Protein	Uniprot accession	ProteinProphet Prob. Score	Unique peptides	Total peptides	Sequence coverage [%]	Fold change ($\log_2$) of ASAPratio	Fold change standard deviation	ASAPratio p-value
Cathepsin L1;	P06797	1	2	2	9.9	-6,644*	-0.001	0.000
Ninein;	Q61043	0.968	2	2	1.1	-6.644	-6.644	0.000
Alpha-actinin-4;	P57780	1	6	6	17.5	0.791	0.146	0.368
Alpha-actinin-2;	Q9JI91	1	5	6	15.5	-4.644	-4.644	0.007
Myosin-4;	Q5SX39	1	24	30	31.5	-4.322	-4.322	0.010
Myosin-1;	Q5SX40	1	16	24	34	-5.644	-2.822	0.000
Myosin, heavy polypeptide 2, skeletal muscle, adult; Uncharacterized protein;	Q5SX41	1	3	3	23.4	-5.059	-1.686	0.000
Mast cell carboxypeptidase A;	P15089	1	5	6	15.8	-3.837	-2.193	0.002
Ig heavy chain V region MOPC 47A;	P01786	0.987	2	2	7.7	-3.644	-0.456	0.000
Chymase;	P21844	1	4	6	25.5	-3.474	-0.386	0.000
Creatine kinase S-type, mitochondrial;	Q6P8J7	1	16	23	31.5	-2.943	-0.906	0.002
Calsequestrin-1;	O09165	1	3	4	22.4	-2.556	-0.451	0.004
Ig kappa chain V-III region CBPC 101;	P01664	1	4	5	30.9	-2.556	-1.353	0.027
Myosin-11;	O08638	1	4	4	1.9	-2.474	-0.825	0.011
Cytochrome b-c1 complex subunit 2, mitochondrial;	Q9DB77	1	6	9	12.6	-2.474	-1.512	0.039
Myosin light chain 1/3, skeletal muscle isoform;	P05977	1	10	30	52.1	-2.474	-0.412	0.004
Reticulon-2;	O70622	1	4	5	7.2	-2.252	-0.536	0.012
Troponin C, skeletal muscle;	P20801	1	12	14	53.8	-2.252	-0.322	0.010
ADP/ATP translocase 1;	P48962	1	19	32	31.2	-2.252	-1.501	0.083
ADP/ATP translocase 2;	P51881	1	4	5	22.8	-0.136	-0.013	0.870
Cytochrome c oxidase subunit 6B1;	P56391	1	5	6	41.9	-2.184	-1.489	0.092
C-type lectin domain family 11 member A;	O88200	1	2	3	3.4	-2.12	-0.461	0.018
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4;	Q62425	1	3	3	26.8	-2.12	-0.737	0.029
Uncharacterized protein;	D3YXF5	1	10	10	30.5	-2.12	-0.645	0.025
Dystrophin;	P11531	1	3	3	3.3	-2	-0.48	0.027
Sarcalumenin;	Q7TQ48	1	10	10	10.7	-2	-0.8	0.045
Mitochondrial 10-formyltetrahydrofolate dehydrogenase;	Q8K009	1	8	8	11	-2	-0.72	0.041
Ig heavy chain V region 441;	P01806	1	4	4	31	-2	-1.36	0.125
Acyl-coenzyme A synthetase ACSM2, mitochondrial;	Q8K0L3	1	4	5	11.5	-2	-0.32	0.022
RIKEN cDNA 8030451F13, isoform CRA_c; Uncharacterized protein;	D3YU50	1	17	24	10.5	-2	-1.44	0.136
Myosin-binding protein C, fast-type;	Q5XKE0	1	22	22	17.3	-1.943	-0.822	0.065
Mast cell protease 4, isoform CRA_a; Uncharacterized protein;	Q3UN88	1	3	3	15.9	-1.943	-0.299	0.026
[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial;	Q9JK42	1	4	4	7.1	-1.889	-0.91	0.084
Uncharacterized protein;	E9Q8T1	1	4	4	2	-1.889	-0.84	0.073
ATP synthase subunit O, mitochondrial;	Q9DB20	1	11	11	41.8	-1.889	-1.749	0.225
Troponin T, fast skeletal muscle;	Q9QZ47	1	3	3	13	-1.889	-0.35	0.031
Ig gamma-1 chain C region secreted form;	P01868	1	9	22	23.5	-1.837	-0.459	0.045
Protein-glutamine gamma-glutamyltransferase 2;	P21981	1	5	5	13.1	-1.837	-0.394	0.042
6-phosphofructokinase, muscle type;	P47857	1	16	17	20.5	-1.837	-0.394	0.039
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial;	P45952	1	8	8	16.6	-1.837	-0.59	0.052
Glycine cleavage system H protein, mitochondrial;	Q91WK5	1	3	3	17.6	-1.837	-1.509	0.210
Keratin, type II cytoskeletal 5;	Q922U2	1	5	6	11	-1.837	-1.115	0.130
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial;	Q99LC3	1	5	5	15.2	-1.786	-0.801	0.087

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Fructose-1,6-bisphosphatase 1;	Q9QXD6	1	2	2	7.4	-1.786	-0.37	0.042
Decorin;	P28654	1	7	8	19.8	-1.737	-0.695	0.084
Ig gamma-2A chain C region, A allele;	P01863	1	5	7	18.5	-1.737	-0.521	0.061
Voltage-dependent anion-selective channel protein 1;	Q60932	1	18	25	49.3	-1.737	-1.1	0.155
Mitochondrial inner membrane protein;	Q8CAQ8	0.998	2	2	7	-1.737	-0.463	0.057
Ig kappa chain V-V region MOPC 173;	P01643	1	4	5	16.7	-1.69	-0.382	0.058
Uncharacterized protein;	E9Q6D8	1	5	5	9.2	-1.69	-0.491	0.072
Myomesin 2; Uncharacterized protein;	Q14BI5	1	27	33	14.8	-1.69	-0.218	0.052
Ig heavy chain V region AC38 205.12;	P06330	1	5	6	36.4	-1.69	-0.491	0.076
Vimentin;	P20152	1	8	8	22.5	-1.69	-1.09	0.180
Desmin;	P31001	1	5	5	10.2	-1.644	-0.308	0.063
Neurofilament medium polypeptide;	P08553	1	2	2	3.5	-1.396	-1.396	0.400
Collagen alpha-2(VI) chain;	Q02788	1	3	3	4.5	-1.644	-0.771	0.128
Synemin;	Q70IV5	1	4	6	6.7	-1.644	-0.719	0.121
ATP synthase subunit delta, mitochondrial;	Q9D3D9	1	2	4	13.7	-1.644	-0.462	0.076
Fatty acid-binding protein, liver;	P12710	1	10	13	48	-1.599	-0.872	0.161
Asporin;	Q99MQ4	1	7	7	24.4	-1.599	-0.436	0.080
Periplakin;	Q9R269	1	4	6	1.7	-1.599	-0.581	0.107
60S ribosomal protein L18a;	P62717	0.991	2	2	4	-1.599	-0.872	0.158
ATP synthase subunit beta, mitochondrial;	P56480	1	42	102	50.5	-1.515	-0.649	0.137
Coagulation factor XIII B chain;	Q07968	1	2	2	1.8	-1.515	-0.13	0.070
Fructose-bisphosphate aldolase B;	Q91Y97	1	12	14	28.6	-1.515	-0.519	0.120
Oxidation resistance protein 1;	Q4KMM3	1	11	13	12.4	-1.515	-1.039	0.242
Vitronectin;	P29788	0.913	2	2	2.9	-1.515	-0.216	0.075
Histone H4;	P62806	1	5	7	29.1	-1.474	-0.532	0.135
A-kinase anchor protein 12;	Q9WTQ5	1	31	43	17.4	-1.474	-0.942	0.239
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	P19783	1	3	5	17.8	-1.434	-0.039	0.082
Plasminogen;	P20918	1	6	12	5.7	-1.434	-0.233	0.100
ES1 protein homolog, mitochondrial;	Q9D172	1	6	7	30.1	-1.434	-1.008	0.273
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2;	Q9DBG6	1	3	3	2.3	-1.434	-0.349	0.113
Myomesin-3;	A2ABU4	1	2	2	1	-1.396	-0.294	0.112
40S ribosomal protein SA;	P14206	1	9	13	35.6	-1.396	-0.331	0.128
Collagen alpha-2(I) chain;	Q01149	1	24	47	16.4	-1.396	-0.404	0.136
Voltage-dependent anion-selective channel protein 3;	Q60931	1	4	5	17.7	-1.396	-0.147	0.104
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial;	Q91VD9	1	10	10	11.8	-1.396	-0.294	0.120
Voltage-dependent L-type calcium channel subunit beta-1;	Q8R3Z5	1	3	3	5.7	-1.396	-0.661	0.201
4-aminobutyrate aminotransferase, mitochondrial;	P61922	1	3	3	3.8	-1.396	-0.404	0.135
Retinal dehydrogenase 1;	P24549	1	27	33	26.7	-1.358	-0.279	0.123
Dynein light chain roadblock-type 1;	P62627	1	3	3	51	-1.358	-0.522	0.171
Keratin, type II cytoskeletal 1b;	Q6IFZ6	1	9	9	16.8	-1.358	-0.731	0.231
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial;	Q7TSQ8	1	6	6	6.4	-1.358	-0.836	0.264
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1;	Q8R429	1	51	111	32.6	-1.358	-0.522	0.176
Adenylosuccinate synthetase isozyme 1;	P28650	1	27	48	38.1	-1.322	-0.529	0.198

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Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial;	Q8K2B3	1	21	24	26.4	-1.322	-0.43	0.167
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6;	Q9CQZ5	1	2	2	13	-1.322	-0.463	0.177
Collagen triple helix repeat-containing protein 1;	Q9D1D6	1	2	4	6.1	-1.322	-0.099	0.112
Microfibril-associated glycoprotein 4;	Q9D1H9	1	5	5	9.7	-1.322	-0.364	0.153
Pigment epithelium-derived factor;	P97298	1	9	12	17.7	-1.322	-0.463	0.177
PDZ and LIM domain protein 7;	Q3TJD7	1	5	10	42.7	-1.322	-0.43	0.166
60S ribosomal protein L14;	Q9CR57	1	2	2	6	-1.286	-0.157	0.131
Collagen alpha-1(I) chain;	P11087	1	30	52	16.2	-1.286	-0.753	0.277
Cytochrome c oxidase subunit 2;	P00405	1	4	4	13.2	-1.252	-0.119	0.134
Nucleobindin-2;	P81117	1	3	3	4.8	-1.252	-0.149	0.144
Haptoglobin;	Q61646	1	4	5	12.7	-1.252	-0.179	0.148
Glycogen [starch] synthase, muscle;	Q9Z1E4	1	4	4	3.3	-1.252	-0.179	0.146
Transforming growth factor-beta-induced protein ig-h3;	P82198	1	8	8	11.1	-1.252	-0.268	0.164
Threonine synthase-like 2;	Q80W22	1	4	4	10.1	-1.252	-0.417	0.188
Cytochrome c oxidase subunit 5A, mitochondrial;	P12787	1	2	2	11	-1.218	-0.142	0.150
Thioredoxin-dependent peroxide reductase, mitochondrial;	P20108	1	11	20	21.4	-1.218	-0.17	0.160
Cystatin-C;	P21460	1	2	2	10.8	-1.218	-0.085	0.151
Tetranectin;	P43025	1	9	14	28.7	-1.218	-0.198	0.158
Acyl-CoA synthetase short-chain family member 3, mitochondrial;	Q14DH7	1	5	5	10.3	-1.218	-0.595	0.267
Neudesin;	Q9CQ45	1	5	5	22.8	-1.218	-1.048	0.416
Mitochondrial 2-oxoglutarate/malate carrier protein;	Q9CR62	1	2	2	14.5	-1.218	-0.085	0.151
Cytochrome b-c1 complex subunit 1, mitochondrial;	Q9CZ13	1	12	17	20.2	-1.218	-0.312	0.178
Glycogen phosphorylase, muscle form;	Q9WUB3	1	59	112	48.2	-1.218	-0.425	0.212
Glycogen phosphorylase, brain form;	Q8CI94	1	13	14	21.9	0.454	0.103	0.613
Nebulin; Uncharacterized protein;	A2AQA9	1	5	7	1.1	-1.218	-0.906	0.365
Histone H1.2;	P15864	0.998	2	2	5.3	-1.218	-0.113	0.154
60S acidic ribosomal protein P2;	P99027	1	2	2	28.7	-1.184	-0.215	0.177
Actin, aortic smooth muscle;	P62737	1	7	19	67.6	-1.184	-0.538	0.266
Actin, alpha skeletal muscle;	P68134	1	7	7	67.6	-1.322	-0.132	0.122
Long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P51174	1	21	26	28.1	-1.152	-0.486	0.267
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial;	Q9WUM5	1	11	14	22.5	-1.152	-0.64	0.319
Uncharacterized protein;	F6UFZ5	0.924	2	2	2	-1.152	-0.077	0.174
Leukemia inhibitory factor receptor;	P42703	1	9	11	7.8	-1.12	-0.317	0.224
Peroxisomal bifunctional enzyme;	Q9DBM2	1	3	3	6	-1.12	-0.122	0.186
ATP synthase subunit gamma, mitochondrial;	Q91VR2	1	11	17	35.7	-1.12	-0.755	0.389
Methylmalonyl-CoA mutase, mitochondrial;	P16332	1	3	3	4.9	-1.089	-0.996	0.490
Peptidyl-prolyl cis-trans isomerase B;	P24369	1	6	6	26.4	-1.089	-0.626	0.353
Heparin cofactor 2;	P49182	1	10	11	14.2	-1.089	-0.394	0.271
Myomesin-1;	Q62234	1	30	35	11.5	-1.089	-0.579	0.335
Acyl-coenzyme A thioesterase 13;	Q9CQR4	1	6	10	25	-1.089	-0.139	0.206
ATP synthase subunit d, mitochondrial;	Q9DCX2	1	2	2	8.7	-1.089	-0.162	0.201
Major urinary protein 2;	P11589	1	22	35	50	-1.089	-0.093	0.192
40S ribosomal protein S12;	Q6ZWZ6	1	9	16	45.5	-1.089	-0.209	0.209

