Table S1: List of all identified and quantified proteins in the quantitative proteome comparision of skin lysates wt and *Ctsb*$^{-/-}$ (replicate 1).

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change (log$_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
Cathepsin B;	P10605	1	8	12	21.8	-6,644*	-0.001	0.000
Betaine--homocysteine S-methyltransferase 1;	O35490	1	6	9	22.1	-6.644	-0.001	0.000
Liver carboxylesterase 31;	Q63880	0.998	2	2	5.8	-6.644	-6.644	0.000
Fructose-bisphosphate aldolase B;	Q91Y97	1	5	7	15.7	-4.644	-2.322	0.000
Glycine N-methyltransferase;	Q9QXF8	1	4	5	19.1	-4.644	-1.161	0.000
Dimethylglycine dehydrogenase, mitochondrial;	Q9DBT9	1	3	3	3.9	-4.322	-0.864	0.000
Disks large-associated protein 4;	B1AZP2	0.985	2	2	1.5	-4.322	-0.864	0.000
Fatty acid-binding protein, liver;	P12710	0.962	2	3	15	-3.837	-2.741	0.000
Surfeit locus protein 4;	Q64310	0.978	2	2	7.1	-2.396	-2.144	0.068
Fatty acid-binding protein, heart;	P11404	1	8	12	35.3	-1.556	-0.87	0.080
IgG receptor FcRn large subunit p51;	Q61559	1	2	2	9.9	-1.515	-0.952	0.131
Sorting nexin-4;	Q91YJ2	1	2	2	4	-1.515	-0.173	0.000
Hydroxymethylglutaryl-CoA synthase, mitochondrial;	P54869	1	4	7	8.1	-1.396	-0.845	0.151
CD 81 antigen, isoform CRA_c; CD81 antigen; Tapa-1 protein; Uncharacterized protein;	Q91V78	1	3	6	19.1	-1.286	-0.125	0.002
V-type proton ATPase 116 kDa subunit a isoform 1;	Q9Z1G4	1	3	3	2.4	-1.252	-0.656	0.148
N-acetylmuramoyl-L-alanine amidase;	Q8VCS0	1	4	7	7.2	-1.252	-0.715	0.165
Uncharacterized protein;	D3YYM6	1	3	3	15.4	-1.252	-0.447	0.053
UPF0696 protein C11orf68 homolog;	Q8VD62	1	2	2	7.2	-1.252	-0.805	0.216
Serpin H1;	P19324	1	18	23	31.4	-1.184	-0.404	0.061
60S ribosomal protein L12;	P35979	1	5	6	39.4	-1.184	-0.7	0.203
Mitochondrial carrier homolog 2;	Q791V5	1	4	4	16.2	-1.184	-1.076	0.386
Ig kappa chain V-II region 26-10;	P01631	1	2	4	11.5	-1.152	-0.154	0.007
Carboxypeptidase B2;	Q9JHH6	1	3	3	9	-1.152	-0.128	0.005
60S acidic ribosomal protein P2;	P99027	1	3	4	45.2	-1.12	-0.17	0.012
Complement C1s-A subcomponent;	Q8CG14	1	3	3	5	-1.12	-0.365	0.069
CD209 antigen-like protein D;	Q91ZW8	1	2	2	9.3	-1.089	-0.162	0.015
Ubiquitin-conjugating enzyme E2 D3;	P61079	0.999	2	2	7.5	-1.089	-0.023	0.005
UDP-N-acetylhexosamine pyrophosphorylase;	Q91YN5	1	7	7	13	-1.059	-0.265	0.045
Ras-related protein Rap-1b;	Q99JI6	1	6	6	19.6	-1.059	-0.11	0.011
Lymphocyte antigen 6 complex locus protein G6c;	Q9Z1Q4	1	3	5	14.3	-1.059	-0.11	0.011
Uncharacterized protein;	E9Q6D8	1	11	11	15.1	-1.059	-0.375	0.094
Angiotensin-converting enzyme;	P09470	1	25	37	17.1	-1.059	-0.309	0.067
Collagen alpha-1(I) chain;	P11087	1	41	67	24.4	-1.059	-0.574	0.225
Pleckstrin;	Q9JHK5	1	2	2	4.3	-1.059	-0.11	0.011
Peptidyl-prolyl cis-trans isomerase FKBP7;	O54998	1	7	12	17.4	-1.029	-0.189	0.033
Ig mu chain C region secreted form;	P01872	1	9	11	14.5	-1.029	-0.126	0.017
Oxidation resistance protein 1;	Q4KMM3	1	4	4	4.9	-1.029	-0.273	0.063
A-kinase anchor protein 12;	Q9WTQ5	1	42	63	19.5	-1.029	-0.693	0.328
CD9 antigen;	P40240	1	3	4	14.2	-1.029	-0.168	0.026
Growth/differentiation factor 8;	O08689	1	2	2	4.8	-1.029	-0.105	0.014

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
Scavenger receptor cysteine-rich type 1 protein M130;	Q2VLH6	1	4	4	3.4	-0.971	-0.095	0.017
Protein Noxp20;	Q9D281	1	3	3	6.3	-0.971	-0.514	0.256
Major urinary protein 8; Novel member of the major urinary protein (Mup) gene family; Uncharacterized protein;	A2BIN1	0.999	2	3	56.7	-0.971	-0.095	0.017
Major urinary protein 2;	P11589	0.998	5	10	55	-0.474	-0.053	0.258
Myosin-binding protein H;	P70402	1	6	6	12	-0.943	-0.671	0.384
Metalloreductase STEAP3;	Q8CI59	1	4	4	10.7	-0.943	-0.363	0.163
UPF0556 protein C19orf10 homolog;	Q9CPT4	1	3	3	12.7	-0.943	-0.381	0.180
Cysteine-rich with EGF-like domain protein 2;	Q9CYA0	1	3	3	6.6	-0.943	-0.326	0.130
Sodium/potassium-transporting ATPase subunit beta-3;	P97370	1	4	4	11.2	-0.943	-0.435	0.214
Myelin basic protein;	P04370	1	2	2	8	-0.916	-0.086	0.025
Complement component C9;	P06683	1	26	31	26.8	-0.916	-0.207	0.069
Myosin-binding protein C, fast-type;	Q5XKE0	1	44	61	28	-0.916	-0.156	0.049
Ubiquitin carboxyl-terminal hydrolase isozyme L1;	Q9R0P9	1	7	9	27.8	-0.916	-0.709	0.438
Carbonyl reductase [NADPH] 2;	P08074	1	18	27	48.4	-0.916	-0.311	0.138
Dipeptidase 1;	P31428	1	4	7	9.8	-0.889	-0.132	0.047
C-type mannose receptor 2;	Q64449	1	15	17	9.7	-0.889	-0.181	0.065
Leukemia inhibitory factor receptor;	P42703	1	6	6	6.7	-0.862	-0.172	0.073
Protein canopy homolog 2;	Q9QXT0	1	3	5	15.4	-0.862	-0.063	0.031
Uncharacterized protein;	D3YXF5	1	9	12	29.2	-0.862	-0.486	0.337
COP9 signalosome complex subunit 1;	Q99LD4	1	2	2	5.5	-0.862	-0.141	0.063
Heterogeneous nuclear ribonucleoprotein L;	Q8R081	0.999	2	2	4.6	-0.862	-0.611	0.432
Equilibrative nucleoside transporter 1;	Q9JIM1	0.998	2	2	9.9	-0.862	-0.047	0.030
Macrophage colony-stimulating factor 1 receptor;	P09581	0.993	2	2	1.8	-0.862	-0.078	0.036
Niemann-Pick C1 protein;	O35604	1	3	5	2	-0.811	-0.085	0.048
SPARC;	P07214	1	7	10	13	-0.811	-0.114	0.062
Murinoglobulin-1;	P28665	1	77	149	30.9	-0.811	-0.299	0.217
Complement component C8 alpha chain;	Q8K182	1	11	13	19.1	-0.811	-0.256	0.167
Hypoxia up-regulated protein 1;	Q9JKR6	1	19	22	16.1	-0.811	-0.47	0.375
Prenylcysteine oxidase;	Q9CQF9	1	2	2	5.9	-0.811	-0.114	0.062
Complement component C8 beta chain;	Q8BH35	1	8	8	15.1	-0.786	-0.122	0.081
Protein phosphatase 1F;	Q8CGA0	1	4	4	6.2	-0.786	-0.461	0.398
Aminopeptidase B;	Q8VCT3	1	11	11	16	-0.786	-0.379	0.316
Mitochondrial-processing peptidase subunit alpha;	Q9DC61	1	4	4	4.3	-0.786	-0.325	0.261
S-formylglutathione hydrolase;	Q9R0P3	1	13	20	29.1	-0.786	-0.081	0.056
UDP-glucose 6-dehydrogenase;	O70475	1	21	22	37.9	-0.786	-0.163	0.104
Adenylosuccinate lyase;	P54822	1	10	11	21.5	-0.786	-0.556	0.475
Malignant T cell-amplified sequence 1;	Q9DB27	1	2	3	19.9	-0.786	-0.054	0.046
Afamin;	O89020	1	22	26	22.2	-0.761	-0.348	0.321
Coagulation factor XIII B chain;	Q07968	1	3	3	5.7	-0.761	-0.271	0.239
Protein PRRC1;	Q3UPH1	1	2	2	7	-0.761	-0.245	0.206
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial;	Q8CHT0	1	8	8	11	-0.761	-0.503	0.456
Thioredoxin domain-containing protein 5;	Q91W90	1	21	35	41.3	-0.761	-0.103	0.081

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
Collagen triple helix repeat-containing protein 1;	Q9D1D6	1	2	2	11	-0.761	-0.103	0.081
Histidine-rich glycoprotein;	Q9ESB3	1	9	10	11.6	-0.761	-0.271	0.239
Nucleobindin-1;	Q02819	1	6	9	11.3	-0.761	-0.439	0.408
Clathrin light polypeptide (Lca); Uncharacterized protein;	B1AWE0	1	4	4	13.9	-0.761	-0.077	0.065
Uncharacterized protein;	E9PV38	1	17	22	29.3	-0.761	-0.348	0.321
Uncharacterized protein;	Q9DBD0	1	26	31	28.7	-0.761	-0.361	0.329
Collagen alpha-1(III) chain;	P08121	1	14	15	8	-0.737	-0.086	0.083
Glutathione peroxidase 7;	Q99LJ6	1	3	4	16.1	-0.737	-0.061	0.069
Hepatitis B virus X-interacting protein homolog;	Q9D1L9	1	2	2	22	-0.737	-0.086	0.083
Prolyl 4-hydroxylase subunit alpha-1;	Q60715	1	5	6	11.2	-0.737	-0.111	0.102
Myeloid-associated differentiation marker;	O35682	1	2	2	5.3	-0.713	-0.082	0.094
Collagen alpha-2(I) chain;	Q01149	1	28	58	17.6	-0.713	-0.199	0.198
Sulfated glycoprotein 1;	Q61207	1	10	15	13.2	-0.713	-0.094	0.103
Poly(ADP-ribose) glycohydrolase ARH3;	Q8CG72	1	2	2	7	-0.713	-0.339	0.374
Ubiquitin-like-conjugating enzyme ATG3;	Q9CPX6	1	4	4	7.3	-0.713	-0.257	0.280
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2;	Q9CQ75	1	2	2	14.1	-0.713	-0.082	0.094
Epidermal growth factor receptor;	Q01279	1	19	26	14.9	-0.713	-0.199	0.198
Protein ERGIC-53;	Q9D0F3	1	3	3	12.2	-0.713	-0.058	0.080
GTPase NRas;	P08556	0.997	2	2	12.2	-0.713	-0.14	0.138
4F2 cell-surface antigen heavy chain;	P10852	1	4	4	6.8	-0.69	-0.312	0.371
Hemopexin;	Q91X72	1	36	204	47.2	-0.69	-0.067	0.098
Vacuolar protein sorting-associated protein 29;	Q9QZ88	1	4	4	25.3	-0.69	-0.045	0.086
Calcium/calmodulin-dependent protein kinase type 1;	Q91YS8	1	4	4	11.2	-0.69	-0.245	0.293
Cytosolic non-specific dipeptidase;	Q9D1A2	1	29	56	37.1	-0.69	-0.078	0.106
Alpha-aminoadipic semialdehyde dehydrogenase;	Q9DBF1	1	17	22	26.2	-0.69	-0.089	0.112
GTP:AMP phosphotransferase, mitochondrial;	Q9WTP7	1	6	6	26.9	-0.69	-0.445	0.499
Uncharacterized protein;	F8VPN4	1	58	72	31	-0.69	-0.234	0.277
SAR1 gene homolog A (S. cerevisiae); SAR1 gene homolog A (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q99JZ4	1	4	6	33.8	-0.69	-0.189	0.212
GTP-binding protein SAR1b;	Q9CQC9	1	2	2	25.8	-0.713	-0.175	0.180
Secretory carrier-associated membrane protein 4;	Q9JKV5	1	2	2	4.8	-0.69	-0.156	0.180
Ubiquitin-like modifier-activating enzyme ATG7;	Q9D906	0.998	2	2	3.6	-0.69	-0.367	0.427
Beta-glucuronidase;	P12265	1	13	16	12.8	-0.667	-0.296	0.382
Splicing factor U2AF 65 kDa subunit;	P26369	1	3	6	8.5	-0.644	-0.07	0.120
Biglycan;	P28653	1	3	4	4.9	-0.644	-0.292	0.398
Coatomer subunit delta;	Q5XJY5	1	11	11	15.9	-0.644	-0.272	0.369
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial;	Q8K2B3	1	17	25	28.5	-0.644	-0.322	0.426
Carboxypeptidase N subunit 2;	Q9DBB9	1	10	11	18.5	-0.644	-0.342	0.452
Sorting nexin-1;	Q9WV80	1	7	7	8.6	-0.644	-0.191	0.258
Phosphoribosylformylglycinamidine synthase;	Q5SUR0	1	8	8	6.2	-0.644	-0.463	0.562
Enoyl-CoA hydratase domain-containing protein 2, mitochondrial;	Q3TLP5	1	2	2	14.3	-0.644	-0.06	0.112
40S ribosomal protein SA;	P14206	1	12	22	40.3	-0.621	-0.134	0.210
Macrophage mannose receptor 1;	Q61830	1	29	37	17.5	-0.621	-0.162	0.241

Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change (log$_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
SEC23-interacting protein;	Q6NZC7	1	3	3	2.6	-0.621	-0.048	0.119
Mannose-1-phosphate guanyltransferase beta;	Q8BTZ7	1	9	10	23.9	-0.621	-0.038	0.114
Cell cycle control protein 50A;	Q8VEK0	1	3	3	7.3	-0.621	-0.287	0.424
Aspartyl-tRNA synthetase, cytoplasmic;	Q922B2	1	4	4	7.2	-0.621	-0.029	0.110
Protein disulfide-isomerase A3;	P27773	1	53	129	56.2	-0.621	-0.239	0.353
N-acylglucosamine 2-epimerase;	P82343	1	5	6	9.5	-0.621	-0.277	0.412
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial;	Q8BH04	1	6	6	8.4	-0.621	-0.277	0.412
UPF0587 protein C1orf123 homolog;	Q8BHG2	1	6	6	38.4	-0.621	-0.449	0.576
MCG21506; Macrophage galactose N-acetyl-galactosamine specific lectin 2 isoform i; Uncharacterized protein;	A9XX86	1	5	6	16.9	-0.621	-0.086	0.156
Paralemmin-1;	Q9Z0P4	1	2	4	4.7	-0.621	-0.105	0.168
Histone deacetylase 2;	P70288	0.999	2	2	10.2	-0.621	-0.124	0.195
Plasma kallikrein;	P26262	1	10	11	17.1	-0.599	-0.163	0.273
Ceruloplasmin;	Q61147	1	47	71	32.1	-0.599	-0.064	0.151
Lon protease homolog, mitochondrial;	Q8CGK3	1	3	3	4.1	-0.599	-0.281	0.442
Cell adhesion molecule 4;	Q8R464	1	2	2	5.4	-0.599	-0.064	0.151
Complement component C8 gamma chain;	Q8VCG4	1	2	2	20.8	-0.599	-0.064	0.151
Disabled homolog 2;	P98078	1	3	4	7.2	-0.599	-0.045	0.135
C-Jun-amino-terminal kinase-interacting protein 4;	Q58A65	1	6	6	4.5	-0.599	-0.254	0.411
Frizzled-7;	Q61090	1	3	3	3.1	-0.599	-0.054	0.142
Alpha-2-antiplasmin;	Q61247	1	8	10	13	-0.599	-0.091	0.167
Coagulation factor XII;	Q80YC5	1	9	9	11.9	-0.599	-0.082	0.169
Uncharacterized protein;	F7DBB3	1	4	4	15.6	-0.599	-0.372	0.541
Phosphoenolpyruvate carboxykinase, cytosolic [GTP];	Q9Z2V4	0.991	2	2	4.2	-0.599	-0.417	0.578
Receptor-type tyrosine-protein phosphatase C;	P06800	1	6	6	5.1	-0.578	-0.276	0.465
Properdin;	P11680	1	3	3	7.1	-0.578	-0.095	0.202
Peptidyl-prolyl cis-trans isomerase C;	P30412	1	7	13	26.4	-0.578	-0.06	0.168
Peroxiredoxin-4;	O08807	1	10	11	43.1	-0.578	-0.069	0.178
Adseverin;	Q60604	1	12	17	13.6	-0.578	-0.242	0.410
Ubiquitin-associated protein 2-like;	Q80X50	1	8	8	7.9	-0.578	-0.336	0.533
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	Q9R0E2	1	6	6	8	-0.578	-0.112	0.229
STE20-like serine/threonine-protein kinase;	O54988	1	3	3	2.1	-0.556	-0.065	0.196
Inorganic pyrophosphatase 2, mitochondrial;	Q91VM9	1	2	2	4	-0.556	-0.065	0.196
Nicotinamide phosphoribosyltransferase;	Q99KQ4	1	13	15	27.1	-0.556	-0.237	0.454
Pterin-4-alpha-carbinolamine dehydratase 2;	Q9CZL5	1	2	2	8.1	-0.556	-0.065	0.195
Coatomer subunit zeta-2;	Q9JHH9	1	3	3	14.1	-0.556	-0.041	0.170
Palmitoyl-protein thioesterase 1;	O88531	1	5	6	16.9	-0.556	-0.237	0.454
Guanine nucleotide-binding protein G(i) subunit alpha-2;	P08752	1	10	13	31.8	-0.556	-0.172	0.354
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;	P63094	1	4	4	11.7	-0.105	-0.008	0.798
AP-1 complex subunit beta-1;	O35643	1	4	5	3.7	-0.515	-0.243	0.505
Antithrombin-III;	P32261	1	25	39	34.4	-0.515	-0.235	0.493
Ran-specific GTPase-activating protein;	P34022	1	3	4	10.8	-0.515	-0.294	0.568
Tetranectin;	P43025	1	10	23	45	-0.515	-0.074	0.227

