting protein with calponin homology and LIM domains;	Q8VDP3	1	6	6	7	0.124	0.026	0.901
Clathrin light polypeptide (Lca); Uncharacterized protein;	B1AWE0	1	5	5	13.4	0.124	0.025	0.900
Epsin-2;	Q8CHU3	0.984	2	2	1.7	0.124	0.027	0.902
Ornithine aminotransferase, mitochondrial;	P29758	1	18	19	28.5	0.138	0.024	0.880
Epoxide hydrolase 2;	P34914	1	6	9	9.9	0.138	0.034	0.884
Hydroxymethylglutaryl-CoA lyase, mitochondrial;	P38060	1	5	5	17.8	0.138	0.085	0.912
Acyl-coenzyme A thioesterase 13;	Q9CQR4	1	2	2	9.3	0.138	0.009	0.876
Bifunctional purine biosynthesis protein PURH;	Q9CWJ9	1	28	55	32.3	0.138	0.015	0.878
Carboxypeptidase N catalytic chain;	Q9JJN5	1	6	6	13.8	0.138	0.018	0.878
GTPase KRas;	P32883	0.998	3	3	20.1	0.138	0.04	0.887
C-terminal-binding protein 2;	P56546	1	6	6	13.8	0.138	0.023	0.880
Proteasome activator complex subunit 2;	P97372	1	4	4	12.6	0.138	0.089	0.914
6-phosphogluconolactonase;	Q9CQ60	1	13	28	41.2	0.138	0.015	0.878
Thioredoxin;	P10639	1	2	3	12.4	0.151	0.012	0.867
Arf-GAP domain and FG repeats-containing protein 1;	Q8K2K6	1	5	5	10	0.151	0.033	0.874
DAZ-associated protein 1;	Q9JII5	1	4	4	18.7	0.151	0.014	0.867
Thiamin pyrophosphokinase 1;	Q9R0M5	1	3	3	15.2	0.151	0.026	0.872
Chloride intracellular channel protein 1;	Q9Z1Q5	1	19	26	44.4	0.151	0.03	0.872
Glutathione S-transferase theta 3; Glutathione S-transferase, theta 3; Uncharacterized protein;	Q99L20	1	2	2	7.9	0.151	0.016	0.868
Pyruvate carboxylase, mitochondrial;	Q05920	1	21	29	18.9	0.151	0.024	0.870
Uncharacterized protein;	E9QJY4	1	4	4	2.4	0.151	0.082	0.898
Non-catalytic region of tyrosine kinase adaptor protein 1, isoform CRA_b; Uncharacterized protein;	Q8BH99	1	2	2	7.7	0.151	0.014	0.867
Proteolipid protein 2;	Q9R1Q7	0.999	2	2	7.9	0.151	0.012	0.867
PDZ and LIM domain protein 3;	O70209	1	3	3	10.4	0.163	0.045	0.869
Target of Myb protein 1;	O88746	1	3	3	8.9	0.163	0.013	0.858
Zinc finger CCCH domain-containing protein 15;	Q3TIV5	1	4	4	3.3	0.163	0.022	0.860
Glycyl-tRNA synthetase;	Q9CZD3	1	13	17	12.9	0.163	0.049	0.871
Isocitrate dehydrogenase 3 (NAD+) beta; Tumor-related protein; Uncharacterized protein;	Q91VA7	1	6	9	15.9	0.163	0.038	0.865
Choline transporter-like protein 1;	Q6X893	1	2	2	2.7	0.163	0.019	0.859
Ras-related protein Rab-2A;	P53994	1	5	6	13.2	0.176	0.025	0.852
Rho GDP-dissociation inhibitor 1;	Q99PT1	1	10	22	27	0.176	0.025	0.851
Interferon gamma induced GTPase; Uncharacterized protein;	Q9DCE9	1	2	2	8.3	0.176	0.036	0.854
Glucosamine-6-phosphate isomerase 1;	O88958	1	3	3	7.3	0.189	0.058	0.854
GDP-L-fucose synthase;	P23591	1	6	6	13.1	0.189	0.061	0.856
Hydroxysteroid dehydrogenase-like protein 2;	Q2TPA8	1	4	4	9.7	0.189	0.048	0.849

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GDP-D-glucose phosphorylase C15orf58 homolog;	Q3TLS3	1	2	2	4.8	0.189	0.027	0.842
Glutaredoxin-related protein 5, mitochondrial;	Q80Y14	1	5	5	21.7	0.189	0.023	0.841
Phostensin;	Q8BQ30	1	2	2	4.2	0.189	0.018	0.830
Gephyrin;	Q8BUV3	1	7	7	5.3	0.189	0.061	0.847
Histidine triad nucleotide-binding protein 2, mitochondrial;	Q9D0S9	1	8	14	29.4	0.189	0.045	0.848
Ubiquitin-like modifier-activating enzyme ATG7;	Q9D906	1	3	3	7.9	0.189	0.116	0.884
AP-2 complex subunit beta;	Q9DBG3	1	8	9	6.5	0.189	0.053	0.852
6-phosphogluconate dehydrogenase, decarboxylating;	Q9DCD0	1	16	24	26.1	0.189	0.04	0.837
Uncharacterized protein;	E9PV24	1	24	39	32.1	0.189	0.051	0.851
Adapter molecule crk;	Q64010	1	8	11	17.1	0.189	0.013	0.829
Prostamide/prostaglandin F synthase;	Q9DB60	1	6	6	21.9	0.189	0.015	0.839
Protein unc-45 homolog A;	Q99KD5	0.999	2	2	3.7	0.189	0.025	0.832
MCG140951; Plexin B2; Plxnb2 protein; Uncharacterized protein;	B2RXS4	0.99	3	4	2.9	0.189	0.038	0.836
Tripeptidyl-peptidase 2;	Q64514	1	3	3	3.5	0.202	0.139	0.878
Uncharacterized protein;	E9Q070	1	7	9	19.2	0.202	0.026	0.823
Versican core protein;	Q62059	1	3	3	4.6	0.202	0.026	0.823
2-aminoethanethiol dioxygenase;	Q6PDY2	0.999	2	2	9.4	0.202	0.021	0.822
Proteasome subunit beta type-1;	O09061	1	13	15	30.8	0.214	0.105	0.850
Calreticulin;	P14211	1	15	20	21.2	0.214	0.085	0.839
Myotrophin;	P62774	1	4	6	14.4	0.214	0.015	0.811
Translationally-controlled tumor protein;	P63028	1	9	38	30.2	0.214	0.018	0.814
Keratin, type I cytoskeletal 17;	Q9QWL7	1	7	9	10.4	0.214	0.142	0.869
Keratin, type I cytoskeletal 15;	Q61414	1	2	2	6.6	-2.474	-0.962	0.019
Uncharacterized protein;	Q3TUE1	1	5	5	10.4	0.214	0.031	0.814
Stress-70 protein, mitochondrial;	P38647	1	35	53	37.6	0.227	0.041	0.809
Vasodilator-stimulated phosphoprotein;	P70460	1	2	2	9.9	0.227	0.039	0.808
Heat shock protein beta-6;	Q5EBG6	1	5	7	21	0.227	0.066	0.819
Golgi reassembly-stacking protein 2;	Q99JX3	1	4	5	8.6	0.227	0.027	0.804
Thioredoxin domain-containing protein 12;	Q9CQU0	1	3	8	17.6	0.227	0.016	0.802
Inositol-3-phosphate synthase 1;	Q9JHU9	1	4	4	3.2	0.227	0.08	0.826
Thioredoxin reductase 1, cytoplasmic;	Q9JMH6	1	8	12	16.5	0.227	0.014	0.799
Lectin, galactose binding, soluble 7; Lectin, galactose binding, soluble 7, isoform CRA_a; Uncharacterized protein;	Q9CRB1	1	19	75	68.4	0.227	0.019	0.803
Transgelin;	P37804	1	16	26	55.7	0.239	0.069	0.809
N-acylglucosamine 2-epimerase;	P82343	1	4	4	8	0.239	0.03	0.796
Heterogeneous nuclear ribonucleoprotein H;	O35737	1	10	14	21.2	0.239	0.051	0.803
Hexokinase-1;	P17710	1	6	6	6	0.239	0.063	0.808
Histone deacetylase 2;	P70288	0.999	3	3	9.9	0.239	0.028	0.796
Heat shock protein 105 kDa;	Q61699	1	16	18	16.9	0.239	0.105	0.830
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1;	Q8R429	1	50	136	29.5	0.239	0.032	0.797
Protein dpy-30 homolog;	Q99LT0	1	2	2	20.2	0.239	0.049	0.802
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	Q64191	0.993	2	5	2.3	0.239	0.016	0.793
Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	P70404	1	7	10	16.5	0.251	0.023	0.786

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Leucine-rich repeat flightless-interacting protein 1;	Q3UZ39	1	3	4	5.2	0.251	0.03	0.787
Rab GDP dissociation inhibitor beta;	Q61598	1	30	48	57.1	0.251	0.025	0.786
Rab GDP dissociation inhibitor alpha;	P50396	1	4	4	16.1	0.275	0.027	0.760
ATPase, Ca++ transporting, plasma membrane 3; Uncharacterized protein;	A2ALL9	1	5	5	3.6	0.251	0.057	0.796
Prothrombin;	P19221	1	12	13	18.3	0.263	0.103	0.804
Tryptophanyl-tRNA synthetase, cytoplasmic;	P32921	1	6	9	13.9	0.263	0.022	0.768
Proteasome subunit beta type-4;	P99026	1	9	9	31.8	0.263	0.101	0.808
60S acidic ribosomal protein P2;	P99027	1	4	4	55.7	0.263	0.05	0.784
UMP-CMP kinase;	Q9DBP5	1	14	19	45.9	0.263	0.162	0.832
Heat shock cognate 71 kDa protein;	P63017	1	36	103	42.7	0.263	0.048	0.783
Heat shock 70 kDa protein 1A;	Q61696	1	35	50	42.4	0.176	0.014	0.848
Heat shock-related 70 kDa protein 2;	P17156	1	3	3	16.9	0.926	0.122	0.315
Putative adenosylhomocysteinase 3;	Q68FL4	1	4	5	4.2	0.263	0.173	0.837
ATP-dependent RNA helicase DDX39A;	Q8VDW0	1	8	10	11.2	0.263	0.018	0.776
ADP-sugar pyrophosphatase;	Q9JKX6	1	3	5	11.9	0.263	0.129	0.822
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical];	P56380	1	3	3	15.6	0.263	0.031	0.771
Cystathionine beta-synthase;	Q91WT9	0.979	2	5	3	0.263	0.153	0.834
Ig heavy chain V region B1-8/186-2;	P01751	0.919	2	2	6	0.263	0.042	0.781
Synaptophysin-like protein 1;	O09117	1	2	2	11.4	0.275	0.034	0.762
Alpha-crystallin B chain;	P23927	1	10	20	60.2	0.275	0.052	0.767
Vitamin K-dependent protein S;	Q08761	1	2	2	2.7	0.275	0.036	0.763
10 kDa heat shock protein, mitochondrial;	Q64433	1	9	17	40.2	0.275	0.034	0.762
Ras-related C3 botulinum toxin substrate 1;	P63001	1	9	16	30.2	0.275	0.032	0.761
Cell division control protein 42 homolog;	P60766	1	9	12	36.6	0.585	0.16	0.552
Fermitin family homolog 2;	Q8CIB5	1	5	5	5.3	0.275	0.027	0.765
Trans-2-enoyl-CoA reductase, mitochondrial;	Q9DCS3	1	4	4	5.4	0.275	0.032	0.763
Calpain-1 catalytic subunit;	O35350	1	19	24	18.9	0.287	0.087	0.773
Adenylosuccinate synthetase isozyme 2;	P46664	1	3	3	7.9	0.287	0.047	0.757
Protein phosphatase 1A;	P49443	1	5	5	21.4	0.287	0.092	0.781
Cathepsin Z;	Q9WUU7	1	5	9	7.8	0.287	0.028	0.752
Uncharacterized protein;	E9PVD2	1	9	10	8.2	0.287	0.087	0.773
LanC-like protein 2;	Q9JJK2	1	2	2	8.4	0.287	0.038	0.754
Peptidyl-prolyl cis-trans isomerase-like 1;	Q9D0W5	1	3	3	14.5	0.287	0.019	0.750
Transcription elongation factor B polypeptide 2;	P62869	1	5	6	35.6	0.299	0.066	0.755
N-acetylglucosamine-6-sulfatase;	Q8BFR4	1	8	9	8.1	0.299	0.061	0.753
Protein Z-dependent protease inhibitor;	Q8R121	1	5	5	7.6	0.299	0.107	0.778
5-hydroxyisourate hydrolase;	Q9CRB3	1	3	4	13.6	0.299	0.019	0.742
ADP-ribosylation factor 3;	P61205	1	4	9	49.2	0.299	0.102	0.771
ADP-ribosylation factor 5;	P84084	0.999	3	9	38.9	2.356	0.225	0.010
Retinol-binding protein 4;	Q00724	1	4	10	10	0.31	0.048	0.739
Galactokinase;	Q9R0N0	1	3	5	6.4	0.31	0.037	0.737
Bisphosphoglycerate mutase;	P15327	1	4	5	18.9	0.31	0.11	0.766
F-actin-capping protein subunit alpha-1;	P47753	1	8	10	24.1	0.31	0.03	0.734