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Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B;	Q3TDQ1	1	2	2	0.9	-1.089	-0.139	0.196
RAC-beta serine/threonine-protein kinase;	Q60823	0.998	2	2	5.5	-1.089	-0.348	0.245
Coproporphyrinogen-III oxidase, mitochondrial;	P36552	1	6	6	11.1	-1.059	-0.154	0.216
Myosin light chain kinase, smooth muscle;	Q6PDN3	1	23	33	8.3	-1.059	-0.485	0.319
Adenylate kinase isoenzyme 1;	Q9R0Y5	1	17	57	51	-1.059	-0.199	0.225
Carnitine O-acetyltransferase;	P47934	1	11	11	11.2	-1.059	-0.419	0.295
Enoyl-CoA hydratase, mitochondrial;	Q8BH95	1	5	7	18.3	-1.059	-0.088	0.208
Coatomer subunit delta;	Q5XJY5	1	9	9	13.3	-1.029	-0.672	0.410
Arginase-1;	Q61176	1	14	18	22.9	-1.029	-0.084	0.216
Complement component C8 gamma chain;	Q8VCG4	1	3	3	16.7	-1.029	-0.126	0.230
Synaptopodin-2;	Q91YE8	1	3	3	2.4	-1.029	-0.084	0.223
Uncharacterized protein;	E9Q2T3	1	5	5	1.5	-1.029	-0.336	0.280
Betaine--homocysteine S-methyltransferase 1;	O35490	1	5	5	15.5	-1.029	-0.189	0.232
Secernin-1;	Q9CZC8	1	7	7	16.2	-1.029	-0.42	0.311
Phosphoglycerate mutase 2;	O70250	1	26	219	45.1	-1	-0.08	0.233
Ig mu chain C region secreted form;	P01872	1	10	10	13	-1	-0.08	0.240
NAD(P)H dehydrogenase [quinone] 1;	Q64669	1	4	4	16.8	-1	-0.24	0.273
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial;	Q9CQA3	1	5	5	12.1	-1	-0.1	0.243
Fructose-bisphosphate aldolase A;	P05064	1	26	360	81	-1	-0.12	0.246
Fructose-bisphosphate aldolase;	Q9CPQ9	1	12	74	48.1	-1	-0.06	0.237
Fructose-bisphosphate aldolase C;	P05063	1	4	4	25.1	0.888	0.091	0.296
Hippocalcin-like protein 1;	P62748	1	5	5	23.8	-1	-0.5	0.365
Nascent polypeptide-associated complex subunit alpha, muscle-specific form;	P70670	1	38	46	16.2	-1	-0.76	0.474
Adseverin;	Q60604	1	5	5	6.3	-1	-0.62	0.416
Serpin B6;	Q60854	1	26	87	50	-1	-0.26	0.280
Phosphotriesterase-related protein;	Q60866	1	4	5	7.4	-1	-0.22	0.261
GDH/6PGL endoplasmic bifunctional protein;	Q8CFX1	1	5	5	6.3	-1	-1	0.549
EH domain-binding protein 1-like protein 1;	Q99MS7	1	3	3	2.3	-1	-0.28	0.284
Vacuolar protein-sorting-associated protein 36;	Q91XD6	1	2	2	6.2	-1	-0.22	0.261
40S ribosomal protein S21;	Q9CQR2	1	2	2	10.8	-1	-0.1	0.243
Transthyretin;	P07309	1	11	30	46.3	-0.971	-0.171	0.267
Carbonic anhydrase 3;	P16015	1	35	527	65.4	-0.971	-0.114	0.255
Fructose-1,6-bisphosphatase isozyme 2;	P70695	1	14	14	26.8	-0.971	-0.209	0.274
Secernin-3;	Q3TMH2	1	6	8	12.2	-0.971	-0.209	0.274
Apolipoprotein A-IV;	P06728	1	13	16	32.7	-0.943	-0.707	0.483
Prothrombin;	P19221	1	6	6	11.3	-0.943	-0.435	0.372
Apolipoprotein A-I;	Q00623	1	14	30	34.5	-0.943	-0.199	0.282
Beta-2-glycoprotein 1;	Q01339	1	7	7	19.7	-0.943	-0.073	0.265
Protein-arginine deiminase type-2;	Q08642	1	12	13	12.9	-0.943	-0.272	0.308
Sulfhydryl oxidase 1;	Q8BND5	1	5	5	11	-0.943	-0.109	0.272
Protein Z-dependent protease inhibitor;	Q8R121	1	3	3	5.8	-0.943	-0.145	0.276
Carbohydrate kinase domain-containing protein;	Q9CZ42	1	5	5	17.2	-0.943	-0.163	0.276
Serine protease inhibitor A3K;	P07759	1	38	568	47.8	-0.943	-0.199	0.282

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Serine protease inhibitor A3N;	Q91WP6	1	5	8	14.4	-0.136	-0.076	0.904
Uncharacterized protein;	D3Z450	1	5	7	12.9	0.526	0.077	0.538
Serine protease inhibitor A3G;	Q5I2A0	1	3	3	15.2	0.642	0.041	0.443
Four and a half LIM domains protein 1;	P97447	1	16	27	41.1	-0.943	-0.435	0.379
Lambda-crystallin homolog;	Q99KP3	1	10	10	24.8	-0.943	-0.29	0.312
Cardiomyopathy-associated protein 5;	Q70KF4	1	2	2	0.6	-0.943	-0.073	0.267
Ig kappa chain V19-17;	P01633	1	2	2	6	-0.943	-0.091	0.260
Methionine aminopeptidase 2;	O08663	1	4	4	8.6	-0.916	-0.363	0.362
Collagen alpha-1(III) chain;	P08121	1	10	10	5.8	-0.916	-0.104	0.279
Histone H2B type 1-F/J/L;	P10853	1	2	2	11.9	-0.916	-0.19	0.298
Lumican;	P51885	1	27	413	38.8	-0.916	-0.19	0.302
Complement component C8 alpha chain;	Q8K182	1	6	8	13.1	-0.916	-0.104	0.279
Kinesin-like protein KIF21B;	Q9QXL1	1	2	2	2.3	-0.916	-0.346	0.358
SH3 and PX domain-containing protein 2B;	A2AAY5	1	3	3	3.1	-0.916	-0.363	0.362
Creatine kinase M-type;	P07310	1	44	1204	58.3	-0.889	-0.066	0.283
Parvalbumin alpha;	P32848	1	8	63	32.7	-0.889	-0.082	0.295
Ribonuclease UK114;	P52760	1	4	4	26.7	-0.889	-0.132	0.302
Calcium-regulated heat stable protein 1;	Q9CR86	1	4	6	18.2	-0.889	-0.642	0.506
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial;	Q9Z2I9	1	20	27	28.9	-0.889	-0.346	0.381
Creatine kinase U-type, mitochondrial;	P30275	1	5	5	22.5	-0.889	-0.23	0.332
Dci protein; Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase); Uncharacterized protein;	Q8QZV3	1	15	25	29.8	-0.889	-0.329	0.361
ATP synthase subunit f, mitochondrial;	P56135	1	2	3	30.3	-0.889	-0.033	0.280
Ig kappa chain C region;	P01837	1	3	11	26.4	-0.862	-0.235	0.348
60S ribosomal protein L12;	P35979	1	3	3	9.1	-0.862	-0.141	0.319
Cytochrome c, somatic;	P62897	1	4	10	18.1	-0.862	-0.063	0.311
Creatine kinase B-type;	Q04447	1	31	57	41.2	-0.862	-0.078	0.313
Complement factor I;	Q61129	1	9	14	10.3	-0.862	-0.078	0.313
Zinc-alpha-2-glycoprotein;	Q64726	1	16	18	32.9	-0.862	-0.298	0.371
UTP--glucose-1-phosphate uridylyltransferase;	Q91ZJ5	1	38	69	41.3	-0.862	-0.141	0.316
Aconitate hydratase, mitochondrial;	Q99KI0	1	62	193	47.3	-0.862	-0.141	0.325
Cell adhesion molecule 3;	Q99N28	1	4	4	17.2	-0.862	-0.094	0.316
Lactoylglutathione lyase;	Q9CPU0	1	10	16	31	-0.862	-0.407	0.424
Dihydrolipoyl dehydrogenase, mitochondrial;	O08749	1	22	34	25.7	-0.862	-0.204	0.337
SPARC;	P07214	1	5	7	13.6	-0.862	-0.204	0.342
Glutamate dehydrogenase 1, mitochondrial;	P26443	1	9	12	11.8	-0.862	-0.125	0.320
Plasma protease C1 inhibitor;	P97290	1	11	14	21.6	-0.862	-0.313	0.376
Phosphoglucomutase-1;	Q9D0F9	1	47	93	50.4	-0.862	-0.125	0.314
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;	Q9R0E2	1	8	8	11	-0.862	-0.188	0.332
Apolipoprotein A-II;	P09813	0.999	2	3	9.8	-0.862	-0.172	0.336
Acid trehalase-like protein 1;	Q8BP56	1	5	5	6.1	-0.837	-0.389	0.434
Uncharacterized protein;	E9QA15	1	3	4	2.7	-0.837	-0.374	0.425
Acetyl-coenzyme A synthetase 2-like, mitochondrial;	Q99NB1	0.998	2	2	3.1	-0.837	-0.09	0.324

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Malate dehydrogenase, mitochondrial;	P08249	1	40	189	59.2	-0.811	-0.043	0.338
Fumarate hydratase, mitochondrial;	P97807	1	31	55	41.6	-0.811	-0.441	0.481
Protein AMBP;	Q07456	1	5	5	10	-0.811	-0.327	0.424
L-asparaginase;	Q8C0M9	1	11	15	27	-0.811	-0.157	0.362
Phosphoglycolate phosphatase;	Q8CHP8	1	10	12	21.2	-0.811	-0.583	0.540
Hemopexin;	Q91X72	1	35	176	36.7	-0.811	-0.071	0.341
Neurolysin, mitochondrial;	Q91YP2	1	10	11	12.6	-0.811	-0.726	0.595
MACRO domain-containing protein 1;	Q922B1	1	9	13	26	-0.811	-0.1	0.346
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial;	Q9D6J6	1	4	4	16.5	-0.811	-0.228	0.384
GMP reductase 1;	Q9DCZ1	1	2	2	7.6	-0.811	-0.057	0.329
Complement factor B;	P04186	1	14	19	11.6	-0.811	-0.285	0.411
Adenylosuccinate lyase;	P54822	1	7	9	10.3	-0.811	-0.114	0.348
Voltage-dependent anion-selective channel protein 2;	Q60930	1	9	9	33.9	-0.811	-0.213	0.378
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial;	Q91YT0	1	6	6	9.2	-0.811	-0.114	0.350
Ig kappa chain V-II region 26-10;	P01631	1	2	2	11.5	-0.811	-0.142	0.357
Complement factor D;	P03953	1	5	5	16.6	-0.786	-0.081	0.353
Complement component C9;	P06683	1	13	36	17.5	-0.786	-0.271	0.415
Alpha-2-HS-glycoprotein;	P29699	1	23	44	45.5	-0.786	-0.041	0.347
Scavenger receptor cysteine-rich domain-containing protein LOC284297 homolog;	Q8BV57	1	3	3	2.3	-0.786	-0.339	0.447
Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase;	Q9DBB8	1	6	9	13.5	-0.786	-0.081	0.352
Histidine-rich glycoprotein;	Q9ESB3	1	3	3	5.1	-0.786	-0.122	0.361
Mitogen-activated protein kinase 12;	O08911	1	4	4	12	-0.786	-0.108	0.357
Isocitrate dehydrogenase [NADP], mitochondrial;	P54071	1	34	61	40.7	-0.786	-0.23	0.400
Citrate lyase subunit beta-like protein, mitochondrial;	Q8R4N0	1	7	7	17.2	-0.786	-0.068	0.350
Uncharacterized protein;	D3YY36	1	22	31	22.7	-0.786	-0.339	0.451
Vesicle-associated membrane protein-associated protein B;	Q9QY76	0.998	2	2	10.7	-0.786	-0.108	0.359
Integrin beta-4;	A2A863	1	4	4	2.3	-0.761	-0.271	0.430
Cell surface glycoprotein MUC18;	Q8R2Y2	1	5	7	6.8	-0.761	-0.258	0.431
Peroxisomal trans-2-enoyl-CoA reductase;	Q99MZ7	1	2	2	34.1	-0.761	-0.103	0.378
Plexin domain-containing protein 2;	Q9DC11	1	3	3	6.1	-0.761	-0.155	0.395
Deoxyguanosine kinase, mitochondrial;	Q9QX60	1	2	2	9	-0.761	-0.064	0.360
cAMP-dependent protein kinase catalytic subunit alpha;	P05132	1	3	3	9.4	-0.761	-0.451	0.524
60S acidic ribosomal protein P0;	P14869	1	4	4	13.6	-0.761	-0.09	0.374
Bisphosphoglycerate mutase;	P15327	1	7	7	15.8	-0.761	-0.103	0.376
Purine nucleoside phosphorylase;	P23492	1	18	22	42.6	-0.761	-0.181	0.396
Prohibitin;	P67778	1	4	4	7.4	-0.761	-0.142	0.378
Histidine triad nucleotide-binding protein 1;	P70349	1	8	11	57.9	-0.761	-0.413	0.509
WW domain-binding protein 2;	P97765	1	3	3	9.2	-0.761	-0.077	0.371
Carboxymethylenebutenolidase homolog;	Q8R1G2	1	7	10	15.1	-0.761	-0.039	0.366
Mannose-6-phosphate isomerase;	Q924M7	1	5	5	9.9	-0.761	-0.039	0.357
Propionyl-CoA carboxylase beta chain, mitochondrial;	Q99MN9	1	26	36	37.7	-0.761	-0.31	0.461
Angiotensinogen;	P11859	1	3	3	11.7	-0.737	-0.098	0.397
Annexin A6;	P14824	1	64	101	50.8	-0.737	-0.283	0.457

