Table S4: List of all identified and quantified proteins in the quantitative proteome comparision of skin lysates wt and *Ctsl*$^{-/-}$ (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 L1;	P06797	1	3	3	12.9	-6,644*	-0.001	0.000
PEST proteolytic signal-containing nuclear protein;	Q6P8I4	0.998	2	3	12.9	-6.644	-0.001	0.000
Probable tRNA (uracil-O(2)-)-methyltransferase;	Q9D2Q2	0.984	2	2	2.7	-6.644	-0.001	0.000
Collagen alpha-1(XIV) chain;	Q80X19	1	3	4	1.6	-5.644	-2.822	0.000
Synaptojanin-1;	Q8CHC4	1	3	4	3.9	-5.644	-2.822	0.000
Pyrroline-5-carboxylate reductase 1, mitochondrial;	Q922W5	1	3	4	22.2	-3.184	-3.184	0.050
Apolipoprotein A-IV;	P06728	1	15	24	34.2	-2.837	-1.216	0.006
Betaine--homocysteine S-methyltransferase 1;	O35490	1	12	16	27.5	-2.837	-2.432	0.065
Dimethylglycine dehydrogenase, mitochondrial;	Q9DBT9	0.999	2	3	2.1	-2.556	-0.15	0.002
Uncharacterized protein;	D3YXF5	1	10	12	33.2	-2.474	-2.062	0.084
4-hydroxyphenylpyruvate dioxygenase;	P49429	1	3	3	11.7	-2.474	-1.924	0.077
Apolipoprotein A-I;	Q00623	1	14	30	27.7	-2.252	-0.322	0.007
Arginase-1;	Q61176	1	12	14	25.4	-2.252	-0.429	0.010
Carbamoyl-phosphate synthase [ammonia], mitochondrial;	Q8C196	1	35	39	16.4	-2.252	-1.501	0.076
Fatty acid-binding protein, liver;	P12710	1	9	14	59.1	-2.184	-1.092	0.048
Fructose-bisphosphate aldolase B;	Q91Y97	1	10	11	28.8	-2.184	-0.596	0.016
Leukemia inhibitory factor receptor;	P42703	1	9	9	8.2	-2.059	-0.601	0.023
Ig heavy chain V region 441;	P01806	1	2	2	13.8	-2.059	-0.343	0.017
3-hydroxyanthranilate 3,4-dioxygenase;	Q78JT3	0.996	2	2	10.8	-2	-0.32	0.019
Regucalcin;	Q64374	1	6	7	17.1	-1.943	-0.598	0.035
Apolipoprotein A-II;	P09813	1	2	4	9.8	-1.889	-0.28	0.026
Estradiol 17 beta-dehydrogenase 5;	P70694	1	2	2	6.8	-1.889	-0.14	0.023
Alpha-2-antiplasmin;	Q61247	1	9	12	13	-1.889	-1.679	0.220
Fructose-1,6-bisphosphatase 1;	Q9QXD6	1	2	2	5.3	-1.889	-0.7	0.050
Dual specificity protein phosphatase 23;	Q6NT99	1	5	5	22	-1.837	-0.197	0.026
Glycine N-methyltransferase;	Q9QXF8	1	10	13	28.3	-1.837	-1.115	0.123
Uncharacterized protein;	E9Q6D8	1	5	5	7.5	-1.837	-0.722	0.063
Sodium/potassium-transporting ATPase subunit beta-1;	P14094	1	3	4	6.6	-1.786	-1.724	0.265
Protein phosphatase 1 regulatory subunit 3A;	Q99MR9	1	11	11	10	-1.737	-1.274	0.190
Carboxypeptidase N catalytic chain;	Q9JJN5	1	4	4	4.8	-1.737	-0.29	0.046
SPARC;	P07214	1	8	9	27.2	-1.737	-0.984	0.137
Apolipoprotein E;	P08226	1	5	6	15.4	-1.737	-1.679	0.280
Oxidation resistance protein 1;	Q4KMM3	1	5	5	9.6	-1.737	-0.695	0.089
Haptoglobin;	Q61646	1	6	7	11.8	-1.69	-0.491	0.071
Aldose 1-epimerase;	Q8K157	1	3	3	8.5	-1.69	-0.654	0.095
Beta-2-glycoprotein 1;	Q01339	1	11	13	23.8	-1.644	-0.257	0.055
Serpin H1;	P19324	1	18	32	25.9	-1.599	-0.775	0.138
Sarcalumenin;	Q7TQ48	1	6	6	8.7	-1.599	-0.775	0.136
UDP-N-acetylhexosamine pyrophosphorylase;	Q91YN5	1	7	9	13.6	-1.599	-0.727	0.125
Major urinary protein 2;	P11589	1	7	19	47.8	-1.599	-0.242	0.060

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
Major urinary protein 8; Novel member of the major urinary protein (Mup) gene family; Uncharacterized protein;	A2BIN1	1	7	16	49.4	-1.943	-0.224	0.020
Uncharacterized protein;	E9Q4Y1	1	2	2	4.6	-1.599	-0.242	0.058
C-type lectin domain family 11 member A;	O88200	1	2	2	8.5	-1.556	-0.275	0.071
Ig kappa chain V-II region 26-10;	P01631	1	4	4	38.9	-1.556	-0.961	0.199
Serum amyloid A-4 protein;	P31532	1	2	2	8.5	-1.515	-0.13	0.070
Nucleobindin-2;	P81117	1	3	3	4.8	-1.474	-0.164	0.076
Collagen alpha-2(I) chain;	Q01149	1	27	49	14.4	-1.474	-0.164	0.080
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial;	Q3UV70	1	4	4	7.4	-1.474	-0.368	0.099
A-kinase anchor protein 12;	Q9WTQ5	1	46	54	21.6	-1.474	-0.491	0.119
Tetranectin;	P43025	1	9	10	38.1	-1.434	-0.814	0.211
Retinal dehydrogenase 1;	P24549	1	25	44	32.9	-1.434	-1.046	0.286
Pigment epithelium-derived factor;	P97298	1	10	15	20.1	-1.434	-0.581	0.154
Hippocalcin-like protein 1;	P62748	1	2	2	11.9	-1.434	-0.233	0.096
Taperin;	A2AI08	0.913	2	3	1.9	-1.434	-1.318	0.355
Cardiomyopathy-associated protein 5;	Q70KF4	1	6	6	1.7	-1.396	-0.551	0.163
Glutathione S-transferase A3;	P30115	1	4	4	15.8	-1.396	-0.257	0.108
Four and a half LIM domains 3; Uncharacterized protein;	A6H6N4	1	2	2	6.6	-1.358	-0.244	0.115
Aldehyde oxidase;	O54754	0.995	2	2	2.1	-1.358	-0.627	0.198
Collagen alpha-1(III) chain;	P08121	1	11	14	6.3	-1.322	-0.132	0.108
Hydroxymethylglutaryl-CoA synthase, mitochondrial;	P54869	1	7	8	9.8	-1.322	-0.231	0.120
UPF0556 protein C19orf10 homolog;	Q9CPT4	1	3	3	12.7	-1.322	-0.595	0.207
Collagen alpha-1(I) chain;	P11087	1	31	57	19	-1.322	-0.264	0.128
Peptidyl-prolyl cis-trans isomerase FKBP7;	O54998	1	5	5	17.4	-1.286	-0.22	0.130
Acyl-coenzyme A thioesterase 13;	Q9CQR4	1	6	8	25	-1.286	-0.282	0.142
Heat shock protein beta-3;	Q9QZ57	1	4	4	16.2	-1.286	-0.596	0.218
Novel anaphylotoxin-like domain containing protein; Uncharacterized protein;	A2AS37	1	2	2	2.9	-1.286	-0.188	0.127
Retinol-binding protein 4;	Q00724	1	4	8	18.9	-1.252	-0.715	0.279
WD repeat, SAM and U-box domain-containing protein 1;	Q9D0I6	1	2	2	5	-1.252	-0.209	0.147
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial;	Q9Z2I8	1	12	14	24.6	-1.252	-1.222	0.446
Disabled homolog 2;	P98078	1	4	7	9.6	-1.252	-0.507	0.215
Secernin-3;	Q3TMH2	1	4	5	12.2	-1.252	-0.149	0.130
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	Q99LD8	1	14	21	35.1	-1.252	-0.417	0.188
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	Q9CWS0	1	2	2	11.9	-0.089	-0.012	0.912
Mitochondrial 10-formyltetrahydrofolate dehydrogenase;	Q8K009	1	9	9	12.2	-1.218	-0.595	0.260
Adenylate kinase isoenzyme 1;	Q9R0Y5	1	18	53	57.7	-1.218	-0.312	0.183
Hematopoietic progenitor cell antigen CD34;	Q64314	1	5	5	11.8	-1.184	-0.161	0.160
UPF0366 protein C11orf67 homolog;	Q8R0P4	1	2	4	13.1	-1.184	-0.242	0.181
EH domain-containing protein 3;	Q9QXY6	1	3	3	5.6	-1.184	-0.646	0.305
Liver carboxylesterase N;	P23953	1	23	46	26	-1.184	-0.404	0.216
Carboxylesterase 3;	Q8VCT4	1	22	36	25.3	-0.234	-0.08	0.810
Uncharacterized protein;	D3Z5G7	1	13	27	18.7	-0.578	-0.06	0.492
N-acetylmuramoyl-L-alanine amidase;	Q8VCS0	1	4	8	7.9	-1.184	-0.054	0.155

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
Protein DJ-1;	Q99LX0	1	12	23	48	-1.184	-0.404	0.218
EH domain-binding protein 1-like protein 1;	Q99MS7	1	5	5	3.6	-1.184	-0.215	0.172
Creatine kinase M-type;	P07310	1	46	1074	60.4	-1.152	-0.23	0.187
Myosin light chain kinase 2, skeletal/cardiac muscle;	Q8VCR8	1	15	16	20.7	-1.152	-0.41	0.236
Ig gamma-2A chain C region, A allele;	P01863	1	8	15	29.1	-1.152	-0.435	0.241
4-aminobutyrate aminotransferase, mitochondrial;	P61922	1	2	2	9.2	-1.152	-0.179	0.176
Ig kappa chain V-III region PC 2880/PC 1229;	P01654	1	4	4	16.2	-1.12	-0.049	0.175
Cofilin-2;	P45591	1	9	27	31.9	-1.12	-0.243	0.205
Alpha-1-syntrophin;	Q61234	1	3	3	6.2	-1.12	-0.122	0.182
Smoothelin-like protein 2;	Q8CI12	1	3	3	4.7	-1.12	-0.536	0.294
D-dopachrome decarboxylase;	O35215	1	9	10	51.7	-1.089	-0.07	0.183
Ig gamma-1 chain C region secreted form;	P01868	1	13	22	42.3	-1.089	-0.07	0.183
Cystatin-C;	P21460	1	2	2	10.8	-1.089	-0.07	0.190
Protein AMBP;	Q07456	1	7	7	10	-1.089	-0.209	0.209
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1;	Q3TW96	1	19	25	28.6	-1.089	-0.973	0.476
Aldo-keto reductase family 1 member C13;	Q8VC28	1	2	2	6.5	-1.089	-0.185	0.206
Putative hydroxypyruvate isomerase;	Q8R1F5	1	3	3	11.6	-1.089	-0.487	0.295
Voltage-dependent L-type calcium channel subunit beta-1;	Q8R3Z5	1	2	2	6.8	-1.089	-0.162	0.195
SH3 and PX domain-containing protein 2B;	A2AAY5	1	2	2	2.9	-1.089	-0.463	0.280
Complement C4-B;	P01029	1	27	36	13.2	-1.059	-0.905	0.474
Programmed cell death protein 6;	P12815	1	6	10	22	-1.059	-0.86	0.458
Creatine kinase B-type;	Q04447	1	27	54	43.3	-1.059	-0.419	0.286
Leucine-rich HEV glycoprotein; Leucine-rich alpha-2-glycoprotein; Leucine-rich alpha-2-glycoprotein 1; Uncharacterized protein;	Q91XL1	1	4	5	7.9	-1.059	-0.132	0.204
Uncharacterized protein;	E9PV38	1	15	21	20.4	-1.059	-0.243	0.230
Phosphoglycerate mutase 2;	O70250	1	24	145	45.1	-1.029	-0.525	0.348
Desmin;	P31001	1	2	2	3.4	-1.029	-0.168	0.226
Phosphatidylinositol transfer protein beta isoform;	P53811	1	6	7	28.4	-1.029	-0.483	0.334
Epidermal growth factor receptor;	Q01279	1	12	21	14.6	-1.029	-0.126	0.225
Complement factor I;	Q61129	1	11	16	13.6	-1.029	-0.315	0.271
Heat shock protein beta-2;	Q99PR8	1	6	8	20.9	-1.029	-0.084	0.219
Sec24 related gene family, member D (S. cerevisiae); Uncharacterized protein;	Q6NXL1	1	11	12	9.7	-1.029	-0.441	0.321
Selenium-binding protein 1;	P17563	1	36	55	49.6	-1.029	-0.504	0.349
Plasma protease C1 inhibitor;	P97290	1	10	15	19.4	-1.029	-0.378	0.293
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial;	Q8BH04	1	8	8	13.6	-1.029	-0.378	0.299
Glycine cleavage system H protein, mitochondrial;	Q91WK5	1	4	4	17.6	-1.029	-0.357	0.285
NEDD4-binding protein 1;	Q6A037	1	3	3	3.9	-1.029	-0.105	0.214
Phosphorylase b kinase regulatory subunit beta;	Q7TSH2	0.998	2	2	2.9	-1.029	-0.588	0.381
Ig mu chain C region secreted form;	P01872	1	10	13	15.4	-1	-0.2	0.250
Transthyretin;	P07309	1	11	38	46.3	-1	-0.3	0.277
Ceruloplasmin;	Q61147	1	51	71	36.8	-1	-0.44	0.341
Protein phosphatase 1F;	Q8CGA0	1	3	3	6.2	-1	-0.42	0.327
Acylpyruvase FAHD1, mitochondrial;	Q8R0F8	1	3	3	19.8	-1	-0.16	0.238

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
Galectin-3-binding protein;	Q07797	1	4	4	4.5	-1	-0.2	0.255
Glyceraldehyde-3-phosphate dehydrogenase;	E9QAC7	1	9	91	59.2	-1	-0.14	0.242
Ig heavy chain V region 108A;	P01758	1	2	2	12.8	-1	-0.04	0.223
Arachidonate 12-lipoxygenase, leukocyte-type;	P39654	1	2	2	3	-0.971	-0.209	0.267
Cyclin-dependent kinase 5;	P49615	1	2	2	2.7	-0.971	-0.095	0.243
TBC1 domain family member 9B;	Q5SVR0	1	3	3	3	-0.971	-0.171	0.259
Steroid receptor RNA activator 1;	Q80VJ2	1	2	3	7.8	-0.971	-0.095	0.243
Microfibril-associated glycoprotein 4;	Q9D1H9	1	4	6	7	-0.971	-0.209	0.274
Ahnak protein; MCG17833, isoform CRA_b; Uncharacterized protein;	Q8R2L7	1	2	2	43.9	-0.971	-0.133	0.255
Alpha-1-antitrypsin 1-1;	P07758	1	14	61	42.5	-0.971	-0.076	0.240
Alpha-1-antitrypsin 1-2;	P22599	1	11	29	41.4	-0.889	-0.148	0.293
Alpha-1-antitrypsin 1-4;	Q00897	1	9	14	39.7	-0.578	-0.267	0.590
Thiosulfate sulfurtransferase;	P52196	1	13	15	35	-0.971	-0.095	0.250
Actin, alpha skeletal muscle;	P68134	1	6	6	65.8	-0.971	-0.495	0.378
Phosphotriesterase-related protein;	Q60866	1	5	5	10.9	-0.971	-0.19	0.271
Alpha-2-macroglobulin;	Q61838	1	90	187	38.4	-0.971	-0.343	0.313
Haloacid dehalogenase-like hydrolase domain-containing protein 2;	Q3UGR5	1	8	15	16.2	-0.943	-0.236	0.290
Interleukin-1 receptor accessory protein;	Q61730	1	5	5	7.2	-0.943	-0.127	0.262
Probable fructose-2,6-bisphosphatase TIGAR;	Q8BZA9	1	8	8	25.7	-0.943	-0.308	0.312
UTP--glucose-1-phosphate uridylyltransferase;	Q91ZJ5	1	41	69	43.5	-0.943	-0.272	0.303
ES1 protein homolog, mitochondrial;	Q9D172	1	10	11	31.2	-0.943	-0.218	0.290
Perilipin-3;	Q9DBG5	1	4	4	9.6	-0.943	-0.834	0.535
Carboxypeptidase B2;	Q9JHH6	1	5	5	11.8	-0.943	-0.127	0.264
Kelch repeat and BTB (POZ) domain containing 10; MCG12931; Uncharacterized protein;	A2AUC9	1	11	11	9.6	-0.943	-0.272	0.303
Nascent polypeptide-associated complex subunit alpha, muscle-specific form;	P70670	1	57	74	25.5	-0.943	-0.435	0.376
Peptidyl-prolyl cis-trans isomerase FKBP10;	Q61576	1	13	20	14.6	-0.943	-0.363	0.338
Protein Noxp20;	Q9D281	1	6	6	6.3	-0.943	-0.326	0.326
3-alpha-hydroxysteroid dehydrogenase type 1; Aldo-keto reductase family 1, member C14; Aldo-keto reductase family 1, member C14, isoform CRA_b; Uncharacterized protein;	Q91WT7	0.995	2	2	3.1	-0.943	-0.109	0.261
Inter-alpha-trypsin inhibitor heavy chain H1;	Q61702	1	8	8	8.9	-0.916	-0.328	0.340
Complement component C8 alpha chain;	Q8K182	1	11	11	17.9	-0.916	-0.294	0.335
Glutathione peroxidase 7;	Q99LJ6	1	4	4	16.1	-0.916	-0.173	0.293
Phosphoacetylglucosamine mutase;	Q9CYR6	1	5	7	9.8	-0.916	-0.277	0.321
Microtubule-associated protein;	F7CK47	1	7	9	6.4	-0.916	-0.156	0.288
Fructose-bisphosphate aldolase A;	P05064	1	44	652	79.1	-0.916	-0.277	0.328
Fructose-bisphosphate aldolase C;	P05063	1	2	2	19.6	0.651	0.104	0.443
Carnitine O-palmitoyltransferase 2, mitochondrial;	P52825	1	7	8	10.3	-0.916	-0.242	0.314
Protein transport protein Sec23A;	Q01405	1	11	13	16.7	-0.916	-0.225	0.307
Protein transport protein Sec23B;	Q9D662	1	3	3	3.9	0.322	0.033	0.698
Abhydrolase domain-containing protein 14B;	Q8VCR7	1	7	8	27.1	-0.916	-0.259	0.314
3-mercaptopyruvate sulfurtransferase;	Q99J99	1	15	24	40.1	-0.916	-0.277	0.322

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 C11orf73 homolog;	Q9DD02	1	3	3	10.2	-0.916	-0.121	0.272
EF hand domain containing 2; Efhd2 protein; Uncharacterized protein;	Q8C845	1	5	5	15	-0.916	-0.363	0.352
Uncharacterized protein;	Q9DBD0	1	20	27	21.9	-0.916	-0.121	0.277
Vitronectin;	P29788	0.999	3	3	6.7	-0.916	-0.311	0.343
Protein S100-A6;	P14069	0.998	3	7	16.9	-0.916	-0.242	0.314
Reticulon-2;	O70622	1	3	3	7.2	-0.889	-0.132	0.296
Putative hydrolase RBBP9;	O88851	1	2	2	15.6	-0.889	-0.181	0.310
Heat shock protein beta-6;	Q5EBG6	1	12	16	29	-0.889	-0.115	0.287
UPF0586 protein C9orf41 homolog;	Q80UY1	1	6	7	11	-0.889	-0.461	0.427
Sulfhydryl oxidase 1;	Q8BND5	1	9	9	13	-0.889	-0.165	0.298
Synaptopodin-2;	Q91YE8	1	2	2	1.3	-0.889	-0.099	0.282
Cell adhesion molecule 3;	Q99N28	1	3	4	10.7	-0.889	-0.099	0.291
Calcium-regulated heat stable protein 1;	Q9CR86	1	5	5	18.2	-0.889	-0.346	0.366
Carboxypeptidase N subunit 2;	Q9DBB9	1	9	9	17.4	-0.889	-0.181	0.305
Plexin domain-containing protein 2;	Q9DC11	1	2	2	2.5	-0.889	-0.115	0.294
Microtubule-associated protein tau;	P10637	1	6	6	7.8	-0.889	-0.132	0.290
Smoothelin-like protein 1;	Q99LM3	1	5	5	9.2	-0.889	-0.576	0.470
Complement C3;	P01027	1	119	178	43.8	-0.862	-0.423	0.430
Alpha-2-HS-glycoprotein;	P29699	1	26	89	45.5	-0.862	-0.078	0.304
Neutral alpha-glucosidase C;	Q8BVW0	1	3	3	2.9	-0.862	-0.502	0.466
L-asparaginase;	Q8C0M9	1	7	7	23.9	-0.862	-0.204	0.329
Arsenite methyltransferase;	Q91WU5	1	8	9	14.9	-0.862	-0.141	0.310
Heme-binding protein 1;	Q9R257	1	7	9	32.1	-0.862	-0.392	0.412
Uncharacterized protein;	E9PYJ9	1	32	52	31.5	-0.862	-0.392	0.418
Serpin B6;	Q60854	1	28	97	50.8	-0.862	-0.251	0.355
Inter-alpha-trypsin inhibitor heavy chain H2;	Q61703	1	14	15	10.6	-0.862	-0.188	0.323
26S proteasome non-ATPase regulatory subunit 9;	Q9CR00	0.944	2	2	10.4	-0.862	-0.11	0.300
Calsequestrin-1;	O09165	1	4	5	22.4	-0.837	-0.359	0.417
Procollagen C-endopeptidase enhancer 1;	Q61398	1	6	10	36.3	-0.837	-0.389	0.434
Creatine kinase S-type, mitochondrial;	Q6P8J7	1	16	17	31.5	-0.837	-0.239	0.369
Protein Z-dependent protease inhibitor;	Q8R121	1	3	4	6.7	-0.837	-0.209	0.346
Vesicle-associated membrane protein-associated protein B;	Q9QY76	1	2	2	5.8	-0.837	-0.06	0.318
Glycogenin-1;	Q9R062	1	7	7	13.2	-0.837	-0.344	0.405
Complement factor B;	P04186	1	22	31	20.6	-0.837	-0.284	0.386
L-lactate dehydrogenase B chain;	P16125	1	14	37	35.6	-0.286	-0.052	0.738
Carbonyl reductase [NADPH] 2;	P08074	1	18	26	51.2	-0.837	-0.269	0.379
Murinoglobulin-1;	P28665	1	75	128	34.8	-0.837	-0.374	0.426
Isocitrate dehydrogenase [NADP], mitochondrial;	P54071	1	39	87	44.7	-0.837	-0.374	0.426
Clusterin;	Q06890	1	6	8	8.5	-0.837	-0.404	0.438
Ubiquitin-like modifier-activating enzyme 5;	Q8VE47	1	7	7	12.2	-0.837	-0.299	0.392
Glyoxylate reductase/hydroxypyruvate reductase;	Q91Z53	1	14	16	35.7	-0.837	-0.12	0.321
Flavin reductase (NADPH);	Q923D2	1	12	19	52.9	-0.837	-0.105	0.317