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Ubiquitin-associated protein 2-like;	Q80X50	1	7	7	7.9	0.31	0.025	0.734
Erythrocyte protein band 4.1; Uncharacterized protein;	A2A838	0.993	3	4	2.5	0.31	0.113	0.767
Dynactin subunit 2;	Q99KJ8	1	9	9	21.9	0.322	0.077	0.742
Glutathione S-transferase omega-1;	O09131	1	3	4	10.4	0.322	0.026	0.726
Proteasome subunit alpha type-4;	Q9R1P0	1	7	9	26.7	0.322	0.036	0.728
Elongation factor 1-beta;	O70251	1	7	8	34.7	0.333	0.05	0.723
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;	P63094	1	3	3	6.3	0.333	0.087	0.729
Drebrin-like protein;	Q62418	1	12	12	19.5	0.333	0.048	0.715
Calmodulin-4;	Q9JM83	1	5	5	31.8	0.333	0.061	0.726
H-2 class II histocompatibility antigen, A-Q beta chain;	P06342	1	7	8	24.2	0.333	0.119	0.744
Galectin-related protein A;	Q8VED9	1	4	4	25	0.333	0.058	0.726
Coronin-7;	Q9D2V7	1	10	13	9.3	0.333	0.174	0.773
CUGBP Elav-like family member 2;	Q9Z0H4	1	3	3	15.6	0.333	0.026	0.718
Uridine diphosphate glucose pyrophosphatase;	Q9D142	0.999	2	2	4.1	0.333	0.034	0.719
E3 ubiquitin-protein ligase RNF181;	Q9CY62	0.975	2	2	6.1	0.333	0.032	0.711
AP2-associated protein kinase 1;	Q3UHJ0	1	2	2	3.9	0.345	0.092	0.723
Protein phosphatase 1 regulatory subunit 7;	Q3UM45	1	7	8	15.8	0.345	0.054	0.709
Succinate-semialdehyde dehydrogenase, mitochondrial;	Q8BWF0	1	3	3	8.2	0.345	0.057	0.710
14 kDa phosphohistidine phosphatase;	Q9DAK9	1	3	3	18.5	0.345	0.035	0.705
Glycogen synthase kinase-3 beta;	Q9WV60	1	6	7	20	0.345	0.06	0.710
C-Jun-amino-terminal kinase-interacting protein 4;	Q58A65	1	8	8	6.4	0.345	0.041	0.704
Sorcin;	Q6P069	1	14	17	41.4	0.345	0.136	0.743
Trk-fused; Uncharacterized protein;	Q8C2C6	1	3	3	8.3	0.345	0.033	0.703
Methionine adenosyltransferase 2 subunit beta;	Q99LB6	1	3	3	14.7	0.345	0.081	0.719
Cytoplasmic dynein 1 intermediate chain 2;	O88487	1	6	6	5.9	0.356	0.028	0.694
Elongation factor 2;	P58252	1	47	74	37.9	0.356	0.064	0.705
Aminopeptidase B;	Q8VCT3	1	8	8	11.9	0.356	0.095	0.715
Citrate synthase, mitochondrial;	Q9CZU6	1	11	16	14.7	0.356	0.044	0.697
Serine/threonine-protein phosphatase 6 catalytic subunit;	Q9CQR6	0.915	2	4	2.6	0.356	0.033	0.695
Thioredoxin domain-containing protein 17;	Q9CQM5	1	3	4	11.4	0.367	0.026	0.686
Tubulin polymerization-promoting protein family member 3;	Q9CRB6	1	3	5	11.9	0.367	0.034	0.687
Serine-threonine kinase receptor-associated protein;	Q9Z1Z2	1	14	18	35.1	0.367	0.08	0.701
Adenosylhomocysteinase;	P50247	1	25	38	36.6	0.367	0.083	0.702
Peroxiredoxin-2;	Q61171	1	15	33	42.4	0.367	0.026	0.686
Alpha-2-macroglobulin;	Q61838	1	92	271	41.1	0.367	0.08	0.701
Bleomycin hydrolase;	Q8R016	1	13	15	25.9	0.367	0.114	0.716
Nicotinate phosphoribosyltransferase;	Q8CC86	0.967	2	2	3.3	0.367	0.046	0.690
Peptidyl-prolyl cis-trans isomerase B;	P24369	0.918	2	2	4.2	0.367	0.043	0.689
Dipeptidase 1;	P31428	1	3	5	7.6	0.379	0.082	0.693
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;	P63330	1	12	17	29.1	0.379	0.044	0.682
Alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB); Uncharacterized protein;	A2BFA6	1	3	3	3.4	0.379	0.023	0.678
Heat shock protein 4; Heat shock protein 4, isoform CRA_a; Uncharacterized protein;	Q3U2G2	1	39	47	33.6	0.379	0.058	0.686
Carbonyl reductase [NADPH] 1;	P48758	1	10	13	36.1	0.39	0.039	0.673

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3-ketoacyl-CoA thiolase, mitochondrial;	Q8BWT1	1	20	25	36	0.39	0.051	0.668
Uncharacterized protein;	Q9CX86	1	5	5	17	0.39	0.089	0.681
Prolyl 4-hydroxylase subunit alpha-1;	Q60715	1	7	9	13.3	0.39	0.042	0.666
Ubiquitin carboxyl-terminal hydrolase 10;	P52479	0.998	2	2	1.8	0.39	0.039	0.673
Delta-aminolevulinic acid dehydratase;	P10518	1	14	30	25.8	0.401	0.046	0.659
Twinfilin-1;	Q91YR1	1	3	3	9.1	0.401	0.058	0.662
Tumor protein D54;	Q9CYZ2	1	2	2	6.2	0.401	0.043	0.659
Long-chain-fatty-acid--CoA ligase 1;	P41216	1	4	4	4.1	0.411	0.034	0.650
Eukaryotic translation initiation factor 4E;	P63073	1	5	7	12.9	0.411	0.093	0.667
Ras GTPase-activating protein-binding protein 1;	P97855	1	2	2	7.3	0.411	0.059	0.655
Fatty acyl-CoA reductase 2;	Q7TNT2	0.998	2	2	3.5	0.411	0.139	0.687
Eukaryotic translation initiation factor 6;	O55135	1	6	6	27.8	0.422	0.044	0.644
Peptidyl-prolyl cis-trans isomerase D;	Q9CR16	1	18	22	28.9	0.422	0.072	0.654
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial;	O88696	1	2	3	6.6	0.433	0.189	0.695
Proteasome subunit beta type-7;	P70195	1	4	5	7.2	0.433	0.055	0.640
Inter-alpha-trypsin inhibitor heavy chain H1;	Q61702	1	6	7	7.8	0.433	0.266	0.732
Cytosolic 5'-nucleotidase 3;	Q9D020	1	3	3	8.8	0.433	0.045	0.636
Ras-related protein Rab-7a;	P51150	1	14	17	38.6	0.444	0.039	0.628
Kynurenine--oxoglutarate transaminase 3;	Q71RI9	1	3	4	5.7	0.444	0.183	0.683
Kynurenine--oxoglutarate transaminase 1;	Q8BTY1	1	3	3	8.6	0.444	0.046	0.629
Transgelin-2;	Q9WVA4	1	17	27	44.7	0.444	0.056	0.632
Peptidyl-prolyl cis-trans isomerase A;	P17742	1	7	12	40.2	0.444	0.163	0.673
Chromobox protein homolog 3;	P23198	1	3	3	12.6	0.444	0.036	0.628
Mitogen-activated protein kinase 1;	P63085	0.999	3	4	13.8	0.444	0.111	0.650
Mitogen-activated protein kinase 3;	Q63844	0.999	2	2	8.4	0.098	0.018	0.919
cAMP-dependent protein kinase type I-alpha regulatory subunit;	Q9DBC7	1	8	8	13.4	0.444	0.085	0.640
COP9 signalosome complex subunit 5;	O35864	0.999	2	2	10.2	0.444	0.127	0.657
Myeloid-associated differentiation marker;	O35682	1	2	2	5.3	0.454	0.07	0.621
Galectin-3;	P16110	1	10	24	27.7	0.454	0.06	0.619
Mimecan;	Q62000	1	7	8	15.4	0.454	0.07	0.621
S-methyl-5'-thioadenosine phosphorylase;	Q9CQ65	1	10	13	26.9	0.454	0.086	0.634
Perilipin-3;	Q9DBG5	1	8	9	15.1	0.454	0.166	0.660
Heat shock 70 kDa protein 4L;	P48722	1	11	11	13.8	0.454	0.215	0.685
Biliverdin reductase A;	Q9CY64	1	5	6	23.7	0.454	0.07	0.628
Acyl-coenzyme A thioesterase 9, mitochondrial;	Q9R0X4	1	5	5	7.7	0.454	0.089	0.629
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial;	P50136	1	2	3	4.5	0.454	0.056	0.618
H-2 class II histocompatibility antigen, A-Q alpha chain;	P04227	0.999	2	2	6.8	0.454	0.106	0.634
Guanylate kinase;	Q64520	1	2	2	6.1	0.465	0.034	0.606
Vacuolar protein sorting-associated protein 35;	Q9EQH3	1	5	5	6.2	0.465	0.229	0.688
Serine/threonine-protein phosphatase;	F7BX26	1	5	9	6.3	0.465	0.135	0.637
Complement component 1, q subcomponent binding protein; Complement component 1, q subcomponent binding protein, isoform CRA_b; Uncharacterized protein; p32-RACK;	Q8R5L1	1	5	8	12.5	0.465	0.142	0.641