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Ceruloplasmin;	Q61147	1	45	61	31.8	-0.737	-0.319	0.484
Mitochondrial carrier homolog 2;	Q791V5	1	2	2	6.9	-0.737	-0.098	0.395
UPF0586 protein C9orf41 homolog;	Q80UY1	1	2	2	2.8	-0.737	-0.074	0.390
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial;	Q8CHT0	1	7	8	6.9	-0.737	-0.074	0.390
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2;	Q99LD8	1	12	19	35.1	-0.737	-0.16	0.404
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial;	Q9D2G2	1	10	12	11	-0.737	-0.061	0.388
Elastase 1, pancreatic; Uncharacterized protein;	Q91X79	1	2	2	8.3	-0.737	-0.135	0.405
Angiotensin-converting enzyme;	P09470	1	17	22	9	-0.737	-0.16	0.416
Triosephosphate isomerase;	P17751	1	36	317	64.7	-0.737	-0.184	0.421
Murinoglobulin-1;	P28665	1	76	133	30.6	-0.737	-0.356	0.496
Adiponectin;	Q60994	1	8	11	18.6	-0.737	-0.135	0.408
Uncharacterized protein;	E9PV38	1	14	16	22.3	-0.737	-0.344	0.495
Uncharacterized protein;	F8VPN4	1	57	67	27.7	-0.737	-0.418	0.526
GTP-binding protein 1;	O08582	1	2	2	1.6	-0.737	-0.123	0.403
Mammalian ependymin-related protein 1;	Q99M71	1	2	2	9.4	-0.737	-0.332	0.484
Acylphosphatase-2;	P56375	1	8	17	37.1	-0.713	-0.21	0.449
Ras suppressor protein 1;	Q01730	1	2	5	6.5	-0.713	-0.094	0.406
Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial;	Q8BMS4	1	2	2	8.9	-0.713	-0.503	0.588
Histidine triad nucleotide-binding protein 2, mitochondrial;	Q9D0S9	1	4	4	21.5	-0.713	-0.07	0.400
2-oxoglutarate dehydrogenase, mitochondrial;	Q60597	1	41	60	32.2	-0.713	-0.187	0.439
Golgi reassembly-stacking protein 2;	Q99JX3	1	8	10	16.2	-0.713	-0.187	0.439
Scavenger mRNA-decapping enzyme DcpS;	Q9DAR7	1	13	13	36.4	-0.713	-0.351	0.514
Beta-hexosaminidase subunit alpha;	P29416	1	2	2	4.2	-0.713	-0.117	0.412
Alpha-amylase 1;	P00687	1	2	2	4.1	-0.69	-0.078	0.413
Epidermal growth factor receptor;	Q01279	1	13	15	17.7	-0.69	-0.078	0.413
Protein cordon-bleu;	Q5NBX1	1	2	2	5.5	-0.69	-0.1	0.427
Mimecan;	Q62000	1	7	9	19.8	-0.69	-0.111	0.429
Sulfite oxidase, mitochondrial;	Q8R086	1	5	6	15.4	-0.69	-0.345	0.528
Filamin-C;	Q8VHX6	1	30	32	12.3	-0.69	-0.39	0.556
Prohibitin-2;	O35129	1	3	8	7	-0.69	-0.078	0.413
Aspartate aminotransferase, cytoplasmic;	P05201	1	28	49	47.5	-0.69	-0.134	0.438
Prelamin-A/C;	P48678	1	7	11	11.7	-0.69	-0.401	0.556
Cytochrome b5;	P56395	1	8	9	41	-0.69	-0.056	0.407
Short-chain specific acyl-CoA dehydrogenase, mitochondrial;	Q07417	1	4	4	10.9	-0.69	-0.345	0.528
Echinoderm microtubule-associated protein-like 2;	Q7TNG5	1	12	12	21.1	-0.69	-0.089	0.426
GDP-fucose protein O-fucosyltransferase 1;	Q91ZW2	1	5	6	10.5	-0.69	-0.167	0.439
Serotransferrin;	Q921I1	1	29	218	56.5	-0.69	-0.1	0.427
Citrate synthase, mitochondrial;	Q9CZU6	1	18	25	23.9	-0.69	-0.056	0.417
Follistatin-related protein 1;	Q62356	0.998	2	2	2.6	-0.69	-0.045	0.406
Acylpyruvase FAHD1, mitochondrial;	Q8R0F8	0.998	2	2	13.2	-0.69	-0.111	0.429
Afamin;	O89020	1	14	16	17.3	-0.667	-0.191	0.472
60S acidic ribosomal protein P1;	P47955	1	2	2	14	-0.667	-0.116	0.445

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Interleukin-1 receptor accessory protein;	Q61730	1	4	4	5.6	-0.667	-0.074	0.432
CCA tRNA nucleotidyltransferase 1, mitochondrial;	Q8K1J6	1	3	3	8.5	-0.667	-0.328	0.542
Mitochondrial peptide methionine sulfoxide reductase;	Q9D6Y7	1	3	3	13.3	-0.667	-0.244	0.501
Glucose-6-phosphate isomerase;	P06745	1	38	111	36.7	-0.667	-0.222	0.487
Galectin-related protein A;	Q8VED9	1	3	3	26.2	-0.667	-0.275	0.514
ATP synthase subunit g, mitochondrial;	Q9CPQ8	1	5	8	27.2	-0.667	-0.032	0.425
Plectin;	Q9QXS1	1	37	39	5.9	-0.667	-0.455	0.605
Complement C4-B;	P01029	1	30	32	17.3	-0.644	-0.362	0.582
Serum albumin;	P07724	1	94	3304	67.8	-0.644	-0.161	0.484
Cofilin-2;	P45591	1	10	28	36.7	-0.644	-0.111	0.462
60S ribosomal protein L13;	P47963	1	2	2	5.8	-0.644	-0.101	0.460
Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	P70404	1	12	13	25.2	-0.644	-0.241	0.512
Retinol-binding protein 4;	Q00724	1	5	6	18.9	-0.644	-0.101	0.448
Myosin light chain kinase 2, skeletal/cardiac muscle;	Q8VCR8	1	16	22	16.2	-0.644	-0.201	0.501
Glycyl-tRNA synthetase;	Q9CZD3	1	19	22	19.9	-0.644	-0.272	0.533
Carboxypeptidase N subunit 2;	Q9DBB9	1	5	5	8.6	-0.644	-0.131	0.471
Thiopurine S-methyltransferase;	O55060	1	3	3	8.3	-0.644	-0.101	0.460
L-lactate dehydrogenase A chain;	P06151	1	28	172	43.4	-0.644	-0.091	0.456
L-lactate dehydrogenase B chain;	P16125	1	21	42	38.3	-0.059	-0.007	0.942
Protein-L-isoaspartate(D-aspartate) O-methyltransferase;	P23506	1	5	6	21.5	-0.644	-0.171	0.478
Collagen alpha-1(VI) chain;	Q04857	1	8	8	7	-0.644	-0.181	0.492
Amine oxidase [flavin-containing] B;	Q8BW75	1	3	3	5	-0.644	-0.091	0.447
Trifunctional enzyme subunit beta, mitochondrial;	Q99JY0	1	10	11	19.2	-0.644	-0.433	0.613
UPF0585 protein C16orf13 homolog;	Q9DCS2	1	5	5	15.7	-0.644	-0.312	0.549
Hydroxysteroid (17-beta) dehydrogenase 10; Uncharacterized protein;	A2AFQ2	1	5	5	26.1	-0.644	-0.252	0.526
Peptidyl-prolyl cis-trans isomerase FKBP7;	O54998	1	5	9	17.4	-0.621	-0.076	0.465
Ig kappa chain V-II region 7S34.1;	P01630	1	2	2	11.5	-0.621	-0.076	0.463
4-hydroxyphenylpyruvate dioxygenase;	P49429	1	2	2	20.1	-0.621	-0.172	0.501
Pyruvate kinase isozymes M1/M2;	P52480	1	69	507	63.3	-0.621	-0.201	0.516
Alpha-aminoadipic semialdehyde dehydrogenase;	Q9DBF1	1	18	21	24.3	-0.621	-0.105	0.469
Apoptosis-inducing factor 1, mitochondrial;	Q9Z0X1	1	2	2	3.5	-0.621	-0.048	0.457
Complement C3;	P01027	1	114	183	39.3	-0.599	-0.145	0.499
Serpin H1;	P19324	1	20	21	26.4	-0.599	-0.154	0.513
Glutathione S-transferase A4;	P24472	1	7	8	13.1	-0.599	-0.209	0.530
Glutathione reductase, mitochondrial;	P47791	1	12	14	25.1	-0.599	-0.1	0.493
Eukaryotic translation initiation factor 5A-1;	P63242	1	3	3	7.8	-0.599	-0.073	0.484
Coatomer subunit zeta-2;	Q9JHH9	1	2	2	9.3	-0.599	-0.136	0.494
Fetuin-B;	Q9QXC1	1	8	14	28.2	-0.599	-0.036	0.477
Alpha-1-antitrypsin 1-1;	P07758	1	12	58	42.5	-0.599	-0.027	0.466
Alpha-1-antitrypsin 1-2;	P22599	1	11	31	41.4	-0.667	-0.095	0.437
Alpha-1-antitrypsin 1-4;	Q00897	1	11	21	39.7	-0.889	-0.148	0.301
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial;	P50544	1	13	13	22.1	-0.599	-0.127	0.492
Glyoxylate reductase/hydroxypyruvate reductase;	Q91Z53	1	15	19	32	-0.599	-0.182	0.518

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Uncharacterized protein;	E9PVD2	1	11	11	11.5	-0.599	-0.336	0.605
Nucleoside diphosphate kinase;	E9PZF0	1	12	41	68.5	-0.599	-0.027	0.475
Aspartate aminotransferase, mitochondrial;	P05202	1	39	90	45.8	-0.578	-0.095	0.512
Superoxide dismutase [Mn], mitochondrial;	P09671	1	11	23	19.4	-0.578	-0.095	0.501
Heat shock protein beta-7;	P35385	1	3	3	19.5	-0.578	-0.112	0.506
182 kDa tankyrase-1-binding protein;	P58871	1	8	8	7.3	-0.578	-0.561	0.721
Extended synaptotagmin-1;	Q3U7R1	1	6	6	4.4	-0.578	-0.078	0.506
Sorbitol dehydrogenase;	Q64442	1	9	9	20.2	-0.578	-0.224	0.572
GDP-fucose protein O-fucosyltransferase 2;	Q8VHI3	1	3	3	5.8	-0.578	-0.06	0.501
Isochorismatase domain-containing protein 1;	Q91V64	1	12	20	29	-0.578	-0.147	0.532
Glutathione S-transferase Mu 5;	P48774	1	11	12	30.8	-0.578	-0.242	0.573
Protein DJ-1;	Q99LX0	1	13	24	66.3	-0.578	-0.19	0.552
Thymidylate kinase;	P97930	1	2	2	10.8	-0.578	-0.423	0.669
Synaptic vesicle membrane protein VAT-1 homolog-like;	Q80TB8	0.96	2	2	5	-0.578	-0.138	0.527
Myc box-dependent-interacting protein 1;	O08539	1	6	8	14	-0.556	-0.204	0.570
Heterogeneous nuclear ribonucleoprotein L;	Q8R081	1	7	7	10.9	-0.556	-0.213	0.580
Isovaleryl-CoA dehydrogenase, mitochondrial;	Q9JHI5	1	10	12	18.2	-0.556	-0.09	0.522
Ribonuclease 4;	Q9JJH1	1	6	8	16.2	-0.556	-0.098	0.524
Band 4.1-like protein 3;	Q9WV92	1	10	12	12.4	-0.556	-0.082	0.518
Uncharacterized protein;	D3Z0Y2	1	30	65	72.5	-0.556	-0.065	0.513
Delta-aminolevulinic acid dehydratase;	P10518	1	15	17	35.5	-0.535	-0.039	0.519
Plasma kallikrein;	P26262	1	7	7	13.3	-0.535	-0.078	0.537
Antithrombin-III;	P32261	1	24	49	35.1	-0.535	-0.14	0.552
Mannose-binding protein C;	P41317	1	3	3	9.8	-0.535	-0.194	0.591
Transcription elongation factor B polypeptide 2;	P62869	1	4	4	35.6	-0.535	-0.163	0.576
Annexin A7;	Q07076	1	21	32	28.3	-0.535	-0.271	0.631
Kynurenine--oxoglutarate transaminase 3;	Q71RI9	1	3	3	5.3	-0.535	-0.256	0.616
Heat shock protein beta-2;	Q99PR8	1	5	7	20.9	-0.535	-0.217	0.604
Spectrin alpha chain, brain;	P16546	1	40	42	14.2	-0.535	-0.419	0.706
Selenium-binding protein 1;	P17563	1	35	48	51.9	-0.535	-0.155	0.568
Quinone oxidoreductase;	P47199	1	6	6	16.9	-0.535	-0.054	0.522
Protein transport protein Sec23A;	Q01405	1	11	11	14.1	-0.535	-0.163	0.573
MCG142264, isoform CRA_a; Uncharacterized protein;	D3Z494	1	7	10	20.5	-0.535	-0.124	0.557
Aldose reductase-related protein 2;	P45377	1	5	5	21.8	0.963	0.267	0.295
Alpha-1-syntrophin;	Q61234	1	3	5	5.2	-0.535	-0.039	0.518
Extracellular superoxide dismutase [Cu-Zn];	O09164	1	10	11	24.7	-0.515	-0.022	0.537
Gamma-synuclein;	Q9Z0F7	1	9	12	54.5	-0.515	-0.206	0.610
Kininogen-1;	O08677	1	31	60	40.4	-0.515	-0.044	0.541
Kng2 protein; LMW kininogen-II; MCG128256, isoform CRA_e; Uncharacterized protein;	Q6S9I0	1	2	2	12.5	-0.556	-0.123	0.534
Annexin A8;	O35640	1	30	57	53.2	-0.515	-0.11	0.565
Rab GDP dissociation inhibitor alpha;	P50396	1	18	19	29.8	-0.515	-0.184	0.597
Alcohol dehydrogenase [NADP+];	Q9JII6	1	18	31	37.2	-0.515	-0.206	0.610