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
Ribonuclease UK114;	P52760	1	2	2	19.3	-0.515	-0.052	0.206
40S ribosomal protein S20;	P60867	1	2	3	10.1	-0.515	-0.029	0.184
Nucleobindin-2;	P81117	1	6	6	14	-0.515	-0.147	0.356
Complement factor I;	Q61129	1	11	20	15.4	-0.515	-0.11	0.296
Sorbitol dehydrogenase;	Q64442	1	6	9	9.8	-0.515	-0.132	0.326
Oligoribonuclease, mitochondrial;	Q9D8S4	1	3	3	9.3	-0.515	-0.11	0.296
Inositol-3-phosphate synthase 1;	Q9JHU9	1	8	8	9.7	-0.515	-0.044	0.197
Uncharacterized protein;	F8VQL5	1	5	11	47.9	-0.515	-0.052	0.206
Dynamin-2;	P39054	1	5	5	7.4	-0.515	-0.191	0.429
CUGBP Elav-like family member 2;	Q9Z0H4	1	3	3	11.5	-0.515	-0.059	0.216
Protein phosphatase 1 regulatory subunit 7;	Q3UM45	1	13	19	27.1	-0.494	-0.174	0.432
Cytosolic purine 5'-nucleotidase;	Q3V1L4	1	4	4	9.5	-0.494	-0.125	0.345
Dipeptidyl peptidase 2;	Q9ET22	1	10	13	14.2	-0.494	-0.125	0.345
Plasma glutamate carboxypeptidase;	Q9WVJ3	1	10	12	19.6	-0.494	-0.125	0.345
ATP synthase subunit alpha, mitochondrial;	Q03265	1	44	90	44.3	-0.494	-0.334	0.637
Peptidyl-prolyl cis-trans isomerase FKBP10;	Q61576	1	12	13	13.8	-0.494	-0.077	0.260
Myoferlin;	Q69ZN7	1	12	12	4.6	-0.494	-0.139	0.375
Sodium/potassium-transporting ATPase subunit alpha-1;	Q8VDN2	1	11	13	17.7	-0.494	-0.23	0.520
Sodium/potassium-transporting ATPase subunit alpha-2;	Q6PIE5	1	6	9	16.2	-0.644	-0.362	0.476
Hsc70-interacting protein;	Q99L47	1	6	12	13.5	-0.494	-0.195	0.472
Complement factor H;	P06909	1	3	3	2.7	-0.494	-0.223	0.508
Reversion-inducing cysteine-rich protein with Kazal motifs;	Q9Z0J1	1	2	2	0.8	-0.494	-0.035	0.210
Peptidyl-prolyl cis-trans isomerase FKBP2;	P45878	0.995	2	4	8.6	-0.494	-0.056	0.237
Dipeptidyl peptidase 4;	P28843	1	8	9	10.1	-0.474	-0.086	0.308
Guanine nucleotide-binding protein subunit beta-2-like 1;	P68040	1	27	35	60.9	-0.474	-0.092	0.322
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial;	Q7TSQ8	1	3	3	4.2	-0.474	-0.092	0.322
Cleavage stimulation factor subunit 2;	Q8BIQ5	1	2	2	6	-0.474	-0.066	0.270
CD209 antigen-like protein B;	Q8CJ91	1	2	2	10.8	-0.474	-0.066	0.270
Mitochondrial 10-formyltetrahydrofolate dehydrogenase;	Q8K009	1	9	9	12.1	-0.474	-0.158	0.436
GDP-fucose protein O-fucosyltransferase 1;	Q91ZW2	1	2	2	4.5	-0.474	-0.039	0.240
Cell adhesion molecule 3;	Q99N28	1	2	4	5.5	-0.474	-0.053	0.258
S-methyl-5'-thioadenosine phosphorylase;	Q9CQ65	1	9	10	24	-0.474	-0.145	0.422
40S ribosomal protein S21;	Q9CQR2	1	3	3	22.9	-0.474	-0.066	0.270
Peptidyl-prolyl cis-trans isomerase FKBP9;	Q9Z247	1	10	11	10.9	-0.474	-0.204	0.512
Uncharacterized protein;	E9Q019	1	3	4	20.8	-0.474	-0.257	0.585
Alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB); Uncharacterized protein;	A2BFA6	1	2	2	1.1	-0.474	-0.033	0.233
Protein S100-A13;	P97352	1	5	7	31.6	-0.454	-0.168	0.493
Probable proline racemase;	Q9CXA2	1	8	10	24	-0.454	-0.112	0.385
Glycyl-tRNA synthetase;	Q9CZD3	1	15	16	15.9	-0.454	-0.236	0.590
ADP-ribosylation factor-like protein 3;	Q9WUL7	1	8	9	34.1	-0.454	-0.037	0.263
Gelsolin;	P13020	1	36	98	25.4	-0.454	-0.323	0.679
SAM domain and HD domain-containing protein 1;	Q60710	1	18	23	30.1	-0.454	-0.106	0.371
Alpha-2-macroglobulin;	Q61838	1	91	235	39.8	-0.454	-0.05	0.281

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
Argininosuccinate lyase;	Q91YI0	1	6	6	11.6	-0.454	-0.025	0.250
Cytosolic acyl coenzyme A thioester hydrolase;	Q91V12	1	2	2	7.1	-0.454	-0.336	0.691
Argininosuccinate synthase;	P16460	0.999	3	4	4.1	-0.454	-0.317	0.673
Tripartite motif-containing protein 72;	Q1XH17	1	11	14	18.2	-0.434	-0.182	0.545
Glycerol-3-phosphate dehydrogenase, mitochondrial;	Q64521	1	4	5	3.4	-0.434	-0.158	0.511
Spermidine synthase;	Q64674	1	7	11	14.6	-0.434	-0.07	0.340
Zinc-alpha-2-glycoprotein;	Q64726	1	6	8	18.6	-0.434	-0.041	0.296
Ribulose-phosphate 3-epimerase;	Q8VEE0	1	3	3	17.5	-0.434	-0.129	0.461
Stomatin-like protein 2;	Q99JB2	1	2	2	4	-0.434	-0.047	0.306
Phosphoacetylglucosamine mutase;	Q9CYR6	1	9	10	15.8	-0.434	-0.076	0.353
Epidermal growth factor receptor substrate 15;	P42567	1	4	5	4.6	-0.434	-0.129	0.461
PDZ and LIM domain protein 7;	Q3TJD7	1	4	5	42.7	-0.434	-0.123	0.448
Pyrroline-5-carboxylate reductase 1, mitochondrial;	Q922W5	1	2	2	11.7	-0.434	-0.065	0.328
UPF0160 protein MYG1, mitochondrial;	Q9JK81	1	6	6	19.3	-0.434	-0.106	0.407
Cathepsin E;	P70269	0.997	2	2	4.9	-0.434	-0.035	0.288
Cathepsin K;	P55097	0.994	2	2	3	-0.434	-0.029	0.281
Leukotriene A-4 hydrolase;	P24527	1	37	46	41.1	-0.415	-0.188	0.592
Ras-related protein Rab-23;	P35288	1	4	4	17.3	-0.415	-0.066	0.364
Immunoglobulin superfamily containing leucine-rich repeat protein;	Q6GU68	1	2	2	3.3	-0.415	-0.028	0.306
14 kDa phosphohistidine phosphatase;	Q9DAK9	1	5	6	28.2	-0.415	-0.055	0.341
Carboxypeptidase N catalytic chain;	Q9JJN5	1	6	6	17.3	-0.415	-0.066	0.364
Catalase;	P24270	1	35	47	45.2	-0.415	-0.227	0.635
Xanthine dehydrogenase/oxidase;	Q00519	1	46	56	28.1	-0.415	-0.1	0.410
Inter-alpha-trypsin inhibitor heavy chain H2;	Q61703	1	11	11	11.6	-0.415	-0.061	0.352
	Q8R164	1	8	8	27.8	-0.415	-0.243	0.658
NEDD9-interacting protein with calponin homology and LIM domains;	Q8VDP3	1	4	4	5.2	-0.415	-0.072	0.376
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial;	Q921G7	1	10	10	15.1	-0.415	-0.177	0.561
Flavin reductase (NADPH);	Q923D2	1	9	11	43.2	-0.415	-0.194	0.602
Vitamin D-binding protein;	P21614	1	31	54	54.6	-0.377	-0.034	0.348
Alpha-2-HS-glycoprotein;	P29699	1	21	52	37.1	-0.377	-0.029	0.340
Protein AMBP;	Q07456	1	7	9	14.3	-0.377	-0.088	0.452
COMM domain-containing protein 3;	Q63829	1	3	3	12.3	-0.377	-0.049	0.367
Prostaglandin reductase 1;	Q91YR9	1	10	14	24.9	-0.377	-0.264	0.725
Serine protease inhibitor A3K;	P07759	1	36	549	50.7	-0.377	-0.024	0.333
Uncharacterized protein;	D3Z450	1	4	6	12.9	0.705	0.221	0.237
Serine protease inhibitor A3N;	Q91WP6	1	4	4	19.4	-0.494	-0.049	0.227
Serine protease inhibitor A3G;	Q5I2A0	1	3	3	15.2	0.566	0.042	0.155
Serine protease inhibitor A3M;	Q03734	0.986	2	2	20.8	0.848	0.033	0.029
Septin-2;	P42208	1	13	15	36.8	-0.377	-0.093	0.464
Thiosulfate sulfurtransferase;	P52196	1	11	12	30.6	-0.377	-0.024	0.333
Isocitrate dehydrogenase [NADP], mitochondrial;	P54071	1	39	72	38.5	-0.377	-0.054	0.378
Prolyl 4-hydroxylase subunit alpha-2;	Q60716	1	9	9	14.2	-0.377	-0.069	0.413
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial;	Q91YT0	1	12	15	24.8	-0.377	-0.201	0.658

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
Prolow-density lipoprotein receptor-related protein 1;	Q91ZX7	1	40	44	7.7	-0.377	-0.132	0.549
Golgi reassembly-stacking protein 2;	Q99JX3	1	6	7	11.4	-0.377	-0.029	0.340
Nucleoside diphosphate kinase;	E9PZF0	1	12	49	74.2	-0.377	-0.152	0.580
Serum albumin;	P07724	1	96	3649	70.2	-0.358	-0.133	0.588
Prothrombin;	P19221	1	13	16	12.5	-0.358	-0.083	0.475
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	Q99LD8	1	18	26	40.7	-0.358	-0.119	0.557
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial;	Q9CQA3	1	10	16	28.7	-0.358	-0.129	0.578
Sorting nexin-5;	Q9D8U8	1	7	10	11.9	-0.358	-0.078	0.463
Glutamate dehydrogenase 1, mitochondrial;	P26443	1	15	16	20.1	-0.358	-0.069	0.451
F-actin-capping protein subunit alpha-1;	P47753	1	5	6	27.6	-0.358	-0.083	0.475
F-actin-capping protein subunit alpha-2;	P47754	0.995	2	2	27.6	-0.515	-0.066	0.229
Ras-related protein Rab-1A;	P62821	1	10	11	41.1	-0.358	-0.064	0.439
Ras-related protein Rab-14;	Q91V41	1	6	10	36.4	-0.089	-0.013	0.848
Ras-related protein Rab-1B;	Q9D1G1	1	4	4	26.9	0.345	0.035	0.401
Ras-related protein Rab-10;	P61027	1	3	5	22.5	0.176	0.023	0.681
Ras-related protein Rab-8A;	P55258	1	2	3	17.4	-0.12	-0.025	0.801
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1;	P62874	1	6	9	29.4	-0.358	-0.055	0.415
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2;	P62880	1	3	4	25.1	-0.358	-0.133	0.588
Aminopeptidase N;	P97449	1	17	20	11.9	-0.358	-0.078	0.463
Leukocyte elastase inhibitor A;	Q9D154	1	22	53	38.5	-0.358	-0.078	0.463
Fetuin-B;	Q9QXC1	1	10	19	24.7	-0.358	-0.032	0.376
Guanine deaminase;	Q9R111	1	20	23	39.6	-0.358	-0.069	0.451
MCG140951; Plexin B2; Plxnb2 protein; Uncharacterized protein;	B2RXS4	1	2	2	2.1	-0.358	-0.023	0.361
Transmembrane emp24 domain-containing protein 10;	Q9D1D4	1	3	3	9.6	-0.358	-0.023	0.361
Acylpyruvase FAHD1, mitochondrial;	Q8R0F8	0.999	3	3	16.7	-0.358	-0.046	0.394
Myc box-dependent-interacting protein 1;	O08539	1	8	12	18	-0.34	-0.245	0.756
Complement C4-B;	P01029	1	30	33	15.5	-0.34	-0.121	0.595
Nuclear transport factor 2;	P61971	1	4	4	23.6	-0.34	-0.06	0.464
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1;	Q3TW96	1	26	31	32.7	-0.34	-0.125	0.607
Sulfhydryl oxidase 1;	Q8BND5	1	8	10	9.8	-0.34	-0.047	0.432
Dihydropyrimidinase-related protein 2;	O08553	1	48	84	55.1	-0.34	-0.052	0.442
Uncharacterized protein;	E9PWE8	1	24	28	35.1	-0.12	-0.018	0.786
Vacuolar protein sorting-associated protein 26A;	P40336	1	4	4	9.2	-0.34	-0.121	0.598
Ras-related protein Rab-2A;	P53994	1	7	8	19.3	-0.34	-0.056	0.453
Endoplasmic reticulum resident protein 29;	P57759	1	7	13	17.6	-0.34	-0.06	0.464
Histidine triad nucleotide-binding protein 1;	P70349	1	8	31	71.4	-0.34	-0.164	0.666
Lysosomal alpha-glucosidase;	P70699	1	3	4	4.8	-0.34	-0.116	0.588
Keratin, type II cytoskeletal 1b;	Q6IFZ6	1	8	8	10.1	-0.34	-0.112	0.578
Clathrin light chain B;	Q6IRU5	1	3	4	7.9	-0.34	-0.034	0.412
Isoleucyl-tRNA synthetase, mitochondrial;	Q8BIJ6	1	10	10	9.1	-0.34	-0.142	0.634
Protein DJ-1;	Q99LX0	1	11	17	43.4	-0.34	-0.159	0.659
Selenocysteine lyase;	Q9JLI6	1	3	3	9.5	-0.34	-0.065	0.476
Extracellular matrix protein 1;	Q61508	1	2	2	11.7	-0.34	-0.082	0.511

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
Beta-hexosaminidase subunit beta;	P20060	0.986	2	2	1.7	-0.34	-0.022	0.391
Lymphocyte antigen 6D;	P35459	1	5	6	48	-0.322	-0.129	0.644
Adenosine kinase;	P55264	1	16	22	25.2	-0.322	-0.101	0.597
Fibulin-1;	Q08879	1	13	13	12.6	-0.322	-0.056	0.491
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1;	Q8R3B1	1	8	8	13.8	-0.322	-0.101	0.594
Alpha-1-antitrypsin 1-1;	P07758	1	11	45	38.3	-0.322	-0.032	0.441
Alpha-1-antitrypsin 1-2;	P22599	1	9	20	35.6	-0.252	-0.018	0.521
Alpha-1-antitrypsin 1-4;	Q00897	1	7	13	33.9	-0.621	-0.038	0.114
Elongation factor 1-alpha 1;	P10126	1	13	30	36.4	-0.322	-0.056	0.491
Elongation factor 1-alpha 2;	P62631	1	11	18	30.2	0.202	0.03	0.636
Selenium-binding protein 1;	P17563	1	36	53	52.5	-0.322	-0.06	0.502
Dipeptidyl peptidase 1;	P97821	1	9	13	12.4	-0.322	-0.076	0.535
Tubulin--tyrosine ligase-like protein 12;	Q3UDE2	1	9	13	11.6	-0.322	-0.205	0.747
Arachidonate 5-lipoxygenase;	P48999	1	2	2	1.3	-0.322	-0.04	0.450
Cartilage-associated protein;	Q9CYD3	1	2	2	2	-0.322	-0.04	0.450
Uncharacterized protein;	E9Q4Y1	1	2	2	4.6	-0.322	-0.02	0.421
Dynactin subunit 3;	Q9Z0Y1	0.999	2	2	5.7	-0.322	-0.04	0.450
D-dopachrome decarboxylase;	O35215	1	11	17	51.7	-0.304	-0.116	0.655
Annexin A3;	O35639	1	13	14	29.4	-0.304	-0.068	0.550
Ectonucleoside triphosphate diphosphohydrolase 2;	O55026	1	4	4	7.1	-0.304	-0.068	0.550
Proteasome subunit alpha type-3;	O70435	1	7	9	18	-0.304	-0.18	0.751
BAG family molecular chaperone regulator 3;	Q9JLV1	1	5	6	6.4	-0.304	-0.023	0.457
Galactokinase;	Q9R0N0	1	6	7	11.5	-0.304	-0.038	0.480
Prostaglandin F2 receptor negative regulator;	Q9WV91	1	3	3	5.8	-0.304	-0.045	0.498
Coatomer subunit epsilon;	O89079	1	3	3	14.1	-0.304	-0.094	0.610
Protein disulfide-isomerase;	P09103	1	37	72	33.2	-0.304	-0.03	0.471
V-type proton ATPase catalytic subunit A;	P50516	1	15	20	19.9	-0.304	-0.049	0.508
Elongation factor 2;	P58252	1	50	82	39.3	-0.304	-0.109	0.647
Retinoid-inducible serine carboxypeptidase;	Q920A5	1	8	10	15	-0.304	-0.083	0.591
Peptidyl-prolyl cis-trans isomerase D;	Q9CR16	1	20	24	31.6	-0.304	-0.049	0.508
Obg-like ATPase 1;	Q9CZ30	1	9	9	16.7	-0.304	-0.173	0.741
Aspartyl aminopeptidase;	Q9Z2W0	1	13	14	28.5	-0.304	-0.034	0.469
Uncharacterized protein;	Q3ULW8	1	7	8	9.7	-0.304	-0.019	0.452
Creatine kinase M-type;	P07310	1	46	1232	60.4	-0.286	-0.042	0.527
Creatine kinase B-type;	Q04447	1	28	54	37.3	-0.286	-0.049	0.546
Synaptic vesicle membrane protein VAT-1 homolog;	Q62465	1	19	34	26.1	-0.286	-0.045	0.536
Neutral alpha-glucosidase AB;	Q8BHN3	1	13	17	12.4	-0.286	-0.049	0.546
Aflatoxin B1 aldehyde reductase member 2;	Q8CG76	1	13	23	26.4	-0.286	-0.049	0.546
Aldose 1-epimerase;	Q8K157	1	4	4	13.2	-0.286	-0.038	0.518
ATP-dependent RNA helicase DDX1;	Q91VR5	1	2	2	1.8	-0.286	-0.017	0.483
6-phosphogluconate dehydrogenase, decarboxylating;	Q9DCD0	1	23	36	32.3	-0.286	-0.091	0.642
Interferon-induced guanylate-binding protein 2;	Q9Z0E6	1	6	6	9.2	-0.286	-0.094	0.650
Epididymal secretory protein E1;	Q9Z0J0	1	7	16	24.8	-0.286	-0.035	0.510

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
Inositol monophosphatase 1;	O55023	1	7	9	22.4	-0.286	-0.073	0.605
Glutathione S-transferase Mu 2;	P15626	1	17	24	70.2	-0.286	-0.024	0.495
Glutathione S-transferase Mu 1;	P10649	1	14	20	52.8	-0.105	-0.017	0.821
Glutathione S-transferase Mu 5;	P48774	1	6	6	24.2	-0.12	-0.035	0.833
Fumarylacetoacetase;	P35505	1	10	13	25.5	-0.286	-0.066	0.585
Nascent polypeptide-associated complex subunit alpha, muscle-specific form;	P70670	1	31	33	11.8	-0.286	-0.038	0.518
Pyruvate dehydrogenase protein X component, mitochondrial;	Q8BKZ9	1	9	11	16.6	-0.286	-0.119	0.697
Bleomycin hydrolase;	Q8R016	1	12	15	25.9	-0.286	-0.059	0.566
Saccharopine dehydrogenase-like oxidoreductase;	Q8R127	1	4	4	8.4	-0.286	-0.052	0.556
Mannose-6-phosphate isomerase;	Q924M7	1	6	6	13.5	-0.286	-0.063	0.575
Eukaryotic translation initiation factor 3 subunit I;	Q9QZD9	1	3	4	12	-0.286	-0.091	0.642
Xin actin-binding repeat-containing protein 1;	O70373	1	3	3	2.7	-0.286	-0.045	0.536
Angiotensinogen;	P11859	1	2	2	4.6	-0.286	-0.017	0.483
Proteasome subunit beta type-10;	O35955	0.999	2	2	7.7	-0.286	-0.129	0.710
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical];	P56380	1	6	6	42.2	-0.269	-0.045	0.558
Steroid receptor RNA activator 1;	Q80VJ2	1	3	7	12.1	-0.269	-0.019	0.499
Reticulocalbin-3;	Q8BH97	1	4	5	11.7	-0.269	-0.042	0.542
Serpin B8;	O08800	1	7	11	9.9	-0.252	-0.015	0.516
Epididymis-specific alpha-mannosidase;	O54782	1	2	3	2.8	-0.252	-0.015	0.516
Dystrophin;	P11531	1	3	3	4.9	-0.252	-0.042	0.574
Indolethylamine N-methyltransferase;	P40936	1	6	8	25.4	-0.252	-0.099	0.709
Heparin cofactor 2;	P49182	1	9	10	11.7	-0.252	-0.039	0.565
Apolipoprotein A-I;	Q00623	1	20	30	34.5	-0.252	-0.018	0.521
Ganglioside GM2 activator;	Q60648	1	2	2	16.6	-0.252	-0.054	0.602
Putative N-acetylglucosamine-6-phosphate deacetylase;	Q8JZV7	1	4	4	10.5	-0.252	-0.039	0.565
Eukaryotic translation initiation factor 3 subunit H;	Q91WK2	1	4	8	27.1	-0.252	-0.039	0.565
Torsin-1B;	Q9ER41	1	3	4	6.2	-0.252	-0.033	0.548
Sec24 related gene family, member D (S. cerevisiae); Uncharacterized protein;	Q6NXL1	1	7	9	6.4	-0.252	-0.033	0.548
Phosphatidylinositol transfer protein alpha isoform;	P53810	1	7	9	21	-0.252	-0.012	0.512
Plasma protease C1 inhibitor;	P97290	1	12	19	16.9	-0.252	-0.039	0.565
Periostin;	Q62009	1	8	8	7.9	-0.252	-0.066	0.638
Zyxin;	Q62523	1	13	16	15.4	-0.252	-0.045	0.583
Major vault protein;	Q9EQK5	1	6	7	8.6	-0.252	-0.063	0.629
Uncharacterized protein;	Q3TUE1	1	11	15	19.5	-0.252	-0.075	0.673
Synaptophysin-like protein 1;	O09117	1	2	2	11.4	-0.252	-0.021	0.527
NADPH:adrenodoxin oxidoreductase, mitochondrial;	Q61578	0.992	2	2	2.6	-0.252	-0.021	0.527
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial;	O88696	1	4	7	15.1	-0.234	-0.047	0.620
Alcohol dehydrogenase 1;	P00329	1	6	7	10.1	-0.234	-0.022	0.565
CD44 antigen;	P15379	1	2	2	2.6	-0.234	-0.033	0.587
T-complex protein 1 subunit theta;	P42932	1	5	5	6.4	-0.234	-0.019	0.559
Ras-related protein Rab-7a;	P51150	1	17	21	40.1	-0.234	-0.019	0.559
Long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P51174	1	17	24	28.1	-0.234	-0.077	0.701
Acyl-CoA synthetase short-chain family member 3, mitochondrial;	Q14DH7	1	6	6	13	-0.234	-0.102	0.746