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MAP kinase-activated protein kinase 3;	Q3UMW7	0.999	2	2	9	0.465	0.057	0.611
Glucose 1,6-bisphosphate synthase;	Q8CAA7	0.994	2	4	1.6	0.465	0.047	0.608
Polyadenylate-binding protein-interacting protein 1;	Q8VE62	0.976	2	2	1.9	0.465	0.057	0.611
Stress-induced-phosphoprotein 1;	Q60864	1	21	28	21.9	0.475	0.092	0.614
Ribulose-phosphate 3-epimerase;	Q8VEE0	1	5	6	17.5	0.475	0.126	0.627
Acyl-coenzyme A thioesterase 1;	O55137	1	10	14	24.3	0.475	0.096	0.617
Acyl-coenzyme A thioesterase 2, mitochondrial;	Q9QYR9	0.999	2	2	12.1	-0.515	-0.103	0.580
TAR DNA-binding protein 43;	Q921F2	1	10	11	20.8	0.475	0.366	0.738
Acid ceramidase;	Q9WV54	1	9	10	18	0.475	0.103	0.618
Dysferlin;	Q9ESD7	1	2	2	0.5	0.475	0.048	0.602
Phosphopantothenate--cysteine ligase;	Q8VDG5	1	2	2	7.7	0.475	0.062	0.605
Hypoxanthine-guanine phosphoribosyltransferase;	P00493	1	11	17	37.6	0.485	0.173	0.641
Peptidyl-prolyl cis-trans isomerase FKBP5;	Q64378	1	5	5	8.8	0.485	0.218	0.663
Cleft lip and palate transmembrane protein 1 homolog;	Q8VBZ3	1	3	3	7.5	0.485	0.073	0.601
Sorting nexin-1;	Q9WV80	1	4	4	7.5	0.485	0.139	0.623
Monoglyceride lipase;	O35678	1	7	7	27.7	0.485	0.184	0.645
Protein lunapark;	Q7TQ95	1	3	3	8.5	0.485	0.104	0.611
Protein PRRC2C;	Q3TLH4	1	2	3	0.7	0.485	0.059	0.598
V-type proton ATPase subunit B, brain isoform;	P62814	1	9	14	12.1	0.496	0.148	0.621
Uroporphyrinogen decarboxylase;	P70697	1	5	5	14.2	0.496	0.053	0.589
Sarcalumenin;	Q7TQ48	1	14	17	15.8	0.496	0.151	0.620
Heat shock protein beta-2;	Q99PR8	1	4	5	24.2	0.496	0.211	0.650
Ras-related protein Rab-11B;	P46638	1	8	9	33	0.496	0.056	0.588
Tubulin--tyrosine ligase-like protein 12;	Q3UDE2	1	6	10	8.5	0.496	0.032	0.586
Protein transport protein Sec31A;	Q3UPL0	1	18	21	15	0.496	0.179	0.638
Proteasome subunit beta type-3;	Q9R1P1	1	6	8	23.9	0.496	0.06	0.591
WW domain-binding protein 11;	Q923D5	1	2	2	4.1	0.496	0.236	0.665
Vacuolar protein-sorting-associated protein 25;	Q9CQ80	1	2	2	14.1	0.496	0.158	0.626
Protein CREG1;	O88668	1	2	3	8.2	0.506	0.039	0.580
Haloacid dehalogenase-like hydrolase domain-containing protein 3;	Q9CYW4	1	4	4	15.9	0.506	0.107	0.591
Interferon-induced guanylate-binding protein 2;	Q9Z0E6	1	6	6	9.5	0.506	0.175	0.625
Galactose-1-phosphate uridylyltransferase;	Q03249	1	3	3	6.9	0.506	0.118	0.601
Uncharacterized protein;	F6RPJ9	1	18	30	12.4	0.506	0.128	0.599
Uncharacterized protein;	F6ZFU0	1	5	8	15	0.506	0.043	0.580
Cellular retinoic acid-binding protein 2;	P22935	1	3	5	21.7	0.506	0.064	0.579
Smoothelin-like protein 1;	Q99LM3	1	2	2	4	0.506	0.043	0.580
Sorting nexin-6;	Q6P8X1	1	7	7	13.1	0.516	0.076	0.579
S-adenosylmethionine synthase isoform type-2;	Q3THS6	1	10	11	29.3	0.516	0.108	0.585
Reticulon-2;	O70622	1	4	4	7.2	0.516	0.498	0.753
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B;	Q3TDQ1	0.992	2	2	0.9	0.516	0.079	0.576
Protein AMBP;	Q07456	1	4	4	7.2	0.526	0.175	0.605
Microtubule-associated protein RP/EB family member 1;	Q61166	1	3	5	11.2	0.526	0.095	0.573
Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2;	Q6ZQK5	1	3	3	3.6	0.526	0.164	0.601

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Equilibrative nucleoside transporter 1;	Q9JIM1	0.996	2	2	9.9	0.526	0.033	0.560
Costars family protein C6orf115 homolog;	Q4KML4	1	4	4	27.2	0.536	0.144	0.584
Adenylyl cyclase-associated protein 1;	P40124	1	18	21	23.8	0.536	0.24	0.628
Ubiquitin carboxyl-terminal hydrolase 5;	P56399	1	15	23	13.1	0.536	0.126	0.577
Acyl-CoA dehydrogenase family member 9, mitochondrial;	Q8JZN5	1	9	11	16.2	0.536	0.144	0.584
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1;	Q60967	1	12	17	15.7	0.546	0.277	0.639
Presequence protease, mitochondrial;	Q8K411	1	17	18	16.6	0.546	0.202	0.603
Reticulon-4;	Q99P72	1	5	6	11.5	0.546	0.082	0.556
Gamma-glutamylcyclotransferase;	Q9D7X8	1	4	4	12.8	0.546	0.217	0.610
Proteasome subunit beta type-5;	O55234	1	6	6	22.3	0.546	0.18	0.590
Polyadenylate-binding protein 1;	P29341	1	22	24	26.9	0.546	0.12	0.568
Ubiquitin-conjugating enzyme E2 L3;	P68037	1	7	11	47.4	0.546	0.284	0.642
Protein arginine N-methyltransferase 1;	Q9JIF0	1	2	2	8.2	0.546	0.056	0.552
60S acidic ribosomal protein P1;	P47955	1	3	3	14	0.556	0.095	0.553
Ubiquitin carboxyl-terminal hydrolase 14;	Q9JMA1	1	7	13	8.5	0.556	0.034	0.541
Elongation factor G, mitochondrial;	Q8K0D5	1	2	2	3.5	0.556	0.049	0.543
Nidogen-1;	P10493	1	8	9	5.2	0.566	0.279	0.626
3'(2'),5'-bisphosphate nucleotidase 1;	Q9Z0S1	1	5	5	23.3	0.566	0.203	0.589
Cofilin-1;	P18760	1	10	27	40.4	0.566	0.084	0.545
Eukaryotic translation initiation factor 5;	P59325	1	3	3	15.1	0.566	0.317	0.644
Ras-related protein Rab-1A;	P62821	1	9	9	35.6	0.566	0.061	0.533
Ras-related protein Rab-1B;	Q9D1G1	1	5	5	29.9	0.782	0.114	0.397
Ras-related protein Rab-14;	Q91V41	1	4	8	24.4	0.263	0.035	0.771
Ras-related protein Rab-10;	P61027	1	3	3	17	0.934	0.171	0.321
Proteasome subunit alpha type-5;	Q9Z2U1	1	7	10	35.7	0.575	0.085	0.534
Myristoylated alanine-rich C-kinase substrate;	P26645	1	11	17	41.7	0.585	0.086	0.526
Gamma-synuclein;	Q9Z0F7	1	7	7	47.2	0.585	0.051	0.521
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P50544	1	9	12	10.8	0.585	0.117	0.535
Ubiquitin-fold modifier 1;	P61961	1	6	6	50.6	0.585	0.094	0.528
Probable ubiquitin carboxyl-terminal hydrolase FAF-X;	P70398	1	2	2	0.9	0.585	0.148	0.547
Mitogen-activated protein kinase 9;	Q9WTU6	1	4	6	5	0.585	0.082	0.525
Palmitoyl-protein thioesterase 1;	O88531	1	3	3	8.9	0.595	0.102	0.525
ATP-binding cassette sub-family E member 1;	P61222	1	3	4	3.3	0.595	0.146	0.539
Annexin A7;	Q07076	1	10	16	17.7	0.595	0.134	0.535
Poly(U)-binding-splicing factor PUF60;	Q3UEB3	1	9	10	14.2	0.595	0.102	0.526
CD166 antigen;	Q61490	1	6	6	9.3	0.595	0.059	0.515
Dual specificity protein phosphatase 3;	Q9D7X3	1	8	8	30.8	0.595	0.051	0.513
Cystatin E/M; Cystatin M/E; Uncharacterized protein;	Q9D1B1	1	3	3	14.1	0.595	0.075	0.518
Proteasome subunit alpha type-6;	Q9QUM9	1	13	18	29.7	0.595	0.095	0.521
Phosphatidylinositol transfer protein alpha isoform;	P53810	1	8	8	24	0.604	0.091	0.515
Protein unc-119 homolog B;	Q8C4B4	0.998	2	2	5.1	0.604	0.072	0.511
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha;	Q61239	1	3	3	4.2	0.614	0.261	0.570
Diphosphomevalonate decarboxylase;	Q99JF5	1	3	3	5.7	0.614	0.068	0.499