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Legumain;	O89017	1	4	4	3.9	-0.494	-0.077	0.569
Inter-alpha-trypsin inhibitor heavy chain H3;	Q61704	1	11	16	14.7	-0.494	-0.118	0.577
Spectrin beta chain, brain 1;	Q62261	1	8	8	3.3	-0.494	-0.097	0.568
UDP-N-acetylhexosamine pyrophosphorylase;	Q91YN5	1	13	16	17.8	-0.494	-0.181	0.618
Beta-lactamase-like protein 2;	Q99KR3	1	4	5	13.2	-0.494	-0.139	0.595
Protein phosphatase 1 regulatory subunit 3A;	Q99MR9	1	5	5	3.2	-0.494	-0.028	0.548
Copper homeostasis protein cutC homolog;	Q9D8X1	1	6	6	20.1	-0.494	-0.035	0.559
Hexokinase-2;	O08528	1	34	39	35.2	-0.494	-0.23	0.645
Hexokinase-1;	P17710	1	25	28	24.9	0.333	0.143	0.752
Hexokinase-3;	Q3TRM8	1	2	2	5.8	-0.168	-0.053	0.865
Annexin A2;	P07356	1	41	126	66.4	-0.494	-0.056	0.553
Annexin A11;	P97384	1	26	33	27.6	-0.494	-0.042	0.560
Xanthine dehydrogenase/oxidase;	Q00519	1	46	61	23.4	-0.494	-0.139	0.597
NEDD8-activating enzyme E1 regulatory subunit;	Q8VBW6	1	7	7	6.9	-0.494	-0.264	0.667
3-mercaptopyruvate sulfurtransferase;	Q99J99	1	13	16	34.7	-0.494	-0.077	0.572
Sodium/potassium-transporting ATPase subunit beta-1;	P14094	1	3	4	8.2	-0.474	-0.033	0.579
Biglycan;	P28653	1	4	5	9.5	-0.474	-0.296	0.697
Heat shock protein beta-6;	Q5EBG6	1	9	17	29	-0.474	-0.092	0.596
Ketosamine-3-kinase;	Q8K274	1	4	4	9.1	-0.474	-0.079	0.592
Arsenite methyltransferase;	Q91WU5	1	6	6	13.8	-0.474	-0.125	0.611
Carboxypeptidase N catalytic chain;	Q9JJN5	1	2	2	3.3	-0.474	-0.086	0.595
Kelch repeat and BTB (POZ) domain containing 10; MCG12931; Uncharacterized protein;	A2AUC9	1	5	6	6.3	-0.474	-0.165	0.622
Tetratricopeptide repeat protein 38;	A3KMP2	1	16	17	25.8	-0.474	-0.092	0.596
Myelin protein P0;	P27573	1	3	5	8.9	-0.474	-0.039	0.580
Aldose reductase;	P45376	1	24	51	48.1	-0.474	-0.046	0.572
Glutathione peroxidase 3;	P46412	1	6	9	18.1	-0.474	-0.046	0.572
Proliferation-associated protein 2G4;	P50580	1	12	12	18	-0.474	-0.072	0.579
Thiosulfate sulfurtransferase;	P52196	1	8	9	22.2	-0.474	-0.072	0.579
Serine/threonine-protein phosphatase 2A activator;	P58389	1	11	16	29.7	-0.474	-0.217	0.660
Peptidyl-prolyl cis-trans isomerase FKBP10;	Q61576	1	15	21	15.1	-0.474	-0.178	0.640
Alpha-2-macroglobulin;	Q61838	1	84	166	37.7	-0.474	-0.072	0.589
C-type mannose receptor 2;	Q64449	1	9	12	5.4	-0.474	-0.072	0.590
Interferon-activable protein 205-A;	Q8CGE8	1	5	5	8.9	-0.474	-0.27	0.690
Inositol (Myo)-1(Or 4)-monophosphatase 1; Inositol (Myo)-1(Or 4)-monophosphatase 1, isoform CRA_a; Myo-inositol monophosphatase 1; Uncharacterized protein;	Q924B0	1	9	13	27.1	-0.474	-0.132	0.615
Protein S100-A6;	P14069	0.994	3	3	16.9	-0.474	-0.033	0.580
Lysozyme C-2;	P08905	1	2	2	27	-0.454	-0.118	0.620
Acylphosphatase-1;	P56376	1	8	10	39.4	-0.454	-0.112	0.618
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1;	Q91YQ5	1	2	3	5.6	-0.454	-0.162	0.643
Uncharacterized protein;	E9Q8E3	1	2	2	2.1	-0.454	-0.075	0.601
Sec24 related gene family, member D (S. cerevisiae); Uncharacterized protein;	Q6NXL1	1	8	8	8.5	-0.454	-0.155	0.641

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Complement factor H;	P06909	1	3	3	2.9	-0.454	-0.05	0.594
Carbonyl reductase [NADPH] 2;	P08074	1	12	17	29.9	-0.454	-0.05	0.593
ATP synthase subunit alpha, mitochondrial;	Q03265	1	32	52	34.9	-0.454	-0.056	0.595
Fumarylacetoacetate hydrolase domain-containing protein 2A;	Q3TC72	1	2	2	10.5	-0.454	-0.05	0.593
Uncharacterized protein;	E9Q0S6	0.999	4	4	3.6	-0.454	-0.093	0.609
Leukotriene A-4 hydrolase;	P24527	1	32	44	32.1	-0.434	-0.293	0.737
Splicing factor U2AF 65 kDa subunit;	P26369	1	4	4	12.7	-0.434	-0.123	0.646
Cellular retinoic acid-binding protein 1;	P62965	1	6	6	36.5	-0.434	-0.152	0.654
Tripartite motif-containing protein 72;	Q1XH17	1	9	9	20.5	-0.434	-0.199	0.685
Synaptic vesicle membrane protein VAT-1 homolog;	Q62465	1	22	36	33.5	-0.434	-0.1	0.624
Choline dehydrogenase, mitochondrial;	Q8BJ64	1	2	2	8.6	-0.434	-0.117	0.631
Phosphopantothenate--cysteine ligase;	Q8VDG5	1	5	5	9.6	-0.434	-0.029	0.610
Probable proline racemase;	Q9CXA2	1	5	6	14.4	-0.434	-0.229	0.704
Inositol-3-phosphate synthase 1;	Q9JHU9	1	5	5	10.6	-0.434	-0.129	0.639
Thioredoxin reductase 1, cytoplasmic;	Q9JMH6	1	9	12	20.6	-0.434	-0.1	0.633
Maleylacetoacetate isomerase;	Q9WVL0	1	15	15	41.2	-0.434	-0.152	0.654
Plasminogen activator inhibitor 2, macrophage;	P12388	1	9	11	15.7	-0.434	-0.065	0.618
Malate dehydrogenase, cytoplasmic;	P14152	1	25	65	31.4	-0.434	-0.029	0.610
Ras-related protein Rab-2A;	P53994	1	9	11	32.1	-0.434	-0.065	0.618
Myosin light polypeptide 6;	Q60605	1	10	20	32.5	-0.434	-0.164	0.666
Valacyclovir hydrolase;	Q8R164	1	7	8	19.6	-0.434	-0.053	0.605
Hydroxyacylglutathione hydrolase, mitochondrial;	Q99KB8	1	8	8	27	-0.434	-0.1	0.624
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	12	15	35.1	-0.434	-0.076	0.624
cAMP-dependent protein kinase type II-beta regulatory subunit;	P31324	1	6	6	18.5	0.506	0.107	0.571
Neural cell adhesion molecule L1-like protein;	P70232	1	2	2	1.6	-0.434	-0.387	0.774
Caspase-6;	O08738	1	3	3	11.2	-0.415	-0.172	0.690
Ferritin heavy chain;	P09528	1	8	11	28.6	-0.415	-0.039	0.622
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial;	P35486	1	19	27	29.5	-0.415	-0.083	0.638
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;	Q64191	1	2	2	12.4	-0.415	-0.127	0.661
WW domain-binding protein 11;	Q923D5	1	4	4	4.2	-0.415	-0.172	0.685
Protein canopy homolog 2;	Q9QXT0	1	7	8	29.1	-0.415	-0.022	0.619
Phosphatidylethanolamine-binding protein 1;	P70296	1	12	24	56.7	-0.415	-0.028	0.620
Abhydrolase domain-containing protein 14B;	Q8VCR7	1	8	8	31.9	-0.415	-0.111	0.649
Annexin A3;	O35639	1	17	22	39	-0.396	-0.047	0.635
Protein PRRC1;	Q3UPH1	1	2	2	2.7	-0.396	-0.031	0.642
Mannose-1-phosphate guanyltransferase beta;	Q8BTZ7	1	9	11	24.4	-0.396	-0.068	0.651
Poly(ADP-ribose) glycohydrolase ARH3;	Q8CG72	1	6	7	16.8	-0.396	-0.172	0.698
Metalloreductase STEAP3;	Q8CI59	1	4	4	7.9	-0.396	-0.078	0.647
Electron transfer flavoprotein subunit beta;	Q9DCW4	1	21	39	48.6	-0.396	-0.042	0.634
Torsin-1B;	Q9ER41	1	4	4	4.2	-0.396	-0.047	0.645
Dysferlin;	Q9ESD7	1	2	2	0.5	-0.396	-0.052	0.647

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N-acetylneuraminic acid synthase (Sialic acid synthase); Uncharacterized protein;	Q99J77	1	8	8	34.5	-0.396	-0.198	0.723
Procollagen C-endopeptidase enhancer 1;	Q61398	1	10	10	33.1	-0.396	-0.13	0.683
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	Q8QZS1	1	17	22	27.8	-0.396	-0.13	0.684
NAD-dependent deacetylase sirtuin-2;	Q8VDQ8	1	4	5	12.1	-0.396	-0.068	0.655
Prolow-density lipoprotein receptor-related protein 1;	Q91ZX7	1	40	47	8.2	-0.396	-0.099	0.666
Trans-2-enoyl-CoA reductase, mitochondrial;	Q9DCS3	1	5	5	11.3	-0.396	-0.193	0.710
Actin-related protein 2/3 complex subunit 1B;	Q9WV32	1	9	12	23.9	-0.396	-0.172	0.698
Actin-related protein 2/3 complex subunit 1A;	Q9R0Q6	1	6	6	18.4	-1.218	-0.198	0.158
Ectonucleoside triphosphate diphosphohydrolase 2;	O55026	1	10	10	14.1	-0.377	-0.113	0.694
COP9 signalosome complex subunit 6;	O88545	1	4	4	10.4	-0.377	-0.264	0.775
Laminin subunit gamma-1;	P02468	1	8	8	4.9	-0.377	-0.083	0.680
Nucleolin;	P09405	1	5	5	6.2	-0.377	-0.078	0.669
Ornithine aminotransferase, mitochondrial;	P29758	1	20	29	26.4	-0.377	-0.118	0.688
Indolethylamine N-methyltransferase;	P40936	1	8	9	29.2	-0.377	-0.137	0.709
Annexin A5;	P48036	1	32	95	56.4	-0.377	-0.073	0.665
Fibulin-1;	Q08879	1	11	11	16.3	-0.377	-0.108	0.683
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1;	Q3TW96	1	16	19	24.5	-0.377	-0.186	0.736
Electron transfer flavoprotein subunit alpha, mitochondrial;	Q99LC5	1	35	66	48	-0.377	-0.054	0.658
Ribosome-recycling factor, mitochondrial;	Q9D6S7	1	2	2	6.5	-0.377	-0.054	0.658
Omega-amidase NIT2;	Q9JHW2	1	22	27	56.2	-0.377	-0.098	0.677
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1;	Q9QUR7	1	2	2	20.6	-0.377	-0.049	0.655
Glutathione S-transferase P 1;	P19157	1	13	27	48.3	-0.377	-0.059	0.660
Fumarylacetoacetase;	P35505	1	12	13	26.5	-0.377	-0.113	0.687
ADP-ribose pyrophosphatase, mitochondrial;	Q8BVU5	1	5	5	8	-0.377	-0.02	0.660
D-2-hydroxyglutarate dehydrogenase, mitochondrial;	Q8CIM3	1	2	2	5.8	-0.377	-0.108	0.683
1,5-anhydro-D-fructose reductase;	Q9DCT1	0.993	2	2	5.7	-0.377	-0.054	0.668
Microfibrillar-associated protein 2;	P55002	1	2	2	5.5	-0.358	-0.05	0.677
Protein dpy-30 homolog;	Q99LT0	1	2	2	16.2	-0.358	-0.055	0.679
Prefoldin subunit 2;	O70591	1	5	7	22.7	-0.358	-0.087	0.693
Hepatoma-derived growth factor;	P51859	1	7	7	21.5	-0.358	-0.17	0.741
Echinoderm microtubule-associated protein-like 1;	Q05BC3	1	5	5	4.1	-0.358	-0.046	0.677
Guanine nucleotide-binding protein subunit alpha-11;	P21278	1	2	2	2.5	-0.358	-0.046	0.677
Proteasome subunit beta type-1;	O09061	1	18	21	42.5	-0.34	-0.228	0.787
Guanidinoacetate N-methyltransferase;	O35969	1	2	2	8.9	-0.34	-0.034	0.684
Periaxin;	O55103	1	13	14	11.1	-0.34	-0.039	0.695
Adenosine kinase;	P55264	1	16	25	27.1	-0.34	-0.099	0.722
Haloacid dehalogenase-like hydrolase domain-containing protein 2;	Q3UGR5	1	6	12	16.2	-0.34	-0.112	0.719
Acetyl-CoA acetyltransferase, mitochondrial;	Q8QZT1	1	13	20	24.3	-0.34	-0.077	0.710
Glutathione peroxidase 7;	Q99LJ6	1	2	2	9.1	-0.34	-0.043	0.686
Plasma glutamate carboxypeptidase;	Q9WVJ3	1	11	12	19.1	-0.34	-0.065	0.704
Serine-threonine kinase receptor-associated protein;	Q9Z1Z2	1	15	23	40.9	-0.34	-0.185	0.765
Glutathione S-transferase Mu 1;	P10649	1	12	19	49.5	-0.34	-0.138	0.735
Glutathione S-transferase Mu 2;	P15626	1	11	12	37.2	-0.152	-0.017	0.859