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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	1	5	8	11.9	-0.837	-0.314	0.397
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	Q64191	0.999	3	3	11.3	-0.837	-0.164	0.340
Hexokinase-3;	Q3TRM8	1	3	3	5	-0.811	-0.37	0.446
Aflatoxin B1 aldehyde reductase member 2;	Q8CG76	1	12	15	27.5	-0.811	-0.185	0.366
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial;	Q8CHT0	1	6	7	11.2	-0.811	-0.171	0.351
Histidine triad nucleotide-binding protein 2, mitochondrial;	Q9D0S9	1	5	5	29.4	-0.811	-0.256	0.381
Ras-related protein Rab-2A;	P53994	1	9	10	32.5	-0.811	-0.057	0.330
PDZ and LIM domain protein 7;	Q3TJD7	1	4	6	34.7	-0.811	-0.028	0.331
Prolyl 4-hydroxylase subunit alpha-2;	Q60716	1	10	12	14.9	-0.811	-0.455	0.481
Lambda-crystallin homolog;	Q99KP3	1	8	8	17.6	-0.811	-0.199	0.364
Phosphoglucomutase-1;	Q9D0F9	1	49	106	54.8	-0.811	-0.157	0.355
Platelet-derived growth factor receptor beta;	P05622	1	2	2	0.8	-0.786	-0.136	0.359
Plasminogen;	P20918	1	11	14	9.7	-0.786	-0.352	0.449
Heparin cofactor 2;	P49182	1	10	16	11.9	-0.786	-0.257	0.407
Myosin-binding protein C, fast-type;	Q5XKE0	1	19	21	17.3	-0.786	-0.149	0.363
Spermidine synthase;	Q64674	1	7	13	14.6	-0.786	-0.054	0.343
Lon protease homolog, mitochondrial;	Q8CGK3	1	6	7	6.1	-0.786	-0.312	0.439
Beta-enolase;	P21550	1	30	340	59	-0.786	-0.176	0.371
Alpha-enolase;	P17182	1	17	60	65.4	0.401	0.064	0.641
Gamma-enolase;	P17183	1	4	4	29.3	-0.105	-0.047	0.923
Enolase;	B0QZL1	1	2	2	70.1	-0.837	-0.12	0.319
Fumarylacetoacetase;	P35505	1	12	13	22.7	-0.786	-0.095	0.348
C-type mannose receptor 2;	Q64449	1	16	17	8.7	-0.786	-0.312	0.434
D-2-hydroxyglutarate dehydrogenase, mitochondrial;	Q8CIM3	1	3	3	5.8	-0.786	-0.095	0.349
C-reactive protein;	P14847	1	2	2	6.2	-0.761	-0.103	0.369
Vitamin D-binding protein;	P21614	1	35	56	55.3	-0.761	-0.271	0.439
Signal transducer and activator of transcription 3;	P42227	1	2	2	3.4	-0.761	-0.129	0.377
Tripartite motif-containing protein 72;	Q1XH17	1	12	13	26	-0.761	-0.271	0.424
Phosphoglycolate phosphatase;	Q8CHP8	1	8	8	19.3	-0.761	-0.258	0.420
MACRO domain-containing protein 1;	Q922B1	1	9	12	26	-0.761	-0.232	0.411
Serine protease inhibitor A3K;	P07759	1	39	605	50.7	-0.761	-0.451	0.520
Uncharacterized protein;	D3Z450	1	8	12	12.9	0.856	0.085	0.305
Serine protease inhibitor A3N;	Q91WP6	1	8	9	23.2	-0.811	-0.341	0.435
Protein kinase C beta type;	P68404	1	3	3	4.3	-0.761	-0.413	0.503
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	Q8QZS1	1	12	15	21.8	-0.761	-0.284	0.434
Golgi reassembly-stacking protein 2;	Q99JX3	1	9	11	16.2	-0.761	-0.116	0.365
Scavenger mRNA-decapping enzyme DcpS;	Q9DAR7	1	19	22	42.6	-0.761	-0.413	0.497
Nicotinate phosphoribosyltransferase;	Q8CC86	0.998	2	2	3.3	-0.761	-0.103	0.361
Mitogen-activated protein kinase 12;	O08911	1	6	6	12.8	-0.737	-0.111	0.381
Plasma kallikrein;	P26262	1	9	9	11.3	-0.737	-0.049	0.367
Cysteine and glycine-rich protein 1;	P97315	1	9	13	30.1	-0.737	-0.172	0.401

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Sorbitol dehydrogenase;	Q64442	1	10	12	12.9	-0.737	-0.295	0.457
Zinc-alpha-2-glycoprotein;	Q64726	1	11	14	23.5	-0.737	-0.246	0.434
Mannose-1-phosphate guanyltransferase beta;	Q8BTZ7	1	7	7	21.1	-0.737	-0.221	0.422
Abhydrolase domain-containing protein 11;	Q8K4F5	1	4	4	22.9	-0.737	-0.111	0.389
Plasminogen activator inhibitor 2, macrophage;	P12388	1	15	17	21.4	-0.737	-0.381	0.505
Myosin-4;	Q5SX39	1	5	5	12.1	-0.737	-0.307	0.471
Myosin-1;	Q5SX40	1	2	4	10.6	0.227	0.066	0.805
Echinoderm microtubule-associated protein-like 2;	Q7TNG5	1	15	17	26	-0.737	-0.491	0.557
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1;	Q8R429	1	42	87	34.9	-0.737	-0.356	0.491
LIM and calponin homology domains-containing protein 1;	Q3UH68	1	2	2	3	-0.737	-0.111	0.379
Growth/differentiation factor 8;	O08689	1	2	2	2.7	-0.713	-0.082	0.399
Malate dehydrogenase, mitochondrial;	P08249	1	44	171	61.5	-0.713	-0.082	0.397
Angiotensinogen;	P11859	1	2	2	3.6	-0.713	-0.105	0.403
Prothrombin;	P19221	1	13	15	19.1	-0.713	-0.304	0.484
F-box only protein 7;	Q3U7U3	1	2	2	5	-0.713	-0.105	0.403
Mimecan;	Q62000	1	10	12	18.5	-0.713	-0.199	0.438
Synaptic vesicle membrane protein VAT-1 homolog;	Q62465	1	22	38	37.7	-0.713	-0.257	0.459
Myosin light chain kinase, smooth muscle;	Q6PDN3	1	24	32	9.9	-0.713	-0.105	0.397
Sorting nexin-2;	Q9CWK8	1	23	25	28.7	-0.713	-0.175	0.422
Electron transfer flavoprotein subunit beta;	Q9DCW4	1	22	31	44.7	-0.713	-0.327	0.503
Ribonuclease 4;	Q9JJH1	1	7	14	27.7	-0.713	-0.164	0.422
Titin;	A2ASS6	1	40	55	1.1	-0.713	-0.421	0.548
Kininogen-1;	O08677	1	31	70	42.3	-0.713	-0.117	0.399
Sorting nexin-3;	O70492	1	6	7	14.8	-0.713	-0.094	0.400
Bisphosphoglycerate mutase;	P15327	1	6	6	18.9	-0.713	-0.07	0.396
Triosephosphate isomerase;	P17751	1	37	512	77.9	-0.713	-0.117	0.401
Aldose reductase;	P45376	1	23	45	41.1	-0.713	-0.234	0.455
Serotransferrin;	Q921I1	1	28	220	57.7	-0.713	-0.21	0.436
Thioredoxin reductase 1, cytoplasmic;	Q9JMH6	1	11	11	25	-0.713	-0.222	0.442
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	Q9R0E2	1	7	7	9.9	-0.713	-0.164	0.414
Voltage-dependent calcium channel subunit alpha-2/delta-1;	O08532	1	3	3	2.3	-0.69	-0.045	0.400
[Protein ADP-ribosylarginine] hydrolase;	P54923	1	6	6	15.7	-0.69	-0.189	0.453
Protein-arginine deiminase type-2;	Q08642	1	7	7	10.5	-0.69	-0.078	0.414
Cytosolic 10-formyltetrahydrofolate dehydrogenase;	Q8R0Y6	1	9	9	11	-0.69	-0.289	0.493
Dual specificity protein phosphatase 3;	Q9D7X3	1	8	10	22.7	-0.69	-0.134	0.431
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial;	Q9Z2I9	1	16	25	26.6	-0.69	-0.223	0.457
Uncharacterized protein;	E9PVD2	1	8	8	7.5	-0.69	-0.211	0.464
Myosin regulatory light chain 2, skeletal muscle isoform;	P97457	1	8	12	37.3	-0.69	-0.134	0.431
Oxysterol-binding protein;	E9QPD4	1	3	3	5.2	-0.69	-0.189	0.453
Peptidase inhibitor 16;	Q9ET66	1	3	3	9.1	-0.69	-0.189	0.456
Afamin;	O89020	1	15	20	17.6	-0.667	-0.286	0.513
Beta-hexosaminidase subunit beta;	P20060	1	4	4	6.5	-0.667	-0.54	0.637
Peptidyl-prolyl cis-trans isomerase C;	P30412	1	7	13	26.4	-0.667	-0.064	0.421

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Antithrombin-III;	P32261	1	24	41	33.5	-0.667	-0.296	0.521
Dynein light chain roadblock-type 1;	P62627	1	3	3	34.4	-0.667	-0.106	0.442
Beta-lactamase-like protein 2;	Q99KR3	1	2	3	6.2	-0.667	-0.021	0.415
[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial;	Q9JK42	1	5	5	10.3	-0.667	-0.148	0.448
Fetuin-B;	Q9QXC1	1	10	13	28.2	-0.667	-0.085	0.425
Plasma glutamate carboxypeptidase;	Q9WVJ3	1	12	15	19.6	-0.667	-0.116	0.445
N-acetylneuraminic acid synthase (Sialic acid synthase); Uncharacterized protein;	Q99J77	1	11	12	29.5	-0.667	-0.307	0.531
Malate dehydrogenase, cytoplasmic;	P14152	1	21	63	31.4	-0.667	-0.339	0.543
Glutathione S-transferase P 1;	P19157	1	13	26	48.3	-0.667	-0.222	0.477
Acylphosphatase-1;	P56376	1	9	11	55.6	-0.667	-0.095	0.437
55 kDa erythrocyte membrane protein;	P70290	1	3	3	7.2	-0.667	-0.328	0.546
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial;	Q7TSQ8	1	2	2	4.8	-0.667	-0.116	0.445
Translational activator of cytochrome c oxidase 1;	Q8K0Z7	1	2	2	4.1	-0.667	-0.074	0.432
Acp1 protein; MCG7808, isoform CRA_c; Uncharacterized protein;	Q561M1	0.992	2	2	35.4	-0.667	-0.032	0.416
Annexin A3;	O35639	1	12	15	32.8	-0.644	-0.282	0.538
Carbonic anhydrase 2;	P00920	1	12	13	38.5	-0.644	-0.101	0.450
Fructose-1,6-bisphosphatase isozyme 2;	P70695	1	8	10	14.5	-0.644	-0.111	0.452
Protein prune homolog;	Q8BIW1	1	6	6	10.8	-0.644	-0.111	0.450
Copper homeostasis protein cutC homolog;	Q9D8X1	1	3	5	13	-0.644	-0.141	0.470
Uncharacterized protein;	D3Z0Y2	1	28	82	69	-0.644	-0.302	0.546
Cullin-4B;	A2A432	1	3	3	7.7	-0.644	-0.292	0.541
Alpha-N-acetylgalactosaminidase;	Q9QWR8	0.996	2	2	3.9	-0.644	-0.131	0.460
Isovaleryl-CoA dehydrogenase, mitochondrial;	Q9JHI5	1	15	18	21.9	-0.621	-0.096	0.467
Hepatocyte growth factor activator;	Q9R098	1	2	2	4.6	-0.621	-0.459	0.643
Histidine triad nucleotide-binding protein 1;	P70349	1	8	24	51.6	-0.621	-0.057	0.456
Sepiapterin reductase;	Q64105	1	19	28	43.3	-0.621	-0.086	0.463
Pre-B-cell leukemia transcription factor-interacting protein 1;	Q3TVI8	0.999	2	2	7.5	-0.621	-0.105	0.468
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2;	O88428	1	3	3	6.8	-0.599	-0.082	0.479
Hydroxymethylglutaryl-CoA lyase, mitochondrial;	P38060	1	5	5	18.8	-0.599	-0.1	0.485
Eukaryotic translation initiation factor 4E;	P63073	1	8	11	18	-0.599	-0.209	0.527
Calcyclin-binding protein;	Q9CXW3	1	2	2	13.1	-0.599	-0.073	0.469
DnaJ homolog subfamily A member 4;	Q9JMC3	1	2	2	2.5	-0.599	-0.118	0.490
Ras-related protein R-Ras;	P10833	1	4	4	17.9	-0.599	-0.2	0.524
Xanthine dehydrogenase/oxidase;	Q00519	1	49	76	27.9	-0.599	-0.299	0.582
L-xylulose reductase;	Q91X52	1	5	6	13.9	-0.599	-0.073	0.482
Prostamide/prostaglandin F synthase;	Q9DB60	1	6	10	22.9	-0.599	-0.2	0.522
Uncharacterized protein;	F8VPN4	1	58	69	30.3	-0.599	-0.218	0.532
SUMO-conjugating enzyme UBC9;	P63280	0.992	2	2	6.3	-0.599	-0.045	0.470
TBC1 domain family member 8B;	A3KGB4	1	2	2	1.6	-0.578	-0.129	0.516
Serpin B8;	O08800	1	7	7	16.3	-0.578	-0.164	0.532
Coagulation factor X;	O88947	1	2	2	3.3	-0.578	-0.078	0.496
Ig heavy chain V region MOPC 104E;	P01756	1	2	5	16.2	-0.578	-0.043	0.480
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;	P13707	1	31	52	57.7	-0.578	-0.224	0.561

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Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	P70404	1	8	9	17.2	-0.578	-0.129	0.506
Aconitate hydratase, mitochondrial;	Q99KI0	1	61	185	47.2	-0.578	-0.19	0.536
Tubulin polymerization-promoting protein family member 3;	Q9CRB6	1	3	6	11.9	-0.578	-0.345	0.623
GMP reductase 1;	Q9DCZ1	1	3	4	16.6	-0.578	-0.069	0.485
Peptidyl-prolyl cis-trans isomerase FKBP9;	Q9Z247	1	8	10	11.6	-0.578	-0.173	0.525
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	11	12	32.1	-0.578	-0.173	0.529
Platelet-activating factor acetylhydrolase IB subunit gamma;	Q61205	1	2	2	6.3	-0.578	-0.043	0.489
Complement factor D;	P03953	1	4	4	20.1	-0.556	-0.286	0.617
Fatty acid-binding protein, heart;	P11404	1	10	14	31.6	-0.556	-0.041	0.505
Adenylosuccinate synthetase isozyme 1;	P28650	1	30	53	40.7	-0.556	-0.245	0.595
Glutathione reductase, mitochondrial;	P47791	1	12	13	20.3	-0.556	-0.049	0.507
ADP-ribosylation factor 6;	P62331	1	6	8	24	-0.556	-0.106	0.515
Platelet-activating factor acetylhydrolase IB subunit beta;	Q61206	1	5	11	18.9	-0.556	-0.147	0.535
NAD(P)H dehydrogenase [quinone] 1;	Q64669	1	4	5	7.3	-0.556	-0.065	0.502
Sorting nexin-6;	Q6P8X1	1	11	11	22.7	-0.556	-0.188	0.556
Dynamin-1-like protein;	Q8K1M6	1	16	16	18.8	-0.556	-0.114	0.521
Lactoylglutathione lyase;	Q9CPU0	1	10	19	27.2	-0.556	-0.106	0.525
Probable C->U-editing enzyme APOBEC-2;	Q9WV35	1	5	7	23.2	-0.556	-0.196	0.568
Leucine carboxyl methyltransferase 1; Leucine carboxyl methyltransferase 1, isoform CRA_b; Uncharacterized protein;	A2RTH5	1	3	3	8.1	-0.556	-0.139	0.538
UDP-glucose 6-dehydrogenase;	O70475	1	22	23	45.4	-0.556	-0.098	0.513
Acyl-protein thioesterase 1;	P97823	1	6	6	24.3	-0.556	-0.139	0.539
Peroxiredoxin-2;	Q61171	1	16	49	47.5	-0.556	-0.221	0.576
Adapter molecule crk;	Q64010	1	10	11	35.8	-0.556	-0.245	0.588
Leukocyte elastase inhibitor A;	Q9D154	1	30	44	43.8	-0.556	-0.213	0.568
3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial;	Q9D404	0.999	2	3	9.4	-0.556	-0.057	0.510
Spartin;	Q8R1X6	0.998	3	3	6.4	-0.556	-0.041	0.506
Carbonic anhydrase 1;	P13634	0.96	2	2	3.8	-0.556	-0.065	0.503
Ectonucleoside triphosphate diphosphohydrolase 2;	O55026	1	7	8	13.7	-0.535	-0.209	0.587
Peptidyl-prolyl cis-trans isomerase FKBP1A;	P26883	1	3	3	13	-0.535	-0.054	0.518
Dipeptidyl peptidase 4;	P28843	1	18	23	18	-0.535	-0.24	0.609
Protein PRRC1;	Q3UPH1	1	3	5	4.3	-0.535	-0.031	0.514
Coatomer subunit delta;	Q5XJY5	1	13	17	20.4	-0.535	-0.264	0.623
Hexokinase-2;	O08528	1	29	37	26	-0.535	-0.24	0.604
Hexokinase-1;	P17710	1	19	21	18.5	0.189	0.101	0.864
Annexin A8;	O35640	1	31	53	62.7	-0.535	-0.178	0.580
Macrophage colony-stimulating factor 1 receptor;	P09581	1	4	4	5.8	-0.535	-0.264	0.621
Annexin A4;	P97429	1	35	51	52.4	-0.535	-0.217	0.594
LIM and cysteine-rich domains protein 1;	Q8VEE1	1	12	12	33.7	-0.535	-0.279	0.636
Trifunctional enzyme subunit beta, mitochondrial;	Q99JY0	1	10	13	18.5	-0.535	-0.202	0.592
Sorting nexin-1;	Q9WV80	1	11	11	16.1	-0.535	-0.124	0.545

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N-acetylglucosamine-6-sulfatase;	Q8BFR4	1	11	12	11.9	-0.515	-0.11	0.565
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial;	Q9EQ20	1	18	29	30.6	-0.515	-0.125	0.571
Coatomer subunit zeta-2;	Q9JHH9	1	3	3	9.3	-0.515	-0.096	0.549
Annexin A11;	P97384	1	19	22	25.4	-0.515	-0.118	0.565
Astrocytic phosphoprotein PEA-15;	Q62048	1	4	4	27.7	-0.515	-0.044	0.543
Dihydropteridine reductase;	Q8BVI4	1	16	21	56.1	-0.515	-0.029	0.531
GDP-fucose protein O-fucosyltransferase 1;	Q91ZW2	1	4	4	6.5	-0.515	-0.074	0.551
Hydroxyacylglutathione hydrolase, mitochondrial;	Q99KB8	1	9	10	27	-0.515	-0.118	0.559
Cytosolic non-specific dipeptidase;	Q9D1A2	1	28	43	40.6	-0.515	-0.199	0.603
Transportin-3;	Q6P2B1	1	2	3	4.9	-0.515	-0.125	0.572
Fumarylacetoacetate hydrolase domain-containing protein 2A;	Q3TC72	0.999	2	2	10.5	-0.515	-0.044	0.542
Vesicle-associated membrane protein-associated protein A;	Q9WV55	0.982	2	2	4.4	-0.515	-0.096	0.551
Ig kappa chain V19-17;	P01633	0.963	2	2	6	-0.515	-0.052	0.535
Dipeptidase 1;	P31428	1	5	6	12.4	-0.494	-0.118	0.579
Deoxyguanosine kinase, mitochondrial;	Q9QX60	1	2	2	9	-0.494	-0.056	0.555
Uncharacterized protein;	D3YV69	1	2	2	12.6	-0.494	-0.097	0.568
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform;	P18826	1	8	8	6.4	-0.494	-0.16	0.599
Fermitin family homolog 2;	Q8CIB5	1	5	5	5.9	-0.494	-0.271	0.669
Citrate synthase, mitochondrial;	Q9CZU6	1	18	35	20.5	-0.494	-0.111	0.577
Alpha-aminoadipic semialdehyde dehydrogenase;	Q9DBF1	1	14	21	20.4	-0.494	-0.153	0.598
Dci protein; Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase); Uncharacterized protein;	Q8QZV3	1	20	24	32.5	-0.494	-0.139	0.588
Myoglobin;	P04247	1	14	23	41.6	-0.474	-0.132	0.605
Aspartate aminotransferase, mitochondrial;	P05202	1	43	93	45.8	-0.474	-0.158	0.614
Galectin-1;	P16045	1	15	48	45.2	-0.474	-0.033	0.559
Cellular retinoic acid-binding protein 1;	P62965	1	7	7	42.3	-0.474	-0.178	0.629
Perilipin-1;	Q8CGN5	1	10	13	17.6	-0.474	-0.066	0.576
Probable proline racemase;	Q9CXA2	1	5	5	15.3	-0.474	-0.039	0.561
Carbohydrate kinase domain-containing protein;	Q9CZ42	1	3	3	13.4	-0.474	-0.086	0.575
Low molecular weight phosphotyrosine protein phosphatase;	Q9D358	1	10	12	31.6	-0.474	-0.059	0.566
Branched-chain-amino-acid aminotransferase, mitochondrial;	O35855	1	12	16	25.3	-0.474	-0.184	0.633
Angiotensin-converting enzyme;	P09470	1	22	28	11	-0.474	-0.072	0.571
Gelsolin;	P13020	1	30	65	22.1	-0.474	-0.23	0.665
Carnitine O-acetyltransferase;	P47934	1	7	9	8.6	-0.474	-0.072	0.580
Pyruvate kinase isozymes M1/M2;	P52480	1	69	454	64.6	-0.474	-0.138	0.609
Phosphatidylethanolamine-binding protein 1;	P70296	1	13	23	62.6	-0.474	-0.105	0.583
Tumor protein D54;	Q9CYZ2	1	3	3	11.2	-0.474	-0.059	0.565
Synaptic vesicle membrane protein VAT-1 homolog-like;	Q80TB8	0.993	2	2	5	-0.474	-0.066	0.577
Dual specificity mitogen-activated protein kinase kinase 1;	P31938	0.933	2	2	4.9	-0.474	-0.099	0.580
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial;	P45952	1	4	4	8.6	-0.454	-0.199	0.657
Lumican;	P51885	1	26	286	38.8	-0.454	-0.112	0.608
Xaa-Pro dipeptidase;	Q11136	1	12	13	17.6	-0.454	-0.187	0.651
Microtubule-associated protein RP/EB family member 1;	Q61166	1	4	4	11.2	-0.454	-0.062	0.585