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Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Q9D6R2	1	10	12	25.7	0.614	0.148	0.528
Periostin;	Q62009	1	16	18	14	0.614	0.124	0.513
Vinculin;	Q64727	1	28	50	20.6	0.614	0.209	0.552
Enoyl-CoA hydratase domain-containing protein 1;	Q9D9V3	1	10	11	21.1	0.614	0.522	0.689
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1;	Q9QUR7	1	3	3	13.9	0.614	0.044	0.502
Glucocorticoid receptor;	P06537	1	3	3	7.8	0.614	0.269	0.580
Sorting nexin-27;	Q3UHD6	1	3	3	9.1	0.614	0.193	0.539
Ganglioside GM2 activator;	Q60648	1	6	6	16.6	0.623	0.061	0.492
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial;	O88986	1	8	8	26.7	0.623	0.093	0.499
Mitogen-activated protein kinase 14;	P47811	1	5	5	20.5	0.623	0.174	0.527
Latexin;	P70202	1	2	3	8.1	0.632	0.069	0.488
Aldehyde dehydrogenase;	E9Q3E1	1	3	3	6.9	0.632	0.281	0.566
[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial;	Q9JK42	0.903	2	2	1.7	0.632	0.037	0.483
AP-1 complex subunit beta-1;	O35643	1	7	7	9.6	0.642	0.21	0.528
Sorting nexin-2;	Q9CWK8	1	11	14	17.9	0.642	0.169	0.510
Prolyl endopeptidase;	Q9QUR6	1	26	32	28.5	0.642	0.095	0.488
SUMO-activating enzyme subunit 1;	Q9R1T2	1	7	8	28	0.642	0.111	0.492
Myosin-Ic;	Q9WTI7	1	3	3	2.6	0.651	0.062	0.475
Prolyl 4-hydroxylase subunit alpha-2;	Q60716	1	6	7	9.7	0.651	0.07	0.477
Oxysterol-binding protein-related protein 9;	A2A8Z1	1	2	3	1.4	0.651	0.033	0.472
Palmdelphin;	Q9JHU2	1	2	2	3.3	0.66	0.067	0.471
Spectrin beta chain, brain 1;	Q62261	1	4	4	2.5	0.669	0.311	0.554
Ubiquitin-like modifier-activating enzyme 1;	Q02053	1	48	61	28.9	0.669	0.084	0.464
Methylosome protein 50;	Q99J09	1	3	5	8.5	0.669	0.189	0.501
Mevalonate kinase;	Q9R008	1	6	6	25.1	0.669	0.126	0.479
Uncharacterized protein;	E9PZZ3	1	3	3	2.8	0.669	0.261	0.530
Proteasome subunit alpha type-2;	P49722	1	15	20	45.7	0.678	0.038	0.453
Ubiquitin carboxyl-terminal hydrolase isozyme L3;	Q9JKB1	1	7	7	30	0.678	0.131	0.470
Staphylococcal nuclease domain-containing protein 1;	Q78PY7	1	2	2	2.6	0.678	0.369	0.568
Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	P23506	1	5	6	15.8	0.687	0.243	0.505
Lipoma-preferred partner homolog;	Q8BFW7	1	5	7	14.2	0.696	0.103	0.452
UV excision repair protein RAD23 homolog B;	P54728	1	6	6	14.4	0.696	0.232	0.495
Hepatoma-derived growth factor;	P51859	1	7	9	26.2	0.705	0.225	0.485
NSFL1 cofactor p47;	Q9CZ44	1	19	23	32.7	0.705	0.082	0.443
Serpin B5;	P70124	1	38	80	59.2	0.714	0.083	0.438
Ubiquitin thioesterase OTUB1;	Q7TQI3	1	10	15	28.2	0.714	0.113	0.444
Opioid growth factor receptor;	Q99PG2	1	3	4	4.8	0.714	0.074	0.432
N-acetyl-D-glucosamine kinase;	Q9QZ08	1	4	4	14	0.714	0.118	0.446
Perilipin-4;	O88492	1	26	45	23.8	0.722	0.223	0.476
Protein canopy homolog 4;	Q8BQ47	1	5	5	13.5	0.722	0.061	0.429
Ubiquitin-like-conjugating enzyme ATG3;	Q9CPX6	1	4	4	7.3	0.722	0.079	0.427
Diphosphoinositol polyphosphate phosphohydrolase 3-alpha;	P0C027	1	2	3	4.3	0.731	0.084	0.423
Serum deprivation-response protein;	Q63918	1	2	2	3.8	0.731	0.062	0.420

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Protein FAM63A;	Q76LS9	1	4	4	10.7	0.731	0.119	0.431
Glucose-6-phosphate 1-dehydrogenase X;	Q00612	1	26	37	36.1	0.731	0.176	0.448
Asparagine synthetase [glutamine-hydrolyzing];	Q61024	1	2	2	5.5	0.731	0.277	0.487
Methylmalonyl-CoA mutase, mitochondrial;	P16332	1	7	7	9.9	0.74	0.071	0.416
Tyrosine-protein phosphatase non-receptor type 23;	Q6PB44	1	2	2	2.2	0.74	0.084	0.418
SEC14-like protein 4;	Q8R0F9	1	4	4	12.2	0.74	0.142	0.432
Niban-like protein 1;	Q8R1F1	1	3	3	4.3	0.74	0.089	0.420
40S ribosomal protein S21;	Q9CQR2	1	4	4	27.7	0.74	0.368	0.521
MKIAA0079 protein; SEC24 related gene family, member C (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q80U83	0.999	2	2	2.6	0.74	0.12	0.427
Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform;	P62715	1	2	2	29.1	0.748	0.111	0.419
Perilipin-1;	Q8CGN5	1	20	24	39.8	0.748	0.329	0.498
Heterogeneous nuclear ribonucleoprotein K;	P61979	1	26	43	36.4	0.748	0.142	0.427
Dipeptidyl peptidase 1;	P97821	1	7	16	9.8	0.748	0.12	0.421
Uncharacterized protein;	E9QK49	1	5	6	6.8	0.748	0.134	0.425
Aspartyl-tRNA synthetase, cytoplasmic;	Q922B2	1	4	4	11.6	0.757	0.179	0.431
Lupus La protein homolog;	P32067	1	6	6	13.3	0.757	0.381	0.514
Adenylate kinase 2, mitochondrial;	Q9WTP6	1	6	8	32.6	0.757	0.26	0.463
Protein DDI1 homolog 2;	A2ADY9	1	7	8	22.3	0.766	0.095	0.406
Steroid receptor RNA activator 1;	Q80VJ2	1	2	5	7.8	0.766	0.095	0.402
Trifunctional purine biosynthetic protein adenosine-3;	Q64737	1	21	22	19.6	0.766	0.257	0.452
Apolipoprotein D;	P51910	1	3	3	12.7	0.774	0.281	0.456
14-3-3 protein gamma;	P61982	1	8	11	32.4	0.774	0.091	0.397
Epithelial cell adhesion molecule;	Q99JW5	1	2	2	14.3	0.774	0.104	0.399
Extracellular matrix protein 2;	Q5FW85	1	2	2	1.6	0.782	0.164	0.409
Thioredoxin-like protein 1;	Q8CDN6	1	8	9	21.5	0.782	0.068	0.389
Elongation factor 1-gamma;	Q9D8N0	1	13	20	17.8	0.782	0.105	0.395
ADP-ribosylation factor 6;	P62331	1	2	2	5.7	0.782	0.077	0.390
26S proteasome non-ATPase regulatory subunit 9;	Q9CR00	1	2	2	10.8	0.782	0.246	0.437
Vesicle-fusing ATPase;	P46460	1	3	3	4.8	0.791	0.233	0.427
Profilin-2;	Q9JJV2	1	3	3	24.5	0.791	0.123	0.394
Histidyl-tRNA synthetase, cytoplasmic;	Q61035	1	2	3	6.3	0.791	0.119	0.394
LIM domain and actin-binding protein 1;	Q9ERG0	0.996	2	2	3.2	0.791	0.069	0.385
Phosphoribosylformylglycinamidine synthase;	Q5SUR0	1	13	14	11	0.799	0.147	0.395
PDZ and LIM domain protein 5;	Q8CI51	1	7	8	10.7	0.799	0.542	0.546
Non-specific lipid-transfer protein;	P32020	1	9	9	8.8	0.807	0.046	0.373
Protein S100-A1;	P56565	1	2	2	16	0.816	0.134	0.384
Haptoglobin;	Q61646	1	6	9	11.8	0.816	0.083	0.370
Trifunctional enzyme subunit alpha, mitochondrial;	Q8BMS1	1	24	31	30.4	0.816	0.334	0.451
60S ribosomal protein L11;	Q9CXW4	1	2	2	8.1	0.816	0.102	0.373
Heterogeneous nuclear ribonucleoprotein A3;	Q8BG05	1	8	13	14.7	0.816	0.111	0.379
Tripeptidyl-peptidase 1;	O89023	1	5	5	9.4	0.824	0.07	0.366
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform;	P18826	1	8	8	8.2	0.824	0.414	0.475

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Filamin-B;	Q80X90	1	12	12	6	0.824	0.344	0.446
Seryl-tRNA synthetase, cytoplasmic;	P26638	1	12	12	22.1	0.832	0.173	0.380
Dynamin-2;	P39054	1	3	3	6	0.832	0.323	0.433
Carbonic anhydrase 2;	P00920	1	13	14	37.3	0.84	0.258	0.403
Chloride intracellular channel protein 4;	Q9QYB1	1	7	9	31.6	0.84	0.15	0.370
Cathepsin L1;	P06797	1	9	9	29.3	0.848	0.16	0.369
Serine/threonine-protein kinase Nek7;	Q9ES74	0.998	2	2	8	0.848	0.057	0.350
Glutamate--cysteine ligase catalytic subunit;	P97494	1	5	8	9.4	0.856	0.227	0.380
GMP synthase [glutamine-hydrolyzing];	Q3THK7	1	5	6	5.6	0.856	0.052	0.346
Aldehyde dehydrogenase family 16 member A1;	Q571I9	1	4	4	6.2	0.856	0.156	0.359
Ran-binding protein 3;	Q9CT10	1	6	8	12.2	0.856	0.199	0.374
Heterogeneous nuclear ribonucleoprotein F;	Q9Z2X1	1	9	12	20.5	0.856	0.09	0.346
Trifunctional enzyme subunit beta, mitochondrial;	Q99JY0	1	7	9	17.1	0.856	0.147	0.357
Interleukin enhancer-binding factor 3;	Q9Z1X4	1	3	3	7.2	0.856	0.293	0.406
Proteasome subunit alpha type-7;	Q9Z2U0	1	14	26	34.3	0.856	0.099	0.352
Polymerase I and transcript release factor;	O54724	1	6	7	17.9	0.872	0.386	0.429
Carbonic anhydrase 1;	P13634	1	4	4	12.6	0.88	0.096	0.336
GTP-binding nuclear protein Ran;	P62827	1	11	28	29.6	0.88	0.33	0.403
Obg-like ATPase 1;	Q9CZ30	1	7	8	16.9	0.888	0.163	0.342
Alanyl-tRNA synthetase domain containing 1; Uncharacterized protein;	A2A4P4	1	5	5	11.2	0.888	0.326	0.396
Ras-related protein Rab-21;	P35282	1	2	2	13.5	0.895	0.188	0.345
Ly6/PLAUR domain-containing protein 5;	Q9D7Z7	1	2	2	6.2	0.895	0.168	0.342
Ubiquinone biosynthesis protein COQ9, mitochondrial;	Q8K1Z0	1	4	4	15.7	0.895	0.14	0.336
Proteasome subunit beta type-6;	Q60692	1	4	5	8.8	0.903	0.063	0.321
mRNA cap guanine-N7 methyltransferase;	Q9D0L8	1	2	2	16.6	0.903	0.13	0.330
Acetoacetyl-CoA synthetase;	Q9D2R0	0.993	2	2	3	0.903	0.121	0.325
Putative ATP-dependent RNA helicase Pl10;	P16381	1	2	3	4.1	0.911	0.116	0.321
Uncharacterized protein;	E9Q394	1	6	6	2	0.911	0.286	0.365
Protein-arginine deiminase type-2;	Q08642	1	6	6	10.5	0.918	0.253	0.350
Farnesyl pyrophosphate synthase;	Q920E5	1	16	16	26.1	0.918	0.175	0.329
DNA damage-binding protein 1;	Q3U1J4	1	8	9	9.2	0.918	0.214	0.339
Serine/threonine-protein kinase PAK 2;	Q8CIN4	1	12	28	16.2	0.918	0.204	0.337
Large proline-rich protein BAG6;	Q9Z1R2	0.962	2	2	3.5	0.926	0.21	0.333
Rho-associated protein kinase 2;	P70336	1	2	2	2.2	0.934	0.186	0.324
Probable E3 ubiquitin-protein ligase HERC4;	Q6PAV2	1	5	6	7.2	0.934	0.337	0.370
Secretory carrier-associated membrane protein 1;	Q8K021	1	2	2	8	0.934	0.117	0.310
Regulator of nonsense transcripts 1;	Q9EPU0	1	7	8	8.5	0.934	0.328	0.369
Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial;	Q8BMS4	1	2	2	4.3	0.941	0.235	0.333
Ras GTPase-activating-like protein IQGAP1;	Q9JKF1	1	21	24	11.9	0.941	0.431	0.398
26S proteasome non-ATPase regulatory subunit 4;	O35226	1	4	8	10.6	0.949	0.113	0.300
Signal transducer and activator of transcription 1;	P42225	1	4	4	5.6	0.949	0.226	0.323
SET and MYND domain-containing protein 1;	P97443	0.999	2	2	4.7	0.949	0.098	0.297
Sodium/potassium-transporting ATPase subunit beta-3;	P97370	1	5	5	43.3	0.956	0.227	0.320