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Ras-related protein Rab-5B;	P61021	1	2	2	16.7	-0.168	-0.019	0.841
Ras-related protein Rab-5A;	Q9CQD1	1	2	2	16.7	0.367	0.051	0.673
Xaa-Pro dipeptidase;	Q11136	1	14	15	19.9	-0.34	-0.112	0.729
Actin-related protein 2/3 complex subunit 2;	Q9CVB6	1	15	21	29.3	-0.34	-0.142	0.745
Dynein light chain 2, cytoplasmic;	Q9D0M5	1	4	4	20.2	-0.34	-0.09	0.717
3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial;	Q9D404	1	5	5	15.7	-0.34	-0.034	0.683
1,4-alpha-glucan-branching enzyme;	Q9D6Y9	1	9	11	11.4	-0.34	-0.142	0.743
Proline synthase co-transcribed bacterial homolog protein;	Q9Z2Y8	1	6	8	19	-0.34	-0.065	0.704
Serine hydrolase-like protein;	Q9EPB5	1	3	3	6.4	-0.34	-0.069	0.697
UDP-glucose:glycoprotein glucosyltransferase 1;	Q6P5E4	1	10	10	5	-0.322	-0.125	0.748
UPF0556 protein C19orf10 homolog;	Q9CPT4	1	4	4	12.7	-0.322	-0.072	0.718
Galectin-3-binding protein;	Q07797	1	2	2	4.5	-0.322	-0.254	0.819
Peroxiredoxin-2;	Q61171	1	16	67	47.5	-0.322	-0.04	0.699
Secernin-2;	Q8VCA8	1	7	7	16.2	-0.322	-0.036	0.700
Inorganic pyrophosphatase 2, mitochondrial;	Q91VM9	1	5	5	17.6	-0.322	-0.105	0.738
PDZ and LIM domain protein 3;	O70209	1	6	7	22.2	-0.304	-0.026	0.722
Carbonic anhydrase 2;	P00920	1	9	9	30	-0.304	-0.105	0.759
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical];	P56380	1	6	8	21.8	-0.304	-0.049	0.719
EH domain-containing protein 2;	Q8BH64	1	5	5	11.1	-0.304	-0.113	0.753
Aminoacylase-1;	Q99JW2	1	8	10	12	-0.304	-0.023	0.721
Low molecular weight phosphotyrosine protein phosphatase;	Q9D358	1	9	11	31.6	-0.304	-0.03	0.723
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Q9D6R2	1	16	26	32	-0.304	-0.094	0.752
Mitochondrial-processing peptidase subunit alpha;	Q9DC61	1	5	5	9.1	-0.304	-0.161	0.791
Galactokinase;	Q9R0N0	1	8	9	14.1	-0.304	-0.143	0.772
Cullin-1;	Q9WTX6	1	3	3	7.3	-0.304	-0.06	0.725
Probable methylthioribulose-1-phosphate dehydratase;	Q9WVQ5	1	4	4	20.7	-0.304	-0.135	0.768
Eukaryotic translation initiation factor 3 subunit G;	Q9Z1D1	1	4	4	11.9	-0.304	-0.038	0.725
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial;	Q9Z2I8	1	10	10	26.1	-0.304	-0.161	0.792
UDP-glucose 6-dehydrogenase;	O70475	1	26	31	43.4	-0.304	-0.038	0.715
Keratin, type I cytoskeletal 17;	Q9QWL7	1	8	9	21.2	1	0.195	0.257
Keratin 15; Keratin 15, isoform CRA_a; Uncharacterized protein;	B1AQ77	1	5	7	18.4	-3.322	-2.99	0.037
Keratin, type I cytoskeletal 10;	P02535	1	3	3	7.4	-1	-0.24	0.273
Cytosolic non-specific dipeptidase;	Q9D1A2	1	28	40	43.8	-0.304	-0.06	0.735
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial;	Q9EQ20	1	27	39	35.1	-0.304	-0.079	0.744
Actin-like protein 6A;	Q9Z2N8	1	4	5	12.4	-0.304	-0.098	0.750
Uncharacterized protein;	E9PYJ9	1	25	39	27.4	-0.304	-0.161	0.791
Glyceraldehyde-3-phosphate dehydrogenase;	E9QAC7	1	18	112	59.2	-0.304	-0.049	0.719
Glyceraldehyde-3-phosphate dehydrogenase;	E9PYX4	1	5	55	32.8	-0.837	-0.523	0.498
Uncharacterized protein;	Q3ULW8	1	7	7	10.8	-0.304	-0.113	0.763
Catechol-O-methyltransferase 1; Uncharacterized protein;	Q91XH4	1	4	4	18.5	-0.304	-0.053	0.731
Platelet-activating factor acetylhydrolase IB subunit gamma;	Q61205	1	2	3	6.3	-0.304	-0.03	0.713
3-hydroxyanthranilate 3,4-dioxygenase;	Q78JT3	0.999	2	2	12.2	-0.304	-0.068	0.737
Integrin alpha-5;	P11688	1	2	2	1	-0.286	-0.031	0.734

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Peptidyl-prolyl cis-trans isomerase C;	P30412	1	9	15	26.4	-0.286	-0.028	0.733
Succinate-semialdehyde dehydrogenase, mitochondrial;	Q8BWF0	1	3	3	8.2	-0.286	-0.066	0.748
Probable fructose-2,6-bisphosphatase TIGAR;	Q8BZA9	1	4	4	15.6	-0.286	-0.133	0.788
Tubulin polymerization-promoting protein family member 3;	Q9CRB6	1	3	6	11.9	-0.286	-0.021	0.731
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial;	Q9D051	1	22	43	34.5	-0.286	-0.035	0.735
Peroxisomal acyl-coenzyme A oxidase 1;	Q9R0H0	1	21	23	25.3	-0.286	-0.105	0.771
Phosphoglycerate kinase 1;	P09411	1	41	143	54.4	-0.286	-0.07	0.749
Putative adenosylhomocysteinase 2;	Q80SW1	1	6	8	9.4	-0.286	-0.056	0.744
Lysophosphatidic acid phosphatase type 6;	Q8BP40	1	9	10	20.6	-0.286	-0.153	0.800
UPF0160 protein MYG1, mitochondrial;	Q9JK81	1	8	8	22.4	-0.286	-0.157	0.802
Spliceosome RNA helicase Ddx39b;	Q9Z1N5	1	12	17	29.7	-0.286	-0.15	0.799
ATP-dependent RNA helicase DDX39A;	Q8VDW0	1	2	2	15.5	-0.396	-0.026	0.630
TOM1-like protein 2;	Q5SRX1	0.998	2	2	3.5	-0.286	-0.01	0.730
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform;	P18826	1	4	4	3.4	-0.269	-0.139	0.809
Dipeptidyl peptidase 4;	P28843	1	12	12	11.8	-0.269	-0.123	0.803
Laminin subunit alpha-4;	P97927	1	3	4	2.4	-0.269	-0.071	0.763
Protein NDRG1;	Q62433	1	2	2	3.6	-0.269	-0.036	0.746
Myoferlin;	Q69ZN7	1	7	7	3	-0.269	-0.091	0.775
Aflatoxin B1 aldehyde reductase member 2;	Q8CG76	1	14	18	24.3	-0.269	-0.036	0.746
PCTP-like protein;	Q9JMD3	1	3	3	10	-0.269	-0.107	0.784
AP-1 complex subunit beta-1;	O35643	1	10	13	11.6	-0.269	-0.104	0.791
Adenosylhomocysteinase;	P50247	1	24	37	39.4	-0.269	-0.058	0.756
Protein phosphatase 1 regulatory subunit 7;	Q3UM45	1	13	14	28.5	-0.269	-0.068	0.771
Sepiapterin reductase;	Q64105	1	19	26	40.6	-0.269	-0.032	0.754
Coagulation factor XIII A chain;	Q8BH61	1	7	8	6.1	-0.269	-0.084	0.770
Dihydropteridine reductase;	Q8BVI4	1	17	21	68.8	-0.269	-0.049	0.750
Carboxylesterase 3;	Q8VCT4	1	22	31	34.2	-0.269	-0.136	0.802
Liver carboxylesterase N;	P23953	1	21	51	20.9	-0.494	-0.035	0.548
Uncharacterized protein;	D3Z5G7	1	13	36	18.2	-1.252	-1.103	0.413
Expressed sequence AU018778; Uncharacterized protein;	Q91WU0	1	4	4	6.8	-2.12	-2.12	0.198
Calcium/calmodulin-dependent protein kinase type 1;	Q91YS8	1	7	7	14.4	-0.269	-0.068	0.762
Lysosome-associated membrane glycoprotein 1;	P11438	1	7	11	8.4	-0.252	-0.063	0.778
Fibulin-2;	P37889	1	3	3	3.7	-0.252	-0.096	0.805
Platelet-activating factor acetylhydrolase IB subunit alpha;	P63005	1	6	9	11.5	-0.252	-0.051	0.782
N-acetylglucosamine-6-sulfatase;	Q8BFR4	1	10	13	10.5	-0.252	-0.009	0.760
Presequence protease, mitochondrial;	Q8K411	1	9	10	9.7	-0.252	-0.024	0.772
Apolipoprotein A-I-binding protein;	Q8K4Z3	1	9	11	22	-0.252	-0.009	0.770
SPRY domain-containing protein 4;	Q91WK1	1	7	7	29.5	-0.252	-0.111	0.808
Iron-sulfur cluster assembly 2 homolog, mitochondrial;	Q9DCB8	1	7	7	40.3	-0.252	-0.027	0.773
Protein NDRG2;	Q9QYG0	1	18	25	52.8	-0.252	-0.033	0.775
S-formylglutathione hydrolase;	Q9R0P3	1	16	23	40.4	-0.252	-0.06	0.777
Glycogen synthase kinase-3 beta;	Q9WV60	1	5	6	15	-0.252	-0.054	0.784

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
Isocitrate dehydrogenase 3 (NAD+) beta; Tumor-related protein; Uncharacterized protein;	Q91VA7	1	11	11	24.2	-0.252	-0.096	0.805
Branched-chain-amino-acid aminotransferase, mitochondrial;	O35855	1	12	14	19.8	-0.252	-0.084	0.800
U6 snRNA-associated Sm-like protein LSm2;	O35900	1	5	5	47.4	-0.252	-0.03	0.774
Spermine synthase;	P97355	1	7	7	12.8	-0.252	-0.09	0.802
Annexin A4;	P97429	1	32	49	50.5	-0.252	-0.036	0.776
Peroxiredoxin-5, mitochondrial;	P99029	1	20	35	44.8	-0.252	-0.018	0.761
Ubiquitin thioesterase OTUB1;	Q7TQI3	1	14	18	31.1	-0.252	-0.141	0.825
Alpha-mannosidase 2C1;	Q91W89	1	5	5	8.9	-0.252	-0.12	0.814
Quinone oxidoreductase-like protein 1;	Q921W4	1	3	3	9.3	-0.252	-0.045	0.769
Flavin reductase (NADPH);	Q923D2	1	10	23	42.7	-0.252	-0.045	0.770
Ras-related protein Rab-34;	Q64008	0.999	2	2	5.5	-0.252	-0.03	0.764
Cytohesin-3;	O08967	0.998	2	2	1.8	-0.252	-0.033	0.766
Interleukin enhancer-binding factor 3;	Q9Z1X4	0.959	2	2	5.5	-0.252	-0.198	0.861
Histamine N-methyltransferase;	Q91VF2	0.952	2	2	14.2	-0.252	-0.036	0.766
D-dopachrome decarboxylase;	O35215	1	12	17	51.7	-0.234	-0.022	0.782
Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta;	O55057	1	3	3	20.7	-0.234	-0.03	0.783
Vacuolar protein sorting-associated protein 26A;	P40336	1	3	5	11.2	-0.234	-0.022	0.782
Small nuclear ribonucleoprotein Sm D3;	P62320	1	2	2	7.9	-0.234	-0.028	0.784
Scavenger receptor cysteine-rich type 1 protein M130;	Q2VLH6	1	5	5	3.6	-0.234	-0.036	0.786
Peptidyl-prolyl cis-trans isomerase FKBP3;	Q62446	1	5	9	14.7	-0.234	-0.017	0.781
NADP-dependent malic enzyme;	P06801	1	28	36	35	-0.234	-0.088	0.813
Arylsulfatase A;	P50428	1	3	3	8.7	-0.234	-0.03	0.780
Propionyl-CoA carboxylase alpha chain, mitochondrial;	Q91ZA3	1	9	9	11.3	-0.234	-0.135	0.842
Obg-like ATPase 1;	Q9CZ30	1	14	17	22.2	-0.234	-0.03	0.784
Plasma membrane Ca++ transporting ATPase 4 variant x/e; Uncharacterized protein;	D1FNM8	1	5	5	3.2	-0.234	-0.072	0.805
Selenide, water dikinase 2;	P97364	0.999	2	2	6.6	-0.234	-0.05	0.792
Transgelin;	P37804	1	18	22	56.7	-0.218	-0.063	0.819
Hydroxymethylglutaryl-CoA lyase, mitochondrial;	P38060	1	5	6	15.7	-0.218	-0.066	0.821
Glutamate--cysteine ligase catalytic subunit;	P97494	1	4	4	3.1	-0.218	-0.094	0.838
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha;	Q61239	1	2	2	6.1	-0.218	-0.129	0.859
Spermidine synthase;	Q64674	1	9	12	21.9	-0.218	-0.071	0.815
PITH domain-containing protein 1;	Q8BWR2	1	2	3	16.9	-0.218	-0.051	0.812
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial;	Q9D0K2	1	29	57	43.6	-0.218	-0.035	0.806
Catenin alpha-1;	P26231	1	6	6	9.4	-0.218	-0.112	0.842
Ras-related protein Rab-11B;	P46638	1	18	20	52.3	-0.218	-0.119	0.853
UPF0366 protein C11orf67 homolog;	Q8R0P4	1	3	3	20.5	-0.218	-0.117	0.851
Guanine deaminase;	Q9R111	1	21	32	38.5	-0.218	-0.041	0.799
Septin-5;	Q9Z2Q6	1	3	3	8.4	-0.218	-0.033	0.805
Complement component 1, q subcomponent binding protein; Complement component 1, q subcomponent binding protein, isoform CRA_b; Uncharacterized protein; p32-RACK;	Q8R5L1	1	7	9	17.2	-0.218	-0.03	0.795
Ferritin;	Q9CPX4	1	23	51	66.1	-0.218	-0.038	0.807

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TIP41-like protein;	Q8BH58	1	2	2	5.5	-0.218	-0.028	0.804
Coatomer subunit alpha;	Q8CIE6	0.999	4	4	4.3	-0.218	-0.033	0.796
Peroxiredoxin-4;	O08807	1	12	14	39.1	-0.201	-0.053	0.825
Ras-related protein R-Ras;	P10833	1	4	6	17.9	-0.201	-0.097	0.852
78 kDa glucose-regulated protein;	P20029	1	41	76	36.8	-0.201	-0.139	0.876
Heat shock cognate 71 kDa protein;	P63017	1	40	93	47.8	-0.168	-0.076	0.878
Heat shock 70 kDa protein 1A;	Q61696	1	35	52	40.6	0	0	0.998
Ras-related protein Rab-6A;	P35279	1	4	5	9.6	-0.201	-0.113	0.862
40S ribosomal protein S7;	P62082	1	2	2	4.2	-0.184	-0.023	0.832
Peptidyl-prolyl cis-trans isomerase FKBP5;	Q64378	1	3	3	6.4	-0.184	-0.069	0.847
Prostaglandin reductase 1;	Q91YR9	1	17	20	37.7	-0.184	-0.036	0.831
Mitochondrial fission 1 protein;	Q9CQ92	1	3	3	7.9	-0.184	-0.052	0.836
Dual specificity protein phosphatase 3;	Q9D7X3	1	13	17	40.5	-0.184	-0.023	0.832
N-acylglucosamine 2-epimerase;	P82343	1	4	4	9.5	-0.184	-0.042	0.831
Isoleucyl-tRNA synthetase, mitochondrial;	Q8BIJ6	1	7	7	6.9	-0.184	-0.092	0.862
Ubiquinone biosynthesis protein COQ9, mitochondrial;	Q8K1Z0	1	5	5	19.2	-0.184	-0.088	0.860
14 kDa phosphohistidine phosphatase;	Q9DAK9	0.999	2	3	8.9	-0.184	-0.027	0.833
Putative ATP-dependent RNA helicase Pl10;	P16381	1	6	7	5.9	-0.168	-0.011	0.839
Nuclear transport factor 2;	P61971	1	7	10	44.9	-0.168	-0.006	0.847
Eukaryotic translation initiation factor 4E;	P63073	1	8	8	18	-0.168	-0.015	0.849
Fibrinogen gamma chain;	Q8VCM7	1	15	20	26.8	-0.168	-0.015	0.839
Tubulin-specific chaperone C;	Q8VCN9	1	2	2	3.8	-0.168	-0.053	0.865
Ribonuclease inhibitor;	Q91VI7	1	50	71	64.9	-0.168	-0.094	0.890
Translationally-controlled tumor protein;	P63028	1	10	34	30.2	-0.168	-0.011	0.838
Trifunctional purine biosynthetic protein adenosine-3;	Q64737	1	20	23	20.6	-0.168	-0.079	0.881
Copine-1;	Q8C166	1	10	13	20	-0.168	-0.036	0.856
Copine-3;	Q8BT60	1	6	7	17.3	-0.474	-0.342	0.720
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1;	Q9CWS0	1	5	5	28.4	-0.168	-0.053	0.858
NIF3-like protein 1;	Q9EQ80	1	2	2	7.2	-0.168	-0.025	0.842
Profilin-2;	Q9JJV2	1	6	7	25	-0.168	-0.07	0.868
Prostaglandin reductase 2;	Q8VDQ1	1	3	3	11.1	-0.168	-0.091	0.883
Carbonic anhydrase 1;	P13634	1	2	2	10.9	-0.168	-0.049	0.855
Dihydropyrimidinase-related protein 5;	Q9EQF6	1	3	3	4.4	-0.168	-0.028	0.844
Mannan-binding lectin serine protease 1;	P98064	0.996	2	2	3	-0.168	-0.03	0.854
Galectin-3;	P16110	1	13	18	36.2	-0.152	-0.008	0.857
Glutathione S-transferase theta-2;	Q61133	1	5	5	18	-0.152	-0.073	0.889
Nicotinamide phosphoribosyltransferase;	Q99KQ4	1	13	14	25.9	-0.152	-0.044	0.871
Filamin-A;	Q8BTM8	1	74	100	23.5	-0.152	-0.088	0.898
V-type proton ATPase 116 kDa subunit a isoform 1;	Q9Z1G4	0.997	2	2	2.4	-0.152	-0.025	0.862
Superoxide dismutase [Cu-Zn];	P08228	1	14	49	32.5	-0.136	-0.018	0.879
Galectin-1;	P16045	1	13	44	37.8	-0.136	-0.016	0.878
Calnexin;	P35564	1	3	3	4.4	-0.136	-0.013	0.877
Macrophage mannose receptor 1;	Q61830	1	17	20	11	-0.136	-0.049	0.886