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
NudC domain-containing protein 2;	Q9CQ48	1	2	2	8.3	-0.234	-0.019	0.559
Calcium-regulated heat stable protein 1;	Q9CR86	1	4	8	18.2	-0.234	-0.022	0.565
Sorting nexin-2;	Q9CWK8	1	17	17	26.8	-0.234	-0.036	0.595
Endoplasmic reticulum resident protein 44;	Q9D1Q6	1	12	14	21.4	-0.234	-0.039	0.603
Phosphoglycerate mutase 1;	Q9DBJ1	1	25	89	50.8	-0.234	-0.017	0.554
Gamma-interferon-inducible lysosomal thiol reductase;	Q9ESY9	1	2	2	5.2	-0.234	-0.019	0.559
Ribonuclease 4;	Q9JJH1	1	6	7	27.7	-0.234	-0.094	0.734
Carbonyl reductase 3; Uncharacterized protein;	Q8K354	1	13	14	39.7	-0.234	-0.036	0.595
N-acetylneuraminic acid synthase (Sialic acid synthase); Uncharacterized protein;	Q99J77	1	7	8	20.6	-0.234	-0.036	0.595
Myosin light chain 1/3, skeletal muscle isoform;	P05977	1	12	132	52.1	-0.234	-0.022	0.565
Lysosomal protective protein;	P16675	1	9	12	10.1	-0.234	-0.047	0.620
Purine nucleoside phosphorylase;	P23492	1	12	12	34.9	-0.234	-0.05	0.629
Cytochrome b5;	P56395	1	5	6	41	-0.234	-0.028	0.572
Heat shock protein 105 kDa;	Q61699	1	12	12	14.8	-0.234	-0.127	0.786
Inorganic pyrophosphatase;	Q9D819	1	17	26	48.4	-0.234	-0.022	0.565
Leucine-rich repeat-containing protein 20;	Q8CI70	0.986	2	2	4.9	-0.234	-0.019	0.559
Voltage-dependent calcium channel subunit alpha-2/delta-1;	O08532	1	2	2	1.3	-0.218	-0.013	0.583
Metallothionein-2;	P02798	1	2	3	19.7	-0.218	-0.025	0.604
Ornithine aminotransferase, mitochondrial;	P29758	1	17	22	30.8	-0.218	-0.081	0.742
182 kDa tankyrase-1-binding protein;	P58871	1	7	7	5.8	-0.218	-0.056	0.687
Far upstream element-binding protein 2;	Q3U0V1	1	21	26	27.8	-0.218	-0.053	0.680
Arginase-1;	Q61176	1	11	13	31.9	-0.218	-0.028	0.611
Phosphoglucomutase-2;	Q7TSV4	1	12	16	13.4	-0.218	-0.048	0.664
Phostensin;	Q8BQ30	1	2	2	4.2	-0.218	-0.018	0.592
Succinate-semialdehyde dehydrogenase, mitochondrial;	Q8BWF0	1	5	5	12	-0.218	-0.071	0.723
ES1 protein homolog, mitochondrial;	Q9D172	1	15	21	39.5	-0.218	-0.053	0.680
4-trimethylaminobutyraldehyde dehydrogenase;	Q9JLJ2	1	26	34	32.4	-0.218	-0.028	0.611
Proline synthase co-transcribed bacterial homolog protein;	Q9Z2Y8	1	4	8	8	-0.218	-0.086	0.754
Glucosamine-6-phosphate isomerase 1;	O88958	1	3	3	8	-0.218	-0.086	0.754
Adenosylhomocysteinase;	P50247	1	30	49	44.4	-0.218	-0.02	0.598
Pyruvate kinase isozymes M1/M2;	P52480	1	68	329	67.6	-0.218	-0.076	0.730
Glyoxylate reductase/hydroxypyruvate reductase;	Q91Z53	1	17	24	35.7	-0.218	-0.033	0.625
Serotransferrin;	Q921I1	1	89	620	58.8	-0.218	-0.02	0.598
Mitochondrial 2-oxoglutarate/malate carrier protein;	Q9CR62	1	4	4	9.8	-0.218	-0.068	0.716
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	Q9CWS0	1	4	4	17.5	-0.218	-0.063	0.702
Phosphoglucomutase-1;	Q9D0F9	1	49	81	53.2	-0.218	-0.035	0.633
Cysteine sulfinic acid decarboxylase;	Q9DBE0	1	8	10	13	-0.218	-0.056	0.687
Choline transporter-like protein 2;	Q8BY89	0.999	2	2	2.4	-0.218	-0.02	0.598
Complement C3;	P01027	1	116	214	41.1	-0.201	-0.049	0.706
Plasminogen;	P20918	1	10	10	6	-0.201	-0.028	0.649
Ras-related protein Rab-21;	P35282	1	4	4	22.5	-0.201	-0.039	0.677
Dynein light chain roadblock-type 1;	P62627	1	5	5	51	-0.201	-0.03	0.656
Stress-induced-phosphoprotein 1;	Q60864	1	23	28	27.3	-0.201	-0.058	0.726

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
Gephyrin;	Q8BUV3	1	4	6	4	-0.201	-0.111	0.824
Probable fructose-2,6-bisphosphatase TIGAR;	Q8BZA9	1	4	4	16.7	-0.201	-0.025	0.643
Arf-GAP domain and FG repeats-containing protein 1;	Q8K2K6	1	5	5	10	-0.201	-0.076	0.768
Neudesin;	Q9CQ45	1	5	6	25.7	-0.201	-0.016	0.626
Tetratricopeptide repeat protein 38;	A3KMP2	1	12	15	20.2	-0.201	-0.102	0.809
COP9 signalosome complex subunit 3;	O88543	1	4	4	16.1	-0.201	-0.102	0.809
	P35492	1	29	41	35.3	-0.201	-0.028	0.649
Myosin regulatory light chain 2, skeletal muscle isoform;	P97457	1	20	49	55.6	-0.201	-0.025	0.643
Junction plakoglobin;	Q02257	1	9	9	12.2	-0.201	-0.085	0.783
Catenin beta-1;	Q02248	0.997	2	2	6.3	0.475	0.284	0.613
Echinoderm microtubule-associated protein-like 2;	Q7TNG5	1	17	18	29.7	-0.201	-0.065	0.745
Peroxisomal acyl-coenzyme A oxidase 3;	Q9EPL9	1	12	18	11.7	-0.201	-0.169	0.876
Uncharacterized protein;	F8WIT2	1	65	117	51.9	-0.201	-0.049	0.706
PDZ and LIM domain protein 1;	O70400	1	3	3	15	-0.201	-0.032	0.656
Catechol O-methyltransferase;	O88587	1	2	2	6.8	-0.201	-0.025	0.643
Amine oxidase [flavin-containing] A;	Q64133	0.997	2	2	5.7	-0.201	-0.012	0.617
Collagen alpha-1(XV) chain;	O35206	1	4	4	12.2	-0.184	-0.067	0.783
Ig heavy chain V region 441;	P01806	1	3	3	13.8	-0.184	-0.017	0.664
ATP synthase subunit beta, mitochondrial;	P56480	1	46	151	43.5	-0.184	-0.025	0.681
Cellular retinoic acid-binding protein 1;	P62965	1	6	7	34.3	-0.184	-0.04	0.719
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);	Q8VC30	1	4	4	4	-0.184	-0.013	0.656
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial;	Q91VD9	1	13	20	16.4	-0.184	-0.027	0.687
Protein SEC13 homolog;	Q9D1M0	1	8	10	18	-0.184	-0.042	0.725
Protein NDRG2;	Q9QYG0	1	17	25	34	-0.184	-0.042	0.725
Probable methylthioribulose-1-phosphate dehydratase;	Q9WVQ5	1	5	5	21.6	-0.184	-0.017	0.664
Ahnak protein; MCG17833, isoform CRA_b; Uncharacterized protein;	Q8R2L7	1	4	4	57.8	-0.184	-0.042	0.725
Integrin beta-1;	P09055	1	9	10	9.4	-0.184	-0.054	0.756
Chromobox protein homolog 3;	P23198	1	4	4	19.1	-0.184	-0.065	0.778
Microtubule-associated protein 4;	P27546	1	25	30	19.7	-0.184	-0.038	0.712
Protein transport protein Sec23A;	Q01405	1	12	19	13.5	-0.184	-0.023	0.675
Pyridoxal kinase;	Q8K183	1	13	14	22.8	-0.184	-0.04	0.719
Endoplasmic reticulum aminopeptidase 1;	Q9EQH2	1	11	12	8.7	-0.184	-0.044	0.732
Uncharacterized protein;	D3Z0Y2	1	28	89	72.5	-0.184	-0.023	0.675
Peptidyl-prolyl cis-trans isomerase-like 1;	Q9D0W5	1	3	4	14.5	-0.184	-0.006	0.647
Sushi domain-containing protein 2;	Q9DBX3	0.999	2	2	2.4	-0.184	-0.038	0.712
Histamine N-methyltransferase;	Q91VF2	0.998	2	2	6.1	-0.184	-0.04	0.719
Dynactin subunit 2;	Q99KJ8	1	6	6	10.2	-0.168	-0.038	0.737
C-1-tetrahydrofolate synthase, cytoplasmic;	Q922D8	1	18	19	19.1	-0.168	-0.102	0.860
Phosphoglycerate mutase 2;	O70250	1	27	185	49	-0.152	-0.019	0.707
Cytoplasmic dynein 1 intermediate chain 2;	O88487	1	7	7	7.5	-0.152	-0.068	0.833
Basigin;	P18572	1	4	6	5.9	-0.152	-0.008	0.687
Myristoylated alanine-rich C-kinase substrate;	P26645	1	8	14	21	-0.152	-0.019	0.707
Cytoplasmic aconitate hydratase;	P28271	1	35	51	28.1	-0.152	-0.042	0.775

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 phosphatase 1A;	P49443	1	7	8	28.2	-0.152	-0.024	0.724
Neural cell adhesion molecule L1-like protein;	P70232	1	3	3	1.5	-0.152	-0.014	0.698
Fructose-1,6-bisphosphatase isozyme 2;	P70695	1	6	6	12.1	-0.152	-0.081	0.855
Hsp90 co-chaperone Cdc37;	Q61081	1	5	5	13.2	-0.152	-0.052	0.800
Myomesin-1;	Q62234	1	32	38	12.4	-0.152	-0.054	0.805
Peptidyl-prolyl cis-trans isomerase FKBP3;	Q62446	1	4	5	14.7	-0.152	-0.03	0.741
Hematopoietic progenitor cell antigen CD34;	Q64314	1	5	5	11.8	-0.152	-0.03	0.741
Ribonuclease inhibitor;	Q91VI7	1	54	69	73.9	-0.152	-0.022	0.718
Electron transfer flavoprotein subunit beta;	Q9DCW4	1	16	32	40.8	-0.152	-0.047	0.790
Profilin-2;	Q9JJV2	1	2	4	12.7	-0.152	-0.012	0.694
Kininogen-1;	O08677	1	34	83	43.8	-0.152	-0.017	0.703
Sorting nexin-3;	O70492	1	7	8	20.4	-0.152	-0.032	0.747
Sorting nexin-12;	O70493	0.948	2	2	15.4	-0.074	-0.003	0.864
Isocitrate dehydrogenase [NADP] cytoplasmic;	O88844	1	37	63	52.4	-0.152	-0.01	0.690
Beta-galactosidase;	P23780	1	13	20	18.5	-0.152	-0.014	0.698
Aldose reductase;	P45376	1	28	54	41.1	-0.152	-0.01	0.690
Profilin-1;	P62962	1	23	100	64.3	-0.152	-0.01	0.690
Clusterin;	Q06890	1	4	6	8.5	-0.152	-0.024	0.724
Serpin B6;	Q60854	1	29	69	49.2	-0.152	-0.02	0.713
Uncharacterized protein;	E9Q9T2	1	10	14	24.6	0.263	0.066	0.613
Plastin-2;	Q61233	1	44	67	47	-0.152	-0.035	0.758
Low molecular weight phosphotyrosine protein phosphatase;	Q9D358	1	8	15	31.6	-0.152	-0.042	0.775
Enoyl-CoA delta isomerase 2, mitochondrial;	Q9WUR2	1	4	5	22.4	-0.152	-0.037	0.764
Transcription elongation factor B polypeptide 1;	P83940	0.997	2	2	10.7	-0.152	-0.007	0.685
AP-2 complex subunit alpha-1;	P17426	0.928	2	2	1	-0.152	-0.017	0.703
Protein disulfide-isomerase A4;	P08003	1	11	12	12.9	-0.136	-0.03	0.786
Lysosome-associated membrane glycoprotein 1;	P11438	1	2	3	5.7	-0.136	-0.052	0.837
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;	P13707	1	36	73	57.7	-0.136	-0.025	0.765
Monocarboxylate transporter 1;	P53986	1	2	2	4.1	-0.136	-0.015	0.736
Isochorismatase domain-containing protein 2A, mitochondrial;	P85094	1	6	6	13.1	-0.136	-0.004	0.719
2,4-dienoyl-CoA reductase, mitochondrial;	Q9CQ62	1	5	5	21.8	-0.136	-0.057	0.844
EH domain-containing protein 4;	Q9EQP2	1	6	6	8.3	-0.136	-0.033	0.790
Hepatoma-derived growth factor;	P51859	1	7	8	22.8	-0.136	-0.061	0.854
Actin, alpha cardiac muscle 1;	P68033	1	8	10	62.1	-0.136	-0.009	0.725
Heat shock 70 kDa protein 4;	Q61316	1	31	37	30.3	-0.136	-0.016	0.740
Heat shock 70 kDa protein 4L;	P48722	1	10	11	17.1	-0.454	-0.193	0.529
NEDD8-activating enzyme E1 regulatory subunit;	Q8VBW6	1	7	7	12	-0.136	-0.046	0.822
Dynein light chain 2, cytoplasmic;	Q9D0M5	1	6	7	20.2	-0.136	-0.01	0.728
StAR-related lipid transfer protein 5;	Q9EPQ7	1	5	5	20.7	-0.136	-0.015	0.736
Transgelin-2;	Q9WVA4	1	21	34	62.8	-0.136	-0.04	0.809
Opioid growth factor receptor;	Q99PG2	0.999	3	3	7.7	-0.136	-0.01	0.730
Alpha-adducin;	Q9QYC0	0.999	3	4	4.5	-0.136	-0.007	0.723
Phosphatidylinositol-binding clathrin assembly protein;	Q7M6Y3	0.999	2	2	2.3	-0.136	-0.022	0.760

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
Chaperone activity of bc1 complex-like, mitochondrial;	Q60936	0.99	2	2	6.5	-0.136	-0.042	0.813
Heterogeneous nuclear ribonucleoprotein H;	O35737	1	10	11	22.9	-0.12	-0.01	0.766
Protein S100-A1;	P56565	1	2	2	16	-0.12	-0.017	0.781
Serrate RNA effector molecule homolog;	Q99MR6	1	2	2	1.5	-0.12	-0.02	0.790
Bifunctional purine biosynthesis protein PURH;	Q9CWJ9	1	34	61	35.1	-0.12	-0.017	0.781
Iron-sulfur cluster assembly 2 homolog, mitochondrial;	Q9DCB8	1	2	2	7.8	-0.12	-0.013	0.770
Prolyl endopeptidase;	Q9QUR6	1	20	27	22.8	-0.12	-0.04	0.844
Myomesin 2; Uncharacterized protein;	Q14BI5	1	44	57	23.2	-0.12	-0.067	0.891
H-2 class I histocompatibility antigen, L-D alpha chain;	P01897	1	13	15	27.3	-0.12	-0.022	0.794
H-2 class I histocompatibility antigen, K-B alpha chain;	P01901	1	3	3	13.4	-0.014	-0.002	0.975
H-2 class I histocompatibility antigen, Q10 alpha chain;	P01898	1	2	3	9.8	-0.889	-0.296	0.147
Phosphoglycerate kinase 1;	P09411	1	43	142	59.5	-0.12	-0.01	0.755
GTP-binding nuclear protein Ran;	P62827	1	19	41	42.6	-0.12	-0.007	0.758
T-complex protein 1 subunit epsilon;	P80316	1	6	7	7	-0.12	-0.013	0.770
Dihydropteridine reductase;	Q8BVI4	1	11	11	39.2	-0.12	-0.013	0.770
UPF0366 protein C11orf67 homolog;	Q8R0P4	1	9	11	36.9	-0.12	-0.02	0.795
Thioredoxin-dependent peroxide reductase, mitochondrial;	P20108	1	13	27	28	-0.105	-0.05	0.895
Peptidyl-prolyl cis-trans isomerase FKBP1A;	P26883	1	3	4	13	-0.105	-0.007	0.796
Transforming growth factor-beta-induced protein ig-h3;	P82198	1	5	5	7.1	-0.105	-0.005	0.792
Xaa-Pro dipeptidase;	Q11136	1	9	10	15.2	-0.105	-0.028	0.850
Hydroxysteroid dehydrogenase-like protein 2;	Q2TPA8	1	2	2	4.5	-0.105	-0.009	0.801
Leukocyte surface antigen CD47;	Q61735	1	3	4	4.6	-0.105	-0.019	0.824
UPF0586 protein C9orf41 homolog;	Q80UY1	1	4	4	5.8	-0.105	-0.007	0.796
D-2-hydroxyglutarate dehydrogenase, mitochondrial;	Q8CIM3	1	2	2	3.6	-0.105	-0.003	0.791
Beta-lactamase-like protein 2;	Q99KR3	1	5	5	12.5	-0.105	-0.035	0.866
Thioredoxin domain-containing protein 17;	Q9CQM5	1	6	8	26.8	-0.105	-0.007	0.796
Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase;	Q9DBB8	1	4	7	12	-0.105	-0.042	0.881
AP-2 complex subunit beta;	Q9DBG3	1	5	5	4.8	-0.105	-0.012	0.807
Glutathione S-transferase kappa 1;	Q9DCM2	1	5	5	16.8	-0.105	-0.052	0.899
Acyl-protein thioesterase 2;	Q9WTL7	1	4	4	12.6	-0.105	-0.015	0.813
Glycogen synthase kinase-3 beta;	Q9WV60	1	4	4	9.8	-0.105	-0.011	0.803
Mitotic checkpoint protein BUB3;	Q9WVA3	1	5	5	13.8	-0.105	-0.036	0.869
C-terminal-binding protein 1;	O88712	1	6	9	15.4	-0.105	-0.011	0.803
C-terminal-binding protein 2;	P56546	1	4	4	9.3	-0.044	-0.002	0.900
Glutathione S-transferase A3;	P30115	0.987	4	4	8.6	-0.105	-0.014	0.810
Heat shock cognate 71 kDa protein;	P63017	1	51	118	48.3	-0.105	-0.012	0.807
Heat shock 70 kDa protein 1A;	Q61696	1	37	62	46.8	0.251	0.023	0.538
78 kDa glucose-regulated protein;	P20029	1	36	59	37.6	-0.786	-0.325	0.261
Secernin-3;	Q3TMH2	1	6	8	12.2	-0.105	-0.014	0.810
Inter-alpha-trypsin inhibitor heavy chain H3;	Q61704	1	9	9	7.4	-0.105	-0.023	0.836
Copine-3;	Q8BT60	1	8	13	14.8	-0.105	-0.014	0.810
Copine-1;	Q8C166	1	7	10	17.5	-0.252	-0.036	0.557
Scavenger mRNA-decapping enzyme DcpS;	Q9DAR7	1	19	25	40.5	-0.105	-0.036	0.869