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Poliovirus receptor-related protein 4;	Q8R007	1	3	3	5.9	0.956	0.094	0.294
Glycogen synthase kinase-3 alpha;	Q2NL51	0.939	2	3	6.8	0.956	0.172	0.307
Valyl-tRNA synthetase;	Q9Z1Q9	1	7	8	6	0.963	0.064	0.287
Glucosidase 2 subunit beta;	O08795	1	4	6	6.7	0.971	0.149	0.296
Cytoplasmic dynein 1 light intermediate chain 2;	Q6PDL0	1	3	3	6.7	0.971	0.263	0.324
Proteasome subunit alpha type-1;	Q9R1P4	1	11	13	26.3	0.986	0.344	0.340
Uncharacterized protein;	E9Q4L8	1	9	16	21.9	0.986	0.478	0.389
Oxysterol-binding protein;	E9QPD4	1	2	2	5.2	0.986	0.085	0.276
Fascin;	Q61553	1	5	5	11.8	0.993	0.364	0.342
Glutathione S-transferase kappa 1;	Q9DCM2	1	4	4	18.6	1	0.325	0.325
Zyxin;	Q62523	1	11	15	16.9	1	0.21	0.292
26S proteasome non-ATPase regulatory subunit 12;	Q9D8W5	1	4	4	5	1	0.35	0.333
Apolipoprotein A-IV;	P06728	1	20	29	42	1.007	0.271	0.304
Alpha-galactosidase A;	P51569	1	2	2	2.9	1.007	0.145	0.276
14-3-3 protein zeta/delta;	P63101	1	15	26	39.2	1.007	0.095	0.269
14-3-3 protein beta/alpha;	Q9CQV8	1	13	13	45.1	1.007	0.175	0.282
Epithelial splicing regulatory protein 1;	Q3US41	1	2	2	7.9	1.014	0.231	0.288
Nardilysin;	Q8BHG1	1	3	3	2.9	1.014	0.873	0.507
RuvB-like 1;	P60122	1	6	6	19.3	1.014	0.472	0.367
14-3-3 protein eta;	P68510	1	5	7	24	1.021	0.146	0.269
Small glutamine-rich tetratricopeptide repeat-containing protein alpha;	Q8BJU0	1	7	8	19.4	1.021	0.106	0.262
COP9 signalosome complex subunit 8;	Q8VBV7	1	3	3	10	1.021	0.101	0.263
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);	Q8VC30	1	4	6	4	1.021	0.091	0.263
E3 SUMO-protein ligase RanBP2;	Q9ERU9	1	3	3	1.1	1.021	0.126	0.267
Splicing factor 1;	Q64213	1	4	4	7.1	1.021	0.342	0.319
CD2-associated protein;	Q9JLQ0	1	6	8	8.6	1.029	0.212	0.277
Nischarin;	Q80TM9	1	3	3	11.6	1.029	0.424	0.338
Sodium/potassium-transporting ATPase subunit alpha-1;	Q8VDN2	1	7	8	15.9	1.029	0.247	0.289
Sodium/potassium-transporting ATPase subunit alpha-2;	Q6PIE5	1	4	4	13.3	0.084	0.009	0.927
Amidophosphoribosyltransferase;	Q8CIH9	0.999	2	2	3.3	1.029	0.136	0.266
Ensconsin;	O88735	1	2	3	1.8	1.036	0.222	0.276
Acylamino-acid-releasing enzyme;	Q8R146	1	5	5	9.7	1.043	0.294	0.290
Tyrosyl-tRNA synthetase, cytoplasmic;	Q91WQ3	1	3	3	7.4	1.043	0.451	0.339
Arfip1 protein; Uncharacterized protein;	A2RSX9	1	3	3	15	1.043	0.253	0.280
Heat shock protein beta-1;	P14602	1	16	46	37.3	1.05	0.091	0.249
Isopentenyl-diphosphate Delta-isomerase 1;	P58044	1	2	2	18.9	1.05	0.117	0.252
Fatty acid synthase;	P19096	1	107	155	33.6	1.064	0.458	0.330
Calcium-binding protein 39;	Q06138	1	3	3	10	1.064	0.341	0.292
V-type proton ATPase subunit H;	Q8BVE3	1	3	4	11.8	1.064	0.199	0.260
SAR1 gene homolog A (S. cerevisiae); SAR1 gene homolog A (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q99JZ4	1	4	5	33.8	1.077	0.071	0.234
Dynamin-1-like protein;	Q8K1M6	1	3	3	6.9	1.084	0.205	0.248
1-acylglycerol-3-phosphate O-acyltransferase ABHD5;	Q9DBL9	1	2	2	11.1	1.084	0.332	0.280

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change (log$_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
SEC23-interacting protein;	Q6NZC7	1	5	5	4	1.091	0.097	0.231
26S protease regulatory subunit 6A;	O88685	1	17	20	36	1.091	0.389	0.295
Glutathione synthetase;	P51855	1	2	2	3.6	1.091	0.072	0.229
Retroviral-like aspartic protease 1;	Q09PK2	1	5	5	19.5	1.104	0.159	0.231
Lon protease homolog, mitochondrial;	Q8CGK3	1	5	5	5.6	1.104	0.154	0.230
Cytosolic 10-formyltetrahydrofolate dehydrogenase;	Q8R0Y6	1	6	6	12.4	1.104	0.211	0.242
Protein S100-A14;	Q9D2Q8	1	4	5	40.4	1.104	0.092	0.223
Deoxyhypusine hydroxylase;	Q99LN9	1	2	2	17.6	1.104	0.246	0.247
Eukaryotic translation initiation factor 3 subunit D;	O70194	1	5	5	7.5	1.111	0.391	0.282
Band 4.1-like protein 1;	Q9Z2H5	1	2	2	3.8	1.111	0.159	0.228
Ppm1b protein; Protein phosphatase 1B2 53 kDa isoform; Uncharacterized protein;	Q99NF7	1	2	2	4.4	1.111	0.293	0.255
Frizzled-7;	Q61090	1	3	3	3.1	1.111	0.113	0.223
Heterogeneous nuclear ribonucleoproteins A2/B1;	O88569	1	15	43	23.3	1.118	0.469	0.303
14-3-3 protein theta;	P68254	1	7	7	30.6	1.118	0.165	0.227
Peptidyl-prolyl cis-trans isomerase FKBP4;	P30416	1	13	14	23.8	1.138	0.528	0.312
60 kDa heat shock protein, mitochondrial;	P63038	1	28	39	37.2	1.138	0.129	0.213
Talin-1;	P26039	1	56	71	21	1.144	0.347	0.252
28S ribosomal protein S36, mitochondrial;	Q9CQX8	1	2	3	21	1.151	0.145	0.210
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase;	Q8C0L6	1	3	3	5.2	1.151	0.275	0.232
Heparan N-sulfatase; N-sulfoglucosamine sulfohydrolase (Sulfamidase); N-sulfoglucosamine sulfohydrolase (Sulfamidase), isoform CRA_b; Uncharacterized protein;	Q9EQ08	1	2	2	6.8	1.151	0.876	0.416
Signal transducing adapter molecule 2;	O88811	0.997	2	2	2.2	1.157	0.187	0.213
Asparaginyl-tRNA synthetase, cytoplasmic;	Q8BP47	1	2	3	4.1	1.17	0.156	0.205
ATP-binding domain-containing protein 4;	Q9CQ28	1	2	2	6.4	1.176	0.208	0.207
Acyl-CoA-binding protein;	P31786	1	6	11	39.1	1.176	0.167	0.202
StAR-related lipid transfer protein 5;	Q9EPQ7	1	5	5	20.7	1.176	0.167	0.201
Hormone-sensitive lipase;	P54310	1	12	13	17	1.183	0.214	0.208
Fibulin-5;	Q9WVH9	1	6	6	19.6	1.183	0.261	0.214
Ubiquitin carboxyl-terminal hydrolase 4;	P35123	1	8	8	12.1	1.183	0.208	0.205
Programmed cell death 6-interacting protein;	Q9WU78	1	14	17	16.9	1.183	0.698	0.340
26S proteasome non-ATPase regulatory subunit 14;	O35593	1	4	4	16	1.189	0.115	0.192
26S proteasome non-ATPase regulatory subunit 6;	Q99JI4	1	7	11	11.8	1.189	0.574	0.296
Ras-related protein Rab-5C;	P35278	1	4	4	17.1	1.189	0.339	0.230
Ras-related protein Rab-5A;	Q9CQD1	1	2	2	17.2	1.124	0.964	0.463
Four and a half LIM domains 3; Uncharacterized protein;	A6H6N4	1	2	2	6.6	1.189	0.188	0.200
60S ribosomal protein L6;	P47911	1	2	2	5.8	1.202	0.904	0.395
Paxillin;	Q8VI36	1	3	3	7.6	1.208	0.669	0.316
Ran-specific GTPase-activating protein;	P34022	1	2	2	5.4	1.214	0.157	0.186
Protein FAM114A2;	Q8VE88	1	3	3	10.3	1.227	0.603	0.284
Protein Niban;	Q3UW53	1	6	7	9.6	1.233	0.567	0.272
COP9 signalosome complex subunit 6;	O88545	1	2	2	10.4	1.239	0.504	0.249
EPM2A-interacting protein 1;	Q8VEH5	0.997	2	2	4.6	1.239	0.095	0.171