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BTB/POZ domain-containing protein KCTD12;	Q6WVG3	1	10	10	26.3	-0.136	-0.066	0.904
Protein phosphatase 1F;	Q8CGA0	1	2	2	4.4	-0.136	-0.019	0.879
Aspartoacylase;	Q8R3P0	1	2	2	7.4	-0.136	-0.028	0.874
Hepatocyte growth factor activator;	Q9R098	1	3	3	6	-0.136	-0.045	0.883
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial;	O35459	1	7	8	14.4	-0.136	-0.027	0.873
Seryl-tRNA synthetase, cytoplasmic;	P26638	1	11	11	17.6	-0.136	-0.06	0.900
Disabled homolog 2;	P98078	1	3	3	8.5	-0.136	-0.021	0.880
Adapter molecule crk;	Q64010	1	17	18	36.2	-0.136	-0.045	0.883
Enoyl-CoA delta isomerase 2, mitochondrial;	Q9WUR2	1	5	9	22.4	-0.136	-0.015	0.868
Phosphate carrier protein, mitochondrial;	Q8VEM8	1	2	2	3.1	-0.136	-0.009	0.867
SET and MYND domain-containing protein 5;	Q3TYX3	0.999	2	2	2.2	-0.136	-0.03	0.874
Desmoplakin;	E9Q557	1	4	4	2	-0.12	-0.021	0.890
Ras-related protein Rab-7a;	P51150	1	21	32	48.8	-0.12	-0.013	0.887
Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1;	Q4LDD4	1	3	3	6.1	-0.12	-0.025	0.892
Platelet-activating factor acetylhydrolase IB subunit beta;	Q61206	1	4	11	18.9	-0.12	-0.003	0.885
Meteorin-like protein;	Q8VE43	1	2	2	5.1	-0.12	-0.025	0.892
Transmembrane emp24 domain-containing protein 10;	Q9D1D4	1	2	2	13.7	-0.12	-0.017	0.888
Magnesium-dependent phosphatase 1;	Q9D967	1	7	7	21.3	-0.12	-0.025	0.892
Protein phosphatase 1 regulatory subunit 12A;	Q9DBR7	1	3	3	3.9	-0.12	-0.018	0.889
Glycine N-methyltransferase;	Q9QXF8	1	4	6	10.9	-0.12	-0.02	0.889
Proteasome subunit beta type-2;	Q9R1P3	1	4	5	17.9	-0.12	-0.035	0.897
ADP-ribosylation factor-like protein 3;	Q9WUL7	1	4	4	28.6	-0.12	-0.014	0.887
Caveolin-1;	P49817	1	3	5	19.7	-0.12	-0.035	0.897
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;	P63328	1	6	7	17.3	-0.12	-0.059	0.912
Coronin-1C;	Q9WUM4	1	7	7	12.4	-0.12	-0.013	0.887
MCG21506; Macrophage galactose N-acetyl-galactosamine specific lectin 2 isoform i; Uncharacterized protein;	A9XX86	1	2	2	11.7	-0.12	-0.046	0.904
Aldehyde dehydrogenase, cytosolic 1;	O35945	1	3	3	17.4	-0.105	-0.059	0.930
Porphobilinogen deaminase;	P22907	1	3	4	10.8	-0.105	-0.041	0.916
Protein S100-A13;	P97352	1	3	3	23.5	-0.105	-0.024	0.910
Sorting nexin-2;	Q9CWK8	1	22	24	26.8	-0.105	-0.024	0.901
AP-2 complex subunit beta;	Q9DBG3	1	11	12	10	-0.105	-0.014	0.897
Proteasome subunit beta type-5;	O55234	1	17	22	31.1	-0.105	-0.024	0.910
Aldehyde dehydrogenase, mitochondrial;	P47738	1	34	90	40.5	-0.105	-0.014	0.906
Glyoxalase domain-containing protein 4;	Q9CPV4	1	15	17	35.8	-0.105	-0.03	0.906
Vacuolar protein sorting-associated protein 45;	P97390	0.999	2	2	4.2	-0.105	-0.006	0.895
Zinc-binding alcohol dehydrogenase domain-containing protein 2;	Q8BGC4	1	8	11	16.2	-0.089	-0.008	0.915
Rho GDP-dissociation inhibitor 1;	Q99PT1	1	8	22	21.6	-0.089	-0.006	0.922
Thioredoxin domain-containing protein 17;	Q9CQM5	1	5	9	26.8	-0.089	-0.013	0.924
Septin-7;	O55131	1	10	13	19.9	-0.089	-0.026	0.930
Annexin A1;	P10107	1	39	84	59.8	-0.089	-0.01	0.914
Inositol polyphosphate 1-phosphatase;	P49442	1	3	3	5.8	-0.089	-0.01	0.915
Ras-related protein Rab-1A;	P62821	1	10	11	45.5	-0.089	-0.02	0.927

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Ras-related protein Rab-14;	Q91V41	1	7	7	23.7	0.098	0.01	0.907
Ras-related protein Rab-10;	P61027	1	6	9	22.5	0.084	0.022	0.929
Ras-related protein Rab-8A;	P55258	1	6	7	23.2	0.714	0.213	0.445
Ras-related protein Rab-1B;	Q9D1G1	1	5	7	35.3	0.333	0.071	0.707
Pyruvate dehydrogenase protein X component, mitochondrial;	Q8BKZ9	1	8	9	15.2	-0.089	-0.029	0.925
Leukocyte elastase inhibitor A;	Q9D154	1	28	49	36.4	-0.089	-0.006	0.922
Ubiquitin carboxyl-terminal hydrolase isozyme L3;	Q9JKB1	1	9	11	29.6	-0.089	-0.034	0.927
Thiomorpholine-carboxylate dehydrogenase;	O54983	1	4	4	12.1	-0.074	-0.015	0.927
Guanine nucleotide-binding protein subunit beta-2-like 1;	P68040	1	17	20	43.2	-0.074	-0.022	0.939
Eukaryotic translation initiation factor 3 subunit B;	Q8JZQ9	1	2	3	4	-0.074	-0.029	0.943
Glutamine synthetase;	P15105	1	8	10	16.6	-0.074	-0.023	0.939
Peptidyl-prolyl cis-trans isomerase FKBP1A;	P26883	1	3	4	27.8	-0.074	-0.019	0.937
Cytoplasmic aconitate hydratase;	P28271	1	30	35	31.5	-0.074	-0.026	0.941
Mitogen-activated protein kinase 14;	P47811	1	7	8	31.4	-0.074	-0.009	0.935
Serine/threonine-protein phosphatase 5;	Q60676	1	6	8	8.4	-0.074	-0.015	0.935
Disks large homolog 1;	Q811D0	1	3	3	4.1	-0.074	-0.016	0.936
UPF0587 protein C1orf123 homolog;	Q8BHG2	1	4	4	26.1	-0.074	-0.025	0.940
Serpin B8;	O08800	1	11	17	21.4	-0.059	-0.009	0.942
F-box only protein 7;	Q3U7U3	1	2	2	5	-0.059	-0.012	0.944
Fibrinogen beta chain;	Q8K0E8	1	23	34	30.4	-0.059	-0.013	0.944
Rab GTPase-binding effector protein 2;	Q91WG2	1	4	4	6.7	-0.059	-0.012	0.952
Calponin-3;	Q9DAW9	1	4	5	10	-0.059	-0.014	0.945
Cadherin-13;	Q9WTR5	1	3	5	4.9	-0.059	-0.009	0.942
Peptidyl-prolyl cis-trans isomerase FKBP9;	Q9Z247	1	6	6	9.1	-0.059	-0.012	0.944
Non-catalytic region of tyrosine kinase adaptor protein 1, isoform CRA_b; Uncharacterized protein;	Q8BH99	1	2	2	4.5	-0.059	-0.008	0.942
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1;	P47856	1	5	5	8.2	-0.059	-0.033	0.957
Pyruvate carboxylase, mitochondrial;	Q05920	1	8	8	6.4	-0.059	-0.02	0.956
Corticosteroid-binding globulin;	Q06770	1	10	10	12.8	-0.059	-0.02	0.956
Prolyl 4-hydroxylase subunit alpha-2;	Q60716	1	9	13	10.8	-0.059	-0.028	0.961
Putative transferase CAF17 homolog, mitochondrial;	Q8CAK1	1	3	3	10.9	-0.059	-0.023	0.948
Nitrilase homolog 1;	Q8VDK1	1	6	6	21.4	-0.059	-0.018	0.955
Peptidyl-prolyl cis-trans isomerase D;	Q9CR16	1	16	25	34.6	-0.059	-0.022	0.948
Putative hydrolase RBBP9;	O88851	1	5	5	28	-0.044	-0.013	0.963
Serine/threonine-protein phosphatase PP1-beta catalytic subunit;	P62141	1	17	19	42.2	-0.044	-0.007	0.960
Cytosolic purine 5'-nucleotidase;	Q3V1L4	1	2	2	7.9	-0.044	-0.008	0.960
Bifunctional purine biosynthesis protein PURH;	Q9CWJ9	1	31	46	35.5	-0.044	-0.004	0.959
Selenocysteine lyase;	Q9JLI6	1	5	5	13.8	-0.044	-0.006	0.959
Leucine carboxyl methyltransferase 1; Leucine carboxyl methyltransferase 1, isoform CRA_b; Uncharacterized protein;	A2RTH5	1	2	2	5.7	-0.044	-0.005	0.958
Target of Myb protein 1;	O88746	1	4	4	6.1	-0.029	-0.004	0.968
Alcohol dehydrogenase class-3;	P28474	1	11	14	21.9	-0.029	-0.004	0.968
Tyrosine-protein phosphatase non-receptor type 11;	P35235	1	6	7	9.2	-0.029	-0.01	0.972

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Cysteine and glycine-rich protein 3;	P50462	1	6	8	18	-0.029	-0.005	0.977
Rab GDP dissociation inhibitor beta;	Q61598	1	40	75	66.1	-0.029	-0.007	0.978
Protein arginine N-methyltransferase 5;	Q8CIG8	1	4	4	5.8	-0.029	-0.007	0.977
C-type lectin domain family 2 member D;	Q91V08	1	2	2	5.3	-0.029	-0.003	0.968
Metalloreductase STEAP4;	Q923B6	1	2	2	2.8	-0.029	-0.004	0.968
Thioredoxin domain-containing protein 12;	Q9CQU0	1	4	4	22.9	-0.029	-0.002	0.976
Vacuolar protein sorting-associated protein 35;	Q9EQH3	1	7	9	5.8	-0.029	-0.007	0.970
Ubiquitin carboxyl-terminal hydrolase 14;	Q9JMA1	1	4	4	8.3	-0.029	-0.002	0.976
Dihydropyrimidinase-related protein 2;	O08553	1	53	76	59.3	-0.029	-0.005	0.968
Dihydropyrimidinase-related protein 3;	Q62188	1	19	22	38.2	0.536	0.044	0.525
Proteasome subunit alpha type-3;	O70435	1	9	11	25.1	-0.029	-0.011	0.972
Isocitrate dehydrogenase [NADP] cytoplasmic;	O88844	1	40	71	57	-0.029	-0.006	0.978
Actin-related protein 2/3 complex subunit 4;	P59999	1	7	9	29.2	-0.029	-0.012	0.980
Ubiquitin-fold modifier 1;	P61961	1	4	5	50.6	-0.029	-0.004	0.968
Acyl-protein thioesterase 1;	P97823	1	5	7	27.8	-0.029	-0.006	0.969
Biliverdin reductase A;	Q9CY64	1	14	17	29.8	-0.029	-0.005	0.969
Uncharacterized protein;	E9PWQ3	1	32	37	10.9	-0.029	-0.025	0.982
Cysteine sulfinic acid decarboxylase;	Q9DBE0	1	3	4	9.1	-0.014	-0.004	0.986
Heme-binding protein 1;	Q9R257	1	5	7	24.2	-0.014	-0.004	0.986
Protein disulfide-isomerase A3;	P27773	1	40	71	50.5	-0.014	-0.001	0.989
Lupus La protein homolog;	P32067	1	4	4	9.9	-0.014	-0.004	0.986
Histidine ammonia-lyase;	P35492	1	33	48	35.9	-0.014	-0.005	0.987
DNA damage-binding protein 1;	Q3U1J4	1	13	15	14.9	-0.014	-0.003	0.986
Kynurenine--oxoglutarate transaminase 1;	Q8BTY1	1	3	3	12.3	-0.014	-0.003	0.986
Pyridoxal kinase;	Q8K183	1	16	17	22.8	-0.014	-0.002	0.985
Plastin-3;	Q99K51	1	28	40	33.3	-0.014	-0.005	0.987
von Willebrand factor A domain-containing protein 5A;	Q99KC8	1	37	63	27.2	-0.014	-0.005	0.987
Lectin, galactose binding, soluble 7; Lectin, galactose binding, soluble 7, isoform CRA_a; Uncharacterized protein;	Q9CRB1	1	20	61	75	-0.014	-0.003	0.986
Myeloid-associated differentiation marker;	O35682	1	3	7	5.3	0	0	0.994
Myoglobin;	P04247	1	13	29	41.6	0	0	0.998
Myotrophin;	P62774	1	4	8	14.4	0	0	0.998
Microtubule-associated protein RP/EB family member 1;	Q61166	1	2	3	7.5	0	0	0.994
Osteoclast-stimulating factor 1;	Q62422	1	13	16	49.3	0	0	0.994
Regucalcin;	Q64374	1	3	3	10.4	0	0	0.994
Cytoplasmic dynein 1 light intermediate chain 2;	Q6PDL0	1	3	3	8.7	0	0	0.999
NEDD8-activating enzyme E1 catalytic subunit;	Q8C878	1	3	5	7.6	0	0	0.998
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial;	Q921G7	1	4	4	5.8	0	0	0.998
Phosphoacetylglucosamine mutase;	Q9CYR6	1	11	24	19.4	0	0	0.995
Mannose-1-phosphate guanyltransferase alpha;	Q922H4	1	2	2	6.4	0	0	0.998
Hydroxyacid-oxoacid transhydrogenase, mitochondrial;	Q8R0N6	0.997	3	3	11.4	0	0	0.998
Protein DDI1 homolog 2;	A2ADY9	1	7	8	18	0.014	0.005	0.984
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial;	Q61425	1	7	13	25.5	0.014	0.001	0.989