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
Mitogen-activated protein kinase 9;	Q9WTU6	1	4	6	5	-0.105	-0.014	0.810
ADP-ribosylation factor-like protein 8B;	Q9CQW2	1	2	5	4.8	-0.105	-0.003	0.791
UPF0364 protein C6orf211 homolog;	A6H630	0.975	2	2	3.4	-0.105	-0.023	0.836
Lysosomal alpha-mannosidase;	O09159	1	7	7	5.3	-0.089	-0.019	0.864
Cathepsin S;	O70370	1	7	10	26.5	-0.089	-0.017	0.857
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2;	O88428	1	3	5	5.3	-0.089	-0.016	0.854
Calreticulin;	P14211	1	14	19	22.6	-0.089	-0.01	0.842
Tryptophanyl-tRNA synthetase, cytoplasmic;	P32921	1	6	7	10.6	-0.089	-0.008	0.835
Na(+)/H(+) exchange regulatory cofactor NHE-RF1;	P70441	1	5	7	13.2	-0.089	-0.007	0.833
T-complex protein 1 subunit delta;	P80315	1	5	5	4.3	-0.089	-0.018	0.859
Vitamin K-dependent protein S;	Q08761	1	2	2	2.7	-0.089	-0.011	0.842
Zinc finger CCCH domain-containing protein 15;	Q3TIV5	1	2	2	3.3	-0.089	-0.009	0.837
Suprabasin;	Q8CIT9	1	7	7	14.4	-0.089	-0.021	0.870
Pyridoxine-5'-phosphate oxidase;	Q91XF0	1	4	4	6.9	-0.089	-0.007	0.833
von Willebrand factor A domain-containing protein 5A;	Q99KC8	1	33	48	24.1	-0.089	-0.031	0.894
Ribosome-binding protein 1;	Q99PL5	1	5	5	3.4	-0.089	-0.023	0.873
Thioredoxin domain-containing protein 12;	Q9CQU0	1	3	7	17.6	-0.089	-0.005	0.829
Mitochondrial peptide methionine sulfoxide reductase;	Q9D6Y7	1	6	6	19.7	-0.089	-0.032	0.896
[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial;	Q9JK42	1	4	4	11.8	-0.089	-0.026	0.881
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial;	Q9WUM5	1	9	15	19.1	-0.089	-0.003	0.827
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial;	Q9Z2I9	1	22	31	29.4	-0.089	-0.016	0.854
Branched-chain-amino-acid aminotransferase, mitochondrial;	O35855	1	16	22	25.3	-0.089	-0.03	0.891
Glutathione S-transferase P 1;	P19157	1	16	31	39.7	-0.089	-0.007	0.833
Aldehyde dehydrogenase, mitochondrial;	P47738	1	34	92	43.9	-0.089	-0.007	0.833
Retinal dehydrogenase 1;	P24549	1	22	38	24	-0.218	-0.02	0.598
Aldehyde dehydrogenase, cytosolic 1;	O35945	1	2	2	11.6	0.345	0.033	0.396
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1;	P47856	1	4	4	4	-0.089	-0.006	0.831
Glycerol-3-phosphate dehydrogenase 1-like protein;	Q3ULJ0	1	15	20	29.3	-0.089	-0.019	0.864
Myosin light polypeptide 6;	Q60605	1	13	27	46.4	-0.089	-0.014	0.851
Nischarin;	Q80TM9	1	4	4	11.6	-0.089	-0.008	0.835
Nitrilase homolog 1;	Q8VDK1	1	4	5	9	-0.089	-0.009	0.837
Thioredoxin reductase 1, cytoplasmic;	Q9JMH6	1	10	12	14.7	-0.089	-0.018	0.860
MCG142264, isoform CRA_a; Uncharacterized protein;	D3Z494	1	6	6	16.7	-0.089	-0.012	0.845
Capping protein (Actin filament), gelsolin-like; Capping protein (Actin filament), gelsolin-like, isoform CRA_a; Uncharacterized protein;	Q99LB4	1	23	56	45.3	-0.089	-0.008	0.835
Rho GTPase-activating protein 1;	Q5FWK3	1	2	2	2.5	-0.089	-0.014	0.851
Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform;	P48453	0.998	2	3	5.8	-0.089	-0.011	0.842
Activator of 90 kDa heat shock protein ATPase homolog 1;	Q8BK64	0.992	2	2	8.9	-0.089	-0.019	0.864
WD repeat-containing protein 1;	O88342	1	22	33	31.5	-0.074	-0.013	0.884
Vitronectin;	P29788	1	3	3	6.7	-0.074	-0.009	0.873
ELAV-like protein 1;	P70372	1	4	4	12.6	-0.074	-0.035	0.932
Fascin;	Q61553	1	3	3	4.1	-0.074	-0.016	0.892
Transaldolase;	Q93092	1	12	33	21.4	-0.074	-0.014	0.887

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
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial;	Q9D0K2	1	34	59	43.2	-0.074	-0.009	0.875
Protein LSM12 homolog;	Q9D0R8	1	2	2	19.5	-0.074	-0.019	0.899
Prostamide/prostaglandin F synthase;	Q9DB60	1	4	5	30.7	-0.074	-0.009	0.873
Omega-amidase NIT2;	Q9JHW2	1	11	12	39.5	-0.074	-0.005	0.866
Serine-threonine kinase receptor-associated protein;	Q9Z1Z2	1	13	15	32.3	-0.074	-0.016	0.894
Sepiapterin reductase;	Q64105	1	23	29	51.3	-0.074	-0.005	0.868
ATP synthase subunit gamma, mitochondrial;	Q91VR2	1	15	21	42.9	-0.074	-0.005	0.868
3-hydroxyisobutyrate dehydrogenase, mitochondrial;	Q99L13	1	15	27	25.4	-0.074	-0.011	0.880
Lysosomal Pro-X carboxypeptidase;	Q7TMR0	1	2	2	9.6	-0.074	-0.02	0.901
Proteolipid protein 2;	Q9R1Q7	0.994	2	3	7.9	-0.074	-0.005	0.866
Proteasome assembly chaperone 1;	Q9JK23	0.974	2	2	2.6	-0.074	-0.006	0.869
Arginyl-tRNA synthetase, cytoplasmic;	Q9D0I9	1	7	7	10.2	-0.059	-0.021	0.931
1,4-alpha-glucan-branching enzyme;	Q9D6Y9	1	10	13	14.4	-0.059	-0.047	0.966
Protein DDI1 homolog 2;	A2ADY9	1	8	10	20.3	-0.044	-0.003	0.918
Glucosidase 2 subunit beta;	O08795	1	7	9	8.8	-0.044	-0.029	0.962
Hypoxanthine-guanine phosphoribosyltransferase;	P00493	1	15	25	42.2	-0.044	-0.012	0.930
NADP-dependent malic enzyme;	P06801	1	17	26	28.6	-0.044	-0.018	0.945
Epoxide hydrolase 2;	P34914	1	12	16	15.7	-0.044	-0.003	0.901
Hydroxymethylglutaryl-CoA lyase, mitochondrial;	P38060	1	7	7	21.2	-0.044	-0.014	0.934
Ras suppressor protein 1;	Q01730	1	8	8	13.1	-0.044	-0.006	0.909
Calcium-binding protein 39;	Q06138	1	2	2	3.2	-0.044	-0.009	0.918
Putative phospholipase B-like 2;	Q3TCN2	1	4	4	5.4	-0.044	-0.024	0.956
Aldehyde dehydrogenase family 16 member A1;	Q571I9	1	5	5	8	-0.044	-0.017	0.942
Guanylate kinase;	Q64520	1	2	2	6.1	-0.044	-0.003	0.902
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial;	Q6P3A8	1	3	3	8.2	-0.044	-0.005	0.905
Trifunctional enzyme subunit alpha, mitochondrial;	Q8BMS1	1	23	31	26	-0.044	-0.02	0.948
Putative hydroxypyruvate isomerase;	Q8R1F5	1	4	4	34.2	-0.044	-0.006	0.911
Protein phosphatase 1 regulatory subunit 3A;	Q99MR9	1	8	10	6.7	-0.044	-0.005	0.906
Protein S100-A14;	Q9D2Q8	1	3	3	26	-0.044	-0.019	0.947
ATP synthase subunit delta, mitochondrial;	Q9D3D9	1	4	10	13.7	-0.044	-0.002	0.900
Apoptosis-inducing factor 1, mitochondrial;	Q9Z0X1	1	5	6	8.7	-0.044	-0.008	0.914
L-lactate dehydrogenase A chain;	P06151	1	22	99	38.3	-0.044	-0.004	0.903
L-lactate dehydrogenase B chain;	P16125	1	19	33	32.3	0.151	0.008	0.708
Cathepsin D;	P18242	1	19	28	23.4	-0.044	-0.005	0.905
Phospholipase A-2-activating protein;	P27612	1	7	7	9.7	-0.044	-0.006	0.909
Creatine kinase U-type, mitochondrial;	P30275	1	8	16	21.1	-0.044	-0.001	0.899
Peroxiredoxin-1;	P35700	1	22	69	72.4	-0.044	-0.002	0.900
S-adenosylmethionine synthase isoform type-2;	Q3THS6	1	6	7	19.5	-0.044	-0.012	0.930
Rho GDP-dissociation inhibitor 2;	Q61599	1	10	11	22	-0.044	-0.009	0.918
D-3-phosphoglycerate dehydrogenase;	Q61753	1	13	16	19.3	-0.044	-0.007	0.913
Ubiquitin thioesterase OTUB1;	Q7TQI3	1	13	15	31.5	-0.044	-0.014	0.934
Hydroxyacylglutathione hydrolase, mitochondrial;	Q99KB8	1	7	10	23.6	-0.044	-0.005	0.908
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial;	Q9EQ20	1	17	28	22.4	-0.044	-0.01	0.923

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;	E9Q616	1	190	241	40.3	-0.044	-0.011	0.927
Oxysterol-binding protein;	E9QPD4	1	4	4	4.7	-0.044	-0.005	0.908
Ketosamine-3-kinase;	Q8K274	1	3	4	9.1	-0.044	-0.005	0.905
GMP synthase [glutamine-hydrolyzing];	Q3THK7	0.998	2	2	3.2	-0.044	-0.003	0.899
Oxysterol-binding protein-related protein 9;	A2A8Z1	0.998	2	2	3	-0.044	-0.01	0.923
Protein unc-119 homolog B;	Q8C4B4	0.997	2	2	5.1	-0.044	-0.005	0.908
NEDD4-binding protein 1;	Q6A037	0.996	2	2	3.9	-0.044	-0.002	0.900
Peptidase inhibitor 16;	Q9ET66	0.986	2	2	4.3	-0.044	-0.005	0.905
Proteasome subunit beta type-5;	O55234	1	5	5	24.6	-0.029	-0.01	0.959
Prefoldin subunit 2;	O70591	1	2	3	7.8	-0.029	-0.002	0.936
Cytochrome c oxidase subunit 6B1;	P56391	1	4	4	29.1	-0.029	-0.002	0.938
SUMO-conjugating enzyme UBC9;	P63280	1	4	5	12	-0.029	-0.001	0.935
T-complex protein 1 subunit beta;	P80314	1	7	9	13.8	-0.029	-0.007	0.950
Osteoclast-stimulating factor 1;	Q62422	1	11	18	42.3	-0.029	-0.007	0.950
Lactoylglutathione lyase;	Q9CPU0	1	11	19	27.2	-0.029	-0.001	0.936
Adenylate kinase isoenzyme 1;	Q9R0Y5	1	19	71	50.5	-0.029	-0.002	0.938
Uncharacterized protein;	E9PVD2	1	9	11	10	-0.029	-0.007	0.950
Septin-7;	O55131	1	7	7	20.1	-0.029	-0.009	0.956
Adenylyl cyclase-associated protein 1;	P40124	1	17	20	22.4	-0.029	-0.008	0.953
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;	P62137	1	14	16	36.4	-0.029	-0.006	0.948
Acyl-protein thioesterase 1;	P97823	1	6	10	20	-0.029	-0.007	0.950
Ubiquitin-like modifier-activating enzyme 1;	Q02053	1	49	65	28.5	-0.029	-0.01	0.961
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Q76MZ3	1	15	18	21.1	-0.029	-0.011	0.963
Alcohol dehydrogenase [NADP+];	Q9JII6	1	22	36	37.5	-0.029	-0.004	0.940
Glutathione reductase, mitochondrial;	P47791	1	12	12	21.8	-0.014	-0.003	0.975
Annexin A5;	P48036	1	36	83	58.9	-0.014	-0.001	0.971
Platelet-activating factor acetylhydrolase IB subunit alpha;	P63005	1	5	7	6.3	-0.014	-0.007	0.985
Vacuolar protein sorting-associated protein 45;	P97390	1	2	2	2.5	-0.014	-0.001	0.971
Beta-2-glycoprotein 1;	Q01339	1	16	21	30.7	-0.014	-0.005	0.982
Rab GDP dissociation inhibitor beta;	Q61598	1	33	55	56.6	-0.014	-0.002	0.972
Transcription factor BTF3;	Q64152	1	2	2	9.3	-0.014	-0.002	0.973
Alanyl-tRNA synthetase, cytoplasmic;	Q8BGQ7	1	14	14	13.3	-0.014	-0.003	0.977
L-asparaginase;	Q8C0M9	1	5	5	16	-0.014	-0.002	0.979
Protein Z-dependent protease inhibitor;	Q8R121	1	3	3	5.8	-0.014	-0.006	0.985
Oxysterol-binding protein-related protein 1;	Q91XL9	1	2	2	5.4	-0.014	-0.003	0.977
Dipeptidyl peptidase 3;	Q99KK7	1	15	17	15.9	-0.014	-0.006	0.983
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial;	Q9D2G2	1	12	17	15.2	-0.014	-0.001	0.972
Uncharacterized protein;	E9PV24	1	16	26	17.8	-0.014	-0.005	0.983
60S acidic ribosomal protein P0;	P14869	1	3	3	10.7	-0.014	-0.003	0.975
Peptidyl-prolyl cis-trans isomerase FKBP4;	P30416	1	6	6	14.8	-0.014	-0.006	0.983
Glutathione peroxidase 3;	P46412	1	7	11	29.1	-0.014	-0.001	0.971
Xaa-Pro aminopeptidase 1;	Q6P1B1	1	14	16	15.2	-0.014	-0.007	0.986

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
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	Q8QZS1	1	14	15	22.9	-0.014	-0.004	0.978
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1;	Q8R429	1	64	173	35.1	-0.014	-0.002	0.975
Protein disulfide-isomerase A6;	Q922R8	1	12	15	18.6	-0.014	-0.006	0.984
3-mercaptopyruvate sulfurtransferase;	Q99J99	1	21	33	42.1	-0.014	-0.003	0.977
5'(3')-deoxyribonucleotidase, cytosolic type;	Q9JM14	1	7	9	20	-0.014	-0.001	0.971
Basal cell adhesion molecule;	Q9R069	1	9	9	12.9	-0.014	-0.001	0.966
Fructose-bisphosphate aldolase;	A6ZI44	1	21	364	75.4	-0.014	-0.002	0.972
Fructose-bisphosphate aldolase;	Q9CPQ9	0.999	2	3	48.1	-0.434	-0.164	0.523
Alpha-amylase 1;	P00687	0.999	2	2	4.1	-0.014	-0.002	0.974
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase;	Q99JT9	0.999	2	2	4.5	-0.014	-0.002	0.973
Carnitine O-palmitoyltransferase 2, mitochondrial;	P52825	0.962	3	3	4.9	-0.014	-0.002	0.974
Transketolase;	P40142	1	46	98	48.2	0	0	0.998
60S acidic ribosomal protein P1;	P47955	1	2	2	14	0	0	0.996
Proteasome subunit beta type-4;	P99026	1	10	11	31.8	0	0	0.997
Retinol-binding protein 1;	Q00915	1	3	3	15.6	0	0	0.997
Mitogen-activated protein kinase 3;	Q63844	1	6	6	13.7	0	0	0.996
10 kDa heat shock protein, mitochondrial;	Q64433	1	9	16	48	0	0	0.995
Phosphoglycolate phosphatase;	Q8CHP8	1	14	17	30.5	0	0	0.996
Apolipoprotein A-I-binding protein;	Q8K4Z3	1	11	15	24.8	0	0	0.995
Anamorsin;	Q8WTY4	1	2	6	8.9	0	0	0.995
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial;	Q9D6J6	1	8	10	24.2	0	0	0.995
Acid ceramidase;	Q9WV54	1	8	8	13.2	0	0	0.998
Chloride intracellular channel protein 1;	Q9Z1Q5	1	20	30	61.4	0	0	0.995
Complement factor B;	P04186	1	20	28	17.7	0	0	0.996
Glucose-6-phosphate isomerase;	P06745	1	39	96	33.9	0	0	0.995
Bisphosphoglycerate mutase;	P15327	1	6	7	18.5	0	0	0.997
Quinone oxidoreductase;	P47199	1	10	13	29.3	0	0	0.997
Phosphatidylethanolamine-binding protein 1;	P70296	1	11	30	56.7	0	0	0.995
2-oxoglutarate dehydrogenase, mitochondrial;	Q60597	1	53	86	35.5	0	0	0.996
Peroxiredoxin-2;	Q61171	1	17	46	47.5	0	0	0.995
Abhydrolase domain-containing protein 14B;	Q8VCR7	1	7	8	27.1	0	0	0.995
NADH-cytochrome b5 reductase 3;	Q9DCN2	1	6	6	13.3	0	0	0.998
DAZ-associated protein 1;	Q9JII5	1	5	5	11.6	0	0	0.996
Afadin;	Q9QZQ1	1	3	3	2	0	0	0.995
Mitochondrial antiviral-signaling protein;	Q8VCF0	1	2	3	2	0	0	0.995
Nucleoside diphosphate kinase 3;	Q9WV85	0.998	2	2	4.1	0	0	0.995
Prohibitin-2;	O35129	1	2	3	7.6	0.014	0.003	0.967
Complement factor D;	P03953	1	8	9	20.1	0.014	0.001	0.961
Tyrosine-protein kinase CSK;	P41241	1	2	3	9.9	0.014	0.003	0.968
Fumarate hydratase, mitochondrial;	P97807	1	30	46	43.8	0.014	0.002	0.963
Retinol-binding protein 4;	Q00724	1	6	12	14.9	0.014	0.001	0.962
Poly(U)-binding-splicing factor PUF60;	Q3UEB3	1	2	2	2.8	0.014	0.001	0.961
Platelet-activating factor acetylhydrolase IB subunit beta;	Q61206	1	5	11	18.9	0.014	0.001	0.960