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change ($\log_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
26S protease regulatory subunit 7;	P46471	1	9	9	22.6	1.245	0.63	0.283
RelA-associated inhibitor;	Q5I1X5	1	2	4	1	1.245	0.189	0.180
Heterogeneous nuclear ribonucleoprotein U;	Q8VEK3	1	8	8	12.1	1.245	0.399	0.219
Heterogeneous nuclear ribonucleoprotein A/B;	Q99020	1	4	5	12	1.245	0.179	0.179
Multiple inositol polyphosphate phosphatase 1;	Q9Z2L6	1	3	3	5.2	1.245	0.294	0.195
Acetyl-CoA acetyltransferase, mitochondrial;	Q8QZT1	1	8	9	19.1	1.251	0.11	0.168
	F6ZQ75	1	3	3	3.2	1.251	0.347	0.204
55 kDa erythrocyte membrane protein;	P70290	1	3	3	7.2	1.251	0.499	0.241
ATP-citrate synthase;	Q91V92	1	22	26	15.9	1.251	0.315	0.197
Multifunctional protein ADE2;	Q9DCL9	1	7	7	16.5	1.257	0.452	0.226
Eukaryotic translation initiation factor 3 subunit B;	Q8JZQ9	1	9	13	15.6	1.263	0.326	0.195
Apolipoprotein A-II;	P09813	1	4	6	18.6	1.269	0.095	0.162
Uncharacterized protein;	E9Q7G0	1	5	5	1.5	1.269	0.479	0.229
Heterogeneous nuclear ribonucleoprotein D-like;	Q9Z130	1	3	3	5.3	1.269	0.111	0.163
Aminoacylase-1;	Q99JW2	0.998	2	2	4.9	1.269	0.916	0.358
Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	Q8JZK9	1	13	16	20.4	1.275	0.479	0.227
Proliferating cell nuclear antigen;	P17918	1	13	16	35.6	1.275	0.184	0.168
Protein disulfide-isomerase A6;	Q922R8	1	12	17	24.1	1.275	0.337	0.193
Histone-binding protein RBBP4;	Q60972	0.982	3	4	3.9	1.275	0.364	0.198
Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	P70441	1	5	8	13.2	1.281	0.738	0.298
Prefoldin subunit 2;	O70591	1	4	5	16.9	1.281	0.111	0.160
Rab GTPase-binding effector protein 1;	O35551	0.988	3	3	2.2	1.281	0.137	0.160
Apolipoprotein A-I;	Q00623	1	11	27	21.6	1.287	0.227	0.169
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1;	Q62077	1	3	3	2.4	1.287	0.105	0.156
Cullin-associated NEDD8-dissociated protein 1;	Q6ZQ38	1	15	19	12.8	1.287	0.754	0.297
Acyl-CoA synthetase family member 2, mitochondrial;	Q8VCW8	1	4	4	10.1	1.293	0.137	0.158
Copper transport protein ATOX1;	O08997	1	6	10	45.6	1.299	0.322	0.181
Protein arginine N-methyltransferase 5;	Q8CIG8	1	7	7	10.5	1.299	0.475	0.214
GTPase-activating protein and VPS9 domain-containing protein 1;	Q6PAR5	1	2	2	2.5	1.299	0.407	0.198
Rab GTPase-activating protein 1;	A2AWA9	1	2	2	2.6	1.305	0.19	0.159
Importin subunit alpha-4;	O35343	1	2	2	5.2	1.305	0.18	0.158
Junction plakoglobin;	Q02257	1	8	8	18.5	1.305	0.597	0.243
Catenin beta-1;	Q02248	1	3	3	6.7	0.202	0.197	0.902
Clusterin;	Q06890	1	10	11	24.3	1.305	0.301	0.175
PDZ and LIM domain protein 1;	O70400	1	3	3	15.9	1.31	0.143	0.152
Phosphatidylinositol-glycan-specific phospholipase D;	O70362	1	6	7	7.6	1.316	0.481	0.206
Ribosomal protein;	Q5XJF6	1	2	2	13.4	1.316	0.19	0.154
60S ribosomal protein L5;	P47962	1	2	3	8.6	1.322	0.19	0.152
Heat shock protein HSP 90-beta;	P11499	1	32	52	40.3	1.322	0.767	0.281
Heat shock protein HSP 90-alpha;	P07901	1	24	38	34.5	1.516	0.572	0.150
Endoplasmin;	P08113	1	19	26	22.3	0.807	0.71	0.602
Eukaryotic translation initiation factor 3 subunit G;	Q9Z1D1	1	4	5	10	1.328	0.127	0.145
Calpain-2 catalytic subunit;	O08529	1	10	16	14.3	1.328	0.307	0.167

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Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform;	P07934	1	3	3	26.5	1.328	0.19	0.151
Ubiquitin-40S ribosomal protein S27a;	P62983	1	6	10	28.2	1.328	0.386	0.182
Far upstream element (FUSE) binding protein 3; MCG130458; Uncharacterized protein;	A2AJ72	1	4	4	11.6	1.328	0.185	0.150
COP9 signalosome complex subunit 3;	O88543	1	3	3	12.3	1.339	0.344	0.169
Inosine-5'-monophosphate dehydrogenase 2;	P24547	1	3	5	9.7	1.345	1.128	0.374
E3 ubiquitin-protein ligase NEDD4;	P46935	1	5	6	7	1.345	0.858	0.297
tRNA (cytosine(34)-C(5))-methyltransferase;	Q1HFZ0	1	7	8	13.1	1.35	0.598	0.220
Small nuclear ribonucleoprotein Sm D1;	P62315	1	2	2	16.8	1.356	0.328	0.160
Cystatin-B;	Q62426	1	4	5	39.8	1.356	0.249	0.149
Uncharacterized protein;	D3YXL3	1	3	4	29.5	1.356	0.143	0.137
Magnesium-dependent phosphatase 1;	Q9D967	0.999	2	2	18.3	1.356	0.503	0.195
Ubiquitin-like modifier-activating enzyme 6;	Q8C7R4	1	7	7	6.6	1.367	0.434	0.177
Uncharacterized protein;	F7CAE1	1	14	55	57.9	1.367	0.069	0.131
14-3-3 protein sigma;	O70456	1	10	47	27	1.379	0.175	0.134
Coatomer subunit alpha;	Q8CIE6	1	6	7	5.8	1.379	0.78	0.256
E3 ubiquitin-protein ligase HUWE1;	Q7TMY8	1	17	24	5.3	1.384	0.764	0.248
Methionine synthase reductase;	Q8C1A3	1	2	5	1.7	1.39	0.133	0.127
AH receptor-interacting protein;	O08915	1	2	2	8.8	1.395	0.191	0.131
GTPase IMAP family member 4;	Q99JY3	1	4	4	13.2	1.395	0.361	0.153
Monofunctional C1-tetrahydrofolate synthase, mitochondrial;	Q3V3R1	1	3	3	2.4	1.401	0.499	0.177
STE20-like serine/threonine-protein kinase;	O54988	1	3	3	4.2	1.406	0.196	0.127
AP-2 complex subunit alpha-2;	P17427	1	7	7	10.9	1.406	0.706	0.222
14-3-3 protein epsilon;	P62259	1	13	24	34.9	1.406	0.355	0.147
Poly(rC)-binding protein 1;	P60335	1	13	25	33.7	1.411	0.244	0.130
Poly(rC)-binding protein 2;	Q61990	1	10	19	22.9	1.406	0.318	0.143
RNA-binding protein 39;	Q8VH51	1	3	4	7.6	1.417	0.929	0.278
Cytidine monophosphate-N-acetylneuraminic acid hydroxylase;	Q61419	1	3	6	6.1	1.417	0.467	0.165
Nuclease-sensitive element-binding protein 1;	P62960	1	2	3	17.1	1.422	0.833	0.250
Bifunctional protein NCOAT;	Q9EQQ9	1	3	3	3.4	1.428	0.271	0.130
T-complex protein 1 subunit epsilon;	P80316	1	12	16	17	1.428	0.319	0.136
Coatomer subunit beta';	O55029	1	3	3	5.4	1.433	0.276	0.129
Alpha-actinin-4;	P57780	1	10	10	17.8	1.433	0.637	0.193
Alpha-actinin-1;	Q7TPR4	1	3	3	10.3	0.856	0.378	0.435
Cathepsin E;	P70269	1	4	6	4.9	1.444	0.25	0.122
Eukaryotic translation initiation factor 3 subunit I;	Q9QZD9	1	8	10	25.2	1.444	0.34	0.133
T-complex protein 1 subunit theta;	P42932	1	15	18	22.4	1.449	1.056	0.294
Transportin-1;	Q8BFY9	1	6	7	6.7	1.454	0.43	0.144
COP9 signalosome complex subunit 4;	O88544	1	7	8	17.5	1.459	0.334	0.129
6-phosphofructokinase, liver type;	P12382	1	6	7	7.9	1.465	0.653	0.186
D-3-phosphoglycerate dehydrogenase;	Q61753	1	14	17	24.4	1.465	0.292	0.122
Serine hydroxymethyltransferase;	Q9CZN7	1	5	6	5.8	1.475	0.164	0.107
Protein diaphanous homolog 1;	O08808	1	3	3	4.6	1.475	0.233	0.112

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Cysteinyl-tRNA synthetase, cytoplasmic;	Q9ER72	1	6	7	8.7	1.475	0.265	0.115
Programmed cell death protein 4;	Q61823	1	6	7	21.1	1.485	0.705	0.188
Anamorsin;	Q8WTY4	1	5	7	16.5	1.491	0.255	0.111
Uncharacterized protein;	E9Q912	1	5	6	13	1.491	0.504	0.145
26S protease regulatory subunit 8;	P62196	1	5	5	18.7	1.496	0.769	0.200
Cytoplasmic dynein 1 light intermediate chain 1;	Q8R1Q8	1	4	4	14.3	1.496	0.504	0.143
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2;	Q9Z2Z9	1	3	3	8.2	1.496	0.684	0.181
Oligoribonuclease, mitochondrial;	Q9D8S4	1	2	2	5.1	1.501	0.265	0.109
Heterogeneous nuclear ribonucleoprotein Q;	Q7TMK9	1	14	18	20.1	1.501	0.44	0.131
Heterogeneous nuclear ribonucleoprotein R; Uncharacterized protein;	Q8VHM5	1	4	5	9.8	1.736	0.297	0.063
DCC-interacting protein 13-alpha;	Q8K3H0	1	3	3	4.5	1.506	0.18	0.100
60S ribosomal protein L4;	Q9D8E6	0.994	2	2	2.4	1.506	0.143	0.098
Proteasome activator complex subunit 4;	Q5SSW2	1	3	3	2.6	1.516	0.207	0.100
Cold shock domain-containing protein E1;	Q91W50	1	4	6	5.4	1.521	0.17	0.097
Histone H2A type 1;	P22752	1	3	5	20.2	1.521	0.111	0.094
Fatty acid-binding protein, epidermal;	Q05816	1	16	34	65.2	1.521	0.159	0.096
Ubiquitin-fold modifier-conjugating enzyme 1;	Q9CR09	0.999	2	3	4.8	1.521	0.079	0.093
TBC1 domain family member 9B;	Q5SVR0	1	2	2	3.3	1.526	0.244	0.100
HSPB1-associated protein 1;	Q8BK58	0.999	2	2	3.3	1.526	0.18	0.096
Suppressor of G2 allele of SKP1 homolog;	Q9CX34	1	5	5	14	1.531	0.45	0.124
Putative GTP-binding protein Parf;	Q5U3K5	0.999	2	3	5.2	1.531	0.185	0.095
POU domain, class 2, transcription factor 1;	P25425	1	2	2	3	1.546	0.365	0.109
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial;	Q9D1L0	1	2	2	23.5	1.546	0.339	0.106
Matrin-3;	Q8K310	1	5	5	6.1	1.57	0.692	0.155
Hemoglobin subunit beta-1;	P02088	1	17	136	87.8	1.57	0.143	0.085
Hemoglobin subunit beta-2;	P02089	1	16	77	83.7	1.803	0.274	0.051
Desmoglein-2;	O55111	1	2	2	3.6	1.58	0.243	0.088
Uncharacterized protein KIAA0564 homolog;	Q8CC88	1	2	2	0.7	1.599	0.227	0.084
Coatomer subunit gamma;	Q9QZE5	1	7	7	10.5	1.599	0.422	0.102
Ubiquitin-conjugating enzyme E2 O;	Q6ZPJ3	1	2	2	2.5	1.599	0.813	0.169
26S proteasome non-ATPase regulatory subunit 7;	P26516	1	8	12	28.3	1.604	0.559	0.119
Hsp90 co-chaperone Cdc37;	Q61081	1	8	11	16.9	1.604	0.259	0.084
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform;	Q7TNP2	1	8	9	11.1	1.604	0.259	0.085
Cytoplasmic dynein 1 heavy chain 1;	Q9JHU4	1	5	6	1.5	1.604	0.174	0.080
T-complex protein 1 subunit gamma;	P80318	1	6	7	12.7	1.604	0.264	0.085
Protein phosphatase inhibitor 2;	Q9DCL8	1	2	2	12.8	1.628	0.126	0.073
Transcription intermediary factor 1-beta;	Q62318	1	6	6	8.4	1.637	0.242	0.077
60S ribosomal protein L24;	Q8BP67	1	2	2	16.5	1.637	0.195	0.074
Inactive tyrosine-protein kinase 7;	Q8BKG3	1	3	4	3.4	1.637	0.342	0.085
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Q76MZ3	1	20	26	27.7	1.642	0.6	0.115
Sarcosine dehydrogenase, mitochondrial;	Q99LB7	1	3	4	5.7	1.642	0.258	0.077
Nuclear autoantigenic sperm protein;	Q99MD9	1	2	3	2.7	1.646	0.431	0.092
Phospholipase A-2-activating protein;	P27612	1	8	9	9.3	1.646	0.794	0.148