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Mitogen-activated protein kinase 10;	Q61831	1	2	2	3.2	-0.454	-0.062	0.593
Scavenger receptor cysteine-rich domain-containing protein LOC284297 homolog;	Q8BV57	1	7	7	5.3	-0.454	-0.068	0.587
Thioredoxin domain-containing protein 5;	Q91W90	1	20	25	34.6	-0.454	-0.056	0.583
Hemopexin;	Q91X72	1	37	233	40.7	-0.454	-0.193	0.659
Phytanoyl-CoA dioxygenase domain-containing protein 1;	Q9DB26	1	2	2	7.2	-0.454	-0.087	0.602
Cysteine sulfinic acid decarboxylase;	Q9DBE0	1	6	7	13.6	-0.454	-0.236	0.684
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial;	Q9WUM5	1	10	13	25.1	-0.454	-0.019	0.589
Phosphoglycerate kinase 1;	P09411	1	41	207	54.4	-0.454	-0.062	0.593
NEDD8-conjugating enzyme Ubc12;	P61082	1	12	13	41.5	-0.454	-0.05	0.594
Valacyclovir hydrolase;	Q8R164	1	9	10	24.7	-0.454	-0.037	0.586
Carboxymethylenebutenolidase homolog;	Q8R1G2	1	8	12	18	-0.454	-0.193	0.660
Programmed cell death 6-interacting protein;	Q9WU78	1	22	29	22.8	-0.454	-0.124	0.622
Hydroxysteroid (17-beta) dehydrogenase 10; Uncharacterized protein;	A2AFQ2	1	10	11	42.5	-0.454	-0.162	0.640
Lipoma-preferred partner homolog;	Q8BFW7	0.998	2	2	6.9	-0.454	-0.187	0.655
Ferritin heavy chain;	P09528	1	11	15	28.6	-0.434	-0.07	0.615
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical];	P56380	1	6	8	32	-0.434	-0.158	0.652
Apolipoprotein A-I-binding protein;	Q8K4Z3	1	10	13	24.8	-0.434	-0.053	0.601
Ester hydrolase C11orf54 homolog;	Q91V76	1	6	6	20.6	-0.434	-0.076	0.613
ADP-ribosylation factor-like protein 3;	Q9WUL7	1	5	6	28	-0.434	-0.141	0.643
Citrate lyase subunit beta-like protein, mitochondrial;	Q8R4N0	1	4	5	13.6	-0.434	-0.059	0.611
NAD-dependent deacetylase sirtuin-2;	Q8VDQ8	1	3	4	9.3	-0.434	-0.053	0.610
Band 4.1-like protein 3;	Q9WV92	1	6	8	8.1	-0.434	-0.076	0.616
Glutamate--cysteine ligase catalytic subunit;	P97494	1	2	2	4.2	-0.434	-0.041	0.597
Signal transducer and activator of transcription 5B;	P42232	1	2	2	2.8	-0.434	-0.041	0.596
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial;	Q9D1L0	0.998	2	2	21.6	-0.434	-0.065	0.604
Myc box-dependent-interacting protein 1;	O08539	1	7	9	18	-0.415	-0.083	0.629
Serum albumin;	P07724	1	95	4099	71.4	-0.415	-0.26	0.732
Carbonic anhydrase 3;	P16015	1	36	917	73.8	-0.415	-0.232	0.723
Ornithine aminotransferase, mitochondrial;	P29758	1	23	33	27.6	-0.415	-0.083	0.629
Cytosolic 5'-nucleotidase III-like protein;	Q3UFY7	1	2	2	4.8	-0.415	-0.044	0.616
SEC23-interacting protein;	Q6NZC7	1	6	8	4	-0.415	-0.083	0.629
Vacuolar protein sorting-associated protein 26B;	Q8C0E2	1	2	2	5.4	-0.415	-0.066	0.632
Cysteine-rich with EGF-like domain protein 2;	Q9CYA0	1	4	4	8.9	-0.415	-0.172	0.688
Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase;	Q9DBB8	1	7	7	18.3	-0.415	-0.155	0.669
Glycogen synthase kinase-3 beta;	Q9WV60	1	4	4	15	-0.415	-0.089	0.642
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P50544	1	13	14	20.6	-0.415	-0.133	0.656
Peroxiredoxin-5, mitochondrial;	P99029	1	19	34	44.8	-0.415	-0.044	0.625
Uncharacterized protein;	F7CAE1	1	14	32	57.9	-0.415	-0.044	0.625
NAD kinase domain-containing protein 1;	Q8C5H8	1	2	2	5.9	-0.415	-0.077	0.627
Alpha-methylacyl-CoA racemase;	O09174	1	3	3	8.7	-0.415	-0.127	0.653
EH domain-containing protein 4;	Q9EQP2	0.996	2	3	4.8	-0.415	-0.105	0.645
Protein unc-119 homolog B;	Q8C4B4	0.974	2	2	5.1	-0.415	-0.05	0.617
Caspase-6;	O08738	1	2	2	7.2	-0.396	-0.302	0.777

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Glutathione peroxidase 1;	P11352	1	20	30	55.7	-0.396	-0.141	0.681
Glutathione S-transferase A4;	P24472	1	5	6	13.1	-0.396	-0.078	0.654
6-phosphofructokinase, muscle type;	P47857	1	7	9	6	-0.396	-0.135	0.676
Supervillin;	Q8K4L3	1	2	2	1.1	-0.396	-0.036	0.632
Twinfilin-1;	Q91YR1	1	2	2	3.7	-0.396	-0.073	0.652
Rho GDP-dissociation inhibitor 1;	Q99PT1	1	8	19	15.2	-0.396	-0.031	0.639
Glycyl-tRNA synthetase;	Q9CZD3	1	18	21	19.2	-0.396	-0.083	0.655
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Q9D6R2	1	18	29	36.9	-0.396	-0.162	0.700
Regulator of microtubule dynamics protein 1;	Q9DCV4	1	2	2	5.2	-0.396	-0.031	0.631
Prostaglandin F2 receptor negative regulator;	Q9WV91	1	5	5	4.6	-0.396	-0.172	0.705
Isocitrate dehydrogenase 3 (NAD+) beta; Tumor-related protein; Uncharacterized protein;	Q91VA7	1	12	14	26.8	-0.396	-0.089	0.653
Glucose-6-phosphate isomerase;	P06745	1	38	116	44.4	-0.396	-0.13	0.675
Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	P23506	1	6	7	18.5	-0.396	-0.141	0.680
Propionyl-CoA carboxylase beta chain, mitochondrial;	Q99MN9	1	20	23	30.7	-0.396	-0.109	0.662
1,4-alpha-glucan-branching enzyme;	Q9D6Y9	1	13	14	16.4	-0.396	-0.109	0.669
Profilin-2;	Q9JJV2	1	5	8	25	-0.396	-0.12	0.672
Aspartyl aminopeptidase;	Q9Z2W0	1	11	13	18.4	-0.396	-0.135	0.685
Thioredoxin-dependent peroxide reductase, mitochondrial;	P20108	1	13	18	28	-0.377	-0.034	0.649
Isochorismatase domain-containing protein 2A, mitochondrial;	P85094	1	8	8	21.4	-0.377	-0.078	0.665
Sulfite oxidase, mitochondrial;	Q8R086	1	4	4	4	-0.377	-0.069	0.660
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2;	Q9Z2Z9	1	4	4	5.4	-0.377	-0.088	0.672
T-cell specific GTPase; Uncharacterized protein;	Q5SVP4	1	2	2	14.4	-0.377	-0.054	0.655
Niban-like protein 1;	Q8R1F1	1	11	12	16.6	-0.377	-0.108	0.685
Inositol (Myo)-1(Or 4)-monophosphatase 1; Inositol (Myo)-1(Or 4)-monophosphatase 1, isoform CRA_a; Myo-inositol monophosphatase 1; Uncharacterized protein;	Q924B0	1	10	13	34.7	-0.377	-0.191	0.730
Ferritin;	Q9CPX4	1	19	50	61.2	-0.377	-0.142	0.702
Ig kappa chain V-V region L7;	P01642	0.998	2	2	13	-0.377	-0.059	0.657
Complement C1s-A subcomponent;	Q8CG14	1	5	5	7.5	-0.358	-0.239	0.778
Electron transfer flavoprotein subunit alpha, mitochondrial;	Q99LC5	1	32	59	51.1	-0.358	-0.092	0.690
Synaptobrevin homolog YKT6;	Q9CQW1	1	8	11	30.8	-0.358	-0.133	0.716
Pterin-4-alpha-carbinolamine dehydratase 2;	Q9CZL5	1	2	2	8.1	-0.358	-0.06	0.667
Protein canopy homolog 2;	Q9QXT0	1	7	12	35.7	-0.358	-0.179	0.742
S-formylglutathione hydrolase;	Q9R0P3	1	19	27	50.7	-0.358	-0.129	0.704
Hemoglobin subunit beta-1;	P02088	1	16	98	76.9	-0.358	-0.032	0.667
Hemoglobin subunit beta-2;	P02089	1	14	52	72.8	-0.494	-0.104	0.573
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;	P63328	1	5	5	16.3	-0.358	-0.069	0.685
Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform;	P48453	1	2	4	11.5	-0.377	-0.01	0.646
Puromycin-sensitive aminopeptidase;	Q11011	1	28	35	21.5	-0.358	-0.138	0.719
Zyxin;	Q62523	1	7	7	15.9	-0.358	-0.129	0.706
N-acetylgalactosamine kinase;	Q68FH4	1	5	5	9.4	-0.358	-0.106	0.692
UPF0587 protein C1orf123 homolog;	Q8BHG2	1	4	5	32.6	-0.358	-0.037	0.668

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Alanyl-tRNA synthetase domain containing 1; Uncharacterized protein;	A2A4P4	1	5	6	11.4	-0.358	-0.124	0.709
Peptidyl-prolyl cis-trans isomerase;	A2BGI8	1	4	6	19.6	-0.358	-0.184	0.744
Ubiquitin-fold modifier 1;	P61961	1	2	4	18.3	-0.358	-0.032	0.658
Protein-glutamine gamma-glutamyltransferase 2;	P21981	1	8	9	13.3	-0.34	-0.077	0.708
Leukotriene A-4 hydrolase;	P24527	1	38	49	41.9	-0.34	-0.095	0.711
Nuclear transport factor 2;	P61971	1	4	5	23.6	-0.34	-0.03	0.684
Platelet-activating factor acetylhydrolase IB subunit alpha;	P63005	1	13	13	27.3	-0.34	-0.082	0.705
Dystroglycan;	Q62165	1	2	2	1.6	-0.34	-0.056	0.684
SPRY domain-containing protein 4;	Q91WK1	1	8	8	31.4	-0.34	-0.116	0.725
Glutaredoxin-3;	Q9CQM9	1	8	10	22.8	-0.34	-0.077	0.700
28S ribosomal protein S36, mitochondrial;	Q9CQX8	1	2	2	21	-0.34	-0.047	0.689
Dynamin-2;	P39054	1	7	7	8.4	-0.34	-0.194	0.765
Translationally-controlled tumor protein;	P63028	1	12	47	34.3	-0.34	-0.034	0.686
Pyridoxal kinase;	Q8K183	1	11	16	22.8	-0.34	-0.056	0.692
Calcium/calmodulin-dependent protein kinase type 1;	Q91YS8	1	6	7	13.9	-0.34	-0.056	0.692
Uncharacterized protein;	E9QL95	1	4	4	7.2	-0.34	-0.047	0.681
Vacuolar protein sorting-associated protein 4B;	P46467	1	2	2	7	-0.34	-0.056	0.684
CB1 cannabinoid receptor-interacting protein 1;	Q5M8N0	0.993	2	2	14	-0.34	-0.09	0.710
Prefoldin subunit 2;	O70591	1	2	3	7.8	-0.322	-0.044	0.699
Annexin A7;	Q07076	1	18	23	26.1	-0.322	-0.101	0.734
Coagulation factor XIII B chain;	Q07968	1	2	3	1.8	-0.322	-0.02	0.700
COP9 signalosome complex subunit 1;	Q99LD4	1	5	5	10.8	-0.322	-0.165	0.768
Sorting nexin-5;	Q9D8U8	1	8	8	14.1	-0.322	-0.097	0.725
Torsin-1B;	Q9ER41	1	4	4	6.2	-0.322	-0.133	0.754
Alpha-crystallin B chain;	P23927	1	13	26	49.1	-0.322	-0.052	0.700
Aldehyde dehydrogenase, mitochondrial;	P47738	1	35	95	46.8	-0.322	-0.105	0.737
Aldehyde dehydrogenase family 1 member A3;	Q9JHW9	0.995	2	2	4.9	0.057	0.047	0.968
Adenosylhomocysteinase;	P50247	1	28	44	40.5	-0.322	-0.085	0.716
Coagulation factor XII;	Q80YC5	1	3	3	4.4	-0.322	-0.04	0.696
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);	Q8VC30	1	6	13	9.5	-0.322	-0.076	0.723
Glyoxalase domain-containing protein 4;	Q9CPV4	1	16	19	49.1	-0.322	-0.04	0.697
Cysteinyl-tRNA synthetase, cytoplasmic;	Q9ER72	1	6	7	5.8	-0.322	-0.133	0.754
Alcohol dehydrogenase [NADP+];	Q9JII6	1	18	23	34.8	-0.322	-0.089	0.728
WD repeat-containing protein 1;	O88342	1	24	37	38.9	-0.304	-0.146	0.775
Cytoplasmic aconitate hydratase;	P28271	1	44	55	37.8	-0.304	-0.143	0.772
DCC-interacting protein 13-alpha;	Q8K3H0	1	4	5	4.5	-0.304	-0.019	0.718
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial;	Q9D2G2	1	12	12	17.4	-0.304	-0.026	0.719
Mitochondrial peptide methionine sulfoxide reductase;	Q9D6Y7	1	4	4	19.3	-0.304	-0.188	0.799
SH3 domain-binding glutamic acid-rich-like protein;	Q9JJU8	1	5	5	30.7	-0.304	-0.09	0.746
Ubiquitin carboxyl-terminal hydrolase isozyme L1;	Q9R0P9	1	5	5	21.1	-0.304	-0.218	0.821
Peroxiredoxin-4;	O08807	1	14	18	43.1	-0.304	-0.038	0.722
ATP synthase subunit alpha, mitochondrial;	Q03265	1	36	66	39.6	-0.304	-0.158	0.788

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Calcineurin-like phosphoesterase domain-containing protein 1;	Q8BFS6	1	6	6	17.3	-0.304	-0.038	0.722
Aspartoacylase;	Q8R3P0	1	4	4	11.5	-0.304	-0.116	0.755
Alpha-mannosidase 2C1;	Q91W89	1	7	8	10.4	-0.304	-0.12	0.758
Argininosuccinate lyase;	Q91YI0	1	11	12	19.6	-0.304	-0.079	0.733
Prolow-density lipoprotein receptor-related protein 1;	Q91ZX7	1	48	51	9.4	-0.304	-0.139	0.771
UPF0160 protein MYG1, mitochondrial;	Q9JK81	1	6	7	13.9	-0.304	-0.06	0.731
Proteasome assembly chaperone 4;	P0C7N9	1	2	2	32.5	-0.304	-0.161	0.790
Superoxide dismutase [Mn], mitochondrial;	P09671	1	10	17	19.4	-0.286	-0.105	0.768
Ras-related protein Rab-7a;	P51150	1	17	26	52.7	-0.286	-0.073	0.749
Aldehyde dehydrogenase family 16 member A1;	Q571I9	1	3	3	6.4	-0.286	-0.153	0.805
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4;	Q62425	1	3	3	26.8	-0.286	-0.024	0.736
Phosphatidylinositol-binding clathrin assembly protein;	Q7M6Y3	1	4	6	5.3	-0.286	-0.052	0.737
Acylamino-acid-releasing enzyme;	Q8R146	1	8	11	10.9	-0.286	-0.059	0.750
Ribulose-phosphate 3-epimerase;	Q8VEE0	1	4	6	17.5	-0.286	-0.066	0.743
Endoplasmic reticulum resident protein 44;	Q9D1Q6	1	16	21	26.6	-0.286	-0.119	0.782
Dihydropyrimidinase-related protein 5;	Q9EQF6	1	3	3	7.1	-0.286	-0.094	0.761
Inositol-3-phosphate synthase 1;	Q9JHU9	1	8	8	9.7	-0.286	-0.038	0.732
Galactokinase;	Q9R0N0	1	9	10	16.9	-0.286	-0.077	0.758
Probable methylthioribulose-1-phosphate dehydratase;	Q9WVQ5	1	6	6	36.1	-0.286	-0.038	0.732
Gamma-synuclein;	Q9Z0F7	1	6	6	36.6	-0.286	-0.042	0.739
Rab GDP dissociation inhibitor alpha;	P50396	1	16	19	22.6	-0.286	-0.119	0.783
Proteasome activator complex subunit 2;	P97372	1	6	9	27.2	-0.286	-0.091	0.755
Mitochondrial inner membrane protein;	Q8CAQ8	1	4	4	9.6	-0.286	-0.073	0.755
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform;	Q6P1F6	1	2	2	3	-0.286	-0.035	0.739
Dual specificity mitogen-activated protein kinase kinase 3;	O09110	1	2	2	3.2	-0.286	-0.038	0.732
Lysosome-associated membrane glycoprotein 1;	P11438	1	4	8	5.7	-0.269	-0.062	0.759
Epoxide hydrolase 2;	P34914	1	13	17	20.4	-0.269	-0.036	0.757
Cytochrome c, somatic;	P62897	1	4	9	31.4	-0.269	-0.075	0.776
Fumarate hydratase, mitochondrial;	P97807	1	26	33	45.6	-0.269	-0.11	0.789
Thioredoxin domain-containing protein 17;	Q9CQM5	1	5	8	26.8	-0.269	-0.032	0.748
Ubiquitin-like modifier-activating enzyme ATG7;	Q9D906	1	4	4	5.2	-0.269	-0.133	0.810
Protein ETHE1, mitochondrial;	Q9DCM0	1	4	6	16.1	-0.269	-0.032	0.756
4-trimethylaminobutyraldehyde dehydrogenase;	Q9JLJ2	1	26	39	37.4	-0.269	-0.088	0.782
Protein NDRG2;	Q9QYG0	1	24	41	46.4	-0.269	-0.078	0.770
Obscurin;	A2AAJ9	1	4	4	0.9	-0.269	-0.143	0.806
Tetratricopeptide repeat protein 38;	A3KMP2	1	13	18	19.1	-0.269	-0.068	0.763
Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform;	P07934	1	3	3	26.5	-0.269	-0.088	0.774
F-actin-capping protein subunit alpha-2;	P47754	1	10	14	39.2	-0.269	-0.1	0.783
Endoplasmic reticulum resident protein 29;	P57759	1	6	11	13.7	-0.269	-0.039	0.750
Prolyl 3-hydroxylase 1;	Q3V1T4	1	4	5	5.4	-0.269	-0.113	0.799
Cullin-associated NEDD8-dissociated protein 1;	Q6ZQ38	1	14	16	12.2	-0.269	-0.126	0.799
Kynurenine--oxoglutarate transaminase 1;	Q8BTY1	1	5	5	18.4	-0.269	-0.065	0.770
6-phosphogluconolactonase;	Q9CQ60	1	15	22	49	-0.269	-0.032	0.756

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
Tryptophanyl-tRNA synthetase, cytoplasmic;	P32921	1	6	7	13.9	-0.252	-0.027	0.762
Adenosine kinase;	P55264	1	19	28	30.5	-0.252	-0.108	0.810
Ras-related protein Rab-11B;	P46638	1	17	20	46.8	-0.252	-0.036	0.767
Prostaglandin reductase 2;	Q8VDQ1	1	5	7	11.7	-0.252	-0.045	0.765
cAMP-dependent protein kinase type I-alpha regulatory subunit;	Q9DBC7	1	5	6	6.6	-0.252	-0.027	0.763
Galectin-3;	P16110	1	14	27	36.2	-0.234	-0.014	0.769
Transgelin;	P37804	1	15	26	51.2	-0.234	-0.066	0.792
Long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P51174	1	17	24	25.1	-0.234	-0.085	0.812
Acylphosphatase-2;	P56375	1	6	12	37.1	-0.234	-0.066	0.801
Kynurenine--oxoglutarate transaminase 3;	Q71RI9	1	4	4	5.5	-0.234	-0.014	0.769
Phosphoglucomutase-2;	Q7TSV4	1	16	17	24.4	-0.234	-0.215	0.877
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial;	Q8K2B3	1	19	25	33	-0.234	-0.099	0.814
Interleukin-1 receptor-associated kinase 4;	Q8R4K2	1	2	2	3.5	-0.234	-0.044	0.787
Pyridoxine-5'-phosphate oxidase;	Q91XF0	1	3	3	6.9	-0.234	-0.025	0.780
Cytochrome b-c1 complex subunit 2, mitochondrial;	Q9DB77	1	10	10	18.8	-0.234	-0.063	0.798
Glutathione S-transferase theta 3; Glutathione S-transferase, theta 3; Uncharacterized protein;	Q99L20	1	7	7	24.1	-0.234	-0.041	0.786
Heat shock protein beta-1;	P14602	1	18	31	42.1	-0.234	-0.077	0.805
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1;	P47856	1	4	4	8	-0.234	-0.063	0.789
Four and a half LIM domains protein 1;	P97447	1	20	28	43.6	-0.234	-0.044	0.780
Glycerol-3-phosphate dehydrogenase 1-like protein;	Q3ULJ0	1	12	14	24.5	-0.234	-0.091	0.813
C-Jun-amino-terminal kinase-interacting protein 4;	Q58A65	1	17	18	11.1	-0.234	-0.11	0.826
Adiponectin;	Q60994	1	6	8	18.6	-0.234	-0.019	0.770
Ras-related protein Rab-14;	Q91V41	1	8	11	34	-0.234	-0.041	0.778
Ras-related protein Rab-1A;	P62821	1	7	8	45.5	-0.415	-0.061	0.630
Ras-related protein Rab-10;	P61027	1	5	8	22.5	-0.234	-0.047	0.781
Ras-related protein Rab-1B;	Q9D1G1	1	4	5	35.3	-0.029	-0.003	0.966
Ras-related protein Rab-8A;	P55258	1	4	4	23.2	0.029	0.005	0.975
Ras-related protein Rab-35;	Q6PHN9	1	2	2	12.4	0.864	0.109	0.306
Glia maturation factor beta;	Q9CQI3	1	4	4	14.1	-0.234	-0.025	0.780
Indolethylamine N-methyltransferase;	P40936	1	10	10	30.3	-0.218	-0.066	0.817
Folate receptor beta;	Q05685	1	3	3	8	-0.218	-0.079	0.825
Peroxisomal coenzyme A diphosphatase NUDT7;	Q99P30	1	2	2	11.4	-0.218	-0.028	0.790
C4b-binding protein;	P08607	1	3	3	9	-0.218	-0.106	0.841
GDH/6PGL endoplasmic bifunctional protein;	Q8CFX1	1	4	4	4.7	-0.218	-0.074	0.822
Coatomer subunit alpha;	Q8CIE6	1	4	4	3.4	-0.218	-0.076	0.816
Nucleoside diphosphate kinase;	E9PZF0	1	30	89	74.2	-0.218	-0.051	0.800
Uncharacterized protein;	Q3ULW8	1	7	7	14	-0.218	-0.041	0.804
ADP-ribosylation factor-like protein 8B;	Q9CQW2	1	2	2	4.8	-0.218	-0.02	0.788
Ferrochelatase, mitochondrial;	P22315	1	3	3	6.8	-0.201	-0.095	0.848
Caspase-1;	P29452	1	7	7	13.4	-0.201	-0.097	0.849
Annexin A5;	P48036	1	32	76	51.1	-0.201	-0.06	0.824
UDP-glucose:glycoprotein glucosyltransferase 1;	Q6P5E4	1	14	16	8.7	-0.201	-0.06	0.831