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
Interleukin-1 receptor accessory protein;	Q61730	1	8	9	13	0.014	0.003	0.970
Selenide, water dikinase 1;	Q8BH69	1	6	7	7.7	0.014	0.001	0.961
Bifunctional aminoacyl-tRNA synthetase;	Q8CGC7	1	7	8	3.5	0.014	0.006	0.979
GDP-mannose 4,6 dehydratase;	Q8K0C9	1	2	2	6.5	0.014	0.003	0.970
Sulfite oxidase, mitochondrial;	Q8R086	1	4	5	9.2	0.014	0.002	0.965
Electron transfer flavoprotein subunit alpha, mitochondrial;	Q99LC5	1	33	63	53.2	0.014	0.001	0.961
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial;	O35459	1	5	5	14.4	0.014	0.001	0.961
Ig kappa chain V-III region PC 3741/TEPC 111;	P01660	1	5	5	26.1	0.014	0.002	0.964
Peptidyl-prolyl cis-trans isomerase A;	P17742	1	13	51	47	0.014	0.002	0.963
Ras-related protein Rab-11B;	P46638	1	14	21	36.7	0.014	0.002	0.967
Rab GDP dissociation inhibitor alpha;	P50396	1	4	5	13.6	0.014	0.001	0.962
60 kDa heat shock protein, mitochondrial;	P63038	1	33	50	38.7	0.014	0.002	0.967
PEST proteolytic signal-containing nuclear protein;	Q6P8I4	1	3	4	21.1	0.014	0.002	0.963
6-phosphogluconolactonase;	Q9CQ60	1	16	25	36.2	0.014	0.001	0.960
Cytochrome b-c1 complex subunit 1, mitochondrial;	Q9CZ13	1	20	31	28.8	0.014	0.001	0.961
Ferritin;	Q9CPX4	1	19	50	54.1	0.014	0.001	0.962
AMP deaminase 1;	Q3V1D3	0.999	2	2	2.6	0.014	0.001	0.969
GDH/6PGL endoplasmic bifunctional protein;	Q8CFX1	0.998	3	3	3.4	0.014	0.002	0.969
Lipoma-preferred partner homolog;	Q8BFW7	0.991	2	3	3.9	0.014	0.001	0.961
Dual specificity protein phosphatase 23;	Q6NT99	1	7	7	32.7	0.029	0.002	0.936
Serine/threonine-protein phosphatase;	F7BX26	1	3	4	6.3	0.029	0.006	0.951
N-acetyl-D-glucosamine kinase;	Q9QZ08	1	3	3	6.4	0.029	0.005	0.952
Proteasome subunit beta type-1;	O09061	1	10	11	30.8	0.043	0.018	0.960
Thioredoxin;	P10639	1	4	9	21	0.043	0.007	0.936
Cytochrome c oxidase subunit 5A, mitochondrial;	P12787	1	4	4	27.4	0.043	0.005	0.931
Glutathione S-transferase A4;	P24472	1	5	6	13.1	0.043	0.017	0.958
Serine hydroxymethyltransferase, cytosolic;	P50431	1	6	6	7.7	0.043	0.028	0.971
Transcription elongation factor B polypeptide 2;	P62869	1	4	4	43.2	0.043	0.01	0.945
Eukaryotic translation initiation factor 4E;	P63073	1	7	8	21.2	0.043	0.003	0.928
Protein FAM63A;	Q76LS9	1	4	4	8.1	0.043	0.003	0.928
Isochorismatase domain-containing protein 1;	Q91V64	1	6	10	8.4	0.043	0.003	0.929
Cytosol aminopeptidase;	Q9CPY7	1	32	37	42.8	0.043	0.009	0.942
Coactosin-like protein;	Q9CQI6	1	5	9	30.3	0.043	0.013	0.949
Isovaleryl-CoA dehydrogenase, mitochondrial;	Q9JHI5	1	16	19	26.4	0.043	0.01	0.945
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial;	O88986	1	6	6	13.5	0.043	0.016	0.957
Aspartate aminotransferase, cytoplasmic;	P05201	1	24	61	37.3	0.043	0.011	0.946
Ubiquitin-conjugating enzyme E2 L3;	P68037	1	10	15	47.4	0.043	0.02	0.963
Glucose-6-phosphate 1-dehydrogenase X;	Q00612	1	23	32	31.5	0.043	0.022	0.966
Voltage-dependent L-type calcium channel subunit alpha-1S;	Q02789	1	3	3	1.9	0.043	0.021	0.964
Puromycin-sensitive aminopeptidase;	Q11011	1	32	38	23.9	0.043	0.011	0.946
Peptidyl-prolyl cis-trans isomerase;	A2BGI8	1	3	4	13.3	0.043	0.005	0.933
Nuclear migration protein nudC;	O35685	1	3	3	6	0.043	0.013	0.949
WW domain-binding protein 11;	Q923D5	0.967	2	2	2.3	0.043	0.006	0.935

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
Extracellular superoxide dismutase [Cu-Zn];	O09164	1	7	8	19.9	0.057	0.002	0.893
Heterogeneous nuclear ribonucleoprotein A1;	P49312	1	7	10	15.3	0.057	0.008	0.906
Calpastatin;	P51125	1	5	6	6.7	0.057	0.031	0.952
CD166 antigen;	Q61490	1	4	4	9.3	0.057	0.003	0.894
Protein canopy homolog 4;	Q8BQ47	1	4	4	13.5	0.057	0.014	0.921
Presequence protease, mitochondrial;	Q8K411	1	12	12	11.7	0.057	0.018	0.929
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A;	Q8R050	1	4	4	3.6	0.057	0.011	0.912
Galectin-related protein A;	Q8VED9	1	4	4	12.2	0.057	0.004	0.896
MACRO domain-containing protein 1;	Q922B1	1	10	13	22.9	0.057	0.003	0.894
Ran-binding protein 3;	Q9CT10	1	4	5	9.4	0.057	0.006	0.899
Perilipin-3;	Q9DBG5	1	6	6	11.2	0.057	0.021	0.937
E3 SUMO-protein ligase RanBP2;	Q9ERU9	1	2	2	0.7	0.057	0.012	0.914
CD2-associated protein;	Q9JLQ0	1	7	8	10.2	0.057	0.032	0.954
Cadherin-13;	Q9WTR5	1	8	10	9.2	0.057	0.004	0.895
Eukaryotic translation initiation factor 4H;	Q9WUK2	1	2	2	5.7	0.057	0.004	0.895
Kelch repeat and BTB (POZ) domain containing 10; MCG12931; Uncharacterized protein;	A2AUC9	1	8	8	9.9	0.057	0.016	0.926
LanC-like protein 1;	O89112	1	2	2	6.5	0.057	0.02	0.934
Apolipoprotein A-II;	P09813	1	5	9	18.6	0.057	0.014	0.921
Triosephosphate isomerase;	P17751	1	37	596	67.5	0.057	0.006	0.899
Proliferating cell nuclear antigen;	P17918	1	7	8	28.4	0.057	0.01	0.911
Protein S100-A11;	P50543	1	8	10	27.6	0.057	0.01	0.911
Poly(rC)-binding protein 1;	P60335	1	9	15	28.7	0.057	0.012	0.914
Poly(rC)-binding protein 2;	Q61990	1	8	14	20.4	-0.105	-0.006	0.794
Serine/threonine-protein kinase PAK 2;	Q8CIN4	1	7	14	8.6	0.057	0.001	0.892
Aldo-keto reductase family 1 member C18;	Q8K023	1	5	9	9.9	0.057	0.003	0.894
Glyceraldehyde-3-phosphate dehydrogenase;	E9QAC7	1	17	141	62.8	0.057	0.007	0.901
Glyceraldehyde-3-phosphate dehydrogenase;	E9PYX4	1	5	92	37.6	0.043	0.005	0.931
Uncharacterized protein;	F6ZFU0	1	2	4	17.2	0.057	0.004	0.895
Elongation factor 1-delta;	P57776	1	2	3	40	-0.029	-0.003	0.938
Protein FAM114A2;	Q8VE88	0.966	2	2	5.6	0.057	0.009	0.907
C-type lectin domain family 11 member A;	O88200	1	7	7	14.9	0.07	0.005	0.863
Delta-aminolevulinic acid dehydratase;	P10518	1	15	23	35.5	0.07	0.022	0.908
Apolipoprotein C-III;	P33622	1	4	9	19.2	0.07	0.008	0.870
ADP-ribosylation factor 6;	P62331	1	4	4	24	0.07	0.013	0.883
Latexin;	P70202	1	4	5	12.2	0.07	0.012	0.880
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1;	Q60967	1	8	11	12	0.07	0.039	0.938
Synemin;	Q70IV5	1	3	5	3.5	0.07	0.015	0.889
Scavenger receptor cysteine-rich domain-containing protein LOC284297 homolog;	Q8BV57	1	6	6	6	0.07	0.021	0.906
Thimet oligopeptidase;	Q8C1A5	1	18	24	19.9	0.07	0.011	0.878
Rho GDP-dissociation inhibitor 1;	Q99PT1	1	8	22	15.2	0.07	0.003	0.860
SUMO-activating enzyme subunit 1;	Q9R1T2	1	8	10	23.7	0.07	0.004	0.862
Ig gamma-2A chain C region, A allele;	P01863	1	6	10	13.3	0.07	0.007	0.868

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
Peroxiredoxin-5, mitochondrial;	P99029	1	21	43	44.8	0.07	0.005	0.863
Tyrosine-protein kinase Yes;	Q04736	1	4	4	4.6	0.07	0.009	0.874
Corticosteroid-binding globulin;	Q06770	1	10	15	11.1	0.07	0.005	0.865
Protein transport protein Sec31A;	Q3UPL0	1	17	23	12.4	0.07	0.019	0.900
Eukaryotic translation initiation factor 2A;	Q8BJW6	1	5	5	6.5	0.07	0.008	0.870
Actin-related protein 2/3 complex subunit 3;	Q9JM76	1	9	15	27.5	0.07	0.013	0.883
Troponin T, fast skeletal muscle;	Q9QZ47	1	4	6	13	0.07	0.032	0.929
Band 4.1-like protein 3;	Q9WV92	1	4	4	8.5	0.07	0.016	0.892
Dci protein; Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase); Uncharacterized protein;	Q8QZV3	1	21	40	29.8	0.07	0.012	0.880
Glycogen synthase kinase-3 alpha;	Q2NL51	0.999	2	2	3.5	0.07	0.005	0.863
Superoxide dismutase [Cu-Zn];	P08228	1	13	25	32.5	0.084	0.009	0.837
Stress-70 protein, mitochondrial;	P38647	1	28	48	26.4	0.084	0.006	0.831
V-type proton ATPase subunit B, brain isoform;	P62814	1	7	11	11.5	0.084	0.027	0.888
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial;	Q61425	1	9	17	22.3	0.084	0.01	0.839
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Q8BMF4	1	24	40	28.2	0.084	0.009	0.837
Tubulin polymerization-promoting protein family member 3;	Q9CRB6	1	4	6	11.9	0.084	0.01	0.842
Histidine triad nucleotide-binding protein 2, mitochondrial;	Q9D0S9	1	11	15	39.9	0.084	0.005	0.830
Elongation factor 1-gamma;	Q9D8N0	1	15	20	20.1	0.084	0.021	0.874
Valyl-tRNA synthetase;	Q9Z1Q9	1	9	9	5.8	0.084	0.025	0.881
Dihydrolipoyl dehydrogenase, mitochondrial;	O08749	1	23	48	26.3	0.084	0.004	0.829
Annexin A2;	P07356	1	42	208	68.4	0.084	0.008	0.835
Cofilin-1;	P18760	1	11	19	43.4	0.084	0.005	0.830
Beta-enolase;	P21550	1	35	289	59	0.084	0.01	0.839
Alpha-enolase;	P17182	1	15	57	59.7	-0.234	-0.069	0.679
Enolase;	B0QZL1	1	4	5	70.1	-0.218	-0.018	0.592
Procollagen C-endopeptidase enhancer 1;	Q61398	1	10	18	40.8	0.084	0.012	0.847
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase;	Q8C0L6	1	5	5	7.3	0.084	0.036	0.908
Septin-11;	Q8C1B7	1	8	9	25.5	0.084	0.01	0.842
Septin-8;	Q8CHH9	1	5	7	11	0.333	0.092	0.550
Septin-6;	Q9R1T4	1	4	4	13.1	-0.621	-0.057	0.126
Secernin-1;	Q9CZC8	1	6	10	9.9	0.084	0.006	0.833
cAMP-dependent protein kinase type I-alpha regulatory subunit;	Q9DBC7	1	6	7	6.6	0.084	0.006	0.833
RuvB-like 1;	P60122	1	2	2	7	0.084	0.012	0.848
Coronin-1B;	Q9WUM3	0.994	2	2	3.9	0.084	0.015	0.867
Glutathione peroxidase 1;	P11352	1	18	28	55.7	0.098	0.048	0.899
Alcohol dehydrogenase class-3;	P28474	1	12	22	21.4	0.098	0.005	0.799
Heterogeneous nuclear ribonucleoprotein H2;	P70333	1	8	9	16	0.098	0.005	0.799
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	Q64191	1	5	6	18.8	0.098	0.01	0.807
N-acetylneuraminate lyase;	Q9DCJ9	1	19	25	40	0.098	0.01	0.807
Protein ETHE1, mitochondrial;	Q9DCM0	1	5	6	18.1	0.098	0.012	0.812
Eukaryotic translation initiation factor 3 subunit G;	Q9Z1D1	1	5	6	10	0.098	0.013	0.815

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
Polyadenylate-binding protein 1;	P29341	1	17	20	24.8	0.098	0.011	0.809
Poly A binding protein, cytoplasmic 4; Uncharacterized protein;	A3KFU5	0.918	2	2	11.2	0.084	0.005	0.830
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P50544	1	14	18	18.3	0.098	0.032	0.869
Annexin A11;	P97384	1	18	20	25.2	0.098	0.035	0.874
Adiponectin;	Q60994	1	5	5	15	0.098	0.009	0.804
Sorcin;	Q6P069	1	12	18	37.4	0.098	0.016	0.824
Sulfatase-modifying factor 2;	Q8BPG6	1	3	4	8.6	0.098	0.006	0.800
Fermitin family homolog 2;	Q8CIB5	1	6	6	6.3	0.098	0.012	0.812
CAP-Gly domain-containing linker protein 1;	Q922J3	1	6	6	4.5	0.098	0.026	0.853
Trans-2-enoyl-CoA reductase, mitochondrial;	Q9DCS3	1	5	5	14.5	0.098	0.024	0.846
Uncharacterized protein;	E9Q2P1	1	12	25	23.4	0.098	0.012	0.812
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	5	9.5	0.098	0.014	0.818
Ribosome maturation protein SBDS;	P70122	1	2	2	9.8	0.098	0.011	0.809
GDP-D-glucose phosphorylase C15orf58 homolog;	Q3TLS3	0.999	2	2	3.3	0.098	0.011	0.809
Copper transport protein ATOX1;	O08997	1	6	8	57.4	0.111	0.022	0.808
Malate dehydrogenase, mitochondrial;	P08249	1	47	174	63.6	0.111	0.021	0.804
Microtubule-associated protein 1B;	P14873	1	2	2	0.9	0.111	0.01	0.774
Serine/threonine-protein kinase WNK1;	P83741	1	2	2	4.4	0.111	0.015	0.790
Neuroplastin;	P97300	1	2	3	3	0.111	0.002	0.763
Acetyl-CoA acetyltransferase, mitochondrial;	Q8QZT1	1	10	12	15.1	0.111	0.036	0.848
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial;	Q9D051	1	24	46	40.9	0.111	0.012	0.780
GMP reductase 1;	Q9DCZ1	1	4	4	13.4	0.111	0.006	0.768
Hexokinase-2;	O08528	1	30	33	24.5	0.111	0.059	0.890
Hexokinase-1;	P17710	1	8	9	9.6	0.333	0.056	0.464
Seryl-tRNA synthetase, cytoplasmic;	P26638	1	8	8	11.5	0.111	0.015	0.790
Methionine adenosyltransferase 2 subunit beta;	Q99LB6	1	2	2	11.1	0.111	0.015	0.790
Diphosphoinositol polyphosphate phosphohydrolase 1;	Q9JI46	1	3	3	10.1	0.111	0.012	0.780
Exportin-2;	Q9ERK4	1	2	2	2.8	0.111	0.014	0.786
Serine/threonine-protein phosphatase 6 catalytic subunit;	Q9CQR6	1	2	4	2.6	0.111	0.01	0.774
Eukaryotic translation initiation factor 3 subunit E;	P60229	1	2	2	4	0.111	0.057	0.889
Methylosome protein 50;	Q99J09	0.999	2	4	20	0.111	0.005	0.766
Laminin subunit gamma-1;	P02468	1	4	4	3	0.138	0.023	0.754
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3;	P51432	1	3	3	1.7	0.138	0.04	0.817
Lumican;	P51885	1	27	207	38.8	0.138	0.014	0.748
Microtubule-associated protein RP/EB family member 1;	Q61166	1	2	2	7.5	0.138	0.013	0.745
Myosin light chain kinase 2, skeletal/cardiac muscle;	Q8VCR8	1	14	17	15.7	0.138	0.046	0.830
Phosphate carrier protein, mitochondrial;	Q8VEM8	1	4	6	8.4	0.138	0.025	0.778
Cytochrome b-c1 complex subunit 7;	Q9D855	1	3	3	18.9	0.138	0.033	0.798
Peroxisomal acyl-coenzyme A oxidase 1;	Q9R0H0	1	6	7	9	0.138	0.046	0.830
Destrin;	Q9R0P5	1	12	24	38.8	0.138	0.018	0.758
Malate dehydrogenase, cytoplasmic;	P14152	1	20	66	26.6	0.138	0.008	0.738

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
Radixin;	P26043	1	7	7	11	0.138	0.015	0.751
Moesin;	P26041	1	6	6	12.1	0.202	0.012	0.601
Ezrin;	P26040	0.962	2	2	4.6	0.623	0.065	0.129
Caveolin-1;	P49817	1	7	8	30.9	0.138	0.026	0.765
Mitogen-activated protein kinase 1;	P63085	1	7	9	15.9	0.138	0.031	0.784
Galactose-1-phosphate uridylyltransferase;	Q03249	1	4	4	6.9	0.138	0.034	0.802
Collagen alpha-1(VI) chain;	Q04857	1	5	5	5.4	0.138	0.034	0.802
Vinculin;	Q64727	1	35	42	20.9	0.138	0.024	0.775
Trifunctional purine biosynthetic protein adenosine-3;	Q64737	1	12	12	15.7	0.138	0.035	0.806
Citrate lyase subunit beta-like protein, mitochondrial;	Q8R4N0	1	6	6	15.7	0.138	0.024	0.774
Glyoxalase domain-containing protein 4;	Q9CPV4	1	21	28	53	0.138	0.019	0.762
Macrophage migration inhibitory factor;	P34884	0.997	2	4	7.8	0.138	0.008	0.738
Biotinidase;	Q8CIF4	0.954	2	2	1.7	0.138	0.014	0.748
Dehydrogenase/reductase SDR family member 7;	Q9CXR1	0.948	2	2	5.9	0.138	0.024	0.774
Aspartate aminotransferase, mitochondrial;	P05202	1	42	95	51.4	0.151	0.026	0.747
Adenylosuccinate synthetase isozyme 1;	P28650	1	35	54	41.8	0.151	0.024	0.743
Small glutamine-rich tetratricopeptide repeat-containing protein alpha;	Q8BJU0	1	4	4	7.9	0.151	0.008	0.708
Phospholipase B-like 1;	Q8VCI0	1	3	3	5.8	0.151	0.018	0.727
Ester hydrolase C11orf54 homolog;	Q91V76	1	9	10	28.6	0.151	0.063	0.836
Aconitate hydratase, mitochondrial;	Q99KI0	1	70	146	48.2	0.151	0.014	0.716
Serine/threonine-protein phosphatase 2A activator;	P58389	1	7	10	17.6	0.151	0.03	0.761
Platelet-activating factor acetylhydrolase IB subunit gamma;	Q61205	1	4	6	13.9	0.151	0.016	0.723
Coronin-7;	Q9D2V7	1	13	15	12.8	0.151	0.019	0.731
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial;	P53395	0.998	4	5	5.4	0.151	0.01	0.711
AH receptor-interacting protein;	O08915	1	2	2	4.2	0.163	0.015	0.688
Ferritin heavy chain;	P09528	1	9	13	21.4	0.163	0.015	0.688
Galectin-3;	P16110	1	13	23	36.2	0.163	0.038	0.750
Cofilin-2;	P45591	1	8	19	36.1	0.163	0.019	0.699
Adenylosuccinate synthetase isozyme 2;	P46664	1	7	7	10.7	0.163	0.022	0.708
Carbonyl reductase [NADPH] 1;	P48758	1	19	21	43.7	0.163	0.019	0.699
Myotrophin;	P62774	1	4	5	14.4	0.163	0.009	0.680
Peptidyl-prolyl cis-trans isomerase FKBP5;	Q64378	1	4	4	8.6	0.163	0.016	0.692
NAD(P)H dehydrogenase [quinone] 1;	Q64669	1	6	6	20.1	0.163	0.032	0.736
Tubulin-specific chaperone C;	Q8VCN9	1	3	3	6.7	0.163	0.045	0.768
Acyl-coenzyme A thioesterase 1;	O55137	1	11	14	23.9	0.163	0.031	0.731
Acyl-coenzyme A thioesterase 2, mitochondrial;	Q9QYR9	0.999	2	2	21.9	-0.252	-0.081	0.672
Myelin protein P0;	P27573	1	6	7	14.1	0.163	0.048	0.777
Cell division control protein 42 homolog;	P60766	1	12	16	36.6	0.163	0.041	0.759
Ras-related C3 botulinum toxin substrate 1;	P63001	1	11	23	34.4	-0.811	-0.185	0.107
Rho-related GTP-binding protein RhoG;	P84096	1	2	2	14.7	-0.434	-0.035	0.288
Septin-9;	Q80UG5	1	6	8	9.2	0.163	0.029	0.726
NEDD8-activating enzyme E1 catalytic subunit;	Q8C878	1	6	6	19.6	0.163	0.029	0.726