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Ribose-phosphate pyrophosphokinase 1;	Q9D7G0	1	5	5	14.8	1.646	0.642	0.121
Phosphatidylinositol transfer protein beta isoform;	P53811	1	5	5	23.2	1.655	0.163	0.069
Transitional endoplasmic reticulum ATPase;	Q01853	1	46	64	41.1	1.664	0.299	0.076
40S ribosomal protein S17;	P63276	1	4	4	40.7	1.664	0.257	0.073
5-oxoprolinase;	Q8K010	1	20	24	19.1	1.669	0.42	0.085
Caspase-1;	P29452	1	2	2	4.7	1.683	0.671	0.115
Reversion-inducing cysteine-rich protein with Kazal motifs;	Q9Z0J1	0.941	2	2	0.8	1.683	0.163	0.065
Serine hydroxymethyltransferase, cytosolic;	P50431	1	5	5	6.3	1.687	0.634	0.108
Eukaryotic initiation factor 4A-I;	P60843	1	5	6	30.5	1.696	0.523	0.092
Eukaryotic initiation factor 4A-II;	P10630	1	4	4	24.9	0.39	0.065	0.680
Ubiquitin carboxyl-terminal hydrolase 8;	Q80U87	1	3	3	2.1	1.705	0.638	0.105
Eukaryotic translation initiation factor 3 subunit F;	Q9DCH4	1	2	2	5.3	1.709	0.23	0.063
Rho GTPase-activating protein 1;	Q5FWK3	1	2	2	5.9	1.709	0.904	0.148
Sorting nexin-3;	O70492	0.993	2	3	5.7	1.718	0.465	0.080
DNA replication licensing factor MCM2;	P97310	1	2	2	2.8	1.722	0.673	0.105
Activator of 90 kDa heat shock protein ATPase homolog 1;	Q8BK64	1	4	5	14.2	1.731	0.339	0.066
Protein prune homolog;	Q8BIW1	1	3	3	8.8	1.736	0.24	0.060
Tripartite motif-containing protein 29;	Q8R2Q0	1	3	8	2.9	1.736	0.094	0.055
Calsequestrin-1;	O09165	1	5	9	11.4	1.736	0.37	0.068
Tubulin-specific chaperone E;	Q8CIV8	0.999	2	2	7.5	1.736	0.198	0.058
Ubiquitin-conjugating enzyme E2 N;	P61089	1	6	7	32.2	1.74	0.287	0.062
Serum amyloid A-4 protein;	P31532	1	2	2	14.6	1.74	0.156	0.056
Calponin-3;	Q9DAW9	1	2	2	12.4	1.848	0.246	0.045
Transportin-3;	Q6P2B1	1	8	8	7.6	1.753	0.359	0.064
Microtubule-actin cross-linking factor 1;	Q9QXZ0	1	2	2	0.8	1.753	0.635	0.093
Cytosol aminopeptidase;	Q9CPY7	1	37	63	47	1.757	0.291	0.059
40S ribosomal protein S20;	P60867	1	3	5	19.3	1.778	0.746	0.101
Proteasomal ubiquitin receptor ADRM1;	Q9JKV1	1	4	10	8.6	1.778	1.218	0.182
Sequestosome-1;	Q64337	1	2	2	11	1.778	0.549	0.077
FAS-associated factor 1;	P54731	1	2	2	3.1	1.778	0.591	0.081
General transcription factor II-I;	Q9ESZ8	1	2	2	1.7	1.782	0.197	0.051
NEDD8-conjugating enzyme Ubc12;	P61082	1	5	5	23	1.799	0.341	0.056
Sulfotransferase family cytosolic 2B member 1;	O35400	1	3	4	11.2	1.803	1.116	0.154
Fructose-1,6-bisphosphatase 1;	Q9QXD6	1	4	5	16.3	1.803	0.723	0.092
Ubiquitin-conjugating enzyme E2 K;	P61087	1	2	2	19.1	1.807	0.227	0.049
Eukaryotic translation initiation factor 4B;	Q8BGD9	0.998	2	3	2.6	1.807	0.263	0.051
T-complex protein 1 subunit beta;	P80314	1	15	18	31	1.816	0.836	0.105
Programmed cell death protein 6;	P12815	1	5	6	15.7	1.82	0.861	0.108
Apolipoprotein E;	P08226	1	6	8	17.4	1.82	0.407	0.057
26S proteasome non-ATPase regulatory subunit 11;	Q8BG32	1	17	26	31	1.82	0.217	0.047
Bifunctional aminoacyl-tRNA synthetase;	Q8CGC7	1	23	28	17.1	1.824	0.917	0.115
Calmodulin;	P62204	1	2	3	6	1.824	0.386	0.055
Ribonuclease T2;	Q9CQ01	1	5	6	19.3	1.848	0.205	0.044

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Uncharacterized protein;	E9PYU6	1	3	3	1.2	1.848	0.755	0.086
Protein phosphatase 2, regulatory subunit B (B56), delta isoform; Protein phosphatase 2, regulatory subunit B (B56), delta isoform, isoform CRA_b; Protein phosphatase 2A B56delta regulatory subunit; Uncharacterized protein;	Q91V89	1	2	2	5.7	1.848	0.447	0.055
Heterogeneous nuclear ribonucleoprotein M;	Q9D0E1	1	3	3	6.7	1.848	0.395	0.052
Putative RNA-binding protein 3;	O89086	1	2	2	14.1	1.852	0.19	0.042
Coatomer subunit beta;	Q9JIF7	1	4	4	5.7	1.86	0.62	0.068
Nucleolysin TIA-1;	P52912	1	2	3	9.4	1.868	0.353	0.047
Phosphatidylinositol-binding clathrin assembly protein;	Q7M6Y3	1	5	6	8.2	1.872	0.399	0.050
Glutaredoxin-3;	Q9CQM9	1	9	12	26.1	1.872	0.348	0.047
Golgi apparatus protein 1;	Q61543	1	2	2	2.7	1.88	0.71	0.074
Uncharacterized protein C6orf132 homolog;	Q91Z58	1	3	3	5.1	1.884	0.495	0.054
Arginyl-tRNA synthetase, cytoplasmic;	Q9D0I9	1	12	17	16.2	1.891	0.209	0.039
26S proteasome non-ATPase regulatory subunit 13;	Q9WVJ2	1	8	10	26.1	1.891	0.377	0.046
6-phosphofructokinase type C;	Q9WUA3	1	8	10	13.8	1.895	0.423	0.047
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;	P31230	1	6	12	25.5	1.899	0.285	0.040
Fibrillin 1; Uncharacterized protein;	A2AQ53	1	18	20	9.2	1.915	0.853	0.084
Cadherin-1;	P09803	1	6	8	6.9	1.918	0.325	0.040
Poly(U)-specific endoribonuclease;	Q3V188	1	3	3	9.7	1.922	0.806	0.076
Phosphatase and actin regulator 4;	Q501J7	1	4	4	8.6	1.93	0.729	0.067
Ribonucleoside-diphosphate reductase large subunit;	P07742	1	2	2	1.5	1.934	0.258	0.036
26S protease regulatory subunit 4;	P62192	1	6	8	13.9	1.945	0.172	0.032
Angio-associated migratory protein; Uncharacterized protein;	Q3TJ22	1	2	2	3	1.949	0.485	0.045
Ubiquitin-protein ligase E3A;	O08759	1	2	2	1	1.952	0.232	0.033
Protein FAM49A;	Q8BHZ0	1	6	6	17.6	1.96	0.605	0.051
26S proteasome non-ATPase regulatory subunit 3;	P14685	1	13	15	22.3	1.978	0.597	0.048
T-complex protein 1 subunit zeta;	P80317	1	8	10	15.3	1.982	1.159	0.108
CLIP-associating protein 1;	Q80TV8	0.974	2	2	1.8	1.982	0.321	0.033
SUMO-activating enzyme subunit 2;	Q9Z1F9	1	7	7	13.2	1.986	0.742	0.059
Uncharacterized protein ENSP00000244321 homolog;	Q9CQD7	1	2	4	6.1	1.993	0.2	0.029
Small ubiquitin-related modifier 2;	P61957	1	2	2	16.9	1.993	0.17	0.028
Transcription factor BTF3;	Q64152	1	3	4	23	1.996	0.235	0.029
26S proteasome non-ATPase regulatory subunit 1;	Q3TXS7	1	18	24	23	1.996	1.731	0.194
Eukaryotic translation initiation factor 2 subunit 3, X-linked;	Q9Z0N1	1	3	3	8.5	2.007	0.18	0.027
Synaptobrevin homolog YKT6;	Q9CQW1	1	5	5	26.3	2.018	0.578	0.042
Involucrin;	P48997	1	4	4	12.2	2.025	0.199	0.026
High mobility group nucleosome-binding domain-containing protein 5;	Q9JL35	1	2	2	3.7	2.036	0.179	0.025
Glycine N-methyltransferase;	Q9QXF8	1	10	12	27.6	2.036	0.596	0.040
26S proteasome non-ATPase regulatory subunit 2;	Q8VDM4	1	21	28	18.9	2.036	0.452	0.033
Peroxisomal carnitine O-octanoyltransferase;	Q9DC50	1	5	5	3.9	2.046	0.996	0.073
Phosphoribosyl pyrophosphate synthase-associated protein 2;	Q8R574	1	2	2	10.6	2.057	0.232	0.025
Mitogen-activated protein kinase kinase kinase MLT;	Q9ESL4	1	2	2	1.9	2.057	0.237	0.025
Tubulin-specific chaperone D;	Q8BYA0	1	2	2	2.8	2.057	0.583	0.037