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Protein FAM49B;	Q921M7	1	6	6	17.3	-0.201	-0.102	0.858
Cytosolic 5'-nucleotidase 3;	Q9D020	1	8	8	22.7	-0.201	-0.067	0.837
Serine/threonine-protein kinase DCLK1;	Q9JLM8	1	2	2	3	-0.201	-0.035	0.819
BAG family molecular chaperone regulator 3;	Q9JLV1	1	3	5	2.4	-0.201	-0.025	0.815
Nucleoside diphosphate kinase 3;	Q9WV85	1	2	2	4.1	-0.201	-0.016	0.804
Quinone oxidoreductase;	P47199	1	6	9	21.1	-0.201	-0.021	0.814
Spermine synthase;	P97355	1	6	7	15	-0.201	-0.106	0.855
Anamorsin;	Q8WTY4	1	3	4	12.6	-0.201	-0.099	0.856
Methionine adenosyltransferase 2 subunit beta;	Q99LB6	1	4	6	18.9	-0.201	-0.044	0.822
3'(2'),5'-bisphosphate nucleotidase 1;	Q9Z0S1	1	6	6	24	-0.201	-0.058	0.831
Importin subunit alpha-3;	O35344	1	2	2	4.4	-0.201	-0.06	0.831
Integrin alpha-5;	P11688	1	3	4	2.5	-0.184	-0.019	0.822
Activator of 90 kDa heat shock protein ATPase homolog 1;	Q8BK64	1	8	8	20.4	-0.184	-0.071	0.855
Calcium/calmodulin-dependent protein kinase type 1D;	Q8BW96	1	8	8	17.2	-0.184	-0.065	0.853
Ribonuclease inhibitor;	Q91VI7	1	50	72	68.4	-0.184	-0.056	0.848
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial;	Q9CQA3	1	6	6	17	-0.184	-0.044	0.841
Maleylacetoacetate isomerase;	Q9WVL0	1	18	26	51.9	-0.184	-0.054	0.846
Aspartate aminotransferase, cytoplasmic;	P05201	1	27	48	45.3	-0.184	-0.073	0.858
Diphosphoinositol polyphosphate phosphohydrolase 3-alpha;	P0C027	1	4	5	9.8	-0.184	-0.054	0.839
Microtubule-associated protein 4;	P27546	1	25	31	22.9	-0.184	-0.073	0.859
Histidine ammonia-lyase;	P35492	1	35	53	45.7	-0.184	-0.046	0.834
Inositol polyphosphate 1-phosphatase;	P49442	1	3	3	10.4	-0.184	-0.05	0.845
Serine/threonine-protein phosphatase 2A activator;	P58389	1	12	17	44.9	-0.184	-0.077	0.861
Ubiquitin-conjugating enzyme E2 D3;	P61079	1	3	5	19.7	-0.184	-0.079	0.856
Sorcin;	Q6P069	1	14	17	41.4	-0.184	-0.033	0.835
Copine-1;	Q8C166	1	11	15	21.7	-0.184	-0.042	0.839
NEDD8-activating enzyme E1 catalytic subunit;	Q8C878	1	8	8	22.3	-0.184	-0.027	0.825
Ubiquinone biosynthesis protein COQ9, mitochondrial;	Q8K1Z0	1	8	10	23	-0.184	-0.119	0.886
Mannose-6-phosphate isomerase;	Q924M7	1	9	10	17.3	-0.184	-0.1	0.869
Cyclin-dependent kinase 6;	Q64261	1	3	3	10.1	-0.184	-0.04	0.839
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	P19783	1	3	6	16.6	-0.168	-0.06	0.868
Troponin C, skeletal muscle;	P20801	1	7	9	43.1	-0.168	-0.013	0.837
10 kDa heat shock protein, mitochondrial;	Q64433	1	10	19	48	-0.168	-0.032	0.845
Elongation factor Tu, mitochondrial;	Q8BFR5	1	6	11	12.8	-0.168	-0.032	0.838
TIP41-like protein;	Q8BH58	1	3	4	10	-0.168	-0.026	0.849
V-type proton ATPase subunit H;	Q8BVE3	1	7	8	17.4	-0.168	-0.038	0.855
Bifunctional purine biosynthesis protein PURH;	Q9CWJ9	1	32	47	38.5	-0.168	-0.026	0.850
ATP synthase subunit delta, mitochondrial;	Q9D3D9	1	4	9	13.7	-0.168	-0.013	0.846
Dual specificity mitogen-activated protein kinase kinase 4;	P47809	1	5	5	14.4	-0.168	-0.094	0.883
Coagulation factor XIII A chain;	Q8BH61	1	10	13	11.7	-0.168	-0.089	0.885
Nitrilase homolog 1;	Q8VDK1	1	4	5	12.8	-0.168	-0.015	0.838
Guanine deaminase;	Q9R111	1	21	23	44.9	-0.168	-0.064	0.870
Peptidyl-prolyl cis-trans isomerase-like 1;	Q9D0W5	1	4	5	21.1	-0.168	-0.042	0.849

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Uncharacterized protein;	E9PWG2	1	2	2	3.6	-0.168	-0.06	0.861
Scavenger receptor cysteine-rich type 1 protein M130;	Q2VLH6	1	4	4	3.2	-0.152	-0.066	0.882
3-ketoacyl-CoA thiolase, mitochondrial;	Q8BWT1	1	24	32	53.7	-0.152	-0.042	0.869
Protein SEC13 homolog;	Q9D1M0	1	8	10	18	-0.152	-0.02	0.862
V-type proton ATPase 116 kDa subunit a isoform 1;	Q9Z1G4	1	2	2	1.3	-0.152	-0.015	0.855
Isocitrate dehydrogenase [NADP] cytoplasmic;	O88844	1	38	71	57	-0.152	-0.056	0.876
Annexin A1;	P10107	1	42	110	59.8	-0.152	-0.024	0.858
Ras-related protein Rab-5C;	P35278	1	4	6	22.2	-0.152	-0.015	0.855
Ras-related protein Rab-5A;	Q9CQD1	1	2	2	16.7	-0.234	-0.03	0.774
Tubulin alpha-1A chain;	P68369	1	13	22	42.6	-0.152	-0.039	0.872
Tubulin alpha-4A chain;	P68368	1	11	11	42.9	-0.136	-0.084	0.911
Glutathione S-transferase theta-1;	Q64471	1	3	3	11.2	-0.152	-0.068	0.884
Xaa-Pro aminopeptidase 1;	Q6P1B1	1	19	24	28.7	-0.152	-0.022	0.861
Serine/threonine-protein kinase PAK 2;	Q8CIN4	1	14	20	22.5	-0.152	-0.014	0.859
Serine/threonine-protein kinase PAK 1;	O88643	1	2	3	5.7	0.422	0.041	0.608
Protein DDI1 homolog 2;	A2ADY9	1	7	8	18	-0.136	-0.033	0.879
Ubiquitin-protein ligase E3A;	O08759	1	3	3	2.6	-0.136	-0.051	0.885
ATP synthase subunit beta, mitochondrial;	P56480	1	39	103	44.6	-0.136	-0.043	0.886
Rab GDP dissociation inhibitor beta;	Q61598	1	37	63	57.5	-0.136	-0.064	0.900
Alanyl-tRNA synthetase, cytoplasmic;	Q8BGQ7	1	12	15	11.8	-0.136	-0.015	0.865
Reticulocalbin-3;	Q8BH97	1	5	9	11.7	-0.136	-0.097	0.917
Gephyrin;	Q8BUV3	1	6	6	5.3	-0.136	-0.057	0.896
Band 4.1-like protein 2;	O70318	1	17	20	20.2	-0.136	-0.051	0.893
Peroxiredoxin-1;	P35700	1	22	51	72.4	-0.136	-0.006	0.870
Nuclear migration protein nudC;	O35685	1	9	11	26.2	-0.12	-0.013	0.888
Macrophage mannose receptor 1;	Q61830	1	33	40	19.6	-0.12	-0.048	0.902
Peptidyl-prolyl cis-trans isomerase FKBP3;	Q62446	1	5	7	18.3	-0.12	-0.027	0.886
Synemin;	Q70IV5	1	6	8	4.7	-0.12	-0.017	0.881
Thioredoxin domain-containing protein 12;	Q9CQU0	1	3	3	14.1	-0.12	-0.012	0.887
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial;	Q9D051	1	20	36	34.3	-0.12	-0.022	0.891
Magnesium-dependent phosphatase 1;	Q9D967	1	4	4	21.3	-0.12	-0.025	0.892
Dysferlin;	Q9ESD7	1	2	4	0.5	-0.12	-0.031	0.896
Protein S100-A11;	P50543	1	8	18	27.6	-0.12	-0.01	0.887
S-adenosylmethionine synthase isoform type-2;	Q3THS6	1	8	11	20.3	-0.12	-0.009	0.879
MAP kinase-activated protein kinase 3;	Q3UMW7	1	3	3	9	-0.12	-0.016	0.880
5-oxoprolinase;	Q8K010	1	18	21	15.7	-0.12	-0.055	0.904
Proline synthase co-transcribed bacterial homolog protein;	Q9Z2Y8	1	6	7	20.1	-0.12	-0.04	0.895
Phosphopantothenate--cysteine ligase;	Q8VDG5	1	2	2	7.7	-0.12	-0.013	0.880
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial;	P35486	1	19	27	34.9	-0.105	-0.052	0.925
Alanine aminotransferase 1;	Q8QZR5	1	19	21	33.5	-0.105	-0.03	0.905
NAD-dependent malic enzyme, mitochondrial;	Q99KE1	1	2	2	7	-0.105	-0.021	0.900
Transportin-2;	Q99LG2	1	4	4	4.5	-0.105	-0.019	0.899
Histidine-rich glycoprotein;	Q9ESB3	1	7	8	9.3	-0.105	-0.028	0.911

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Palmitoyl-protein thioesterase 1;	O88531	1	5	8	16.9	-0.105	-0.073	0.933
Purine nucleoside phosphorylase;	P23492	1	15	17	45.3	-0.105	-0.035	0.916
Band 4.1-like protein 1;	Q9Z2H5	1	2	2	3.8	-0.105	-0.015	0.897
Arfip1 protein; Uncharacterized protein;	A2RSX9	1	2	2	11.7	-0.105	-0.019	0.907
Peptidyl-prolyl cis-trans isomerase FKBP2;	P45878	0.998	2	3	8.6	-0.105	-0.026	0.910
Sorting nexin-12;	O70493	1	5	5	14.2	-0.089	-0.04	0.929
Superoxide dismutase [Cu-Zn];	P08228	1	13	36	32.5	-0.089	-0.007	0.919
Parvalbumin alpha;	P32848	1	8	25	32.7	-0.089	-0.033	0.924
MOB kinase activator 1B;	Q8BPB0	1	5	5	10.6	-0.089	-0.009	0.911
Isochorismatase domain-containing protein 1;	Q91V64	1	9	11	21.5	-0.089	-0.034	0.932
Dihydropyrimidinase-related protein 2;	O08553	1	43	73	55.8	-0.089	-0.027	0.921
Dihydropyrimidinase-related protein 3;	Q62188	1	22	28	36.3	0.251	0.049	0.770
NADP-dependent malic enzyme;	P06801	1	21	30	29.2	-0.089	-0.032	0.924
F-actin-capping protein subunit beta;	P47757	1	5	5	12.7	-0.089	-0.009	0.919
ADP-ribosylation factor 3;	P61205	1	6	14	53.6	-0.089	-0.006	0.919
ADP-ribosylation factor 5;	P84084	1	6	12	46.7	-0.269	-0.023	0.754
Biliverdin reductase A;	Q9CY64	1	14	15	44.7	-0.089	-0.038	0.928
Obg-like ATPase 1;	Q9CZ30	1	13	14	24.5	-0.089	-0.024	0.926
Protein ERGIC-53;	Q9D0F3	1	2	2	10.1	-0.089	-0.003	0.910
Adenylate kinase 2, mitochondrial;	Q9WTP6	1	7	8	28.5	-0.089	-0.031	0.923
Capping protein (Actin filament), gelsolin-like; Capping protein (Actin filament), gelsolin-like, isoform CRA_a; Uncharacterized protein;	Q99LB4	1	21	51	43.3	-0.089	-0.009	0.911
PDZ and LIM domain protein 3;	O70209	1	5	5	27.8	-0.074	-0.022	0.943
Alcohol dehydrogenase class-3;	P28474	1	11	19	24.3	-0.074	-0.028	0.945
Oxysterol-binding protein-related protein 1;	Q91XL9	1	2	2	5.4	-0.074	-0.015	0.938
Asporin;	Q99MQ4	1	5	8	16.9	-0.074	-0.023	0.935
S-methyl-5'-thioadenosine phosphorylase;	Q9CQ65	1	8	8	26.5	-0.074	-0.016	0.938
Omega-amidase NIT2;	Q9JHW2	1	13	14	42	-0.074	-0.039	0.951
Rho GTPase-activating protein 1;	Q5FWK3	1	5	6	15.9	-0.074	-0.019	0.938
Inter-alpha-trypsin inhibitor heavy chain H3;	Q61704	1	8	8	6.1	-0.074	-0.034	0.949
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial;	Q91YT0	1	7	10	16.3	-0.074	-0.041	0.952
Opioid growth factor receptor;	Q99PG2	1	3	3	6.8	-0.074	-0.01	0.928
Coronin-7;	Q9D2V7	1	14	15	16.2	-0.074	-0.032	0.941
ATP synthase subunit O, mitochondrial;	Q9DB20	1	9	12	29.6	-0.074	-0.007	0.935
Peroxisomal acyl-coenzyme A oxidase 3;	Q9EPL9	1	9	11	13.9	-0.074	-0.032	0.941
Uncharacterized protein;	E9Q0S6	1	4	4	3.6	-0.074	-0.012	0.929
Copper transport protein ATOX1;	O08997	1	8	11	57.4	-0.059	-0.01	0.944
Crk-like protein;	P47941	1	6	7	21.5	-0.059	-0.01	0.952
Carbonyl reductase [NADPH] 1;	P48758	1	17	23	52.7	-0.059	-0.012	0.945
N-acylglucosamine 2-epimerase;	P82343	1	3	3	8	-0.059	-0.038	0.962
NHL repeat-containing protein 2;	Q8BZW8	1	4	4	5.4	-0.059	-0.006	0.950
Poly(ADP-ribose) glycohydrolase ARH3;	Q8CG72	1	2	2	6.2	-0.059	-0.006	0.951
Epididymal secretory protein E1;	Q9Z0J0	1	7	10	24.8	-0.059	-0.015	0.947

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Protein 4.1;	P48193	1	5	5	6.9	-0.059	-0.003	0.950
V-type proton ATPase subunit B, brain isoform;	P62814	1	11	18	22.3	-0.059	-0.018	0.949
Ubiquitin-like modifier-activating enzyme 1;	Q02053	1	58	84	37.7	-0.059	-0.026	0.961
Protein transport protein Sec31A;	Q3UPL0	1	31	39	22	-0.059	-0.016	0.947
TOM1-like protein 2;	Q5SRX1	1	3	5	9	-0.059	-0.028	0.955
Disks large homolog 1;	Q811D0	1	3	3	6.5	-0.059	-0.009	0.951
Vacuolar protein-sorting-associated protein 25;	Q9CQ80	1	4	4	14.1	-0.059	-0.02	0.956
5'(3')-deoxyribonucleotidase, cytosolic type;	Q9JM14	1	6	8	20	-0.059	-0.006	0.943
Toll-interacting protein;	Q9QZ06	1	4	4	16.4	-0.059	-0.009	0.951
Galectin-related protein A;	Q8VED9	1	3	3	11.6	-0.059	-0.012	0.945
Ketosamine-3-kinase;	Q8K274	1	3	3	9.1	-0.059	-0.057	0.970
Target of Myb protein 1;	O88746	1	4	7	12.4	-0.044	-0.012	0.962
Peptidyl-prolyl cis-trans isomerase FKBP5;	Q64378	1	2	2	4.4	-0.044	-0.006	0.959
Presequence protease, mitochondrial;	Q8K411	1	15	16	13.9	-0.044	-0.007	0.953
Carbonyl reductase 3; Uncharacterized protein;	Q8K354	1	20	27	59.6	-0.044	-0.015	0.965
Guanine nucleotide-binding protein G(i) subunit alpha-2;	P08752	1	11	15	31.3	-0.044	-0.023	0.965
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;	P63094	1	5	5	11.7	-0.059	-0.013	0.953
Guanine nucleotide-binding protein G(k) subunit alpha;	Q9DC51	1	3	4	17.8	0.356	0.083	0.690
Guanine nucleotide-binding protein G(i) subunit alpha-1;	B2RSH2	1	4	6	18.6	-0.434	-0.059	0.611
Plastin-3;	Q99K51	1	31	49	37.8	-0.044	-0.028	0.969
Proteasome subunit beta type-3;	Q9R1P1	1	9	10	30.7	-0.044	-0.005	0.958
Neuronal proto-oncogene tyrosine-protein kinase Src;	P05480	1	2	2	1.6	-0.029	-0.005	0.967
Proteasome subunit alpha type-2;	P49722	1	14	16	48.7	-0.029	-0.012	0.978
Cysteine and glycine-rich protein 3;	P50462	1	6	7	18	-0.029	-0.005	0.974
Myomesin-1;	Q62234	1	29	32	17.8	-0.029	-0.005	0.979
Dipeptidyl peptidase 2;	Q9ET22	1	8	10	15	-0.029	-0.005	0.967
SUMO-activating enzyme subunit 1;	Q9R1T2	1	8	9	19.4	-0.029	-0.009	0.970
Uncharacterized protein;	E9Q4K7	1	4	4	1.6	-0.029	-0.004	0.967
Calpain-2 catalytic subunit;	O08529	1	15	21	16.4	-0.029	-0.006	0.970
Glutathione S-transferase Mu 2;	P15626	1	18	26	60.6	-0.029	-0.007	0.968
Glutathione S-transferase Mu 1;	P10649	1	12	22	53.7	0.07	0.026	0.946
Mitogen-activated protein kinase 3;	Q63844	1	6	6	19.2	-0.029	-0.005	0.974
Mitogen-activated protein kinase 1;	P63085	0.998	3	3	13.7	1.07	0.392	0.272
Enoyl-CoA hydratase, mitochondrial;	Q8BH95	1	8	10	18.6	-0.029	-0.005	0.967
Proteasome subunit beta type-10;	O35955	0.997	2	2	4	-0.029	-0.002	0.966
Corticosteroid-binding globulin;	Q06770	1	6	7	8.6	-0.014	-0.003	0.989
Guanylate kinase;	Q64520	1	2	2	6.1	-0.014	-0.001	0.981
Glycerol-3-phosphate dehydrogenase, mitochondrial;	Q64521	1	3	3	3.4	-0.014	-0.003	0.982
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Q8BMF4	1	24	30	30.8	-0.014	-0.007	0.986
Nicotinamide phosphoribosyltransferase;	Q99KQ4	1	10	11	16.9	-0.014	-0.005	0.982
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial;	Q9D0K2	1	36	75	45.3	-0.014	-0.003	0.989
AP-3 complex subunit beta-1;	Q9Z1T1	1	3	3	3.4	-0.014	-0.006	0.991