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
Actin-related protein 3;	Q99JY9	1	17	22	38.3	0.163	0.036	0.745
Proteasome subunit alpha type-5;	Q9Z2U1	1	12	16	47.7	0.163	0.036	0.745
Uncharacterized protein;	F6RPJ9	1	22	33	13.8	0.163	0.044	0.764
Sodium channel protein type 4 subunit alpha;	Q9ER60	0.998	2	2	1.6	0.163	0.031	0.731
Histone-binding protein RBBP4;	Q60972	0.991	2	2	4.1	0.163	0.031	0.731
Ig alpha chain C region;	P01878	1	3	4	7	0.176	0.019	0.668
Transthyretin;	P07309	1	11	37	46.3	0.176	0.012	0.657
Uroporphyrinogen decarboxylase;	P70697	1	4	4	12.3	0.176	0.017	0.664
Eukaryotic translation initiation factor 3 subunit B;	Q8JZQ9	1	5	5	6.6	0.176	0.023	0.681
Glycine cleavage system H protein, mitochondrial;	Q91WK5	1	2	2	5.9	0.176	0.003	0.646
Leucine carboxyl methyltransferase 1; Leucine carboxyl methyltransferase 1, isoform CRA_b; Uncharacterized protein;	A2RTH5	1	3	3	5.4	0.176	0.025	0.681
Calcium/calmodulin-dependent protein kinase type II subunit alpha;	P11798	1	7	9	8.4	0.176	0.009	0.652
ADP-ribosylation factor 3;	P61205	1	5	10	53.6	0.176	0.022	0.677
ADP-ribosylation factor 5;	P84084	1	5	10	46.7	0.057	0.019	0.932
Translationally-controlled tumor protein;	P63028	1	8	27	30.2	0.176	0.017	0.669
Trifunctional enzyme subunit beta, mitochondrial;	Q99JY0	1	10	13	18.5	0.176	0.031	0.701
Actin-related protein 2/3 complex subunit 5;	Q9CPW4	1	4	5	29.1	0.176	0.047	0.741
Calcium channel, voltage-dependent, beta 1 subunit; Uncharacterized protein;	A2A542	1	4	4	6.3	0.176	0.011	0.654
Epoxide hydrolase 1;	Q9D379	1	2	2	7.3	0.176	0.017	0.664
Calponin-2;	Q08093	1	2	2	9	0.176	0.009	0.652
Apolipoprotein A-IV;	P06728	1	25	37	42.8	0.189	0.041	0.702
Galectin-1;	P16045	1	15	37	45.2	0.189	0.028	0.661
Haloacid dehalogenase-like hydrolase domain-containing protein 2;	Q3UGR5	1	8	13	16.2	0.189	0.023	0.651
28S ribosomal protein S36, mitochondrial;	Q9CQX8	1	2	2	21	0.189	0.018	0.638
Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform;	P07934	1	3	3	6.4	0.189	0.017	0.643
Fatty acid-binding protein, epidermal;	Q05816	1	21	38	71.9	0.189	0.07	0.770
Adapter molecule crk;	Q64010	1	12	18	19.4	0.189	0.013	0.630
Carboxylesterase 3;	Q8VCT4	1	25	46	28.7	0.189	0.056	0.739
Liver carboxylesterase N;	P23953	1	17	40	20.9	-0.074	-0.006	0.869
Uncharacterized protein;	D3Z5G7	1	12	28	16.6	-0.152	-0.017	0.703
Enoyl-CoA hydratase domain-containing protein 1;	Q9D9V3	1	11	13	23.9	0.189	0.086	0.800
ATP synthase subunit O, mitochondrial;	Q9DB20	1	14	18	46.5	0.189	0.012	0.627
Chloride channel calcium activated 2; Endothelial chloride channel; MCG120735; Uncharacterized protein;	Q9EQR4	1	7	8	8.8	0.189	0.01	0.625
Signal transducer and activator of transcription 5B;	P42232	1	3	3	4.2	0.189	0.03	0.667
TIP41-like protein;	Q8BH58	1	2	2	4.4	0.189	0.023	0.651
Ubiquitin-fold modifier-conjugating enzyme 1;	Q9CR09	0.999	2	4	4.8	0.189	0.008	0.622
S-phase kinase-associated protein 1;	Q9WTX5	0.994	2	2	8.3	0.189	0.01	0.625
Crk-like protein;	P47941	1	2	2	5.9	0.202	0.012	0.601
40S ribosomal protein S14;	P62264	1	2	2	8.6	0.202	0.018	0.608
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;	P63330	1	13	19	32.7	0.202	0.018	0.608
Glutaredoxin-related protein 5, mitochondrial;	Q80Y14	1	4	4	21.7	0.202	0.023	0.621

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
Vigilin;	Q8VDJ3	1	4	5	3.5	0.202	0.081	0.766
Brain acid soluble protein 1;	Q91XV3	1	3	8	19.9	0.202	0.049	0.692
UMP-CMP kinase;	Q9DBP5	1	14	21	52	0.202	0.044	0.675
Ubiquitin carboxyl-terminal hydrolase 14;	Q9JMA1	1	6	11	8.5	0.202	0.012	0.601
Heat shock protein HSP 90-beta;	P11499	1	33	50	40.7	0.202	0.033	0.647
Heat shock protein HSP 90-alpha;	P07901	1	19	31	31.2	0.227	0.043	0.640
Endoplasmin;	P08113	1	10	13	11	0.098	0.034	0.872
BTB/POZ domain-containing protein KCTD12;	Q6WVG3	1	12	13	25.7	0.202	0.091	0.783
Alpha-soluble NSF attachment protein;	Q9DB05	1	4	4	8.8	0.202	0.018	0.608
Uncharacterized protein;	E9PYJ9	1	28	34	23.1	0.202	0.049	0.692
Uncharacterized protein;	E9Q0S6	1	4	4	2.9	0.202	0.023	0.621
40S ribosomal protein S12;	Q6ZWZ6	1	9	19	45.5	0.202	0.049	0.692
Complement component 1, q subcomponent binding protein; Complement component 1, q subcomponent binding protein, isoform CRA_b; Uncharacterized protein; p32-RACK;	Q8R5L1	1	6	7	17.2	0.202	0.011	0.598
Ribosomal protein S6 kinase alpha-1;	P18653	0.998	3	3	5.1	0.202	0.042	0.669
Annexin A4;	P97429	1	28	42	45.1	0.214	0.02	0.591
Proteasome subunit beta type-9;	P28076	1	3	3	14.2	0.227	0.037	0.623
Tyrosine-protein phosphatase non-receptor type 6;	P29351	1	2	2	2	0.227	0.021	0.586
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial;	P35486	1	19	28	31.8	0.227	0.058	0.676
Haptoglobin;	Q61646	1	7	10	11.8	0.227	0.027	0.601
Cytochrome b-c1 complex subunit 2, mitochondrial;	Q9DB77	1	17	19	26.5	0.227	0.033	0.611
Phosphotriesterase-related protein;	Q60866	1	4	4	9.5	0.227	0.072	0.709
Acetyl-CoA acetyltransferase, cytosolic;	Q8CAY6	1	11	13	32.5	0.227	0.074	0.714
Programmed cell death 6-interacting protein;	Q9WU78	1	9	12	8.7	0.227	0.041	0.634
Calpain-1 catalytic subunit;	O35350	1	21	23	22.6	0.239	0.022	0.562
Proteasome subunit beta type-8;	P28063	1	4	5	8	0.239	0.049	0.624
Lysophosphatidic acid phosphatase type 6;	Q8BP40	1	4	7	9.8	0.239	0.03	0.582
Asporin;	Q99MQ4	1	8	8	23.9	0.239	0.03	0.574
ADP/ATP translocase 1;	P48962	1	23	62	34.2	0.239	0.059	0.640
ADP/ATP translocase 2;	P51881	1	4	6	22.8	0.202	0.012	0.601
Heterogeneous nuclear ribonucleoprotein K;	P61979	1	24	35	34.2	0.239	0.036	0.593
Carboxymethylenebutenolidase homolog;	Q8R1G2	1	10	11	22	0.239	0.024	0.567
TAR DNA-binding protein 43;	Q921F2	1	8	8	31.3	0.239	0.081	0.699
Rab GTPase-binding effector protein 2;	Q91WG2	0.998	2	3	3.8	0.239	0.085	0.715
ADP-ribose pyrophosphatase, mitochondrial;	Q8BVU5	0.995	2	2	13.9	0.239	0.079	0.699
Calumenin;	O35887	0.99	2	2	7.3	0.239	0.01	0.545
Cytochrome c oxidase subunit 2;	P00405	1	4	5	13.2	0.251	0.017	0.530
Programmed cell death protein 6;	P12815	1	6	7	22.5	0.251	0.089	0.696
Protein-glutamine gamma-glutamyltransferase 2;	P21981	1	6	6	8.7	0.251	0.097	0.711
Costars family protein C6orf115 homolog;	Q4KML4	1	3	4	16	0.251	0.051	0.602
Alcohol dehydrogenase class 4 mu/sigma chain;	Q64437	1	12	15	24.9	0.251	0.072	0.658
UDP-glucose:glycoprotein glucosyltransferase 1;	Q6P5E4	1	6	6	3.9	0.251	0.078	0.669

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
Elongation factor Tu, mitochondrial;	Q8BFR5	1	6	6	8.8	0.251	0.017	0.530
Alanine aminotransferase 1;	Q8QZR5	1	13	16	29	0.251	0.044	0.589
Microfibril-associated glycoprotein 4;	Q9D1H9	1	3	5	7	0.251	0.055	0.614
Ribosome-recycling factor, mitochondrial;	Q9D6S7	1	2	2	6.5	0.251	0.025	0.543
Heterogeneous nuclear ribonucleoprotein F;	Q9Z2X1	1	7	10	15.4	0.251	0.021	0.534
H-2 class II histocompatibility antigen, A-Q beta chain;	P06342	1	6	6	24.2	0.251	0.013	0.524
Cathepsin L1;	P06797	1	4	4	12.9	0.251	0.046	0.595
14-3-3 protein zeta/delta;	P63101	1	12	18	42	0.251	0.067	0.646
Spermine synthase;	P97355	1	8	9	25.4	0.251	0.051	0.602
EGF-containing fibulin-like extracellular matrix protein 1;	Q8BPB5	1	15	18	25.4	0.251	0.059	0.627
ATP synthase subunit g, mitochondrial;	Q9CPQ8	1	3	5	27.2	0.251	0.008	0.519
Proteasome subunit alpha type-6;	Q9QUM9	1	18	21	37.8	0.251	0.032	0.559
Lectin, galactose binding, soluble 7; Lectin, galactose binding, soluble 7, isoform CRA_a; Uncharacterized protein;	Q9CRB1	1	21	63	75	0.251	0.013	0.524
Dual specificity mitogen-activated protein kinase kinase 4;	P47809	0.995	2	2	2.8	0.251	0.021	0.534
Arylsulfatase B;	P50429	1	4	5	5.4	0.263	0.164	0.787
Ubiquitin-conjugating enzyme E2 E1;	P52482	1	2	2	7.7	0.263	0.022	0.511
Acylphosphatase-1;	P56376	1	9	11	48.5	0.263	0.103	0.699
Synaptobrevin homolog YKT6;	Q9CQW1	1	4	4	19.7	0.263	0.053	0.580
Chloride intracellular channel protein 4;	Q9QYB1	1	5	8	10.7	0.263	0.033	0.536
Calpain-2 catalytic subunit;	O08529	1	6	7	7.6	0.263	0.022	0.511
Talin-1;	P26039	1	43	47	15.6	0.263	0.059	0.600
Heterogeneous nuclear ribonucleoprotein A3;	Q8BG05	1	11	15	18.3	0.263	0.031	0.530
Early endosome antigen 1;	Q8BL66	1	6	6	3.5	0.263	0.085	0.662
Propionyl-CoA carboxylase alpha chain, mitochondrial;	Q91ZA3	1	15	16	19.1	0.263	0.136	0.753
Ethanolamine-phosphate cytidylyltransferase;	Q922E4	1	2	2	7.8	0.263	0.033	0.536
26S proteasome non-ATPase regulatory subunit 4;	O35226	1	5	6	10.6	0.275	0.025	0.493
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;	P63328	1	3	3	11.6	0.275	0.034	0.514
Sorting nexin-6;	Q6P8X1	1	8	9	11.1	0.275	0.148	0.746
Kynurenine--oxoglutarate transaminase 3;	Q71RI9	1	3	3	7.9	0.275	0.045	0.539
Fibrinogen beta chain;	Q8K0E8	1	25	53	32	0.275	0.02	0.484
Reticulon-4;	Q99P72	1	4	4	11.5	0.275	0.055	0.559
Na(+)/H(+) exchange regulatory cofactor NHE-RF3;	Q9JIL4	1	2	2	2.7	0.275	0.016	0.481
SH3 domain-binding glutamic acid-rich-like protein;	Q9JJU8	1	4	6	20.2	0.275	0.032	0.508
Band 4.1-like protein 2;	O70318	1	12	15	12.1	0.275	0.045	0.539
Glia maturation factor beta;	Q9CQI3	1	3	3	21.1	0.275	0.107	0.681
Glia maturation factor gamma;	Q9ERL7	1	2	2	19.8	-0.014	-0.001	0.971
EF-hand domain-containing protein D2;	Q9D8Y0	1	3	3	9.6	0.275	0.045	0.539
SPRY domain-containing protein 4;	Q91WK1	1	2	2	4.3	0.275	0.023	0.488
Uridine diphosphate glucose pyrophosphatase;	Q9D142	1	2	2	4.1	0.275	0.027	0.497
Uncharacterized protein;	E9Q8T1	1	6	6	1.6	0.287	0.071	0.575
Ferrochelatase, mitochondrial;	P22315	1	2	2	3.5	0.299	0.024	0.466
Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform;	P62715	1	2	2	32.7	0.299	0.036	0.492

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
Cytochrome c, somatic;	P62897	1	4	6	18.1	0.299	0.032	0.481
Eukaryotic translation initiation factor 5A-1;	P63242	1	4	4	19	0.299	0.041	0.498
Annexin A7;	Q07076	1	12	14	17.7	0.299	0.046	0.511
Myosin light chain kinase, smooth muscle;	Q6PDN3	1	14	20	5.6	0.299	0.141	0.707
Fibrinogen gamma chain;	Q8VCM7	1	22	34	29.8	0.299	0.046	0.511
Neurolysin, mitochondrial;	Q91YP2	1	6	6	9.7	0.299	0.097	0.631
Copper homeostasis protein cutC homolog;	Q9D8X1	1	3	3	7.1	0.299	0.027	0.471
Calpain small subunit 1;	O88456	1	6	6	13.3	0.299	0.041	0.498
Voltage-dependent anion-selective channel protein 2;	Q60930	1	7	7	15.6	0.299	0.027	0.471
Cullin-associated NEDD8-dissociated protein 1;	Q6ZQ38	1	10	11	6.6	0.299	0.061	0.545
E3 ubiquitin-protein ligase HUWE1;	Q7TMY8	1	9	9	2.4	0.299	0.058	0.538
Plastin-3;	Q99K51	1	32	48	36.2	0.299	0.066	0.559
Ubiquitin carboxyl-terminal hydrolase isozyme L3;	Q9JKB1	1	3	3	12.6	0.299	0.09	0.612
Toll-interacting protein;	Q9QZ06	1	4	5	16.8	0.299	0.027	0.471
NEDD8-conjugating enzyme Ubc12;	P61082	1	4	4	16.9	0.299	0.066	0.553
Large proline-rich protein BAG6;	Q9Z1R2	0.995	2	2	3.7	0.299	0.022	0.462
Heterogeneous nuclear ribonucleoproteins A2/B1;	O88569	1	10	26	19	0.31	0.03	0.455
Ubiquitin-fold modifier 1;	P61961	1	3	4	18.3	0.31	0.028	0.450
Sarcalumenin;	Q7TQ48	1	10	12	11.5	0.31	0.048	0.490
Cold shock domain-containing protein E1;	Q91W50	1	3	3	3.9	0.31	0.025	0.445
Ribonuclease T2;	Q9CQ01	1	3	3	9.7	0.31	0.052	0.504
Glutaredoxin-3;	Q9CQM9	1	7	9	14.5	0.31	0.03	0.455
ATP synthase subunit d, mitochondrial;	Q9DCX2	1	6	7	37.7	0.31	0.043	0.477
Glutathione S-transferase omega-1;	O09131	1	6	8	19.6	0.31	0.102	0.619
Eukaryotic initiation factor 4A-II;	P10630	1	13	13	24.9	0.31	0.045	0.484
Eukaryotic initiation factor 4A-I;	P60843	0.964	2	2	18.5	0.39	0.054	0.372
Voltage-dependent anion-selective channel protein 1;	Q60932	1	20	29	49.3	0.31	0.083	0.573
Transportin-3;	Q6P2B1	1	4	6	4.9	0.31	0.077	0.560
Calcineurin-like phosphoesterase domain-containing protein 1;	Q8BFS6	1	3	3	6.4	0.31	0.125	0.658
Adenylate kinase 2, mitochondrial;	Q9WTP6	1	8	9	27.2	0.31	0.063	0.525
Ras GTPase-activating protein-binding protein 1;	P97855	1	2	2	2.3	0.31	0.033	0.460
RING finger protein 114;	Q9ET26	1	2	2	8.4	0.31	0.033	0.460
T-complex protein 1 subunit zeta;	P80317	1	2	2	7	0.31	0.055	0.511
Small ubiquitin-related modifier 2;	P61957	0.991	2	2	16.9	0.31	0.025	0.445
Cystatin-B;	Q62426	0.99	2	2	11.2	0.31	0.018	0.438
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial;	P45952	1	4	4	7.8	0.322	0.1	0.588
Creatine kinase S-type, mitochondrial;	Q6P8J7	1	28	41	44.6	0.322	0.098	0.582
Troponin C, skeletal muscle;	P20801	1	17	25	53.8	0.322	0.036	0.445
Elongation factor G, mitochondrial;	Q8K0D5	1	5	5	4.7	0.322	0.147	0.673
Gamma-butyrobetaine dioxygenase;	Q924Y0	1	4	4	11.9	0.322	0.07	0.519
Cytoplasmic protein NCK1;	Q99M51	1	5	5	10.3	0.322	0.103	0.595
COP9 signalosome complex subunit 4;	O88544	1	4	4	13.1	0.322	0.134	0.653
BolA-like protein 2;	Q8BGS2	0.999	2	2	32.6	0.322	0.191	0.733