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NAD-dependent malic enzyme, mitochondrial;	Q99KE1	1	3	3	7.8	0.014	0.003	0.982
Prostaglandin F2 receptor negative regulator;	Q9WV91	1	4	4	7.1	0.014	0.003	0.982
Fatty acid-binding protein, adipocyte;	P04117	1	18	272	64.4	0.014	0.006	0.991
Heat shock protein beta-1;	P14602	1	16	35	33.5	0.014	0.001	0.981
Glutathione synthetase;	P51855	1	4	4	8	0.014	0.001	0.981
Elongation factor 2;	P58252	1	57	103	39.2	0.014	0.006	0.984
Heterogeneous nuclear ribonucleoprotein D0;	Q60668	1	4	10	31.8	0.014	0.006	0.991
Hypoxia up-regulated protein 1;	Q9JKR6	1	21	22	18.2	0.014	0.007	0.992
Sorting nexin-1;	Q9WV80	1	9	10	10.6	0.014	0.001	0.981
EF hand domain containing 2; Efhd2 protein; Uncharacterized protein;	Q8C845	1	6	7	19.2	0.014	0.002	0.989
Protein phosphatase 1G;	Q61074	0.998	2	2	3.7	0.014	0.002	0.989
Protein disulfide-isomerase A4;	P08003	1	15	20	14.7	0.029	0.008	0.975
Parkinson disease 7 domain-containing protein 1;	Q8BFQ8	1	2	2	20	0.029	0.003	0.972
Myosin-9;	Q8VDD5	1	2	2	0.6	0.029	0.004	0.973
Ester hydrolase C11orf54 homolog;	Q91V76	1	8	8	20.6	0.029	0.003	0.972
Ubiquitin-fold modifier-conjugating enzyme 1;	Q9CR09	1	3	3	10.2	0.029	0.004	0.973
Calcineurin-like phosphoesterase domain-containing protein 1;	Q8BFS6	1	5	7	18.9	0.029	0.003	0.972
Vacuolar protein sorting-associated protein 29;	Q9QZ88	1	7	7	25	0.029	0.011	0.977
Proteasome subunit alpha type-4;	Q9R1P0	1	14	22	58.1	0.029	0.005	0.974
Biotinidase;	Q8CIF4	1	2	2	7.7	0.043	0.005	0.964
GDP-mannose 4,6 dehydratase;	Q8K0C9	1	2	2	6.7	0.043	0.022	0.975
Mitochondrial antiviral-signaling protein;	Q8VCF0	1	4	4	4.4	0.043	0.004	0.955
Ribulose-phosphate 3-epimerase;	Q8VEE0	1	3	4	8.3	0.043	0.004	0.956
Pyridoxine-5'-phosphate oxidase;	Q91XF0	1	3	3	6.9	0.043	0.005	0.956
Ubiquitin carboxyl-terminal hydrolase isozyme L1;	Q9R0P9	1	8	9	31.4	0.043	0.014	0.968
Eukaryotic translation initiation factor 4H;	Q9WUK2	1	2	2	11.7	0.043	0.014	0.961
Paralemmin-1;	Q9Z0P4	1	4	4	5	0.043	0.01	0.966
Protein disulfide-isomerase;	P09103	1	39	74	47	0.043	0.014	0.968
Alpha-crystallin B chain;	P23927	1	11	19	28	0.043	0.002	0.955
LIM and cysteine-rich domains protein 1;	Q8VEE1	1	5	5	14.5	0.043	0.02	0.971
TAR DNA-binding protein 43;	Q921F2	1	8	9	23.8	0.043	0.02	0.969
Peroxisomal acyl-coenzyme A oxidase 3;	Q9EPL9	1	15	19	16.9	0.043	0.01	0.958
Basal cell adhesion molecule;	Q9R069	1	7	7	10.3	0.043	0.012	0.959
Glutathione peroxidase 1;	P11352	1	16	21	55.7	0.057	0.003	0.947
Histidyl-tRNA synthetase, cytoplasmic;	Q61035	1	3	3	8.1	0.057	0.01	0.949
Tripeptidyl-peptidase 2;	Q64514	1	7	7	5.1	0.057	0.021	0.955
Signal transducer and activator of transcription 3;	P42227	1	3	3	5.2	0.057	0.011	0.942
Reticulocalbin-3;	Q8BH97	1	5	5	13.5	0.057	0.008	0.948
Protein transport protein Sec24A;	Q3U2P1	1	5	6	13.7	0.07	0.006	0.939
BAG family molecular chaperone regulator 1;	Q60739	1	9	14	12.1	0.07	0.011	0.940
NmrA-like family domain-containing protein 1;	Q8K2T1	1	2	2	5.4	0.07	0.009	0.940
CD109 antigen;	Q8R422	1	6	6	3.6	0.07	0.025	0.940
Serine/threonine-protein kinase DCLK1;	Q9JLM8	1	2	2	3	0.07	0.011	0.932

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S-phase kinase-associated protein 1;	Q9WTX5	1	3	3	15.3	0.07	0.007	0.932
Probable C->U-editing enzyme APOBEC-2;	Q9WV35	1	10	11	31.2	0.07	0.028	0.942
Dynactin subunit 1;	O08788	1	2	2	3	0.07	0.018	0.943
Protein canopy homolog 4;	Q8BQ47	1	4	4	17.6	0.07	0.009	0.932
L-xylulose reductase;	Q91X52	1	7	8	18.9	0.07	0.022	0.936
MAGUK p55 subfamily member 6;	Q9JLB0	1	3	3	3.4	0.07	0.021	0.938
Adenine phosphoribosyl transferase; Adenine phosphoribosyl transferase, isoform CRA_b; Uncharacterized protein;	Q6PK77	1	5	6	34.4	0.07	0.027	0.942
Nucleoside diphosphate kinase 3;	Q9WV85	0.999	2	2	4.1	0.07	0.008	0.939
Thioredoxin;	P10639	1	8	15	46.7	0.084	0.021	0.928
Isochorismatase domain-containing protein 2A, mitochondrial;	P85094	1	4	4	7.8	0.084	0.012	0.924
Phosphoglucomutase-2;	Q7TSV4	1	14	15	12.7	0.084	0.025	0.927
Cytosolic 5'-nucleotidase 3;	Q9D020	1	10	10	24.2	0.084	0.009	0.915
Eukaryotic translation initiation factor 3 subunit I;	Q9QZD9	1	3	3	11.5	0.084	0.015	0.925
Destrin;	Q9R0P5	1	11	25	40.6	0.084	0.012	0.924
Uncharacterized protein;	E9PV24	1	11	14	19.9	0.084	0.017	0.926
Beta-galactosidase;	P23780	1	14	16	16.9	0.084	0.017	0.929
Peroxiredoxin-1;	P35700	1	22	49	72.4	0.084	0.016	0.918
3-hydroxyisobutyrate dehydrogenase, mitochondrial;	Q99L13	1	16	23	37.6	0.084	0.015	0.917
NSFL1 cofactor p47;	Q9CZ44	1	17	21	33.8	0.084	0.018	0.919
Malignant T cell-amplified sequence 1;	Q9DB27	1	4	5	25.4	0.084	0.016	0.925
CUGBP Elav-like family member 2;	Q9Z0H4	1	6	6	14	0.084	0.035	0.939
3'(2'),5'-bisphosphate nucleotidase 1;	Q9Z0S1	1	8	8	25.3	0.084	0.031	0.927
Glucosidase 2 subunit beta;	O08795	1	8	8	12.7	0.098	0.01	0.908
Cysteine and glycine-rich protein 1;	P97315	1	9	10	30.1	0.098	0.024	0.913
Alanine aminotransferase 1;	Q8QZR5	1	16	18	26	0.098	0.022	0.910
Lysosomal alpha-glucosidase;	P70699	1	8	8	7	0.098	0.014	0.908
Uncharacterized protein;	Q3TUE1	1	5	5	10.3	0.098	0.029	0.916
COP9 signalosome complex subunit 5;	O35864	1	5	6	16.8	0.111	0.029	0.899
Fatty acid-binding protein, heart;	P11404	1	10	14	47.4	0.111	0.032	0.901
Proteasome subunit beta type-8;	P28063	1	7	11	16.3	0.111	0.024	0.896
Crk-like protein;	P47941	1	4	4	5.9	0.111	0.009	0.899
Desmocollin-3;	P55850	1	3	3	4.5	0.111	0.024	0.896
Proteasome subunit beta type-4;	P99026	1	9	11	32.6	0.111	0.015	0.900
Proteasome subunit beta type-6;	Q60692	1	4	6	8.8	0.111	0.012	0.891
Peptidyl-prolyl cis-trans isomerase F, mitochondrial;	Q99KR7	1	2	2	24.8	0.111	0.035	0.903
Calcyclin-binding protein;	Q9CXW3	1	2	2	13.1	0.111	0.01	0.891
Dipeptidyl peptidase 2;	Q9ET22	1	7	9	9.7	0.111	0.011	0.891
Translin-associated protein X;	Q9QZE7	1	5	5	18.3	0.111	0.011	0.891
Tyrosine-protein kinase Lyn;	P25911	1	3	3	3.9	0.111	0.056	0.916
Actin-related protein 3;	Q99JY9	1	18	28	33.3	0.111	0.015	0.892
Glia maturation factor beta;	Q9CQI3	1	5	7	21.1	0.111	0.009	0.899
WD repeat-containing protein 91;	Q7TMQ7	1	2	2	3.1	0.111	0.022	0.895

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Heterogeneous nuclear ribonucleoprotein H2;	P70333	1	9	9	24.3	0.124	0.027	0.889
Cytosolic 10-formyltetrahydrofolate dehydrogenase;	Q8R0Y6	1	15	15	14.7	0.124	0.044	0.899
Septin-2;	P42208	1	17	22	41.6	0.124	0.023	0.892
C-1-tetrahydrofolate synthase, cytoplasmic;	Q922D8	1	11	11	11.1	0.124	0.051	0.903
Multifunctional protein ADE2;	Q9DCL9	1	11	13	21.6	0.124	0.024	0.888
ATPase Asna1;	O54984	1	2	2	6	0.138	0.016	0.869
Calreticulin;	P14211	1	16	25	26.7	0.138	0.018	0.869
Vitamin D-binding protein;	P21614	1	38	46	54.6	0.138	0.023	0.873
Rho GTPase-activating protein 25;	Q8BYW1	1	3	3	3.9	0.138	0.018	0.869
Mitotic checkpoint protein BUB3;	Q9WVA3	1	3	3	7.4	0.138	0.07	0.899
Polymerase I and transcript release factor;	O54724	1	8	8	15.1	0.138	0.078	0.909
Diphosphoinositol polyphosphate phosphohydrolase 3-alpha;	P0C027	1	4	4	9.8	0.138	0.02	0.877
Prolyl 3-hydroxylase 1;	Q3V1T4	1	2	2	3.2	0.138	0.026	0.872
Glutathione S-transferase theta-1;	Q64471	1	4	4	5.8	0.138	0.011	0.875
Vinculin;	Q64727	1	33	38	28	0.138	0.021	0.878
Xaa-Pro aminopeptidase 1;	Q6P1B1	1	23	27	26.2	0.138	0.013	0.875
Major vault protein;	Q9EQK5	1	9	9	11	0.138	0.046	0.891
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;	P13707	1	29	53	54.6	0.151	0.041	0.871
Glutathione S-transferase kappa 1;	Q9DCM2	1	11	13	35	0.151	0.052	0.878
Guanine nucleotide-binding protein G(i) subunit alpha-2;	P08752	1	13	15	38	0.151	0.054	0.880
Guanine nucleotide-binding protein G(k) subunit alpha;	Q9DC51	1	4	5	17.2	0.614	0.088	0.474
Ras-related protein Rap-2b;	P61226	0.983	2	2	6	0.151	0.015	0.860
GDP-L-fucose synthase;	P23591	1	6	6	13.1	0.163	0.036	0.853
Actin-related protein 2;	P61161	1	17	17	26.9	0.163	0.048	0.860
Survival of motor neuron-related-splicing factor 30;	Q8BGT7	1	2	2	4.2	0.163	0.016	0.853
Abl interactor 1;	Q8CBW3	1	2	2	2.3	0.163	0.007	0.851
Acylamino-acid-releasing enzyme;	Q8R146	1	14	16	15.2	0.163	0.055	0.871
Dipeptidyl peptidase 3;	Q99KK7	1	18	23	21	0.163	0.051	0.869
Glucosamine-6-phosphate isomerase 1;	O88958	1	4	4	17.6	0.163	0.051	0.868
Chromobox protein homolog 3;	P23198	1	3	3	14.8	0.163	0.044	0.865
F-actin-capping protein subunit beta;	P47757	1	7	7	23.1	0.163	0.073	0.875
Glucose-6-phosphate 1-dehydrogenase X;	Q00612	1	27	34	32.4	0.163	0.031	0.851
Lysosomal acid phosphatase;	P24638	0.978	2	2	8.5	0.163	0.02	0.846
Synaptophysin-like protein 2;	O89104	1	2	2	10.6	0.176	0.03	0.834
Nucleosome assembly protein 1-like 4;	Q78ZA7	1	5	5	10.1	0.176	0.076	0.862
Thioredoxin-like protein 1;	Q8CDN6	1	8	9	24.6	0.176	0.03	0.842
Perilipin-1;	Q8CGN5	1	11	11	27.1	0.176	0.056	0.849
Endoplasmic reticulum resident protein 44;	Q9D1Q6	1	13	13	23.6	0.176	0.036	0.844
Prolargin;	Q9JK53	1	16	24	24.1	0.176	0.012	0.829
Integrin beta-1;	P09055	1	4	4	4.9	0.176	0.092	0.878
Protein 4.1;	P48193	1	4	5	5.3	0.176	0.069	0.856
Aminopeptidase N;	P97449	1	20	23	15.8	0.176	0.059	0.858
Ubiquitin-like modifier-activating enzyme 1;	Q02053	1	54	83	27.6	0.176	0.042	0.840