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Ubiquitin-conjugating enzyme E2 K;	P61087	1	6	6	27.5	-0.014	-0.005	0.984
Ubiquitin-conjugating enzyme E2 N;	P61089	1	9	10	46.7	-0.014	-0.003	0.982
Aminopeptidase N;	P97449	1	26	32	20.9	-0.014	-0.007	0.991
Serine/threonine-protein kinase 4;	Q9JI11	0.997	2	2	4.5	-0.014	-0.007	0.991
Guanylate-binding protein 9; MCG142489, isoform CRA_a; Uncharacterized protein; Gbp6 protein; Guanylate binding protein 7; MCG141961, isoform CRA_a;	Q8BTS3	1	2	2	5.2	-0.014	-0.004	0.990
Uncharacterized protein;	Q91Z40	0.994	2	2	5.3	0.151	0.018	0.862
Uncharacterized protein;	F8WI09	0.993	2	2	2.8	-0.014	-0.004	0.983
Ubiquitin-fold modifier-conjugating enzyme 1;	Q9CR09	0.975	2	2	10.2	-0.014	-0.001	0.981
Macrophage migration inhibitory factor;	P34884	1	2	6	7.8	0	0	0.996
26S protease regulatory subunit 8;	P62196	1	6	8	26.6	0	0	0.997
Acetyl-CoA acetyltransferase, mitochondrial;	Q8QZT1	1	15	17	29	0	0	0.997
Serine/threonine-protein kinase 38;	Q91VJ4	1	3	3	5.6	0	0	1.000
Ubiquitin-like-conjugating enzyme ATG3;	Q9CPX6	1	3	3	7.3	0	0	0.996
Prolyl endopeptidase;	Q9QUR6	1	31	41	35.9	0	0	0.997
Proteasome subunit beta type-2;	Q9R1P3	1	4	4	10.4	0	0	0.997
Lysosomal alpha-glucosidase;	P70699	1	5	6	7.6	0	0	0.999
Copine-3;	Q8BT60	1	11	12	24.8	0	0	0.997
Ubiquitin-conjugating enzyme E2 variant 1;	Q9CZY3	1	6	7	30.6	0	0	0.997
ADP-sugar pyrophosphatase;	Q9JKX6	1	7	8	23.9	0	0	0.996
Uncharacterized protein;	D3Z7P3	1	6	8	10.9	0	0	0.995
SAR1 gene homolog A (S. cerevisiae); SAR1 gene homolog A (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q99JZ4	1	4	7	37.4	0	0	0.997
GTP-binding protein SAR1b;	Q9CQC9	1	4	6	33.3	-0.12	-0.039	0.894
Mitogen-activated protein kinase 14;	P47811	1	5	5	22.7	0.014	0.004	0.990
Serpin B5;	P70124	1	41	76	61.6	0.014	0.004	0.983
Oxysterol-binding protein-related protein 11;	Q8CI95	1	4	4	7.1	0.014	0.002	0.981
Calpain small subunit 1;	O88456	1	8	10	13.3	0.014	0.003	0.989
Annexin A2;	P07356	1	39	166	66.4	0.014	0.004	0.983
F-actin-capping protein subunit alpha-1;	P47753	1	8	11	26.6	0.014	0.002	0.989
Ubiquitin carboxyl-terminal hydrolase 5;	P56399	1	17	19	15.6	0.014	0.002	0.989
Poly(A) polymerase alpha;	Q61183	1	2	2	6.4	0.014	0.004	0.983
Protein canopy homolog 4;	Q8BQ47	1	5	6	17.6	0.014	0.002	0.982
Peptidyl-prolyl cis-trans isomerase D;	Q9CR16	1	17	22	37	0.014	0.004	0.994
Vacuolar protein sorting-associated protein 29;	Q9QZ88	1	5	5	29	0.014	0.002	0.989
Suppressor of G2 allele of SKP1 homolog;	Q9CX34	0.997	3	3	6	0.014	0.001	0.989
Lysosomal alpha-mannosidase;	O09159	1	10	10	8.8	0.029	0.01	0.978
Methylmalonyl-CoA mutase, mitochondrial;	P16332	1	7	7	12.3	0.029	0.011	0.981
Ras-related protein Rab-23;	P35288	1	5	5	13.5	0.029	0.003	0.967
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1;	Q8R3B1	1	8	10	10.4	0.029	0.009	0.977
Exportin-2;	Q9ERK4	1	2	2	3.4	0.029	0.004	0.974
Dihydrolipoyl dehydrogenase, mitochondrial;	O08749	1	22	40	27.3	0.029	0.011	0.972
26S protease regulatory subunit 6A;	O88685	1	14	14	32.5	0.029	0.015	0.981

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Protein Niban;	Q3UW53	1	10	10	13.4	0.029	0.014	0.974
Nischarin;	Q80TM9	1	3	4	11.6	0.029	0.003	0.974
Serine/threonine-protein phosphatase;	F7BX26	1	4	5	8.8	0.029	0.003	0.967
Trk-fused; Uncharacterized protein;	Q8C2C6	1	3	3	7.8	0.029	0.01	0.978
Thioredoxin;	P10639	1	6	10	46.7	0.043	0.01	0.960
60S acidic ribosomal protein P2;	P99027	1	2	2	28.7	0.043	0.007	0.960
Filamin-B;	Q80X90	1	18	18	9.1	0.043	0.034	0.977
Succinate-semialdehyde dehydrogenase, mitochondrial;	Q8BWF0	1	3	3	8.6	0.043	0.014	0.964
THO complex subunit 4;	O08583	1	3	3	14.1	0.043	0.019	0.967
Phosphatidylinositol transfer protein alpha isoform;	P53810	1	8	13	26.6	0.043	0.025	0.972
GTP-binding nuclear protein Ran;	P62827	1	15	28	39.4	0.043	0.006	0.960
Voltage-dependent anion-selective channel protein 1;	Q60932	1	17	26	55.7	0.043	0.005	0.963
Ras-related protein Rab-21;	P35282	1	10	10	36.9	0.057	0.018	0.952
Serine/threonine-protein kinase OSR1;	Q6P9R2	1	2	2	5.5	0.057	0.005	0.945
Selenide, water dikinase 1;	Q8BH69	1	4	6	7.7	0.057	0.009	0.953
GDP-fucose protein O-fucosyltransferase 2;	Q8VHI3	1	3	3	5.8	0.057	0.005	0.952
Ubiquitin-conjugating enzyme E2 L3;	P68037	1	7	11	41.6	0.057	0.01	0.954
2-oxoglutarate dehydrogenase, mitochondrial;	Q60597	1	39	72	36.2	0.057	0.029	0.955
Adseverin;	Q60604	1	8	8	10.9	0.057	0.019	0.958
Myoferlin;	Q69ZN7	1	13	14	6.8	0.057	0.026	0.956
Ubiquitin carboxyl-terminal hydrolase isozyme L3;	Q9JKB1	1	9	9	29.6	0.057	0.009	0.946
Delta-aminolevulinic acid dehydratase;	P10518	1	12	20	35.2	0.07	0.029	0.944
Hormone-sensitive lipase;	P54310	1	11	13	13	0.07	0.024	0.940
UPF0368 protein Cxorf26 homolog;	Q9D0B6	1	4	4	15.7	0.07	0.017	0.935
Peroxisomal carnitine O-octanoyltransferase;	Q9DC50	1	3	3	2.5	0.07	0.023	0.939
Translin-associated protein X;	Q9QZE7	1	2	3	3.1	0.07	0.009	0.939
Fatty acid-binding protein, adipocyte;	P04117	1	18	137	64.4	0.07	0.006	0.938
Glutathione peroxidase 3;	P46412	1	5	7	21.6	0.07	0.011	0.932
Heterogeneous nuclear ribonucleoprotein D0;	Q60668	1	5	10	31.8	0.07	0.027	0.941
Phenylalanyl-tRNA synthetase beta chain;	Q9WUA2	1	3	3	5.6	0.07	0.004	0.930
Haloacid dehalogenase-like hydrolase domain-containing protein 3;	Q9CYW4	0.999	2	2	9.6	0.07	0.02	0.944
Cytochrome c oxidase subunit 6B1;	P56391	1	6	7	41.9	0.084	0.017	0.924
Leukocyte surface antigen CD47;	Q61735	1	3	4	8.9	0.084	0.006	0.923
5-hydroxyisourate hydrolase;	Q9CRB3	1	3	5	31.4	0.084	0.017	0.927
Calponin-3;	Q9DAW9	1	3	4	10	0.084	0.029	0.927
DAZ-associated protein 1;	Q9JII5	1	6	9	18.7	0.084	0.01	0.924
AP-2 complex subunit alpha-2;	P17427	1	6	6	11.7	0.084	0.04	0.935
AP-2 complex subunit alpha-1;	P17426	1	2	2	3.3	0.956	0.128	0.256
Catalase;	P24270	1	35	54	43.5	0.084	0.041	0.937
Septin-2;	P42208	1	13	14	39.1	0.084	0.04	0.935
ATP synthase subunit gamma, mitochondrial;	Q91VR2	1	11	16	36.4	0.084	0.013	0.919
Propionyl-CoA carboxylase alpha chain, mitochondrial;	Q91ZA3	1	14	14	18.8	0.084	0.032	0.935
Malignant T cell-amplified sequence 1;	Q9DB27	1	4	4	29.8	0.084	0.013	0.918

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GTP:AMP phosphotransferase, mitochondrial;	Q9WTP7	1	7	7	28.2	0.084	0.012	0.925
Enoyl-CoA delta isomerase 2, mitochondrial;	Q9WUR2	1	7	8	31.8	0.084	0.022	0.930
Ig alpha chain C region;	P01878	1	2	5	7	0.084	0.057	0.950
Extracellular superoxide dismutase [Cu-Zn];	O09164	1	3	4	16.3	0.098	0.029	0.917
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial;	Q61425	1	15	32	37.6	0.098	0.025	0.910
5'-nucleotidase;	Q61503	1	5	5	5.6	0.098	0.015	0.911
Trifunctional enzyme subunit alpha, mitochondrial;	Q8BMS1	1	32	37	33.8	0.098	0.015	0.904
COP9 signalosome complex subunit 8;	Q8VBV7	1	5	5	23	0.098	0.008	0.909
Neurolysin, mitochondrial;	Q91YP2	1	8	9	12.1	0.098	0.019	0.913
Prostaglandin reductase 1;	Q91YR9	1	10	14	31	0.098	0.011	0.903
Arginyl-tRNA synthetase, cytoplasmic;	Q9D0I9	1	21	26	26.2	0.098	0.056	0.935
UMP-CMP kinase;	Q9DBP5	1	13	21	45.9	0.098	0.036	0.922
Elongation factor 1-alpha 2;	P62631	1	10	31	28.5	-0.889	-0.214	0.318
Seryl-tRNA synthetase, cytoplasmic;	P26638	1	13	17	27.9	0.098	0.038	0.921
Protein disulfide-isomerase A3;	P27773	1	46	93	50.7	0.098	0.016	0.915
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;	P63330	1	12	18	32.7	0.098	0.046	0.924
Trifunctional purine biosynthetic protein adenosine-3;	Q64737	1	25	26	20.6	0.098	0.02	0.914
Calcium/calmodulin-dependent protein kinase type II subunit delta;	Q6PHZ2	1	4	5	5.8	0.098	0.067	0.941
Protein disulfide-isomerase A6;	Q922R8	1	17	20	38.6	0.098	0.018	0.916
Actin-related protein 3;	Q99JY9	1	26	34	43.3	0.098	0.017	0.912
Cytochrome b-c1 complex subunit 1, mitochondrial;	Q9CZ13	1	14	17	25.8	0.098	0.035	0.919
Actin-related protein 2/3 complex subunit 1B;	Q9WV32	1	11	13	27.7	0.098	0.027	0.912
Actin-related protein 2/3 complex subunit 1A;	Q9R0Q6	0.999	2	3	10.8	-0.434	-0.094	0.616
Protein LZIC;	Q8K3C3	1	2	2	17.4	0.098	0.021	0.908
Choline transporter-like protein 2;	Q8BY89	0.999	3	3	4.4	0.098	0.021	0.914
26S proteasome non-ATPase regulatory subunit 4;	O35226	1	5	9	10.6	0.111	0.016	0.892
Phosphoglycerate mutase 1;	Q9DBJ1	1	22	69	45.7	0.111	0.009	0.890
Small ubiquitin-related modifier 2;	P61957	1	2	4	16.9	0.111	0.009	0.889
26S proteasome non-ATPase regulatory subunit 14;	O35593	0.992	2	2	5.3	0.111	0.013	0.889
C-terminal-binding protein 1;	O88712	1	5	5	11.1	0.124	0.015	0.883
Basigin;	P18572	1	4	4	8.2	0.124	0.009	0.881
Small ubiquitin-related modifier 1;	P63166	1	4	4	18.8	0.124	0.067	0.908
Vacuolar protein sorting-associated protein 35;	Q9EQH3	1	7	7	7.3	0.124	0.072	0.911
Beta-galactosidase;	P23780	1	17	21	20.2	0.124	0.034	0.886
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1;	P62874	1	7	11	22.4	0.124	0.042	0.897
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2;	P62880	1	5	7	33.5	-0.454	-0.317	0.728
Profilin-1;	P62962	1	25	120	64.3	0.124	0.023	0.886
Rho-related GTP-binding protein RhoC;	Q62159	1	7	7	36.8	0.124	0.009	0.874
NEDD8-activating enzyme E1 regulatory subunit;	Q8VBW6	1	9	9	10.8	0.124	0.03	0.893
Uncharacterized protein;	E9QK49	1	5	6	6.6	0.124	0.05	0.902
Uncharacterized protein;	F7DBB3	1	4	4	15.8	0.124	0.053	0.907
Hypoxanthine-guanine phosphoribosyltransferase;	P00493	1	12	15	46.3	0.138	0.035	0.878
Histidyl-tRNA synthetase, cytoplasmic;	Q61035	1	3	3	8.1	0.138	0.04	0.885

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Probable E3 ubiquitin-protein ligase HERC4;	Q6PAV2	1	4	4	5.6	0.138	0.028	0.874
UDP-glucose 4-epimerase;	Q8R059	1	5	5	9.5	0.138	0.019	0.873
Protein disulfide-isomerase;	P09103	1	42	93	50.1	0.138	0.079	0.906
V-type proton ATPase catalytic subunit A;	P50516	1	14	18	18.5	0.138	0.031	0.876
RNA-binding protein 12;	Q8R4X3	1	3	3	4.5	0.138	0.053	0.893
Microtubule-associated protein 1B;	P14873	1	4	5	3.2	0.151	0.015	0.862
GDP-L-fucose synthase;	P23591	1	4	4	7.2	0.151	0.026	0.859
Neutrophil cytosol factor 1;	Q09014	1	4	4	4.6	0.151	0.029	0.867
Ganglioside GM2 activator;	Q60648	1	6	7	20.7	0.151	0.02	0.858
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Q76MZ3	1	26	29	34.3	0.151	0.071	0.883
CCA tRNA nucleotidyltransferase 1, mitochondrial;	Q8K1J6	1	3	3	4.1	0.151	0.068	0.890
Acyl-CoA synthetase family member 2, mitochondrial;	Q8VCW8	1	14	14	21	0.151	0.053	0.881
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1;	Q91YQ5	1	3	3	7.2	0.151	0.048	0.871
Threonyl-tRNA synthetase, cytoplasmic;	Q9D0R2	1	6	7	8.6	0.151	0.067	0.883
Non-specific lipid-transfer protein;	P32020	1	14	18	19.2	0.151	0.079	0.897
Poly(rC)-binding protein 1;	P60335	1	17	27	45.8	0.151	0.019	0.863
Poly(rC)-binding protein 2;	Q61990	1	9	14	25.7	0.251	0.034	0.763
Glucose-6-phosphate 1-dehydrogenase X;	Q00612	1	33	45	36.1	0.151	0.022	0.864
Stromal membrane-associated protein 1;	Q91VZ6	1	5	6	5.5	0.151	0.01	0.861
Actin-related protein 2/3 complex subunit 2;	Q9CVB6	1	11	13	33	0.151	0.026	0.862
Basal cell adhesion molecule;	Q9R069	1	5	5	10.1	0.151	0.019	0.857
RING finger protein 114;	Q9ET26	1	2	2	8.4	0.151	0.027	0.866
Methylosome protein 50;	Q99J09	0.997	2	3	18.6	0.151	0.029	0.861
Peroxisomal multifunctional enzyme type 2;	P51660	1	16	18	15.6	0.163	0.012	0.843
Proteasome activator complex subunit 1;	P97371	1	8	10	28.5	0.163	0.017	0.849
Cleft lip and palate transmembrane protein 1 homolog;	Q8VBZ3	1	3	3	7.5	0.163	0.026	0.846
Transaldolase;	Q93092	1	14	26	22.6	0.163	0.022	0.843
Dipeptidyl peptidase 3;	Q99KK7	1	14	18	17.5	0.163	0.036	0.857
Secretory carrier-associated membrane protein 4;	Q9JKV5	1	2	2	4.8	0.163	0.02	0.843
Glucosamine-6-phosphate isomerase 1;	O88958	1	3	3	19.7	0.163	0.076	0.881
Glucosamine-6-phosphate isomerase 2;	Q9CRC9	1	2	2	21.5	-0.474	-0.323	0.706
Myosin light chain 1/3, skeletal muscle isoform;	P05977	1	13	46	52.1	0.163	0.039	0.857
Calpastatin;	P51125	1	7	8	14.8	0.163	0.065	0.874
Elongation factor G, mitochondrial;	Q8K0D5	1	2	2	3.5	0.163	0.028	0.846
Gamma-butyrobetaine dioxygenase;	Q924Y0	1	5	6	13.2	0.163	0.031	0.854
SEC14-like protein 2;	Q99J08	1	3	3	12.2	0.163	0.028	0.846
Uncharacterized protein;	E9Q912	1	9	11	17	0.163	0.076	0.880
Calpain-1 catalytic subunit;	O35350	1	28	34	30	0.176	0.086	0.873
Coproporphyrinogen-III oxidase, mitochondrial;	P36552	1	5	5	10.4	0.176	0.014	0.835
Transcription elongation factor B polypeptide 2;	P62869	1	4	4	52.5	0.176	0.006	0.827
Serine-threonine kinase receptor-associated protein;	Q9Z1Z2	1	16	18	38.6	0.176	0.04	0.839
ADP/ATP translocase 1;	P48962	1	19	44	34.2	0.176	0.048	0.847
ADP/ATP translocase 2;	P51881	1	4	10	22.8	1.098	0.077	0.185

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
CAP-Gly domain-containing linker protein 1;	Q922J3	1	6	6	5.2	0.176	0.087	0.867
NSFL1 cofactor p47;	Q9CZ44	1	20	25	39.2	0.176	0.062	0.858
Glycolipid transfer protein;	Q9JL62	1	4	5	10	0.176	0.02	0.836
N-acetyl-D-glucosamine kinase;	Q9QZ08	1	4	5	8.5	0.176	0.011	0.830
Interferon-induced guanylate-binding protein 2;	Q9Z0E6	1	16	17	22.9	0.176	0.036	0.845
COP9 signalosome complex subunit 7a;	Q9CZ04	1	2	2	13.6	0.176	0.025	0.832
Uridine diphosphate glucose pyrophosphatase;	Q9D142	1	2	2	4.1	0.176	0.02	0.836
Cytochrome c oxidase subunit 2;	P00405	1	4	5	13.2	0.189	0.035	0.828
Echinoderm microtubule-associated protein-like 1;	Q05BC3	1	3	3	3.4	0.189	0.045	0.834
Costars family protein C6orf115 homolog;	Q4KML4	1	4	7	27.2	0.189	0.058	0.836
Fascin;	Q61553	1	8	10	14.2	0.189	0.035	0.829
Drebrin-like protein;	Q62418	1	15	15	28.9	0.189	0.035	0.822
Ubiquitin carboxyl-terminal hydrolase 47;	Q8BY87	1	2	2	2	0.189	0.04	0.831
Myomesin 2; Uncharacterized protein;	Q14BI5	1	21	24	11.8	0.189	0.08	0.855
Proteasome subunit beta type-5;	O55234	1	9	12	27.3	0.189	0.081	0.850
Heat shock protein HSP 90-beta;	P11499	1	36	81	42.5	0.189	0.091	0.863
Endoplasmin;	P08113	1	28	42	25.8	0.379	0.23	0.757
Heat shock protein HSP 90-alpha;	P07901	1	26	47	38.1	0.623	0.202	0.506
Heat shock cognate 71 kDa protein;	P63017	1	37	81	46.6	0.189	0.053	0.832
78 kDa glucose-regulated protein;	P20029	1	35	67	39.5	-0.201	-0.139	0.879
Heat shock 70 kDa protein 1A;	Q61696	1	32	45	41.7	0.454	0.126	0.623
Biglycan;	P28653	1	6	7	16.8	0.202	0.151	0.882
Transketolase;	P40142	1	45	101	45.1	0.202	0.042	0.814
UPF0585 protein C16orf13 homolog;	Q9DCS2	1	2	2	16.8	0.202	0.044	0.820
Bifunctional protein NCOAT;	Q9EQQ9	1	4	5	7.9	0.202	0.025	0.811
Chloride intracellular channel protein 4;	Q9QYB1	1	14	17	45.8	0.202	0.044	0.820
Chloride intracellular channel protein 1;	Q9Z1Q5	1	23	34	64.7	0.202	0.037	0.816
General vesicular transport factor p115;	Q9Z1Z0	1	5	5	7.1	0.202	0.039	0.811
Actin-related protein 2/3 complex subunit 5;	Q9CPW4	1	4	5	29.1	0.202	0.1	0.854
Glycogen phosphorylase, muscle form;	Q9WUB3	1	53	102	50.7	0.202	0.118	0.860
Glycogen phosphorylase, brain form;	Q8CI94	1	12	16	23.5	0.536	0.081	0.531
Glycogen phosphorylase, liver form;	Q9ET01	1	8	9	16.1	-0.184	-0.052	0.845
Epididymis-specific alpha-mannosidase;	O54782	1	2	2	2.8	0.214	0.07	0.821
Stress-induced-phosphoprotein 1;	Q60864	1	21	25	26.7	0.214	0.087	0.829
Thimet oligopeptidase;	Q8C1A5	1	21	29	26.9	0.214	0.09	0.835
Protein phosphatase Slingshot homolog 3;	Q8K330	1	2	2	4.8	0.214	0.065	0.818
Di-N-acetylchitobiase;	Q8R242	1	3	3	8.2	0.214	0.079	0.827
Reticulon-4;	Q99P72	1	4	4	16.9	0.214	0.026	0.799
Trans-2-enoyl-CoA reductase, mitochondrial;	Q9DCS3	1	9	9	28.4	0.214	0.068	0.816
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial;	O88696	1	2	3	6.6	0.227	0.019	0.790
Voltage-dependent anion-selective channel protein 3;	Q60931	1	5	5	22.3	0.227	0.107	0.831
GDP-mannose 4,6 dehydratase;	Q8K0C9	1	3	3	6.7	0.227	0.056	0.806
Guanine nucleotide-binding protein subunit alpha-13;	P27601	1	2	2	5.3	0.227	0.054	0.804