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
PDZ and LIM domain protein 3;	O70209	1	4	5	25	0.333	0.071	0.500
Caspase-14;	O89094	1	5	7	14.8	0.333	0.034	0.420
Superoxide dismutase [Mn], mitochondrial;	P09671	1	9	20	19.4	0.333	0.085	0.529
GDP-L-fucose synthase;	P23591	1	5	5	7.2	0.333	0.069	0.493
Catenin delta-1;	P30999	1	4	4	8.9	0.333	0.069	0.493
Neutral amino acid transporter B(0);	P51912	1	2	2	2.4	0.333	0.037	0.426
Cysteine and glycine-rich protein 1;	P97315	1	13	20	35.2	0.333	0.074	0.507
N-acetylglucosamine-6-sulfatase;	Q8BFR4	1	12	16	13.4	0.333	0.079	0.515
Thioredoxin-like protein 1;	Q8CDN6	1	7	7	19.4	0.333	0.034	0.420
Acylamino-acid-releasing enzyme;	Q8R146	1	6	6	7.4	0.333	0.085	0.529
5-hydroxyisourate hydrolase;	Q9CRB3	1	7	10	29.7	0.333	0.032	0.415
Isoamyl acetate-hydrolyzing esterase 1 homolog;	Q9DB29	1	6	7	20.9	0.333	0.103	0.571
ADP-sugar pyrophosphatase;	Q9JKX6	1	2	5	6.9	0.333	0.066	0.479
Peroxisomal acyl-coenzyme A oxidase 2;	Q9QXD1	1	2	2	4.4	0.333	0.238	0.760
General vesicular transport factor p115;	Q9Z1Z0	1	3	3	3.3	0.333	0.032	0.415
Plasminogen activator inhibitor 2, macrophage;	P12388	1	11	14	17.6	0.333	0.058	0.471
Mitogen-activated protein kinase 14;	P47811	1	7	7	17.1	0.333	0.04	0.431
Protein Niban;	Q3UW53	1	3	3	4.6	0.333	0.032	0.415
Propionyl-CoA carboxylase beta chain, mitochondrial;	Q99MN9	1	18	18	24.2	0.333	0.058	0.471
Aldehyde dehydrogenase;	E9Q3E1	1	9	9	14.6	0.333	0.05	0.451
Coatomer subunit beta;	Q9JIF7	1	2	3	2.2	0.333	0.034	0.420
Glutathione S-transferase theta-1;	Q64471	0.998	2	3	8.3	0.333	0.251	0.773
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha;	Q61239	0.998	2	2	4.2	0.333	0.04	0.431
Ear5 protein; Eosinophil-associated ribonuclease 5; Eosinophil-associated, ribonuclease A family, member 5; Uncharacterized protein;	Q8K416	0.998	2	2	14.8	0.333	0.092	0.550
COP9 signalosome complex subunit 5;	O35864	1	3	3	10.2	0.345	0.209	0.714
Catenin alpha-1;	P26231	1	6	6	6.7	0.345	0.101	0.539
Kynurenine--oxoglutarate transaminase 1;	Q8BTY1	1	4	4	8.6	0.345	0.03	0.391
V-type proton ATPase subunit H;	Q8BVE3	1	3	4	8.7	0.345	0.052	0.432
Uncharacterized protein;	E9Q8E3	1	4	4	2.4	0.345	0.019	0.379
Annexin A8;	O35640	1	32	51	48.6	0.345	0.035	0.401
Apolipoprotein E;	P08226	1	7	7	21.2	0.345	0.12	0.579
Polypyrimidine tract-binding protein 1;	P17225	1	6	10	16.1	0.345	0.03	0.391
Ras-related protein Rab-5C;	P35278	1	3	3	26.9	0.345	0.054	0.438
UV excision repair protein RAD23 homolog B;	P54728	1	5	5	14.1	0.345	0.095	0.532
Tubulin beta-5 chain;	P99024	1	6	10	51.4	0.345	0.046	0.419
Tubulin beta-4B chain;	P68372	1	6	6	47.4	0.791	0.059	0.049
Tubulin beta-2A chain;	Q7TMM9	0.998	2	2	35.3	0.163	0.015	0.688
Cardiomyopathy-associated protein 5;	Q70KF4	1	9	10	3.3	0.345	0.128	0.598
Ubiquitin-conjugating enzyme E2 variant 1;	Q9CZY3	0.986	4	5	16	0.345	0.024	0.383
Spliceosome RNA helicase Ddx39b;	Q9Z1N5	1	10	11	17.3	0.345	0.084	0.504
Uncharacterized protein;	E9PWQ3	1	10	10	4.4	0.345	0.247	0.754
Cyclin-dependent kinase 6;	Q64261	1	2	2	4.9	0.345	0.035	0.401

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
Tyrosine-protein phosphatase non-receptor type 11;	P35235	1	3	3	6.9	0.345	0.033	0.396
Target of Myb protein 1;	O88746	1	5	5	11	0.356	0.259	0.746
Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	P23506	1	5	7	15.8	0.356	0.042	0.394
Serpin B5;	P70124	1	43	90	60.8	0.356	0.053	0.413
Mimecan;	Q62000	1	7	12	15.1	0.356	0.117	0.556
Versican core protein;	Q62059	1	5	5	6.7	0.356	0.047	0.400
Protein arginine N-methyltransferase 5;	Q8CIG8	1	2	2	3.1	0.356	0.042	0.394
NADH dehydrogenase [ubiquinone] 1 subunit C2;	Q9CQ54	1	2	2	10.8	0.356	0.017	0.358
Acyl-coenzyme A thioesterase 13;	Q9CQR4	1	3	3	16.4	0.356	0.017	0.358
E3 ubiquitin-protein ligase ARIH1;	Q9Z1K5	1	2	2	2	0.356	0.031	0.373
Proliferation-associated protein 2G4;	P50580	1	5	5	12.4	0.356	0.036	0.383
ATP-binding cassette sub-family E member 1;	P61222	1	3	3	3.8	0.356	0.07	0.449
COP9 signalosome complex subunit 2;	P61202	1	3	3	5.7	0.356	0.022	0.362
Ubiquitin-like modifier-activating enzyme 6;	Q8C7R4	1	4	4	3.5	0.379	0.117	0.526
Nuclear receptor-binding protein;	Q99J45	1	2	2	2.8	0.379	0.067	0.416
Transportin-2;	Q99LG2	1	3	4	3	0.379	0.117	0.526
Ly6/PLAUR domain-containing protein 5;	Q9D7Z7	1	2	2	6.2	0.379	0.073	0.431
3-ketoacyl-CoA thiolase A, peroxisomal;	Q921H8	1	19	25	38	0.379	0.058	0.402
Glutathione S-transferase theta 3; Glutathione S-transferase, theta 3; Uncharacterized protein;	Q99L20	1	6	8	14.1	0.379	0.076	0.438
Transitional endoplasmic reticulum ATPase;	Q01853	1	34	41	30	0.39	0.113	0.495
Cytoplasmic dynein 1 light intermediate chain 2;	Q6PDL0	1	4	4	6.7	0.39	0.101	0.473
3-ketoacyl-CoA thiolase, mitochondrial;	Q8BWT1	1	25	46	44.3	0.39	0.033	0.338
Carbonic anhydrase 13;	Q9D6N1	1	5	5	23.7	0.39	0.074	0.414
Proteasomal ubiquitin receptor ADRM1;	Q9JKV1	1	3	11	6.1	0.39	0.054	0.372
Serine/threonine-protein kinase DCLK1;	Q9JLM8	1	2	2	3	0.39	0.119	0.510
Annexin A1;	P10107	1	39	88	57.5	0.39	0.033	0.338
Protein RCC2;	Q8BK67	1	9	10	15.8	0.39	0.113	0.495
Phosphoserine aminotransferase;	Q99K85	1	18	19	43.5	0.39	0.057	0.378
Ubiquitin carboxyl-terminal hydrolase isozyme L5;	Q9WUP7	1	2	2	4.3	0.39	0.033	0.338
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1;	Q62077	0.999	2	2	2.4	0.39	0.033	0.338
Interleukin-1 receptor antagonist protein;	P25085	0.977	2	2	8.1	0.39	0.039	0.348
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	P19783	1	5	11	23.7	0.401	0.046	0.343
Uncharacterized protein;	E9Q043	1	2	5	1.5	0.401	0.058	0.361
Heterogeneous nuclear ribonucleoprotein Q;	Q7TMK9	1	10	12	12.8	0.401	0.061	0.368
NSFL1 cofactor p47;	Q9CZ44	1	17	19	33.2	0.401	0.055	0.355
Hydroxysteroid (17-beta) dehydrogenase 10; Uncharacterized protein;	A2AFQ2	1	5	5	21.1	0.401	0.07	0.382
Inactive tyrosine-protein kinase 7;	Q8BKG3	1	2	4	6.5	0.401	0.058	0.361
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial;	P50136	1	3	3	6.6	0.411	0.071	0.366
Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	P70404	1	13	15	30.3	0.411	0.043	0.322
Echinoderm microtubule-associated protein-like 1;	Q05BC3	1	5	5	5	0.411	0.127	0.485
Retroviral-like aspartic protease 1;	Q09PK2	1	3	4	10.6	0.411	0.071	0.366
Drebrin-like protein;	Q62418	1	10	10	17.9	0.411	0.108	0.448

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
Farnesyl pyrophosphate synthase;	Q920E5	1	11	13	19.3	0.411	0.046	0.327
Heterogeneous nuclear ribonucleoprotein A/B;	Q99020	1	4	4	8	0.411	0.034	0.306
tRNA-splicing ligase RtcB homolog;	Q99LF4	1	3	3	5.3	0.411	0.124	0.477
Integrin beta-4;	A2A863	1	3	3	2.4	0.411	0.077	0.380
Glutamine synthetase;	P15105	1	7	7	16.6	0.411	0.093	0.410
Ras-related protein R-Ras;	P10833	1	3	5	10.6	0.422	0.06	0.330
Lysosome-associated membrane glycoprotein 2;	P17047	1	5	5	8.7	0.422	0.044	0.308
Calnexin;	P35564	1	2	2	1.7	0.422	0.035	0.291
Transgelin;	P37804	1	15	29	43.3	0.422	0.047	0.312
Acylphosphatase-2;	P56375	1	7	11	39.2	0.422	0.06	0.330
14-3-3 protein theta;	P68254	1	7	7	27.8	0.422	0.057	0.323
Platelet glycoprotein 4;	Q08857	1	8	14	11	0.422	0.06	0.330
Zinc transporter SLC39A7;	Q31125	1	2	2	2.7	0.422	0.041	0.301
Perilipin-1;	Q8CGN5	1	16	16	25	0.422	0.192	0.577
Acetoacetyl-CoA synthetase;	Q9D2R0	1	7	8	9.4	0.422	0.151	0.511
Prolyl-tRNA synthetase associated domain-containing protein 1;	Q9D820	1	3	3	15.4	0.422	0.072	0.350
Isocitrate dehydrogenase 3 (NAD+) beta; Tumor-related protein; Uncharacterized protein;	Q91VA7	1	8	10	20.3	0.422	0.06	0.330
Protein diaphanous homolog 1;	O08808	1	2	2	3	0.422	0.299	0.697
NADPH--cytochrome P450 reductase;	P37040	1	4	4	4	0.422	0.145	0.497
Lambda-crystallin homolog;	Q99KP3	1	11	12	25.4	0.422	0.117	0.440
Alpha-galactosidase A;	P51569	1	2	2	2.9	0.444	0.049	0.297
Zinc-binding alcohol dehydrogenase domain-containing protein 2;	Q8BGC4	1	9	10	18.3	0.444	0.049	0.297
CD109 antigen;	Q8R422	1	4	4	2.2	0.444	0.036	0.277
Serine/threonine-protein kinase 24;	Q99KH8	1	2	2	3	0.444	0.065	0.321
Probable C->U-editing enzyme APOBEC-2;	Q9WV35	1	3	3	6.7	0.444	0.062	0.315
SUMO-activating enzyme subunit 2;	Q9Z1F9	1	5	5	8.8	0.444	0.039	0.281
Protein S100-A4;	P07091	1	4	6	15.8	0.444	0.059	0.309
Actin-related protein 2/3 complex subunit 4;	P59999	1	4	5	16.7	0.444	0.069	0.328
Heterogeneous nuclear ribonucleoprotein D0;	Q60668	1	4	5	20.6	0.444	0.101	0.386
Proteasome subunit alpha type-4;	Q9R1P0	1	9	14	31.4	0.444	0.124	0.432
Uncharacterized protein;	E9QJY4	1	2	2	2.4	0.444	0.042	0.283
E3 ubiquitin-protein ligase NEDD4;	P46935	1	4	4	4.5	0.444	0.131	0.447
Ig heavy chain V region MOPC 104E;	P01756	1	2	5	16.2	0.454	0.03	0.256
Coatomer subunit gamma;	Q9QZE5	1	3	3	5.9	0.454	0.093	0.356
Secernin-2;	Q8VCA8	1	6	8	13.2	0.454	0.169	0.495
Actin-related protein 2/3 complex subunit 2;	Q9CVB6	1	5	5	13	0.454	0.099	0.364
Protein arginine N-methyltransferase 1;	Q9JIF0	1	2	2	11	0.454	0.04	0.268
Proteasome subunit alpha type-7;	Q9Z2U0	1	14	26	37.5	0.454	0.02	0.250
Proteasome subunit beta type-7;	P70195	1	6	7	11.2	0.465	0.078	0.306
Vasodilator-stimulated phosphoprotein;	P70460	1	3	3	6.7	0.465	0.078	0.306
Voltage-dependent anion-selective channel protein 3;	Q60931	1	5	5	15.5	0.465	0.084	0.320
Calponin-3;	Q9DAW9	1	3	3	6.7	0.465	0.246	0.589

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
1-acylglycerol-3-phosphate O-acyltransferase ABHD5;	Q9DBL9	1	3	3	11.1	0.465	0.216	0.547
Acyl-CoA dehydrogenase family member 9, mitochondrial;	Q8JZN5	1	13	14	19.4	0.465	0.091	0.334
Uncharacterized protein;	E9Q7G0	1	3	4	1.2	0.465	0.35	0.687
Dual specificity mitogen-activated protein kinase kinase 6;	P70236	1	2	2	5.5	0.465	0.054	0.269
Thiopurine S-methyltransferase;	O55060	1	2	2	8.3	0.465	0.388	0.713
Carbohydrate kinase domain-containing protein;	Q9CZ42	1	2	2	10.2	0.465	0.202	0.530
UPF0554 protein C2orf43 homolog;	Q8BVA5	0.996	2	2	4	0.465	0.061	0.280
Ig kappa chain C region;	P01837	1	7	23	44.3	0.475	0.058	0.261
Methylmalonyl-CoA mutase, mitochondrial;	P16332	1	5	5	5.6	0.475	0.229	0.551
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Q9D6R2	1	16	24	32.2	0.475	0.137	0.402
Calmodulin-4;	Q9JM83	1	9	9	41.2	0.475	0.034	0.234
Cathepsin Z;	Q9WUU7	1	5	9	7.8	0.475	0.048	0.251
Gamma-synuclein;	Q9Z0F7	1	6	7	47.2	0.475	0.031	0.231
Uncharacterized protein;	Q9CX86	1	3	4	12.1	0.475	0.024	0.228
26S proteasome non-ATPase regulatory subunit 13;	Q9WVJ2	1	4	4	10	0.475	0.055	0.256
Histidyl-tRNA synthetase, cytoplasmic;	Q61035	1	2	2	5.9	0.475	0.031	0.230
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial;	Q99LC3	1	4	4	9	0.485	0.371	0.676
Dual specificity protein phosphatase 3;	Q9D7X3	1	10	10	32.4	0.485	0.055	0.243
Apoptosis-associated speck-like protein containing a CARD;	Q9EPB4	1	9	11	35.2	0.485	0.059	0.249
Maleylacetoacetate isomerase;	Q9WVL0	1	17	21	51.9	0.485	0.097	0.314
Glycogen phosphorylase, muscle form;	Q9WUB3	1	54	107	48.1	0.485	0.09	0.300
Glycogen phosphorylase, brain form;	Q8CI94	1	15	19	21.8	0.07	0.01	0.875
Glycogen phosphorylase, liver form;	Q9ET01	1	4	4	9.4	-0.152	-0.01	0.690
T-complex protein 1 subunit eta;	P80313	1	3	3	3.1	0.496	0.165	0.418
Eukaryotic peptide chain release factor subunit 1;	Q8BWY3	1	2	2	2.3	0.496	0.06	0.237
DCC-interacting protein 13-alpha;	Q8K3H0	1	3	3	4.5	0.496	0.032	0.207
UTP--glucose-1-phosphate uridylyltransferase;	Q91ZJ5	1	33	56	37	0.496	0.12	0.337
Cystatin E/M; Cystatin M/E; Uncharacterized protein;	Q9D1B1	1	7	9	35.6	0.496	0.186	0.452
Titin;	A2ASS6	1	37	48	1.1	0.496	0.324	0.624
Monoglyceride lipase;	O35678	1	7	7	26.4	0.496	0.106	0.317
Tubulin alpha-1B chain;	P05213	1	10	13	38.8	0.496	0.056	0.231
Tubulin alpha-4A chain;	P68368	1	5	5	34.6	0.546	0.224	0.440
Acyl-CoA-binding protein;	P31786	1	7	8	39.1	0.496	0.042	0.218
Coronin-1C;	Q9WUM4	1	7	7	12.2	0.496	0.032	0.207
Proteasome subunit alpha type-2;	P49722	1	12	14	39.7	0.516	0.094	0.264
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial;	Q3UV70	1	3	3	4.6	0.516	0.036	0.199
5'-nucleotidase;	Q61503	1	4	4	5.6	0.516	0.382	0.654
Filamin-B;	Q80X90	1	11	11	5.2	0.516	0.108	0.286
Heme-binding protein 1;	Q9R257	1	5	7	14.7	0.516	0.051	0.215
Coagulation factor XIII A chain;	Q8BH61	1	6	6	7.2	0.516	0.076	0.248
Pantetheinase;	Q9Z0K8	1	3	3	5.1	0.526	0.026	0.184
H-2 class II histocompatibility antigen, A-Q alpha chain;	P04227	1	4	4	11.8	0.526	0.062	0.214
Perilipin-2;	P43883	1	5	6	11.5	0.526	0.27	0.533