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Lipopolysaccharide-responsive and beige-like anchor protein;	Q9ESE1	0.99	2	3	1.4	2.057	0.816	0.054
Nuclear migration protein nudC;	O35685	1	3	4	6	2.064	0.489	0.032
Pyridoxal-dependent decarboxylase domain-containing protein 1;	Q99K01	1	3	3	5.7	2.067	0.469	0.031
Adenylate kinase isoenzyme 4, mitochondrial;	Q9WUR9	0.999	2	2	16.3	2.067	0.306	0.026
Eukaryotic translation initiation factor 3 subunit H;	Q91WK2	1	5	13	10.2	2.074	0.488	0.031
Dihydrofolate reductase;	P00375	1	3	4	13.9	2.077	0.207	0.023
Desmocollin-3;	P55850	0.996	2	2	4.8	2.077	1.088	0.077
40S ribosomal protein S9;	Q6ZWN5	1	4	4	17.5	2.084	1.165	0.085
Importin-5;	Q8BKC5	1	11	12	11.4	2.084	1.155	0.083
Serine/threonine-protein phosphatase 6 regulatory subunit 1;	Q7TSI3	1	2	2	4.8	2.094	1.785	0.169
40S ribosomal protein S3a;	P97351	1	5	6	18.6	2.094	1.456	0.120
DNA replication licensing factor MCM3;	P25206	0.981	2	2	3.4	2.094	0.324	0.024
Cornifin-A;	Q62266	1	7	10	37.5	2.134	0.365	0.022
Treacle protein;	O08784	1	2	3	3.6	2.138	0.355	0.022
NmrA-like family domain-containing protein 1;	Q8K2T1	1	3	3	14.4	2.144	0.364	0.022
Cartilage-associated protein;	Q9CYD3	1	2	2	2	2.144	0.291	0.020
Transcriptional repressor p66 alpha;	Q8CHY6	0.984	2	2	5.1	2.154	0.276	0.019
26S protease regulatory subunit 6B;	P54775	1	8	11	11.5	2.157	0.295	0.019
Chondroitin sulfate proteoglycan 4;	Q8VHY0	1	3	3	2.1	2.173	0.747	0.035
T-complex protein 1 subunit eta;	P80313	1	8	9	11.9	2.176	0.895	0.044
26S proteasome non-ATPase regulatory subunit 5;	Q8BJY1	1	7	7	17.9	2.198	0.407	0.019
Caspase-14;	O89094	1	10	12	22.6	2.205	0.823	0.035
26S protease regulatory subunit 10B;	P62334	1	14	20	25.7	2.205	0.493	0.021
Rho-associated protein kinase 1;	P70335	1	3	3	2.2	2.217	0.486	0.020
Eif2b3 protein; Uncharacterized protein;	A4FUS0	1	3	3	14	2.22	0.853	0.036
4F2 cell-surface antigen heavy chain;	P10852	1	6	9	7	2.223	0.505	0.020
Poly(A) polymerase alpha;	Q61183	1	2	2	5	2.245	0.677	0.025
Kinesin-1 heavy chain;	Q61768	1	13	16	12	2.257	0.269	0.014
Protein unc-45 homolog B;	Q8CGY6	1	3	3	3.7	2.26	0.316	0.014
Serine/threonine-protein phosphatase 4 regulatory subunit 2;	Q0VGB7	1	2	2	7.9	2.263	0.49	0.018
Clathrin heavy chain 1;	Q68FD5	1	29	38	21.1	2.266	1.018	0.041
Uridine 5'-monophosphate synthase;	P13439	1	3	3	6.7	2.275	0.71	0.024
Dual specificity mitogen-activated protein kinase kinase 4;	P47809	1	2	2	7.1	2.278	0.329	0.014
Ribonucleoprotein PTB-binding 1;	Q9CW46	1	3	3	7.1	2.284	0.521	0.017
Nucleophosmin;	Q61937	1	3	3	13.2	2.287	0.351	0.014
T-complex protein 1 subunit delta;	P80315	1	11	13	16.9	2.29	0.304	0.013
Leucine-rich PPR motif-containing protein, mitochondrial;	Q6PB66	1	9	9	9.1	2.29	1.719	0.104
Vacuolar protein sorting-associated protein 4B;	P46467	1	4	4	15.1	2.313	0.526	0.016
ATP-dependent RNA helicase DDX19A;	Q61655	1	2	3	2.1	2.322	0.237	0.011
Nucleosome assembly protein 1-like 4;	Q78ZA7	1	6	6	10.1	2.325	1.021	0.035
Inosine triphosphate pyrophosphatase;	Q9D892	1	5	5	21.2	2.325	0.274	0.011
Importin subunit beta-1;	P70168	1	11	15	11.6	2.339	0.837	0.024
Apolipoprotein C-III;	P33622	1	3	12	19.2	2.350	0.405	0.012

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Argininosuccinate synthase;	P16460	1	5	7	10.7	2.381	0.795	0.020
Tubulin alpha-1C chain;	P68373	1	12	26	44.3	2.384	0.233	0.009
Tubulin alpha-4A chain;	P68368	1	9	11	40	2.032	0.656	0.045
MARCKS-related protein;	P28667	1	6	8	14	2.398	0.296	0.009
Protein KIAA1967 homolog;	Q8VDP4	1	5	5	5.5	2.417	0.991	0.025
Importin-7;	Q9EPL8	1	7	8	9.2	2.436	1.175	0.032
General vesicular transport factor p115;	Q9Z1Z0	1	5	8	5.4	2.472	0.646	0.011
Serine/threonine-protein phosphatase 6 regulatory subunit 3;	Q922D4	1	2	4	1.4	2.493	0.297	0.007
Ubiquitin-conjugating enzyme E2 Z;	Q3UE37	0.998	2	2	5.1	2.493	0.562	0.009
Cytosolic 5'-nucleotidase III-like protein;	Q3UFY7	1	2	3	4.8	2.498	0.221	0.006
Prostaglandin E synthase 3;	Q9R0Q7	1	4	4	28.5	2.506	0.154	0.006
Nucleosome assembly protein 1-like 1;	P28656	1	7	8	14.6	2.524	0.773	0.012
Protein FAM206A;	Q80ZQ9	1	2	2	37.8	2.524	0.241	0.006
Proteasome-associated protein ECM29 homolog;	Q6PDI5	1	4	4	3.8	2.536	1.106	0.021
Metastasis-associated protein MTA2;	Q9R190	1	4	7	5.4	2.570	1.376	0.031
Stathmin;	P54227	1	5	7	31.4	2.585	0.840	0.011
Leucyl-tRNA synthetase, cytoplasmic;	Q8BMJ2	1	11	16	14.4	2.602	2.431	0.108
Glutamate--cysteine ligase regulatory subunit;	O09172	1	2	2	11.7	2.606	0.689	0.008
DNA-(apurinic or apyrimidinic site) lyase;	P28352	1	2	2	15.3	2.618	0.307	0.004
Vacuolar protein sorting-associated protein 13C;	Q8BX70	0.999	2	2	1.1	2.637	1.217	0.019
Eukaryotic translation initiation factor 3 subunit E;	P60229	1	5	5	10.3	2.676	0.557	0.005
Exportin-2;	Q9ERK4	1	7	7	7.1	2.689	0.359	0.004
Thiomorpholine-carboxylate dehydrogenase;	O54983	1	9	17	24	2.694	0.833	0.007
Eukaryotic translation initiation factor 4 gamma 1;	Q6NZJ6	1	7	7	6.3	2.751	0.993	0.008
40S ribosomal protein S18;	P62270	1	3	3	21.1	2.778	0.316	0.002
Cullin-4B;	A2A432	1	5	6	8	2.785	0.550	0.003
Heat shock protein 75 kDa, mitochondrial;	Q9CQN1	1	6	6	15.2	2.846	0.831	0.004
AP-2 complex subunit mu;	P84091	1	2	2	5.8	2.862	0.480	0.002
Protein-arginine deiminase type-3;	Q9Z184	1	2	2	4.1	2.884	0.379	0.002
Carboxypeptidase M;	Q80V42	1	2	2	6.5	2.888	0.363	0.002
Gasdermin-A;	Q9EST1	1	11	18	26.7	2.897	1.295	0.009
Tubulin beta-5 chain;	P99024	1	6	16	56.1	2.899	0.268	0.001
Tubulin beta-2A chain;	Q7TMM9	1	3	3	52.4	1.922	0.872	0.084
RING finger protein 114;	Q9ET26	1	2	2	8.4	2.934	0.338	0.001
40S ribosomal protein S27;	Q6ZWU9	0.999	2	2	13.1	2.949	0.837	0.003
T-complex protein 1 subunit alpha;	P11983	1	10	11	14.7	2.973	0.564	0.002
CTP synthase 1;	P70698	1	7	8	18.4	2.976	0.718	0.002
Protein-glutamine gamma-glutamyltransferase E;	Q08189	1	11	11	19.9	3.025	1.015	0.003
Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase, isoform CRA_c; Uncharacterized protein;	B2RQC6	1	2	3	4.6	3.030	1.228	0.005
Acetyl-CoA carboxylase 1;	Q5SWU9	1	4	5	2.4	3.067	1.241	0.004
Serum paraoxonase/arylesterase 1;	P52430	1	2	2	8.5	3.086	0.702	0.001

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Glutaminyl-tRNA synthetase; Uncharacterized protein;	Q8BML9	1	8	10	15.6	3.129	1.774	0.010
Uncharacterized protein;	D3YYM6	1	3	5	8.2	3.141	0.434	0.001
Uncharacterized protein;	D3YUU6	1	3	3	11.9	3.146	0.796	0.001
40S ribosomal protein S7;	P62082	1	4	4	26	3.176	0.773	0.001
Uncharacterized protein;	E9Q2E9	1	3	4	15.3	3.233	0.409	0.000
Cytosolic phospholipase A2 beta;	P0C871	1	2	2	3.6	3.246	0.527	0.000
40S ribosomal protein S3;	P62908	1	8	9	34.2	3.406	1.452	0.002
Translation initiation factor eIF-2B subunit alpha;	Q99LC8	1	2	3	7.5	3.410	0.430	0.000
40S ribosomal protein S15a;	P62245	1	4	4	40	3.442	0.940	0.000
Constitutive coactivator of PPAR-gamma-like protein 1;	Q6A0A9	1	3	3	4.6	3.503	1.381	0.001
40S ribosomal protein S14;	P62264	1	3	5	15.2	3.608	0.462	0.000
Cadherin-3;	P10287	0.999	2	2	1.7	3.732	1.494	0.000
Trichohyalin-like protein 1;	Q9D3P1	1	14	14	28.1	3.782	1.421	0.000
Eukaryotic translation initiation factor 3 subunit C;	Q8R1B4	1	3	5	4	3.806	1.107	0.000
Isoleucyl-tRNA synthetase, cytoplasmic;	Q8BU30	1	4	4	3.6	3.977	1.300	0.000
E3 ubiquitin-protein ligase UBR4;	A2AN08	1	4	5	1.6	4.001	0.685	0.000
40S ribosomal protein S11;	P62281	1	3	3	18.4	4.335	0.638	0.000
40S ribosomal protein S4, X isoform;	P62702	1	5	5	17.6	4.475	1.048	0.000
Uncharacterized protein;	E9QNN1	1	4	6	3.3	4.591	1.271	0.000
40S ribosomal protein S16;	P14131	1	3	3	20.5	4.702	1.966	0.000
Protein S100-A3;	P62818	1	3	3	24.8	4.943	1.489	0.000
40S ribosomal protein S13;	P62301	1	3	3	19.3	5.042	2.604	0.000
L-dopachrome tautomerase;	P29812	1	2	2	7.5	5.100	0.833	0.000
40S ribosomal protein S6;	P62754	1	2	3	9.6	5.140	2.338	0.000
Proline-rich protein 9;	Q8BV84	0.999	2	2	26.7	5.459	1.754	0.000
HIRA-interacting protein 3;	Q8BLH7	1	4	6	5.5	7.316	3.378	0.000
Transcriptional activator protein Pur-beta;	O35295	1	2	2	6.5	9.727	0.469	0.000
Eukaryotic translation initiation factor 3 subunit A;	P23116	1	2	2	3.8	9.727	0.469	0.000
Endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 4; Lysophosphatidic acid receptor 2; Uncharacterized protein;	Q6P290	0.954	2	2	6.3	9.727	0.469	0.000