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
60 kDa heat shock protein, mitochondrial;	P63038	1	29	49	42.6	0.227	0.062	0.809
Protein phosphatase 1 regulatory subunit 7;	Q3UM45	1	12	14	34.3	0.227	0.091	0.820
Calcium-binding mitochondrial carrier protein Aralar1;	Q8BH59	1	3	4	4	0.227	0.089	0.825
Inorganic pyrophosphatase 2, mitochondrial;	Q91VM9	1	5	5	21.5	0.227	0.136	0.852
MAGUK p55 subfamily member 6;	Q9JLB0	1	2	2	4.5	0.227	0.07	0.807
Ubiquitin carboxyl-terminal hydrolase isozyme L5;	Q9WUP7	0.998	2	2	7.6	0.227	0.029	0.793
Vasodilator-stimulated phosphoprotein;	P70460	1	3	3	13.3	0.239	0.053	0.785
Ubiquitin-like modifier-activating enzyme 6;	Q8C7R4	1	13	13	12.1	0.239	0.093	0.808
Cadherin-13;	Q9WTR5	1	7	7	8.4	0.239	0.02	0.778
Chromobox protein homolog 3;	P23198	1	4	4	12.6	0.239	0.081	0.801
Talin-1;	P26039	1	79	96	30.9	0.239	0.087	0.810
Talin-2;	Q71LX4	1	6	6	5.5	0.07	0.028	0.949
Isoleucyl-tRNA synthetase, mitochondrial;	Q8BIJ6	1	7	7	7.4	0.239	0.132	0.835
EGF-containing fibulin-like extracellular matrix protein 1;	Q8BPB5	1	14	21	27.4	0.239	0.132	0.832
ATP synthase subunit g, mitochondrial;	Q9CPQ8	1	6	14	27.2	0.239	0.036	0.783
Platelet glycoprotein 4;	Q08857	1	7	10	11	0.251	0.03	0.762
Proteasome subunit beta type-6;	Q60692	1	6	9	13	0.251	0.021	0.766
Ubiquitin domain-containing protein UBFD1;	Q78JW9	1	2	2	15.9	0.251	0.034	0.763
Cell surface glycoprotein MUC18;	Q8R2Y2	1	7	7	12.3	0.251	0.051	0.776
AP-2 complex subunit beta;	Q9DBG3	1	14	14	14.2	0.251	0.053	0.778
Polyubiquitin-B;	P0CG49	1	6	8	44.6	0.251	0.03	0.762
Extracellular matrix protein 1;	Q61508	0.993	2	2	6.5	0.251	0.04	0.771
AP-1 complex subunit beta-1;	O35643	1	13	15	15.1	0.263	0.142	0.812
Protein dpy-30 homolog;	Q99LT0	1	4	4	36.4	0.263	0.028	0.755
ATP synthase subunit d, mitochondrial;	Q9DCX2	1	6	8	37.7	0.263	0.064	0.771
Bifunctional aminoacyl-tRNA synthetase;	Q8CGC7	1	19	21	13	0.263	0.059	0.768
Uncharacterized protein;	E9Q070	1	3	3	12.3	0.263	0.035	0.752
Protein S100-A4;	P07091	0.997	2	2	15.8	0.263	0.055	0.759
Osteoclast-stimulating factor 1;	Q62422	1	13	19	46	0.275	0.061	0.754
Ras-related protein Rap-1b;	Q99JI6	1	7	7	25	0.275	0.032	0.744
Cytosol aminopeptidase;	Q9CPY7	1	33	44	46.8	0.275	0.08	0.761
Septin-7;	O55131	1	6	7	14.8	0.275	0.107	0.778
UV excision repair protein RAD23 homolog B;	P54728	1	5	5	16.8	0.275	0.066	0.759
UV excision repair protein RAD23 homolog A;	P54726	1	2	2	20.2	-0.474	-0.132	0.604
Ubiquitin thioesterase OTUB1;	Q7TQI3	1	12	17	37.6	0.275	0.086	0.771
von Willebrand factor A domain-containing protein 5A;	Q99KC8	1	36	56	27.2	0.275	0.114	0.782
MCG21506; Macrophage galactose N-acetyl-galactosamine specific lectin 2 isoform i; Uncharacterized protein;	A9XX86	1	6	9	19.9	0.275	0.093	0.770
Proteasome subunit beta type-4;	P99026	1	10	12	28.8	0.287	0.085	0.751
GTPase NRas;	P08556	1	4	4	16.9	0.287	0.045	0.730
Integrin beta-1;	P09055	1	8	8	11.3	0.287	0.049	0.739
Acyl-CoA-binding protein;	P31786	1	4	6	39.1	0.287	0.125	0.782
Epidermal growth factor receptor substrate 15;	P42567	1	8	8	13.4	0.287	0.094	0.763

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Hypoxia up-regulated protein 1;	Q9JKR6	1	22	24	20.1	0.287	0.071	0.750
Proteasome subunit alpha type-7;	Q9Z2U0	1	14	24	41.1	0.287	0.056	0.736
Uncharacterized protein;	F7AM67	1	2	2	1.7	0.287	0.101	0.761
Ras-related protein Ral-A;	P63321	0.909	2	2	8.7	0.287	0.165	0.801
Hsp90 co-chaperone Cdc37;	Q61081	1	7	9	16.9	0.299	0.051	0.727
Glucocorticoid receptor;	P06537	1	4	4	6.4	0.299	0.066	0.733
Proteasome subunit alpha type-4;	Q9R1P0	1	15	23	62.4	0.299	0.036	0.723
Nebulin; Uncharacterized protein;	A2AQA9	1	5	6	1.2	0.299	0.061	0.731
T-complex protein 1 subunit theta;	P42932	1	12	12	17.2	0.31	0.195	0.798
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial;	Q91VD9	1	8	8	13.8	0.31	0.04	0.717
Amidophosphoribosyltransferase;	Q8CIH9	1	2	2	3.3	0.31	0.07	0.730
Eukaryotic initiation factor 4A-II;	P10630	1	3	3	27.1	-0.105	-0.016	0.897
Heat shock protein 105 kDa;	Q61699	1	17	17	24	0.31	0.16	0.776
Importin-5;	Q8BKC5	1	8	9	5.1	0.31	0.19	0.797
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase;	Q8C0L6	1	9	10	11.1	0.31	0.045	0.712
Proteasome subunit alpha type-5;	Q9Z2U1	1	12	18	47.7	0.31	0.11	0.747
Clathrin light polypeptide (Lca); Uncharacterized protein;	B1AWE0	1	4	4	13.4	0.31	0.033	0.709
Uncharacterized protein;	E9QPB2	1	8	10	14.4	0.31	0.123	0.752
Collagen alpha-1(XV) chain;	O35206	1	2	2	5.4	0.31	0.04	0.711
Serpin B12;	Q9D7P9	0.989	2	2	4	0.31	0.155	0.776
Putative GTP-binding protein Parf;	Q5U3K5	1	3	3	6.5	0.322	0.157	0.765
Zinc-binding alcohol dehydrogenase domain-containing protein 2;	Q8BGC4	1	12	15	25.5	0.322	0.111	0.734
Membrane primary amine oxidase;	O70423	1	12	19	19.2	0.322	0.144	0.758
COP9 signalosome complex subunit 2;	P61202	1	7	10	13.5	0.322	0.106	0.732
3-hydroxyisobutyrate dehydrogenase, mitochondrial;	Q99L13	1	14	24	32.2	0.322	0.121	0.746
Perilipin-4;	O88492	1	35	48	35	0.333	0.151	0.748
Transcription factor p65;	Q04207	1	4	4	9.3	0.333	0.029	0.691
Phospholysine phosphohistidine inorganic pyrophosphate phosphatase;	Q9D7I5	1	5	8	13	0.333	0.032	0.685
Transgelin-2;	Q9WVA4	1	15	24	52.3	0.333	0.14	0.742
Cell division control protein 42 homolog;	P60766	1	14	20	42.4	0.333	0.069	0.700
Ras-related C3 botulinum toxin substrate 1;	P63001	1	11	16	34.4	0.546	0.172	0.561
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;	P62137	1	5	5	39.4	0.333	0.037	0.693
Epidermal growth factor receptor substrate 15-like 1;	Q60902	1	3	3	7.3	0.333	0.145	0.749
ATPase Asna1;	O54984	1	2	2	6	0.345	0.049	0.679
Cathepsin B;	P10605	1	19	28	35.7	0.345	0.111	0.717
182 kDa tankyrase-1-binding protein;	P58871	1	4	4	2.6	0.345	0.185	0.761
Myotrophin;	P62774	1	5	6	20.3	0.345	0.076	0.697
Vitamin K-dependent protein S;	Q08761	1	2	2	2.7	0.345	0.054	0.687
Gamma-glutamylcyclotransferase;	Q9D7X8	1	7	7	27.1	0.345	0.054	0.682
Multifunctional protein ADE2;	Q9DCL9	1	8	9	16.7	0.345	0.201	0.766
Glutathione S-transferase kappa 1;	Q9DCM2	1	7	8	28.3	0.345	0.177	0.755
Uncharacterized protein;	E9Q2T3	1	5	5	1.9	0.345	0.136	0.727
Vinculin;	Q64727	1	46	86	31.2	0.345	0.166	0.750

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Protein disulfide-isomerase A4;	P08003	1	23	29	27.1	0.356	0.214	0.762
Thioredoxin-like protein 1;	Q8CDN6	1	8	8	23.9	0.356	0.097	0.697
Farnesyl pyrophosphate synthase;	Q920E5	1	14	18	20.4	0.356	0.064	0.674
Pyruvate carboxylase, mitochondrial;	Q05920	1	9	9	7.5	0.356	0.039	0.665
Selenocysteine lyase;	Q9JLI6	1	4	4	10.9	0.356	0.167	0.733
Acyl-coenzyme A thioesterase 2, mitochondrial;	Q9QYR9	1	7	7	16.6	0.356	0.039	0.671
Acyl-coenzyme A thioesterase 1;	O55137	1	4	6	19.3	0.124	0.022	0.879
Tyrosine-protein phosphatase non-receptor type 11;	P35235	1	5	5	8.9	0.367	0.102	0.688
Nucleosome assembly protein 1-like 4;	Q78ZA7	1	4	4	10.1	0.367	0.043	0.661
Heterogeneous nuclear ribonucleoprotein L;	Q8R081	1	4	5	8.5	0.367	0.265	0.782
Heat shock protein 75 kDa, mitochondrial;	Q9CQN1	1	6	6	12.3	0.367	0.057	0.666
Isoamyl acetate-hydrolyzing esterase 1 homolog;	Q9DB29	1	8	9	22.9	0.367	0.168	0.726
Cathepsin Z;	Q9WUU7	1	6	9	7.8	0.367	0.04	0.660
Adenylyl cyclase-associated protein 1;	P40124	1	17	22	28.9	0.367	0.068	0.673
Aldo-keto reductase family 1 member C18;	Q8K023	1	5	9	14.6	0.367	0.105	0.689
Mitochondrial 2-oxoglutarate/malate carrier protein;	Q9CR62	1	3	3	8.9	0.367	0.139	0.709
Lymphocyte-specific protein 1;	P19973	1	3	3	17.7	0.379	0.125	0.689
Proteasome subunit beta type-8;	P28063	1	7	10	22.1	0.379	0.163	0.718
Proteasome subunit beta type-9;	P28076	1	5	5	25.1	0.379	0.137	0.696
Inosine triphosphate pyrophosphatase;	Q9D892	1	5	6	21.2	0.379	0.117	0.685
MCG140951; Plexin B2; Plxnb2 protein; Uncharacterized protein;	B2RXS4	1	3	3	3.4	0.379	0.055	0.654
C-terminal-binding protein 2;	P56546	1	3	3	6.9	0.379	0.038	0.654
Elongation factor 2;	P58252	1	62	105	41.4	0.379	0.16	0.710
BTB/POZ domain-containing protein KCTD12;	Q6WVG3	1	10	13	28.4	0.379	0.128	0.696
Filamin-A;	Q8BTM8	1	87	112	32.5	0.379	0.23	0.752
C-1-tetrahydrofolate synthase, cytoplasmic;	Q922D8	1	8	9	8.6	0.379	0.096	0.672
Glutaminyl-tRNA synthetase; Uncharacterized protein;	Q8BML9	1	14	14	21.4	0.379	0.085	0.670
Cytochrome c oxidase subunit 7A1, mitochondrial;	P56392	1	2	2	16.2	0.379	0.044	0.656
T-complex protein 1 subunit eta;	P80313	1	6	6	9.4	0.39	0.191	0.719
Serine/threonine-protein phosphatase 6 regulatory subunit 1;	Q7TSI3	1	2	2	4.8	0.39	0.083	0.661
Ubiquitin carboxyl-terminal hydrolase 14;	Q9JMA1	1	6	11	8.5	0.39	0.042	0.639
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial;	O35459	1	6	6	16.8	0.39	0.104	0.671
Tyrosine-protein kinase CSK;	P41241	1	3	3	8.4	0.39	0.039	0.644
Adenylosuccinate lyase;	P54822	1	6	7	18.6	0.39	0.083	0.661
Junction plakoglobin;	Q02257	1	8	9	15.3	0.39	0.214	0.732
Myosin light polypeptide 6;	Q60605	1	12	24	37.7	0.39	0.113	0.671
Prolyl 4-hydroxylase subunit alpha-1;	Q60715	1	13	16	21	0.39	0.074	0.653
Pyruvate dehydrogenase protein X component, mitochondrial;	Q8BKZ9	1	6	7	14.8	0.39	0.131	0.681
STE20-like serine/threonine-protein kinase;	O54988	1	4	4	6.2	0.401	0.182	0.700
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1;	Q60967	1	8	12	11.5	0.401	0.046	0.630
Parkinson disease 7 domain-containing protein 1;	Q8BFQ8	1	3	3	31.4	0.401	0.131	0.670
NHL repeat-containing protein 3;	Q8CCH2	1	3	3	11	0.401	0.191	0.706
26S proteasome non-ATPase regulatory subunit 3;	P14685	1	14	16	20.9	0.401	0.17	0.699

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Nucleobindin-1;	Q02819	1	3	4	7	0.401	0.036	0.627
Prenylcysteine oxidase;	Q9CQF9	1	4	4	8.7	0.401	0.176	0.702
Cytosolic purine 5'-nucleotidase;	Q3V1L4	0.998	2	2	6.4	0.401	0.055	0.637
Fibulin-2;	P37889	1	5	5	4.1	0.411	0.046	0.625
26S protease regulatory subunit 6B;	P54775	1	8	9	28.2	0.411	0.213	0.709
Putative N-acetylglucosamine-6-phosphate deacetylase;	Q8JZV7	1	2	2	10.5	0.411	0.244	0.730
Coactosin-like protein;	Q9CQI6	1	7	9	46.5	0.411	0.077	0.630
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial;	Q9D6J6	1	5	6	24.2	0.411	0.096	0.645
Vacuolar protein sorting-associated protein 26A;	P40336	1	4	4	15.3	0.411	0.043	0.619
Cytochrome b5;	P56395	1	7	8	41	0.411	0.049	0.626
Ras suppressor protein 1;	Q01730	1	4	5	13.7	0.411	0.034	0.621
N-alpha-acetyltransferase 38, NatC auxiliary subunit;	Q6ZWM4	1	3	3	16.7	0.422	0.05	0.611
40S ribosomal protein S21;	Q9CQR2	1	5	6	39.8	0.422	0.151	0.665
Creatine kinase U-type, mitochondrial;	P30275	1	8	13	24.2	0.422	0.183	0.682
Aldose reductase-related protein 2;	P45377	1	6	7	18.7	0.422	0.117	0.644
Eukaryotic translation initiation factor 3 subunit I;	Q9QZD9	1	5	5	21.5	0.422	0.076	0.626
Uncharacterized protein;	E9Q2P1	1	11	17	23.4	0.422	0.063	0.620
Ig gamma-3 chain C region;	P03987	1	6	6	13.8	0.433	0.08	0.616
Arylsulfatase B;	P50429	1	5	6	5.4	0.433	0.192	0.678
T-complex protein 1 subunit beta;	P80314	1	15	16	28.8	0.433	0.202	0.685
Transmembrane 9 superfamily member 2;	P58021	1	3	4	3.9	0.433	0.138	0.646
DNA damage-binding protein 1;	Q3U1J4	1	9	12	9.3	0.433	0.061	0.609
Metalloreductase STEAP3;	Q8CI59	1	4	4	11.3	0.433	0.071	0.611
Uncharacterized protein;	F6RT34	1	4	5	21.2	0.433	0.035	0.597
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;	P31230	1	8	12	29.4	0.444	0.065	0.600
Coiled-coil and C2 domain-containing protein 1B;	Q8BRN9	1	2	2	3.2	0.444	0.075	0.609
Cytoplasmic dynein 1 light intermediate chain 2;	Q6PDL0	1	3	3	9.3	0.444	0.072	0.608
Cytoplasmic dynein 1 light intermediate chain 1;	Q8R1Q8	1	3	3	15.5	0.766	0.365	0.474
GTPase IMAP family member 4;	Q99JY3	1	3	3	18.7	0.444	0.134	0.632
1-acylglycerol-3-phosphate O-acyltransferase ABHD5;	Q9DBL9	0.961	2	3	9.7	0.444	0.069	0.602
ATP-binding cassette sub-family E member 1;	P61222	1	3	4	3.8	0.454	0.219	0.672
Eukaryotic translation initiation factor 6;	O55135	1	5	5	37.1	0.454	0.06	0.593
Exportin-1;	Q6P5F9	1	2	2	3.2	0.454	0.222	0.673
Lysophosphatidic acid phosphatase type 6;	Q8BP40	1	9	13	16.5	0.454	0.149	0.630
UPF0364 protein C6orf211 homolog;	A6H630	1	2	2	5.9	0.454	0.295	0.715
Coatomer subunit beta';	O55029	1	4	4	7.6	0.465	0.128	0.613
Serine/threonine-protein kinase WNK1;	P83741	1	2	2	4.4	0.465	0.084	0.592
CD166 antigen;	Q61490	1	3	3	9.3	0.465	0.047	0.580
SEC14-like protein 4;	Q8R0F9	1	17	21	34.2	0.465	0.179	0.637
Peptidyl-prolyl cis-trans isomerase A;	P17742	1	12	42	47	0.465	0.29	0.706
Glutamate dehydrogenase 1, mitochondrial;	P26443	1	11	12	21.5	0.465	0.044	0.575
Endoplasmic reticulum aminopeptidase 1;	Q9EQH2	1	11	13	9.8	0.465	0.064	0.580
Mevalonate kinase;	Q9R008	1	5	5	19.2	0.465	0.118	0.608

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;	E9Q8T1	1	9	9	4.8	0.465	0.179	0.636
Lectin, galactose binding, soluble 7; Lectin, galactose binding, soluble 7, isoform CRA_a; Uncharacterized protein;	Q9CRB1	1	18	67	75	0.465	0.118	0.608
Lysosome membrane protein 2;	O35114	0.962	2	2	5.6	0.465	0.125	0.612
Isoleucyl-tRNA synthetase, cytoplasmic;	Q8BU30	1	6	6	5.2	0.475	0.116	0.598
Ubiquitin carboxyl-terminal hydrolase 4;	P35123	1	5	6	5.2	0.475	0.082	0.577
Uncharacterized protein;	E9QA15	1	2	2	2.7	0.475	0.096	0.582
Serine hydroxymethyltransferase;	Q9CZN7	1	3	3	3.6	0.475	0.082	0.577
Glucosidase 2 subunit beta;	O08795	1	7	10	13.8	0.485	0.09	0.573
Spectrin beta chain, brain 1;	Q62261	1	7	7	4	0.485	0.215	0.642
Tissue alpha-L-fucosidase;	Q99LJ1	1	3	3	8.2	0.485	0.118	0.582
Signal transducer and activator of transcription 1;	P42225	1	6	6	7.3	0.485	0.194	0.626
S-phase kinase-associated protein 1;	Q9WTX5	1	3	3	20.2	0.485	0.066	0.562
Tubulin-folding cofactor B;	Q9D1E6	1	2	2	4.5	0.485	0.09	0.575
Uncharacterized protein KIAA0564 homolog;	Q8CC88	0.996	2	2	1.6	0.485	0.111	0.580
N-acetylgalactosamine-6-sulfatase;	Q571E4	0.99	2	2	4.8	0.485	0.426	0.750
Thy-1 membrane glycoprotein;	P01831	1	6	7	31.5	0.496	0.134	0.586
Eukaryotic peptide chain release factor subunit 1;	Q8BWY3	1	3	3	5	0.496	0.063	0.555
Keratin, type II cytoskeletal 1b;	Q6IFZ6	1	12	13	16.1	0.496	0.148	0.596
Septin-5;	Q9Z2Q6	1	5	6	13.6	0.496	0.12	0.575
Ig kappa chain C region;	P01837	1	5	8	36.8	0.506	0.267	0.652
Putative transferase CAF17 homolog, mitochondrial;	Q8CAK1	1	2	2	7.5	0.506	0.061	0.546
Interferon-activable protein 205-A;	Q8CGE8	1	2	2	5.7	0.506	0.103	0.562
Arachidonate 12-lipoxygenase, epidermal-type;	P55249	1	2	2	3.3	0.506	0.235	0.632
Decorin;	P28654	1	8	14	19.8	0.516	0.126	0.562
U6 snRNA-associated Sm-like protein LSm2;	O35900	1	3	4	47.4	0.516	0.115	0.561
COP9 signalosome complex subunit 3;	O88543	1	6	6	24.1	0.516	0.213	0.613
Plasma membrane Ca++ transporting ATPase 4 variant x/e; Uncharacterized protein;	D1FNM8	0.999	6	7	5.6	0.516	0.058	0.537
MCG21235; Uncharacterized protein;	Q9D1Q5	1	15	19	38.2	0.516	0.227	0.622
40S ribosomal protein S20;	P60867	1	2	2	10.1	0.516	0.032	0.531
Stress-70 protein, mitochondrial;	P38647	1	36	51	39.8	0.526	0.153	0.572
IgG receptor FcRn large subunit p51;	Q61559	1	2	2	6.6	0.526	0.073	0.536
Transmembrane emp24 domain-containing protein 10;	Q9D1D4	1	4	4	24.2	0.526	0.15	0.570
Glutathione S-transferase Mu 5;	P48774	1	12	17	34.4	0.526	0.259	0.630
Inorganic pyrophosphatase;	Q9D819	1	16	26	48.1	0.526	0.219	0.607
Uncharacterized protein;	E9Q4Z2	1	5	5	3.6	0.526	0.336	0.672
Acetyl-CoA carboxylase 1;	Q5SWU9	0.999	4	4	3.2	1.299	0.195	0.126
Complement component 1, q subcomponent binding protein; Complement component 1, q subcomponent binding protein, isoform CRA_b; Uncharacterized protein; p32-RACK;	Q8R5L1	1	7	12	17.2	0.526	0.095	0.544
Arachidonate 5-lipoxygenase;	P48999	1	2	2	1.3	0.526	0.077	0.537
Probable ATP-dependent RNA helicase DDX6;	P54823	1	2	2	6.8	0.526	0.113	0.550
Integrin beta-5;	O70309	1	2	3	3	0.526	0.062	0.529