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
Rho-related GTP-binding protein RhoC;	Q62159	1	7	8	36.8	0.526	0.102	0.275
Four and a half LIM domains 1; Four and a half LIM domains 1, isoform CRA_b; Uncharacterized protein;	A2AEX8	1	23	49	41.2	0.526	0.124	0.311
Ufm1-specific protease 1;	Q9CZP0	1	3	3	13.8	0.526	0.329	0.592
26S proteasome non-ATPase regulatory subunit 7;	P26516	1	8	9	21.2	0.536	0.166	0.364
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial;	Q9CXZ1	1	3	3	14.3	0.536	0.092	0.243
Cytosolic 5'-nucleotidase 3;	Q9D020	1	7	7	17.8	0.536	0.1	0.257
26S proteasome non-ATPase regulatory subunit 12;	Q9D8W5	1	2	2	3.1	0.536	0.1	0.257
Proteasome subunit alpha type-1;	Q9R1P4	1	16	18	35.9	0.536	0.311	0.560
Twinfilin-2;	Q9Z0P5	1	4	4	12.9	0.536	0.055	0.190
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial;	Q9Z2I8	1	15	16	37.9	0.536	0.362	0.609
Lupus La protein homolog;	P32067	1	2	2	6	0.536	0.177	0.386
Pigment epithelium-derived factor;	P97298	1	4	4	9.6	0.536	0.078	0.225
5-oxoprolinase;	Q8K010	1	17	18	10.9	0.536	0.137	0.313
14-3-3 protein beta/alpha;	Q9CQV8	1	8	10	34.1	0.536	0.059	0.198
14-3-3 protein eta;	P68510	1	2	2	14.6	0.604	0.06	0.140
Dysferlin;	Q9ESD7	1	3	3	0.9	0.546	0.034	0.167
26S protease regulatory subunit 6A;	O88685	1	16	16	31.2	0.546	0.217	0.433
Ubiquitin carboxyl-terminal hydrolase 5;	P56399	1	13	14	12.1	0.546	0.243	0.464
Proteasome subunit beta type-3;	Q9R1P1	1	4	4	15.1	0.546	0.093	0.232
Actin-related protein 2/3 complex subunit 1B;	Q9WV32	1	10	10	21	0.546	0.067	0.198
Carbonic anhydrase 2;	P00920	1	12	12	37.3	0.556	0.253	0.464
6-phosphofructokinase, liver type;	P12382	1	11	12	13.8	0.556	0.219	0.415
Carbonic anhydrase 3;	P16015	1	35	868	65.4	0.556	0.045	0.167
Cytosolic 10-formyltetrahydrofolate dehydrogenase;	Q8R0Y6	1	7	7	8.4	0.556	0.091	0.215
COP9 signalosome complex subunit 8;	Q8VBV7	1	2	2	17.2	0.556	0.386	0.602
2-aminoethanethiol dioxygenase;	Q6PDY2	1	2	2	4.3	0.556	0.072	0.193
U6 snRNA-associated Sm-like protein LSm2;	O35900	1	2	2	20	0.566	0.119	0.243
Niban-like protein 1;	Q8R1F1	1	6	6	6.9	0.566	0.134	0.271
Ig kappa chain V-V region L6;	P01638	1	3	3	22.6	0.566	0.076	0.188
Polyubiquitin-B;	P0CG49	1	5	6	32.8	0.566	0.317	0.522
Galectin-3-binding protein;	Q07797	1	3	3	7.5	0.566	0.302	0.507
Ig gamma-2B chain C region;	P01867	1	4	5	13.4	0.585	0.062	0.161
Thiamin pyrophosphokinase 1;	Q9R0M5	1	3	3	15.2	0.585	0.078	0.179
Proteasome subunit beta type-2;	Q9R1P3	1	3	5	12.9	0.585	0.105	0.213
Phospholysine phosphohistidine inorganic pyrophosphate phosphatase;	Q9D7I5	0.999	3	3	8.1	0.585	0.039	0.144
Protein phosphatase 1B;	P36993	1	5	5	7.9	0.595	0.118	0.216
ATP synthase subunit f, mitochondrial;	P56135	1	3	5	30.3	0.595	0.039	0.136
14-3-3 protein gamma;	P61982	1	5	8	25.1	0.595	0.051	0.145
Importin subunit beta-1;	P70168	1	6	8	6.2	0.595	0.307	0.479
V-type proton ATPase subunit E 1;	P50518	1	3	3	8.4	0.595	0.067	0.156
Cytochrome P450 2F2;	P33267	1	2	2	3.9	0.595	0.063	0.152
Ig gamma-1 chain C region secreted form;	P01868	1	12	35	23.8	0.604	0.02	0.121

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
Peroxisomal multifunctional enzyme type 2;	P51660	1	8	9	10.1	0.604	0.06	0.141
MAP kinase-activated protein kinase 3;	Q3UMW7	1	2	2	4.5	0.604	0.056	0.141
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4;	Q62425	1	4	4	26.8	0.604	0.044	0.132
Membrane primary amine oxidase;	O70423	1	14	21	15.8	0.604	0.155	0.259
Ubiquinone biosynthesis protein COQ9, mitochondrial;	Q8K1Z0	1	6	6	19.5	0.604	0.095	0.177
Multifunctional protein ADE2;	Q9DCL9	1	10	10	17.6	0.604	0.199	0.321
Mitogen-activated protein kinase 12;	O08911	1	5	5	13.9	0.614	0.096	0.172
Sulfotransferase family cytosolic 2B member 1;	O35400	1	3	3	5.9	0.614	0.076	0.149
Pyruvate carboxylase, mitochondrial;	Q05920	1	29	42	21.7	0.614	0.128	0.209
EH domain-containing protein 2;	Q8BH64	1	3	4	3.7	0.614	0.181	0.282
Tumor protein D54;	Q9CYZ2	1	2	2	6.2	0.614	0.076	0.149
Alpha-methylacyl-CoA racemase;	O09174	1	7	7	12.3	0.623	0.312	0.441
Diphosphomevalonate decarboxylase;	Q99JF5	1	3	3	5.7	0.623	0.057	0.126
Coronin-1A;	O89053	1	10	14	12.6	0.623	0.065	0.129
Enoyl-CoA hydratase, mitochondrial;	Q8BH95	1	7	8	18.6	0.623	0.073	0.137
ATP-citrate synthase;	Q91V92	1	36	42	22.4	0.623	0.121	0.187
T-complex protein 1 subunit alpha;	P11983	1	2	2	9.7	0.623	0.053	0.123
Non-specific lipid-transfer protein;	P32020	1	9	14	10.8	0.642	0.115	0.173
Prostaglandin reductase 2;	Q8VDQ1	1	4	5	11.7	0.642	0.099	0.152
ATP synthase protein 8;	P03930	0.999	2	2	14.9	0.642	0.025	0.103
Alanyl-tRNA editing protein Aarsd1;	Q3THG9	0.981	2	2	6.8	0.642	0.099	0.152
Tripeptidyl-peptidase 1;	O89023	1	3	4	6.2	0.651	0.249	0.337
Decorin;	P28654	1	4	7	5.9	0.651	0.075	0.123
Hormone-sensitive lipase;	P54310	1	6	6	7.8	0.651	0.108	0.154
Gamma-glutamylcyclotransferase;	Q9D7X8	1	7	7	21.8	0.651	0.141	0.194
Keratin, type I cytoskeletal 17;	Q9QWL7	1	5	5	12.5	0.651	0.166	0.225
Keratin 15; Keratin 15, isoform CRA_a; Uncharacterized protein;	B1AQ77	1	5	5	22.1	1.014	0.432	0.165
Acyl-coenzyme A thioesterase 9, mitochondrial;	Q9R0X4	1	5	5	7.7	0.651	0.141	0.196
26S proteasome non-ATPase regulatory subunit 1;	Q3TXS7	1	8	8	10.6	0.66	0.071	0.113
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial;	O09111	0.996	2	2	6.6	0.66	0.1	0.137
Epidermal growth factor receptor kinase substrate 8-like protein 1;	Q8R5F8	1	5	5	5.3	0.669	0.063	0.101
Heat shock protein beta-2;	Q99PR8	1	6	8	30.8	0.669	0.189	0.233
Desmoglein-3;	O35902	0.986	2	2	1.8	0.669	0.042	0.091
Mevalonate kinase;	Q9R008	1	5	8	16.7	0.678	0.114	0.137
Carnitine O-palmitoyltransferase 1, muscle isoform;	Q924X2	1	3	3	3.6	0.678	0.042	0.086
Acyl-CoA synthetase family member 2, mitochondrial;	Q8VCW8	1	8	8	14.5	0.687	0.205	0.233
Cytochrome c1, heme protein, mitochondrial;	Q9D0M3	1	4	4	5.8	0.687	0.055	0.087
Sorting nexin-27;	Q3UHD6	0.933	2	2	7.2	0.687	0.422	0.474
Fatty acid-binding protein, adipocyte;	P04117	1	17	79	64.4	0.705	0.03	0.073
Acetyl-coenzyme A synthetase, cytoplasmic;	Q9QXG4	1	5	5	6.4	0.705	0.277	0.307
6-phosphofructokinase type C;	Q9WUA3	1	9	10	15.6	0.705	0.061	0.085
Ubiquitin-protein ligase E3A;	O08759	1	3	3	2.6	0.714	0.139	0.136
Gasdermin-A;	Q9EST1	1	4	6	7.6	0.714	0.083	0.091

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 S100-A10;	P08207	0.994	2	2	7.2	0.714	0.017	0.067
Ras GTPase-activating-like protein IQGAP1;	Q9JKF1	1	21	22	11.4	0.722	0.429	0.442
14-3-3 protein epsilon;	P62259	1	12	17	39.2	0.722	0.123	0.116
PDZ and LIM domain protein 5;	Q8CI51	1	6	6	14.7	0.722	0.07	0.078
Citrate synthase, mitochondrial;	Q9CZU6	1	15	31	20.9	0.722	0.166	0.153
Four and a half LIM domains 3; Uncharacterized protein;	A6H6N4	1	4	4	12.8	0.722	0.372	0.388
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	7	8	23.9	0.722	0.031	0.065
cAMP-dependent protein kinase catalytic subunit alpha;	P05132	0.98	3	3	5.4	0.722	0.061	0.076
Cytochrome c oxidase subunit 7A1, mitochondrial;	P56392	1	2	2	16.2	0.731	0.044	0.064
MCG21235; Uncharacterized protein;	Q9D1Q5	1	12	17	21.4	0.731	0.154	0.138
NHL repeat-containing protein 3;	Q8CCH2	0.999	2	2	6.1	0.731	0.181	0.165
Fatty acid synthase;	P19096	1	114	184	34.2	0.74	0.323	0.315
Prolargin;	Q9JK53	1	18	34	23.8	0.74	0.133	0.109
26S proteasome non-ATPase regulatory subunit 14;	O35593	1	2	2	5.3	0.74	0.058	0.065
Long-chain-fatty-acid--CoA ligase 5;	Q8JZR0	0.964	2	2	2.9	0.74	0.044	0.061
Parvalbumin alpha;	P32848	1	12	180	45.5	0.757	0.112	0.088
26S protease regulatory subunit 7;	P46471	1	4	4	10.9	0.757	0.202	0.167
Prohibitin;	P67778	1	3	3	7.7	0.757	0.085	0.073
26S proteasome non-ATPase regulatory subunit 11;	Q8BG32	1	16	18	24.4	0.757	0.04	0.056
ATP-dependent RNA helicase DDX19A;	Q61655	0.999	2	2	2.1	0.757	0.054	0.060
Alanine aminotransferase 2;	Q8BGT5	1	3	3	4.4	0.766	0.149	0.111
Leucyl-tRNA synthetase, cytoplasmic;	Q8BMJ2	1	4	4	3.8	0.766	0.063	0.060
Neurobeachin;	Q9EPN1	0.909	2	2	1.6	0.766	0.086	0.069
Cadherin-1;	P09803	1	5	7	6.2	0.774	0.077	0.060
Clathrin heavy chain 1;	Q68FD5	1	25	29	14.2	0.774	0.154	0.110
Cell surface glycoprotein MUC18;	Q8R2Y2	1	4	4	8.2	0.774	0.349	0.305
Short-chain specific acyl-CoA dehydrogenase, mitochondrial;	Q07417	1	2	2	8.3	0.782	0.091	0.064
Heat shock protein beta-1;	P14602	1	20	49	46.4	0.782	0.045	0.048
Spectrin alpha chain, brain;	P16546	1	23	25	10.5	0.782	0.259	0.201
Nidogen-1;	P10493	1	6	6	4	0.791	0.046	0.046
Long-chain-fatty-acid--CoA ligase 1;	P41216	1	7	8	8.3	0.791	0.142	0.088
Carnitine O-acetyltransferase;	P47934	1	2	2	19.7	0.791	0.087	0.058
Proteasome activator complex subunit 1;	P97371	1	3	4	10.4	0.791	0.119	0.074
Vacuolar protein sorting-associated protein 35;	Q9EQH3	1	4	4	4.1	0.791	0.229	0.161
Filamin-A;	Q8BTM8	1	75	102	27	0.791	0.274	0.210
Beta-1-syntrophin;	Q99L88	1	2	2	2.2	0.791	0.087	0.058
Suppressor of G2 allele of SKP1 homolog;	Q9CX34	0.992	2	2	7.1	0.791	0.32	0.255
26S proteasome non-ATPase regulatory subunit 6;	Q99JI4	1	4	5	6.2	0.799	0.073	0.049
Proteasome activator complex subunit 2;	P97372	1	4	4	16.3	0.799	0.298	0.231
14-3-3 protein sigma;	O70456	1	10	21	29.8	0.832	0.056	0.037
SEC14-like protein 4;	Q8R0F9	1	7	7	17.9	0.832	0.065	0.040

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
Alpha-crystallin B chain;	P23927	1	13	42	34.3	0.832	0.037	0.034
RNA-binding protein FUS;	P56959	0.999	2	2	2.8	0.832	0.042	0.034
Calcium-binding mitochondrial carrier protein SCaMC-1;	Q8BMD8	0.993	2	2	1.9	0.848	0.085	0.039
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform;	P18826	1	3	3	2	0.856	0.407	0.274
Ig kappa chain V-V region HP R16.7;	P01644	1	4	4	36.1	0.856	0.189	0.086
Calcineurin subunit B type 1;	Q63810	1	2	3	12.9	0.856	0.151	0.063
Uncharacterized protein;	F7CAE1	1	14	43	57.9	0.872	0.152	0.060
Chondroitin sulfate proteoglycan 4;	Q8VHY0	0.997	2	2	1.5	0.872	0.124	0.047
Hemoglobin subunit beta-1;	P02088	1	19	100	87.8	0.888	0.096	0.034
Hemoglobin subunit beta-2;	P02089	1	18	60	83.7	0.824	0.098	0.053
Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	Q8JZK9	1	12	12	14.4	0.895	0.212	0.081
Heat shock 70 kDa protein 12A;	Q8K0U4	0.979	2	2	1.5	0.895	0.077	0.027
Myozenin-1;	Q9JK37	0.946	2	2	2.7	0.895	0.101	0.033
Glycolipid transfer protein;	Q9JL62	1	3	3	14.7	0.903	0.14	0.044
Laminin subunit alpha-4;	P97927	0.999	2	2	0.6	0.903	0.077	0.025
Ig gamma-3 chain C region;	P03987	0.991	3	3	8.3	0.911	0.111	0.031
26S protease regulatory subunit 6B;	P54775	1	6	8	10.8	0.918	0.165	0.050
MCG117626; Odorant binding protein Ia; Uncharacterized protein;	Q9D3H2	0.998	2	2	9.2	0.918	0.044	0.020
40S ribosomal protein S3;	P62908	1	3	3	11	0.926	0.297	0.127
Angio-associated migratory protein; Uncharacterized protein;	Q3TJ22	1	2	2	3	0.926	0.122	0.032
Calcium-binding mitochondrial carrier protein Aralar1;	Q8BH59	1	9	9	9.9	0.934	0.504	0.281
Perilipin-4;	O88492	1	27	38	36.5	0.949	0.462	0.237
26S proteasome non-ATPase regulatory subunit 2;	Q8VDM4	1	14	15	13.8	0.956	0.256	0.079
Periplakin;	Q9R269	1	6	6	2.1	0.971	0.154	0.030
tRNA (cytosine(34)-C(5))-methyltransferase;	Q1HFZ0	1	2	2	3.6	0.978	0.333	0.117
Myosin-4;	Q5SX39	1	21	22	22.1	0.978	0.124	0.022
Myosin-1;	Q5SX40	1	9	12	22.5	3.401	1.311	0.000
Myosin, heavy polypeptide 2, skeletal muscle, adult; Uncharacterized protein;	Q5SX41	1	3	3	16.3	3.406	1.671	0.000
Threonyl-tRNA synthetase, cytoplasmic;	Q9D0R2	0.996	3	3	3.5	0.978	0.05	0.013
Calsequestrin-1;	O09165	1	4	6	22.4	0.993	0.16	0.028
UDP-glucose 4-epimerase;	Q8R059	1	5	5	6.1	1	0.275	0.071
Ribose-phosphate pyrophosphokinase 1;	Q9D7G0	1	4	4	10.7	1	0.4	0.149
Heat shock protein beta-3;	Q9QZ57	0.994	2	2	17.5	1.036	0.091	0.011
	O54724	1	4	6	11.2	1.043	0.137	0.016
ATPase Asna1;	O54984	1	2	2	6	1.064	0.137	0.014
Ubiquitin carboxyl-terminal hydrolase 4;	P35123	1	2	3	3.1	1.064	0.86	0.384
Fibulin-5;	Q9WVH9	1	7	8	14.1	1.07	0.168	0.017
Nebulin; Uncharacterized protein;	A2AQA9	1	6	7	1.5	1.07	0.627	0.246
26S protease regulatory subunit 4;	P62192	1	6	7	16.8	1.077	0.454	0.135
Spectrin beta chain, brain 1;	Q62261	1	4	4	2.4	1.084	0.332	0.065
Phosphoserine phosphatase;	Q99LS3	1	2	2	10.7	1.084	0.205	0.022
Alpha-actinin-4;	P57780	1	5	5	5.8	1.091	0.359	0.073
Alpha-actinin-3;	O88990	1	4	4	6.4	1.757	0.587	0.005

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
Glutaredoxin-1;	Q9QUH0	1	3	4	22.4	1.098	0.267	0.035
Heat shock protein beta-6;	Q5EBG6	1	7	11	29	1.111	0.206	0.019
Protein S100-A6;	P14069	0.994	4	5	24.7	1.118	0.752	0.282
Asparagine synthetase [glutamine-hydrolyzing];	Q61024	1	2	2	1.6	1.151	0.202	0.013
Carbonic anhydrase 1;	P13634	1	2	2	12.3	1.163	0.244	0.018
26S protease regulatory subunit 8;	P62196	1	4	4	14.7	1.17	0.697	0.215
Myoglobin;	P04247	1	16	44	41.6	1.183	0.177	0.008
RelA-associated inhibitor;	Q5I1X5	1	2	2	1	1.195	0.13	0.004
Monofunctional C1-tetrahydrofolate synthase, mitochondrial;	Q3V3R1	1	3	3	2.4	1.202	0.157	0.005
26S protease regulatory subunit 10B;	P62334	1	8	10	12.3	1.208	0.267	0.016
Tripartite motif-containing protein 29;	Q8R2Q0	1	2	5	1.7	1.214	0.037	0.002
Kinesin-1 heavy chain;	Q61768	1	11	13	10.5	1.275	0.232	0.006
Plectin;	Q9QXS1	1	15	17	3.6	1.299	0.76	0.161
Heat shock protein beta-7;	P35385	1	5	6	26	1.322	0.243	0.005
Uncharacterized protein;	E9PXU6	0.903	2	2	4.1	1.328	0.069	0.001
RIKEN cDNA 8030451F13, isoform CRA_c; Uncharacterized protein;	D3YU50	1	35	40	23.8	1.362	0.472	0.031
Filamin-C;	Q8VHX6	1	16	16	9	1.379	0.536	0.043
Myomesin-3;	A2ABU4	1	4	4	3.5	1.39	0.377	0.012
6-phosphofructokinase, muscle type;	P47857	1	38	59	34.1	1.411	0.286	0.004
Vimentin;	P20152	1	9	9	18.5	1.485	0.727	0.064
Keratin, type II cytoskeletal 5;	Q922U2	1	2	2	4.8	1.59	0.417	0.003
Uncharacterized protein;	E9Q4Z2	1	2	2	1.2	1.614	0.195	0.000
Syntaxin 17; Syntaxin 17, isoform CRA_b; Uncharacterized protein;	Q9D614	0.971	2	2	3.3	1.637	0.153	0.000
Protein CREG1;	O88668	1	6	9	13.2	1.674	0.184	0.000
DnaJ homolog subfamily A member 4;	Q9JMC3	1	2	2	2.5	1.778	0.202	0.000
Rho-associated protein kinase 2;	P70336	1	3	3	2.2	1.791	0.223	0.000
Histone H2A type 1;	P22752	1	3	3	20.2	1.937	0.137	0.000
Protein-arginine deiminase type-2;	Q08642	1	12	12	18.9	2.057	0.722	0.001
Histone H4;	P62806	1	6	6	21.4	2.384	0.516	0.000
Absent in melanoma 1-like; Uncharacterized protein;	B7ZCC2	0.986	2	2	0.7	3.089	0.236	0.000
Homeobox protein Hox-D8;	P23463	0.934	2	2	4.3	3.981	3.678	0.004
Fumarylacetoacetate hydrolase domain-containing protein 2A;	Q3TC72	0.995	2	2	9.6	5.396	0.926	0.000
Structural maintenance of chromosomes protein 5;	Q8CG46	0.999	2	2	0.9	9.964	0.202	0.000
Histone H2B type 1-F/J/L;	P10853	0.999	2	2	15.9	9.964	0.202	0.000
Microtubule-actin cross-linking factor 1;	Q9QXZ0	0.994	2	2	0.5	9.964	0.202	0.000