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LanC-like protein 1;	O89112	1	2	2	9	0.536	0.048	0.521
14-3-3 protein gamma;	P61982	1	5	8	24.3	0.536	0.281	0.633
Short-chain specific acyl-CoA dehydrogenase, mitochondrial;	Q07417	1	2	2	8.3	0.536	0.037	0.519
Glutaredoxin-related protein 5, mitochondrial;	Q80Y14	1	3	3	21.7	0.536	0.03	0.514
Protein MEMO1;	Q91VH6	1	2	2	5.1	0.536	0.092	0.529
Periaxin;	O55103	1	8	8	9.3	0.536	0.303	0.645
Plectin;	Q9QXS1	1	24	25	6.4	0.536	0.24	0.608
Uncharacterized protein;	E9Q8E3	1	4	4	3.7	0.536	0.303	0.644
Muscle-related coiled-coil protein;	A2AMM0	1	2	2	3.9	0.546	0.097	0.522
Legumain;	O89017	1	2	2	3.9	0.546	0.097	0.523
26S protease regulatory subunit 10B;	P62334	1	16	19	43.4	0.546	0.176	0.559
Protein arginine N-methyltransferase 5;	Q8CIG8	1	5	5	8	0.546	0.075	0.515
Troponin T, fast skeletal muscle;	Q9QZ47	1	2	2	6.7	0.546	0.105	0.530
Heterogeneous nuclear ribonucleoprotein K;	P61979	1	23	41	30.4	0.546	0.097	0.522
Nuclear protein localization protein 4 homolog;	P60670	1	2	2	4.4	0.556	0.057	0.502
Tax1-binding protein 3;	Q9DBG9	1	3	3	13.7	0.556	0.034	0.502
MKIAA0079 protein; SEC24 related gene family, member C (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q80U83	1	6	6	7.1	0.556	0.098	0.518
Eukaryotic translation initiation factor 4 gamma 3;	Q80XI3	1	3	3	2.4	0.556	0.095	0.519
Eukaryotic translation initiation factor 4 gamma 1;	Q6NZJ6	1	2	2	2.7	0.934	0.147	0.271
Bleomycin hydrolase;	Q8R016	1	13	15	29.5	0.556	0.318	0.634
Neuroplastin;	P97300	1	2	4	3	0.556	0.023	0.500
Proteasome subunit beta type-1;	O09061	1	15	19	38.8	0.566	0.214	0.566
Ig gamma-2B chain C region;	P01867	1	8	8	17.6	0.566	0.161	0.539
6-phosphogluconate dehydrogenase, decarboxylating;	Q9DCD0	1	19	31	30.8	0.566	0.18	0.548
Phospholipid scramblase 3;	Q9JIZ9	0.992	2	2	2.4	0.566	0.099	0.511
Arf-GAP domain and FG repeats-containing protein 1;	Q8K2K6	1	3	3	10	0.575	0.178	0.541
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial;	Q921G7	1	5	7	9.5	0.575	0.096	0.504
Aspartyl-tRNA synthetase, cytoplasmic;	Q922B2	1	9	9	17	0.575	0.154	0.526
CD2-associated protein;	Q9JLQ0	1	5	5	6.4	0.575	0.085	0.495
Destrin;	Q9R0P5	1	10	22	34.5	0.575	0.297	0.607
Glutathione S-transferase omega-1;	O09131	1	9	9	26.2	0.575	0.178	0.537
Tubulin beta-4B chain;	P68372	1	9	11	56.2	0.575	0.039	0.490
Tubulin beta-5 chain;	P99024	1	6	10	54.1	0.239	0.075	0.803
Tubulin beta-2A chain;	Q7TMM9	1	2	2	38	0.333	0.024	0.684
T-complex protein 1 subunit zeta;	P80317	1	5	5	13.6	0.575	0.235	0.567
26S proteasome non-ATPase regulatory subunit 5;	Q8BJY1	1	5	5	16.3	0.575	0.197	0.548
Heat shock protein 4; Heat shock protein 4, isoform CRA_a; Uncharacterized protein;	Q3U2G2	1	42	54	39.5	0.575	0.293	0.605
Heat shock 70 kDa protein 4L;	P48722	1	10	10	20.2	0.903	0.241	0.319
Secretory carrier-associated membrane protein 1;	Q8K021	1	2	2	8	0.585	0.086	0.493
Serine/threonine-protein kinase 24;	Q99KH8	1	2	2	7.4	0.585	0.133	0.506
Uncharacterized protein;	E9PV24	1	20	27	28.5	0.585	0.296	0.593
Collagen alpha-1(VI) chain;	Q04857	1	6	7	8.9	0.585	0.215	0.549

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Peroxisomal acyl-coenzyme A oxidase 1;	Q9R0H0	1	16	19	30.3	0.585	0.199	0.537
Coronin-1C;	Q9WUM4	1	4	4	8.2	0.585	0.168	0.528
Uncharacterized protein;	E9Q616	1	235	341	48.7	0.585	0.292	0.595
Tripeptidyl-peptidase 1;	O89023	1	6	9	9.4	0.595	0.205	0.536
Tyrosine-protein phosphatase non-receptor type 6;	P29351	1	6	8	10.3	0.595	0.205	0.537
Ran-specific GTPase-activating protein;	P34022	1	2	2	5.4	0.595	0.055	0.477
Actin-related protein 2;	P61161	1	11	11	22.6	0.595	0.146	0.508
Transportin-1;	Q8BFY9	1	7	9	6.1	0.595	0.177	0.520
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating;	Q9R1J0	1	2	2	8.6	0.595	0.091	0.482
GMP reductase 2;	Q99L27	0.999	2	2	7.5	0.595	0.099	0.489
Long-chain-fatty-acid--CoA ligase 1;	P41216	0.991	2	2	5	0.084	0.037	0.940
Secretory carrier-associated membrane protein 2;	Q9ERN0	1	2	2	9.7	0.604	0.27	0.561
Dihydrofolate reductase;	P00375	0.999	2	2	8.6	0.604	0.075	0.474
E3 ubiquitin-protein ligase NEDD4;	P46935	0.995	3	3	2.1	0.604	0.056	0.466
Uroporphyrinogen decarboxylase;	P70697	1	7	8	21.5	0.614	0.076	0.466
Fibrinogen beta chain;	Q8K0E8	1	23	39	39.3	0.614	0.084	0.468
Acetyl-coenzyme A synthetase, cytoplasmic;	Q9QXG4	1	8	8	10.3	0.614	0.189	0.511
26S proteasome non-ATPase regulatory subunit 7;	P26516	1	6	10	25.2	0.623	0.113	0.471
Transforming growth factor-beta-induced protein ig-h3;	P82198	1	8	11	13.2	0.623	0.138	0.480
Ribose-phosphate pyrophosphokinase 1;	Q9D7G0	1	7	8	14.8	0.623	0.105	0.468
Putative adenosylhomocysteinase 3;	Q68FL4	1	3	3	7.2	0.623	0.243	0.531
Uncharacterized protein;	E9Q6R7	1	4	4	1.6	0.623	0.085	0.457
E3 ubiquitin-protein ligase HUWE1;	Q7TMY8	1	17	18	5.8	0.632	0.216	0.511
RIKEN cDNA 8030451F13, isoform CRA_c; Uncharacterized protein;	D3YU50	1	17	19	12.5	0.632	0.163	0.482
40S ribosomal protein SA;	P14206	1	10	12	39.7	0.642	0.193	0.489
T-complex protein 1 subunit gamma;	P80318	1	5	5	11.8	0.642	0.226	0.509
Proteasome subunit alpha type-6;	Q9QUM9	1	20	27	44.7	0.642	0.263	0.529
Choline-phosphate cytidylyltransferase A;	P49586	1	2	2	5.7	0.642	0.091	0.447
Adenosine deaminase;	P03958	1	3	3	14.8	0.651	0.323	0.553
Integrin beta-2;	P11835	1	5	5	7.8	0.651	0.087	0.439
Actin-related protein 2/3 complex subunit 4;	P59999	1	4	5	16.1	0.651	0.195	0.481
Inactive tyrosine-protein kinase 7;	Q8BKG3	1	4	4	4	0.651	0.091	0.444
Eukaryotic translation initiation factor 5A-1;	P63242	1	5	7	19	0.66	0.359	0.559
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha;	Q61239	1	6	6	17.2	0.66	0.138	0.448
Glycogen [starch] synthase, muscle;	Q9Z1E4	1	3	3	5.3	0.66	0.171	0.462
Glutamate--cysteine ligase regulatory subunit;	O09172	1	2	2	11.7	0.66	0.046	0.427
COP9 signalosome complex subunit 4;	O88544	1	11	13	34	0.66	0.163	0.462
Myelin protein P0;	P27573	1	7	12	14.1	0.66	0.267	0.511
Rho-associated protein kinase 2;	P70336	1	5	6	2.4	0.66	0.221	0.491
Phosphoribosylformylglycinamidine synthase;	Q5SUR0	1	10	10	9.2	0.66	0.263	0.508
Aminopeptidase B;	Q8VCT3	1	12	12	14.3	0.66	0.288	0.523
	F6ZQ75	0.999	2	2	2.5	0.66	0.226	0.493
60S ribosomal protein L11;	Q9CXW4	1	2	2	8.1	0.669	0.072	0.420

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AH receptor-interacting protein;	O08915	1	7	7	23.9	0.669	0.181	0.460
V-type proton ATPase subunit E 1;	P50518	1	4	4	14.2	0.669	0.063	0.424
Moesin;	P26041	1	10	10	25	0.678	0.212	0.471
Ezrin;	P26040	1	8	9	19.3	0.722	0.267	0.462
Radixin;	P26043	1	7	8	17.7	0.202	0.084	0.844
Dynein light chain 2, cytoplasmic;	Q9D0M5	1	5	5	57.3	0.678	0.254	0.489
Programmed cell death protein 4;	Q61823	0.999	2	2	5.8	0.678	0.102	0.424
Heat shock protein beta-7;	P35385	1	4	4	14.8	0.687	0.346	0.532
Protein PRRC2C;	Q3TLH4	1	4	5	2.3	0.687	0.273	0.493
Protein diaphanous homolog 1;	O08808	1	6	6	5.6	0.687	0.427	0.573
Hydroxysteroid dehydrogenase-like protein 2;	Q2TPA8	1	5	5	10.8	0.687	0.405	0.559
3-ketoacyl-CoA thiolase A, peroxisomal;	Q921H8	1	20	33	51.9	0.687	0.183	0.450
COP9 signalosome complex subunit 6;	O88545	1	5	5	18.2	0.696	0.249	0.474
Fatty acid synthase;	P19096	1	134	217	39.4	0.696	0.288	0.493
26S proteasome non-ATPase regulatory subunit 2;	Q8VDM4	1	21	28	20.2	0.696	0.339	0.519
Phosphoserine phosphatase;	Q99LS3	1	5	7	16.4	0.696	0.211	0.457
Uncharacterized protein;	E9PZ00	1	16	22	26.1	0.696	0.322	0.511
Uncharacterized protein;	E9Q1Y3	0.946	2	4	0.6	0.696	0.095	0.409
Voltage-dependent anion-selective channel protein 2;	Q60930	1	8	11	29.8	0.705	0.411	0.547
26S proteasome non-ATPase regulatory subunit 11;	Q8BG32	1	20	27	38.2	0.705	0.277	0.482
Integrin beta-4;	A2A863	1	3	3	2.7	0.705	0.208	0.447
Cellular retinoic acid-binding protein 2;	P22935	1	6	7	36.2	0.714	0.061	0.389
D-3-phosphoglycerate dehydrogenase;	Q61753	1	16	20	26.1	0.714	0.157	0.420
Major vault protein;	Q9EQK5	1	7	7	9.5	0.714	0.257	0.464
ELAV-like protein 1;	P70372	1	10	11	24.5	0.722	0.271	0.460
Laminin subunit alpha-4;	P97927	1	2	2	1.3	0.722	0.096	0.389
26S proteasome non-ATPase regulatory subunit 1;	Q3TXS7	1	11	17	14.3	0.722	0.359	0.505
CD109 antigen;	Q8R422	1	9	9	7.8	0.722	0.298	0.474
ATP synthase subunit b, mitochondrial;	Q9CQQ7	1	3	3	7.8	0.722	0.061	0.382
Caveolin-1;	P49817	1	4	5	29.2	0.722	0.109	0.393
Early endosome antigen 1;	Q8BL66	1	8	8	5.1	0.722	0.267	0.459
Phosphoserine aminotransferase;	Q99K85	1	21	27	43.5	0.722	0.219	0.435
Actin-related protein 2/3 complex subunit 3;	Q9JM76	1	10	16	27.5	0.722	0.333	0.495
40S ribosomal protein S12;	Q6ZWZ6	1	10	12	53	0.722	0.162	0.411
14-3-3 protein eta;	P68510	1	8	9	45.9	0.731	0.348	0.497
SUMO-activating enzyme subunit 2;	Q9Z1F9	1	10	11	14.7	0.731	0.181	0.415
Retinoid-inducible serine carboxypeptidase;	Q920A5	1	11	13	16.6	0.731	0.181	0.412
Neutral alpha-glucosidase AB;	Q8BHN3	1	27	31	23.8	0.74	0.23	0.425
Dynactin subunit 2;	Q99KJ8	1	8	8	16.9	0.74	0.226	0.428
Collagen alpha-2(VI) chain;	Q02788	1	3	3	5.1	0.74	0.439	0.529
Phospholipase D4;	Q8BG07	1	2	2	5.2	0.748	0.142	0.387
COP9 signalosome complex subunit 5;	O35864	1	6	6	20.7	0.757	0.3	0.449
Asparagine synthetase [glutamine-hydrolyzing];	Q61024	1	3	3	3.6	0.757	0.282	0.440

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Leucyl-tRNA synthetase, cytoplasmic;	Q8BMJ2	1	8	9	9.8	0.757	0.188	0.399
Sideroflexin-3;	Q91V61	1	4	4	16.4	0.757	0.121	0.374
Cullin-1;	Q9WTX6	1	4	4	7.3	0.757	0.081	0.364
Golgi apparatus protein 1;	Q61543	1	4	4	5.1	0.757	0.219	0.410
PDZ and LIM domain protein 5;	Q8CI51	1	7	8	13.7	0.757	0.291	0.448
Mothers against decapentaplegic homolog 4;	P97471	1	2	2	3.4	0.757	0.143	0.380
Chymase;	P21844	1	2	2	6.1	0.766	0.158	0.382
Interleukin-1 receptor antagonist protein;	P25085	1	4	4	29.4	0.766	0.338	0.464
Calponin-2;	Q08093	1	5	5	18.7	0.766	0.122	0.368
Tubulin--tyrosine ligase-like protein 12;	Q3UDE2	1	8	13	13.3	0.766	0.315	0.449
BAG family molecular chaperone regulator 1;	Q60739	1	3	3	5.4	0.766	0.086	0.361
Catenin alpha-1;	P26231	1	9	10	15.8	0.774	0.475	0.520
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1;	Q62077	1	2	2	1.8	0.774	0.204	0.394
Calcineurin subunit B type 1;	Q63810	1	2	2	12.9	0.774	0.317	0.446
60S ribosomal protein L14;	Q9CR57	1	2	2	6	0.774	0.122	0.362
Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase, isoform CRA_c; Uncharacterized protein;	B2RQC6	1	3	3	5.8	0.774	0.557	0.560
Acetyl-CoA acetyltransferase, cytosolic;	Q8CAY6	1	13	19	38	0.774	0.258	0.417
26S proteasome non-ATPase regulatory subunit 13;	Q9WVJ2	1	7	7	21.5	0.774	0.312	0.439
Vigilin;	Q8VDJ3	1	6	6	5.4	0.782	0.336	0.444
Carbonic anhydrase 13;	Q9D6N1	1	4	4	23.7	0.782	0.273	0.415
Host cell factor 1;	Q61191	1	5	6	2.8	0.782	0.136	0.364
Ras GTPase-activating-like protein IQGAP1;	Q9JKF1	1	33	43	22.5	0.782	0.386	0.475
Sodium/potassium-transporting ATPase subunit beta-3;	P97370	1	5	7	19.1	0.791	0.155	0.363
Cytoplasmic dynein 1 intermediate chain 2;	O88487	1	7	9	9.5	0.799	0.211	0.377
Periplakin;	Q9R269	1	2	2	1.1	0.799	0.142	0.353
Ribosome-binding protein 1;	Q99PL5	1	14	14	8.7	0.807	0.235	0.380
Prohibitin-2;	O35129	1	6	8	15.7	0.807	0.277	0.402
Beta-glucuronidase;	P12265	1	17	23	22.7	0.807	0.392	0.457
Aldehyde dehydrogenase;	E9Q3E1	1	9	10	20.9	0.807	0.36	0.439
NADPH:adrenodoxin oxidoreductase, mitochondrial;	Q61578	1	4	5	9.3	0.816	0.158	0.348
V-type proton ATPase subunit d 1;	P51863	0.999	2	2	9.4	0.816	0.417	0.462
Cadherin-1;	P09803	1	8	10	10.6	0.824	0.256	0.380
Cytosolic acyl coenzyme A thioester hydrolase;	Q91V12	1	3	3	10.2	0.824	0.182	0.351
Uncharacterized protein;	E9PYU6	0.995	2	2	0.9	0.824	0.242	0.372
Neurofilament medium polypeptide;	P08553	1	2	2	2.5	0.832	0.514	0.493
Nidogen-1;	P10493	1	9	10	8.4	0.832	0.224	0.362
Lysosome-associated membrane glycoprotein 2;	P17047	1	5	5	8.7	0.832	0.276	0.380
Cyclin-dependent kinase 4 inhibitor C;	Q60772	1	2	2	7.1	0.832	0.131	0.327
Cytoplasmic dynein 1 heavy chain 1;	Q9JHU4	1	11	11	3	0.832	0.453	0.466
Plastin-2;	Q61233	1	54	84	54.1	0.832	0.346	0.415
T-complex protein 1 subunit epsilon;	P80316	1	6	6	10.7	0.84	0.094	0.313

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
Myeloid-associated differentiation marker;	O35682	1	3	4	5.3	0.848	0.226	0.347
14-3-3 protein theta;	P68254	1	8	9	42	0.848	0.278	0.373
Sulfotransferase family cytosolic 2B member 1;	O35400	1	4	5	14.5	0.856	0.355	0.397
Putative RNA-binding protein 3;	O89086	1	2	4	14.1	0.864	0.033	0.296
Sialoadhesin;	Q62230	1	2	2	1.6	0.864	0.066	0.296
N-acetylneuraminate lyase;	Q9DCJ9	1	13	18	36.6	0.864	0.271	0.358
Ubiquitin carboxyl-terminal hydrolase 8;	Q80U87	1	3	3	2.1	0.864	0.161	0.316
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3;	P51432	1	2	2	2.4	0.864	0.252	0.350
Histone H4;	P62806	1	3	3	31.1	0.872	0.157	0.313
Cytochrome b-c1 complex subunit 7;	Q9D855	1	3	3	18.9	0.872	0.224	0.334
Septin-9;	Q80UG5	1	12	14	21.1	0.872	0.191	0.323
Pleckstrin;	Q9JHK5	1	2	2	4.3	0.872	0.162	0.314
Transcription elongation factor SPT5;	O55201	0.998	2	2	2.8	0.872	0.195	0.324
CD44 antigen;	P15379	1	2	2	2.6	0.88	0.124	0.297
Calnexin;	P35564	1	3	3	8	0.888	0.154	0.302
GMP synthase [glutamine-hydrolyzing];	Q3THK7	1	9	10	16.2	0.888	0.24	0.329
Heterogeneous nuclear ribonucleoprotein A/B;	Q99020	1	5	6	18.5	0.888	0.125	0.292
Uncharacterized protein;	E9Q9T2	1	13	17	30.2	0.888	0.24	0.329
H-2 class II histocompatibility antigen, A-Q beta chain;	P06342	1	10	13	34.7	0.888	0.096	0.289
StAR-related lipid transfer protein 5;	Q9EPQ7	1	4	5	24.4	0.888	0.403	0.396
Acid ceramidase;	Q9WV54	1	10	13	25.4	0.888	0.35	0.372
Proteasome subunit beta type-7;	P70195	1	5	6	11.2	0.895	0.111	0.289
UPF0317 protein C14orf159 homolog, mitochondrial;	Q8BH86	1	2	2	3.9	0.895	0.236	0.322
Fibulin-5;	Q9WVH9	1	8	9	26.1	0.895	0.082	0.280
Glutamine synthetase;	P15105	1	5	6	16.6	0.903	0.092	0.279
Uridine 5'-monophosphate synthase;	P13439	1	2	2	4.4	0.903	0.155	0.292
Versican core protein;	Q62059	1	4	4	6.7	0.911	0.262	0.321
Diphosphomevalonate decarboxylase;	Q99JF5	1	4	4	15	0.911	0.3	0.339
Prelamin-A/C;	P48678	1	4	4	10.2	0.918	0.549	0.439
E3 SUMO-protein ligase RanBP2;	Q9ERU9	1	4	4	1.6	0.918	0.248	0.311
Lysosomal protective protein;	P16675	1	20	29	22.6	0.918	0.243	0.312
Uncharacterized protein;	Q3TUE1	1	8	8	13.9	0.918	0.17	0.286
Latexin;	P70202	1	4	6	17.6	0.926	0.224	0.298
Far upstream element-binding protein 2;	Q3U0V1	1	13	15	24.1	0.926	0.19	0.289
Small glutamine-rich tetratricopeptide repeat-containing protein alpha;	Q8BJU0	1	7	10	22.2	0.926	0.429	0.381
Na(+)/H(+) exchange regulatory cofactor NHE-RF3;	Q9JIL4	1	2	3	2.7	0.926	0.068	0.262
Sec24 related gene family, member B (S. cerevisiae); Uncharacterized protein;	Q80ZX0	1	3	3	1.4	0.926	0.521	0.421
Alpha-ketoglutarate-dependent dioxygenase FTO;	Q8BGW1	1	2	2	5.7	0.934	0.152	0.273
Dehydrogenase/reductase SDR family member 1;	Q99L04	1	3	3	13.4	0.934	0.152	0.276
Clathrin heavy chain 1;	Q68FD5	1	49	58	30.2	0.934	0.518	0.417
Septin-11;	Q8C1B7	1	13	16	32.5	0.934	0.377	0.352
Septin-8;	Q8CHH9	1	5	6	14.9	0.176	0.059	0.856
Septin-6;	Q9R1T4	1	5	6	20	0.433	0.186	0.674

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Prohibitin;	P67778	1	2	2	7.4	0.934	0.186	0.282
60S ribosomal protein L12;	P35979	1	4	4	27.9	0.941	0.333	0.328
Ubiquitin-associated protein 2-like;	Q80X50	1	5	5	8.7	0.941	0.123	0.262
Elongation factor 1-gamma;	Q9D8N0	1	21	40	24.7	0.949	0.187	0.276
Phosphomannomutase 2;	Q9Z2M7	1	3	3	14.9	0.949	0.103	0.257
Dipeptidyl peptidase 1;	P97821	1	12	17	15.4	0.949	0.128	0.259
Phosphate carrier protein, mitochondrial;	Q8VEM8	1	4	5	7.8	0.956	0.394	0.345
Putative ATP-dependent RNA helicase Pl10;	P16381	1	4	4	5.9	0.971	0.168	0.258
Pterin-4-alpha-carbinolamine dehydratase;	P61458	1	2	2	9.6	0.971	0.099	0.243
T-complex protein 1 subunit delta;	P80315	1	10	13	23.9	0.971	0.367	0.324
Cold shock domain-containing protein E1;	Q91W50	1	6	6	7.4	0.971	0.431	0.353
Afadin;	Q9QZQ1	1	3	4	2.4	0.971	0.609	0.429
PDZ and LIM domain protein 1;	O70400	1	6	7	24.2	0.978	0.377	0.323
CD 81 antigen, isoform CRA_c; CD81 antigen; Tapa-1 protein; Uncharacterized protein;	Q91V78	1	2	3	19.1	0.978	0.511	0.379
Extended synaptotagmin-1;	Q3U7R1	1	2	2	3.5	0.978	0.477	0.367
Transcriptional activator protein Pur-alpha;	P42669	1	2	2	7.8	0.978	0.149	0.249
Guanine nucleotide-binding protein subunit beta-2-like 1;	P68040	1	22	26	63.7	0.986	0.508	0.374
ERO1-like protein alpha;	Q8R180	1	3	3	8	0.986	0.418	0.337
Polymerase I and transcript release factor;	O54724	1	4	7	10.5	0.986	0.134	0.242
Proliferation-associated protein 2G4;	P50580	1	8	9	18.5	0.986	0.269	0.279
Nuclear-interacting partner of ALK;	Q80YV2	1	3	3	8	0.986	0.134	0.242
WW domain-binding protein 11;	Q923D5	1	2	2	2.3	0.986	0.159	0.248
Ectonucleoside triphosphate diphosphohydrolase 1;	P55772	0.996	2	2	11.8	0.986	0.154	0.246
Methionine aminopeptidase 2;	O08663	0.972	2	2	5.6	0.986	0.129	0.242
Calreticulin;	P14211	1	17	29	26.4	0.993	0.095	0.232
Valyl-tRNA synthetase;	Q9Z1Q9	1	14	16	11	0.993	0.274	0.275
Sodium/potassium-transporting ATPase subunit alpha-1;	Q8VDN2	1	11	12	21.4	0.993	0.324	0.295
Sodium/potassium-transporting ATPase subunit alpha-2;	Q6PIE5	1	5	7	18.2	-0.322	-0.105	0.728
NADH-cytochrome b5 reductase 3;	Q9DCN2	1	7	8	27.9	0.993	0.304	0.287
26S proteasome non-ATPase regulatory subunit 6;	Q99JI4	1	8	12	15.4	1	0.445	0.339
Proteolipid protein 2;	Q9R1Q7	0.96	2	3	7.9	1	0.085	0.228
RelA-associated inhibitor;	Q5I1X5	1	2	3	1	1.007	0.11	0.228
Acetoacetyl-CoA synthetase;	Q9D2R0	1	10	11	18.2	1.007	0.321	0.286
Uncharacterized protein;	F6ZFU0	1	3	6	15.4	1.007	0.13	0.231
Hsp70-binding protein 1;	Q99P31	0.998	2	2	8.1	1.007	0.23	0.256
Syntaxin-binding protein 3;	Q60770	0.996	2	2	2.9	1.007	0.14	0.233
Caspase-3;	P70677	1	3	3	11.9	1.014	0.211	0.245
RNA-binding protein FUS;	P56959	1	3	3	7	1.014	0.261	0.259
Spliceosome RNA helicase Ddx39b;	Q9Z1N5	1	9	12	25.2	1.014	0.462	0.334
H-2 class I histocompatibility antigen, K-B alpha chain;	P01901	1	2	2	16.2	1.021	0.231	0.246
H-2 class I histocompatibility antigen, Q10 alpha chain;	P01898	0.999	2	2	15.7	0.202	0.025	0.811
Polyadenylate-binding protein 1;	P29341	1	24	27	26.7	1.021	0.367	0.291

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Importin subunit beta-1;	P70168	1	13	17	12.4	1.029	0.419	0.309
Transcription intermediary factor 1-beta;	Q62318	1	3	3	8.6	1.029	0.187	0.231
Lysyl-tRNA synthetase;	Q99MN1	1	3	3	5.4	1.029	0.121	0.218
Alpha-actinin-4;	P57780	1	7	8	16.1	1.029	0.247	0.247
Alpha-actinin-1;	Q7TPR4	1	3	3	11.3	1.070	0.148	0.206
Eukaryotic translation initiation factor 2A;	Q8BJW6	1	4	4	10	1.029	0.232	0.244
Alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB); Uncharacterized protein;	A2BFA6	1	3	3	2.8	1.036	0.091	0.211
Ferric-chelate reductase 1;	Q8K385	1	2	2	3.5	1.036	0.101	0.214
Calcium-binding protein 39;	Q06138	1	3	3	9.1	1.043	0.223	0.236
14 kDa phosphohistidine phosphatase;	Q9DAK9	1	4	5	18.5	1.057	0.229	0.230
Vimentin;	P20152	1	6	6	15.5	1.057	0.793	0.439
26S protease regulatory subunit 4;	P62192	1	9	10	17.5	1.064	0.336	0.257
WD repeat-containing protein 61;	Q9ERF3	1	5	5	17.7	1.064	0.153	0.208
Uncharacterized protein;	F6RPJ9	1	31	37	26	1.064	0.361	0.267
Glutaredoxin-1;	Q9QUH0	1	2	2	10.3	1.077	0.066	0.192
Protein phosphatase 1A;	P49443	1	5	5	20.2	1.077	0.383	0.264
Protein phosphatase 1B;	P36993	1	2	2	7.9	0.163	0.023	0.844
Coatomer subunit gamma;	Q9QZE5	1	5	5	5.3	1.091	0.384	0.258
Poly [ADP-ribose] polymerase 1;	P11103	0.995	2	2	2.6	1.091	0.164	0.199
CD9 antigen;	P40240	1	2	2	14.2	1.098	0.180	0.199
Tripeptidyl-peptidase 2;	Q64514	1	7	7	4.1	1.098	0.585	0.328
Protein XRP2;	Q9EPK2	1	2	2	5.5	1.098	0.190	0.200
Protein argonaute-2;	Q8CJG0	1	3	3	4.4	1.098	0.139	0.192
14-3-3 protein beta/alpha;	Q9CQV8	1	12	15	52	1.098	0.405	0.261
Protein CREG1;	O88668	1	4	8	13.2	1.104	0.154	0.192
Pantetheinase;	Q9Z0K8	1	4	5	12.1	1.111	0.098	0.182
Eukaryotic translation initiation factor 3 subunit L;	Q8QZY1	0.991	2	2	3.7	1.111	0.195	0.195
Catechol O-methyltransferase;	O88587	0.997	2	2	12.1	1.118	0.155	0.185
Cofilin-1;	P18760	1	11	23	45.2	1.124	0.763	0.379
Beta-hexosaminidase subunit alpha;	P29416	1	4	4	8.8	1.131	0.413	0.247
Peptidyl-prolyl cis-trans isomerase FKBP4;	P30416	1	10	12	22.9	1.131	0.150	0.179
UDP-glucuronosyltransferase 1-1;	Q63886	1	2	2	6.9	1.131	0.269	0.203
Nucleoside diphosphate-linked moiety X motif 17;	Q9CWD3	0.998	2	2	12.8	1.138	0.202	0.184
Phostensin;	Q8BQ30	1	2	5	4.2	1.144	0.207	0.185
Fermitin family homolog 3;	Q8K1B8	1	2	2	3.2	1.144	0.233	0.191
ATP-dependent RNA helicase DDX42;	Q810A7	0.998	2	2	3.7	1.144	0.771	0.369
Transitional endoplasmic reticulum ATPase;	Q01853	1	35	44	35.7	1.151	0.524	0.275
Gasdermin-A;	Q9EST1	1	10	16	20.9	1.151	0.757	0.359
Eukaryotic translation initiation factor 3 subunit B;	Q8JZQ9	1	7	7	11.8	1.157	0.368	0.217
Cathepsin S;	O70370	1	9	13	30.6	1.163	0.421	0.232
Fatty acid-binding protein, epidermal;	Q05816	1	16	50	71.9	1.163	0.234	0.180
Chitotriosidase-1;	Q9D7Q1	0.941	2	2	3.9	1.163	0.119	0.162
Importin-7;	Q9EPL8	1	5	5	6.1	1.170	0.343	0.203

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Polypyrimidine tract-binding protein 1;	P17225	1	9	14	22.7	1.170	0.130	0.162
AP-2 complex subunit mu;	P84091	1	2	2	5.8	1.170	0.421	0.227
14-3-3 protein epsilon;	P62259	1	13	18	41.2	1.195	0.376	0.203
Transcription elongation factor B polypeptide 1;	P83940	1	3	4	23.2	1.208	0.204	0.158
Elongation factor 1-beta;	O70251	1	6	10	34.7	1.220	0.560	0.246
Retinol-binding protein 1;	Q00915	1	3	3	15.6	1.220	0.225	0.158
Tubulin-specific chaperone D;	Q8BYA0	1	3	3	2.7	1.220	0.283	0.168
Protein RCC2;	Q8BK67	1	12	15	24.8	1.233	0.619	0.262
6-phosphofructokinase type C;	Q9WUA3	1	11	12	16.7	1.233	0.126	0.139
Sorting nexin-27;	Q3UHD6	1	3	3	9.1	1.233	0.084	0.135
Cytochrome b-c1 complex subunit 9;	Q8R1I1	1	2	2	26.6	1.251	0.158	0.136
Monocarboxylate transporter 1;	P53986	1	3	3	6.1	1.257	0.279	0.153
Splicing factor 3A subunit 1;	Q8K4Z5	1	3	3	5.2	1.263	0.268	0.149
H-2 class II histocompatibility antigen, A-Q alpha chain;	P04227	1	5	6	17.2	1.275	0.590	0.227
Serine hydroxymethyltransferase, cytosolic;	P50431	1	2	4	4.2	1.275	0.306	0.151
Uncharacterized protein;	E9PWQ3	1	16	18	8.1	1.293	0.565	0.212
Phospholipase B-like 1;	Q8VCI0	1	14	19	20.2	1.299	0.407	0.166
Alpha-soluble NSF attachment protein;	Q9DB05	1	3	3	13.2	1.299	0.164	0.122
Cystatin-B;	Q62426	1	5	8	39.8	1.305	0.159	0.121
40S ribosomal protein S3;	P62908	1	4	5	15.6	1.305	0.137	0.119
Splicing factor 1;	Q64213	0.997	2	2	4.2	1.328	0.185	0.116
Involucrin;	P48997	1	3	3	9.2	1.345	0.233	0.117
Nuclear autoantigenic sperm protein;	Q99MD9	1	2	2	9.4	1.373	0.838	0.255
Serine/threonine-protein phosphatase 6 catalytic subunit;	Q9CQR6	0.954	3	3	6.6	1.373	0.265	0.113
Leucyl-cystinyl aminopeptidase;	Q8C129	1	2	2	3.1	1.379	0.318	0.121
N-alpha-acetyltransferase 15, NatA auxiliary subunit;	Q80UM3	0.985	2	2	1.3	1.379	0.122	0.097
Enoyl-CoA hydratase domain-containing protein 1;	Q9D9V3	1	11	14	26.1	1.384	0.578	0.173
Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	Q8JZK9	1	16	20	25	1.390	0.653	0.192
Serine/threonine-protein phosphatase 6 regulatory subunit 3;	Q922D4	1	5	7	5.9	1.395	0.223	0.101
Histone-binding protein RBBP4;	Q60972	1	4	4	6	1.411	0.223	0.097
26S proteasome non-ATPase regulatory subunit 12;	Q9D8W5	1	3	4	5.7	1.417	0.478	0.137
Pantothenate kinase 1;	Q8K4K6	0.998	2	2	6	1.428	0.356	0.110
Monoglyceride lipase;	O35678	1	15	18	49.8	1.449	0.642	0.163
E3 ubiquitin-protein ligase UBR4;	A2AN08	1	4	4	1.4	1.454	0.133	0.080
Putative phospholipase B-like 2;	Q3TCN2	1	6	6	9.3	1.454	0.377	0.107
Nesprin-2;	Q6ZWQ0	0.995	3	3	0.8	1.454	0.769	0.194
Bcl-2-like protein 13;	P59017	1	2	2	2.5	1.459	0.387	0.107
Retroviral-like aspartic protease 1;	Q09PK2	1	7	10	28	1.459	0.207	0.085
Cornifin-A;	Q62266	1	4	7	37.5	1.459	0.223	0.085
Prolargin;	Q9JK53	1	19	39	32.3	1.465	0.186	0.082
Heterogeneous nuclear ribonucleoprotein Q;	Q7TMK9	1	15	16	30.7	1.465	0.632	0.155
Large proline-rich protein BAG6;	Q9Z1R2	0.978	2	2	4	1.475	0.260	0.086
Protein arginine N-methyltransferase 1;	Q9JIF0	1	4	5	17.3	1.485	0.445	0.110

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60S ribosomal protein L8;	P62918	0.994	2	2	10.5	1.491	0.271	0.084
Chloride channel calcium activated 2; Endothelial chloride channel; MCG120735; Uncharacterized protein;	Q9EQR4	1	12	13	18.5	1.501	0.324	0.087
Alpha-centractin;	P61164	0.997	2	2	8.8	1.506	0.249	0.078
Prostaglandin E synthase 3;	Q9R0Q7	1	5	6	34.6	1.511	0.520	0.116
Periostin;	Q62009	1	12	13	18.9	1.511	0.355	0.089
Epithelial cell adhesion molecule;	Q99JW5	1	3	3	23.2	1.516	0.355	0.088
Alcohol dehydrogenase class 4 mu/sigma chain;	Q64437	1	14	20	32.1	1.521	0.249	0.075
Asparaginyl-tRNA synthetase, cytoplasmic;	Q8BP47	0.994	2	2	1.4	1.526	0.297	0.078
14-3-3 protein sigma;	O70456	1	10	40	33.1	1.531	0.657	0.136
Cathepsin D;	P18242	1	25	56	40	1.541	0.291	0.075
Lupus La protein homolog;	P32067	1	6	6	18.3	1.546	0.852	0.177
Kallikrein related-peptidase 10; Uncharacterized protein;	Q99M20	0.996	2	2	10.8	1.551	0.132	0.061
Ribonucleoside-diphosphate reductase large subunit;	P07742	1	3	3	4.7	1.556	0.175	0.063
Laminin subunit alpha-2;	Q60675	1	4	4	1.3	1.561	0.513	0.100
Isopentenyl-diphosphate Delta-isomerase 1;	P58044	1	6	6	41	1.566	0.418	0.084
Importin subunit alpha-4;	O35343	1	5	5	8.4	1.566	0.407	0.082
Protein S100-A14;	Q9D2Q8	1	3	4	33.7	1.590	0.486	0.088
6-phosphofructokinase, liver type;	P12382	1	6	8	8.8	1.595	0.364	0.072
Mitotic checkpoint protein BUB3;	Q9WVA3	1	4	4	13.8	1.599	0.406	0.075
Biotinidase;	Q8CIF4	0.948	2	2	1.7	1.609	0.179	0.054
Heterogeneous nuclear ribonucleoprotein H;	O35737	1	10	14	30.3	1.628	0.522	0.085
TAR DNA-binding protein 43;	Q921F2	1	9	11	18.1	1.651	0.189	0.049
Pro-interleukin-16;	O54824	1	2	2	0.8	1.655	0.289	0.054
Putative RNA-binding protein Luc7-like 2;	Q7TNC4	1	2	2	8.8	1.674	0.304	0.052
Carboxypeptidase E;	Q00493	1	5	6	17	1.678	0.713	0.101
Protein capicua homolog;	Q924A2	0.992	2	2	3.1	1.692	0.283	0.048
Coronin-1B;	Q9WUM3	1	4	4	7.6	1.700	0.235	0.044
Eif2b3 protein; Uncharacterized protein;	A4FUS0	1	3	3	13.7	1.709	0.282	0.045
Histone deacetylase 1;	O09106	1	3	3	9.1	1.709	0.167	0.040
Inosine-5'-monophosphate dehydrogenase 2;	P24547	1	2	2	6	1.714	0.334	0.048
Regulator of nonsense transcripts 1;	Q9EPU0	1	7	7	8	1.722	0.350	0.048
UBX domain-containing protein 4;	Q8VCH8	1	2	2	9.3	1.736	0.339	0.046
Apoptosis-associated speck-like protein containing a CARD;	Q9EPB4	1	8	10	43	1.766	0.961	0.120
Ubiquilin-1;	Q8R317	1	2	2	4.8	1.766	0.628	0.068
WASH complex subunit FAM21;	Q6PGL7	1	2	2	1.3	1.766	0.571	0.061
Proliferating cell nuclear antigen;	P17918	1	8	9	33.3	1.770	0.114	0.032
UPF0568 protein C14orf166 homolog;	Q9CQE8	0.905	2	2	8.2	1.782	0.461	0.048
Treacle protein;	O08784	1	3	3	4.7	1.807	0.434	0.042
Heterogeneous nuclear ribonucleoprotein F;	Q9Z2X1	1	10	12	24.6	1.824	0.716	0.067
Carboxypeptidase A4;	Q6P8K8	1	6	8	21.2	1.848	0.436	0.038
Heterogeneous nuclear ribonucleoproteins A2/B1;	O88569	1	13	33	23.3	1.876	0.976	0.092
RNA-binding protein EWS;	Q61545	1	2	2	2.3	1.876	0.307	0.028

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Heterogeneous nuclear ribonucleoprotein A3;	Q8BG05	1	9	17	29	1.895	0.637	0.047
Cystatin E/M; Cystatin M/E; Uncharacterized protein;	Q9D1B1	1	7	8	49	1.918	0.655	0.045
Polyadenylate-binding protein 2;	Q8CCS6	0.994	2	3	9.3	1.922	0.066	0.019
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial;	P53395	0.991	2	2	2.3	1.926	0.416	0.028
Nucleolin;	P09405	1	5	6	7.8	1.937	0.344	0.024
Annexin A6;	P14824	1	2	2	56.2	1.937	0.475	0.030
Receptor-type tyrosine-protein phosphatase C;	P06800	1	4	4	3.8	1.952	0.373	0.024
Poly(U)-binding-splicing factor PUF60;	Q3UEB3	1	10	12	20.2	1.978	0.758	0.046
Poly(U)-specific endoribonuclease;	Q3V188	1	6	6	18.2	2.007	1.268	0.102
Uncharacterized protein;	Q9CX86	1	3	7	22.6	2.025	0.856	0.048
Protein KIAA1967 homolog;	Q8VDP4	1	5	6	7.5	2.029	1.069	0.070
Uncharacterized protein;	D3Z2Y6	0.997	2	2	32.9	2.029	0.512	0.024
Uncharacterized protein;	E9PZZ3	1	2	2	1.7	2.057	0.297	0.015
Metastasis-associated protein MTA2;	Q9R190	1	3	3	7	2.067	0.597	0.025
Keratin, type I cytoskeletal 14;	Q61781	1	9	10	26.2	2.081	1.673	0.143
Keratin, type I cytoskeletal 17;	Q9QWL7	1	3	4	15.7	3.053	0.666	0.001
Keratin, type I cytoskeletal 10;	P02535	1	3	3	7.4	0.379	0.099	0.675
Epithelial splicing regulatory protein 1;	Q3US41	1	2	2	5.4	2.094	0.387	0.015
ATP-binding cassette sub-family D member 3;	P55096	1	3	3	7.7	2.118	0.815	0.033
Perilipin-2;	P43883	1	11	14	27.1	2.118	1.327	0.083
Monofunctional C1-tetrahydrofolate synthase, mitochondrial;	Q3V3R1	0.987	2	2	2.1	2.189	0.547	0.015
Lymphocyte antigen 6D;	P35459	1	4	4	48	2.202	0.321	0.009
Nardilysin;	Q8BHG1	1	2	2	2	2.220	0.248	0.008
Nuclease-sensitive element-binding protein 1;	P62960	1	2	3	17.1	2.257	0.359	0.008
DNA-binding protein A;	Q9JKB3	1	2	2	18.8	1.705	0.309	0.048
Heterogeneous nuclear ribonucleoprotein U-like protein 2;	Q00PI9	1	4	4	7.8	2.260	0.387	0.008
ATP-citrate synthase;	Q91V92	1	31	42	29	2.299	0.477	0.009
Nucleophosmin;	Q61937	0.998	2	4	13.2	2.325	1.091	0.029
Peroxisomal acyl-coenzyme A oxidase 2;	Q9QXD1	1	2	3	2.8	2.336	0.486	0.007
Caspase-14;	O89094	1	9	13	30.4	2.359	2.331	0.152
Adipocyte enhancer-binding protein 1;	Q640N1	1	3	3	2.2	2.359	0.299	0.005
Uncharacterized protein;	F8WIT2	1	61	114	55.8	2.359	0.543	0.00764
Latent-transforming growth factor beta-binding protein 4;	Q8K4G1	1	8	10	9.5	2.428	1.11	0.021
DNA-(apurinic or apyrimidinic site) lyase;	P28352	1	2	2	15.3	2.43	0.442	0.00481
Fatty acyl-CoA reductase 2;	Q7TNT2	1	4	4	7.2	2.511	0.709	0.00615
Heterogeneous nuclear ribonucleoprotein M;	Q9D0E1	1	4	4	14	2.534	0.551	0.00393
Short-chain dehydrogenase/reductase family 16C member 6;	Q05A13	1	2	2	8.2	2.566	0.338	0.00232
3-keto-steroid reductase;	O88736	0.998	2	2	7.2	2.599	0.266	0.00182
Ear5 protein; Eosinophil-associated ribonuclease 5; Eosinophil-associated, ribonucleas	Q8K416	1	5	7	29.7	2.611	0.415	0.00218
28S ribosomal protein S27, mitochondrial;	Q8BK72	1	2	2	4.8	2.637	0.449	0.0021
Rho-associated protein kinase 1;	P70335	1	4	4	3	2.774	1.367	0.0107
Tripartite motif-containing protein 29;	Q8R2Q0	1	2	2	1.7	2.799	0.189	0.000705

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Uncharacterized protein;	D3Z4B0	1	3	3	13	2.807	0.778	0.0021
Heterogeneous nuclear ribonucleoprotein A1;	P49312	1	9	14	24.4	2.969	2.139	0.025
Splicing factor U2AF 65 kDa subunit;	P26369	1	2	3	9.4	3.246	1.635	0.00307
Uncharacterized protein;	F6TL02	1	3	6	19.6	3.374	1.171	0.000451
Long-chain-fatty-acid--CoA ligase 4;	Q9QUJ7	1	4	4	7	3.379	2.138	0.00592
Gamma-glutamyl hydrolase;	Q9Z0L8	1	3	4	13.6	3.502	1.617	0.000923
Desmoglein-1-alpha;	Q61495	1	2	2	3.6	3.52	0.522	0.0000331
Uncharacterized protein;	E9Q7G0	1	7	7	5.2	3.584	1.082	0.000115
Aldehyde oxidase 4; Uncharacterized protein;	Q3TYQ9	1	7	7	8.6	3.979	2.044	0.000321
Laminin subunit beta-1;	P02469	1	2	2	1.2	4.052	0.784	0.00000295
Uncharacterized protein;	E9Q394	1	3	4	2	4.629	2.618	0.0000635
MARCKS-related protein;	P28667	1	2	2	7.5	9.081	0.18	0
Transcriptional repressor p66-beta;	Q8VHR5	1	2	2	7.6	9.081	0.18	0
Choroidermia; Uncharacterized protein;	A2AD03	1	2	2	6.1	9.081	0.18	0
Protein FRG1;	P97376	0.999	2	2	6.2	9.081	0.18	0