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Versican core protein;	Q62059	1	8	8	8.7	0.176	0.03	0.834
cAMP-dependent protein kinase type I-alpha regulatory subunit;	Q9DBC7	1	7	8	9.4	0.176	0.016	0.837
N-acetyl-D-glucosamine kinase;	Q9QZ08	1	4	4	11.1	0.176	0.019	0.830
Apoptosis inhibitor 5;	O35841	1	2	2	4.2	0.176	0.028	0.834
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase;	Q99JT9	1	2	2	11.7	0.176	0.031	0.835
Platelet glycoprotein 4;	Q08857	1	6	8	12.9	0.189	0.038	0.830
Transcription factor BTF3;	Q64152	1	4	4	23	0.189	0.025	0.824
N-alpha-acetyltransferase 38, NatC auxiliary subunit;	Q6ZWM4	1	3	4	27.1	0.189	0.075	0.851
Eukaryotic translation initiation factor 2 subunit 1;	Q6ZWX6	1	3	3	7	0.189	0.022	0.823
ATP-dependent RNA helicase DDX42;	Q810A7	1	2	3	2.6	0.189	0.012	0.821
Neutral alpha-glucosidase AB;	Q8BHN3	1	17	20	11.2	0.189	0.017	0.822
Prolyl endopeptidase;	Q9QUR6	1	30	33	39.9	0.189	0.04	0.831
DnaJ homolog subfamily B member 2;	Q9QYI5	1	3	3	7.9	0.189	0.086	0.858
Proteasome subunit beta type-3;	Q9R1P1	1	16	18	38.5	0.189	0.017	0.822
Capping protein (Actin filament), gelsolin-like; Capping protein (Actin filament), gelsolin-like, isoform CRA_a; Uncharacterized protein;	Q99LB4	1	23	53	45.3	0.189	0.012	0.821
Transketolase;	P40142	1	41	74	42.5	0.202	0.042	0.815
Peroxisomal multifunctional enzyme type 2;	P51660	1	14	18	15.8	0.202	0.069	0.838
Filamin-B;	Q80X90	1	22	23	8.8	0.202	0.104	0.859
Ubiquitin-like modifier-activating enzyme 5;	Q8VE47	1	4	4	5.2	0.202	0.03	0.811
Resistin-like alpha;	Q9EP95	1	2	2	13.5	0.202	0.061	0.827
Glutathione S-transferase theta 3; Glutathione S-transferase, theta 3; Uncharacterized protein;	Q99L20	1	6	7	24.1	0.202	0.032	0.812
Band 4.1-like protein 2;	O70318	1	10	10	8.4	0.202	0.067	0.837
Proteasome activator complex subunit 2;	P97372	1	6	6	23.4	0.202	0.077	0.844
Nischarin;	Q80TM9	1	2	2	11.6	0.202	0.037	0.821
Methionine adenosyltransferase 2 subunit beta;	Q99LB6	1	6	6	18.9	0.202	0.04	0.823
Actin-related protein 2/3 complex subunit 5;	Q9CPW4	1	6	8	29.1	0.202	0.019	0.815
Toll-interacting protein;	Q9QZ06	1	3	5	10.5	0.202	0.014	0.807
Heat shock protein 4; Heat shock protein 4, isoform CRA_a; Uncharacterized protein;	Q3U2G2	1	39	58	33	0.202	0.067	0.838
Heat shock 70 kDa protein 4L;	P48722	1	10	11	16.7	0.872	0.248	0.350
Trk-fused; Uncharacterized protein;	Q8C2C6	1	3	3	7.8	0.202	0.104	0.860
Stress-70 protein, mitochondrial;	P38647	1	38	53	35.5	0.214	0.028	0.803
DCC-interacting protein 13-alpha;	Q8K3H0	1	5	6	8.3	0.214	0.09	0.839
Heterogeneous nuclear ribonucleoprotein A/B;	Q99020	1	6	7	21.4	0.214	0.05	0.812
Calpain-1 catalytic subunit;	O35350	1	23	27	24.4	0.227	0.027	0.794
10 kDa heat shock protein, mitochondrial;	Q64433	1	11	27	54.9	0.227	0.114	0.842
Elongation factor G, mitochondrial;	Q8K0D5	1	3	3	3.8	0.227	0.045	0.802
Thioredoxin domain-containing protein 5;	Q91W90	1	18	25	33.1	0.227	0.089	0.820
UPF0368 protein Cxorf26 homolog;	Q9D0B6	1	5	5	22.7	0.227	0.043	0.794
Sorting nexin-5;	Q9D8U8	1	8	11	14.6	0.227	0.12	0.840
Epididymal secretory protein E1;	Q9Z0J0	1	5	5	24.8	0.227	0.023	0.787
Peptidyl-prolyl cis-trans isomerase A;	P17742	1	13	50	47	0.227	0.017	0.793

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Endoplasmic reticulum resident protein 29;	P57759	1	8	10	17.6	0.227	0.031	0.789
Profilin-1;	P62962	1	24	217	64.3	0.227	0.012	0.792
Endoplasmic reticulum aminopeptidase 1;	Q9EQH2	1	17	18	12.9	0.227	0.072	0.816
MCG140951; Plexin B2; Plxnb2 protein; Uncharacterized protein;	B2RXS4	1	3	3	2.7	0.227	0.047	0.803
WD repeat-containing protein 1;	O88342	1	27	38	44.1	0.239	0.115	0.822
Thy-1 membrane glycoprotein;	P01831	1	7	8	22.2	0.239	0.022	0.773
AP-2 complex subunit alpha-2;	P17427	1	8	8	10.4	0.239	0.085	0.811
[Protein ADP-ribosylarginine] hydrolase;	P54923	1	4	4	13.8	0.239	0.022	0.779
Mitochondrial-processing peptidase subunit beta;	Q9CXT8	1	3	3	4.5	0.239	0.038	0.778
4-trimethylaminobutyraldehyde dehydrogenase;	Q9JLJ2	1	23	30	35	0.239	0.047	0.788
Heterogeneous nuclear ribonucleoprotein K;	P61979	1	23	32	30.4	0.239	0.095	0.815
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1;	P62874	1	12	22	29.4	0.239	0.113	0.827
Proteasome subunit alpha type-7;	Q9Z2U0	1	19	34	45.6	0.239	0.036	0.777
Endophilin-A2;	Q62419	0.991	2	2	4.3	0.239	0.067	0.792
Epsin-1;	Q80VP1	0.977	3	3	6.1	0.239	0.087	0.810
Heterogeneous nuclear ribonucleoproteins A2/B1;	O88569	1	13	20	20.5	0.251	0.084	0.794
Gelsolin;	P13020	1	25	46	20.4	0.251	0.049	0.780
Hsc70-interacting protein;	Q99L47	1	10	10	20.2	0.251	0.049	0.774
26S proteasome non-ATPase regulatory subunit 4;	O35226	1	4	5	13.6	0.263	0.028	0.753
Ig gamma-2B chain C region;	P01867	1	4	6	13.4	0.263	0.072	0.779
Basigin;	P18572	1	5	5	9.8	0.263	0.129	0.810
Rho GTPase-activating protein 1;	Q5FWK3	1	4	5	14.7	0.263	0.094	0.785
CB1 cannabinoid receptor-interacting protein 1;	Q5M8N0	1	3	3	23.8	0.263	0.033	0.761
Serine/threonine-protein kinase OSR1;	Q6P9R2	1	7	7	11.2	0.263	0.184	0.838
Selenide, water dikinase 1;	Q8BH69	1	4	5	11	0.263	0.035	0.756
Small glutamine-rich tetratricopeptide repeat-containing protein alpha;	Q8BJU0	1	7	7	15.9	0.263	0.182	0.842
Transaldolase;	Q93092	1	14	26	22.3	0.263	0.127	0.806
Ubiquitin-like modifier-activating enzyme ATG7;	Q9D906	1	3	3	3.4	0.263	0.037	0.763
Guanylate binding protein 1; Uncharacterized protein;	A4UUI2	1	3	3	4.2	0.263	0.044	0.758
Serine/threonine-protein kinase PAK 2;	Q8CIN4	1	13	18	23.9	0.263	0.031	0.760
Cysteinyl-tRNA synthetase, cytoplasmic;	Q9ER72	1	2	3	2.8	0.263	0.033	0.754
Aspartyl aminopeptidase;	Q9Z2W0	1	8	8	15.4	0.263	0.092	0.783
Coatomer subunit beta;	Q9JIF7	0.994	2	2	3.9	0.263	0.153	0.827
Membrane primary amine oxidase;	O70423	1	10	13	18.3	0.275	0.041	0.750
Gamma-butyrobetaine dioxygenase;	Q924Y0	1	4	4	10.9	0.275	0.093	0.776
Glutaredoxin-3;	Q9CQM9	1	12	17	25.5	0.275	0.068	0.762
Ribonuclease T2;	Q9CQ01	0.999	2	2	9.7	0.275	0.025	0.745
C-reactive protein;	P14847	1	2	2	12	0.287	0.094	0.762
Microtubule-associated protein 4;	P27546	1	21	23	13.9	0.287	0.038	0.735
Thioredoxin, mitochondrial;	P97493	1	2	2	14.1	0.287	0.019	0.730
Tissue alpha-L-fucosidase;	Q99LJ1	1	3	3	6.2	0.287	0.104	0.774
5-hydroxyisourate hydrolase;	Q9CRB3	1	5	6	37.3	0.287	0.082	0.755
Cytoglobin;	Q9CX80	1	4	5	14.7	0.287	0.038	0.735

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SH3 domain-binding glutamic acid-rich-like protein;	Q9JJU8	1	7	10	53.5	0.287	0.016	0.736
Hemoglobin subunit beta-1;	P02088	1	16	83	76.9	0.287	0.024	0.731
Hemoglobin subunit beta-2;	P02089	1	14	52	72.8	0.614	0.161	0.502
ATP-dependent RNA helicase DDX19A;	Q61655	1	3	4	4.4	0.287	0.111	0.778
Prostamide/prostaglandin F synthase;	Q9DB60	1	8	9	17.9	0.287	0.024	0.737
Proteasome subunit beta type-9;	P28076	1	4	6	18.3	0.299	0.039	0.728
Guanylate kinase;	Q64520	1	3	4	17.2	0.299	0.049	0.725
Protein FAM63A;	Q76LS9	1	2	2	6.4	0.299	0.068	0.734
Ran-binding protein 3;	Q9CT10	1	4	5	6.7	0.299	0.049	0.725
Phytanoyl-CoA dioxygenase domain-containing protein 1;	Q9DB26	1	2	2	7.2	0.299	0.053	0.727
Guanine nucleotide-binding protein subunit alpha-13;	P27601	1	4	4	12.7	0.299	0.058	0.729
Septin-11;	Q8C1B7	1	8	10	22.2	0.299	0.046	0.724
Septin-8;	Q8CHH9	1	6	7	16.3	0	0	0.998
Septin-6;	Q9R1T4	1	6	7	24.7	0.275	0.02	0.744
Argininosuccinate lyase;	Q91YI0	1	9	11	17.9	0.299	0.1	0.758
Uncharacterized protein;	E9Q616	1	246	370	46	0.299	0.143	0.784
Uncharacterized protein;	F7CAE1	1	14	34	57.9	0.299	0.019	0.717
Eukaryotic translation initiation factor 4 gamma 1;	Q6NZJ6	1	2	2	2.1	0.299	0.233	0.828
Phosphatidylinositol-glycan-specific phospholipase D;	O70362	1	8	9	6.2	0.31	0.12	0.756
14-3-3 protein gamma;	P61982	1	3	5	20.2	0.31	0.107	0.748
Elongation factor Tu, mitochondrial;	Q8BFR5	1	7	9	11.7	0.31	0.028	0.712
Heterogeneous nuclear ribonucleoprotein U;	Q8VEK3	1	7	7	10.9	0.31	0.087	0.737
S-methyl-5'-thioadenosine phosphorylase;	Q9CQ65	1	9	10	26.5	0.31	0.03	0.712
AP-2 complex subunit alpha-1;	P17426	1	3	3	4.8	0.31	0.095	0.742
Serpin B12;	Q9D7P9	1	6	6	13	0.31	0.258	0.835
Actin-related protein 2/3 complex subunit 3;	Q9JM76	1	9	12	23.6	0.31	0.068	0.727
Uncharacterized protein;	E9QK49	1	6	6	6.5	0.31	0.1	0.744
Protein S100-A4;	P07091	1	2	2	7.9	0.322	0.028	0.705
ADP-ribosylation factor 6;	P62331	1	4	5	28	0.322	0.041	0.709
Alpha-parvin;	Q9EPC1	1	5	5	11.3	0.322	0.111	0.736
Chloride intracellular channel protein 1;	Q9Z1Q5	1	22	32	53.9	0.322	0.064	0.717
Golgi apparatus protein 1;	Q61543	1	2	2	2.8	0.322	0.052	0.714
Heat shock protein 105 kDa;	Q61699	1	19	21	18.1	0.322	0.07	0.713
Protein Noxp20;	Q9D281	1	4	4	8.3	0.322	0.031	0.699
Serine/threonine-protein phosphatase 4 catalytic subunit;	P97470	1	2	2	14.3	0.322	0.041	0.702
Adenylosuccinate synthetase isozyme 2;	P46664	1	9	10	17.8	0.333	0.116	0.735
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase;	Q8C0L6	1	5	12	20.8	0.333	0.034	0.693
Arf-GAP domain and FG repeats-containing protein 1;	Q8K2K6	1	2	2	5.9	0.333	0.193	0.778
Dynactin subunit 2;	Q99KJ8	1	11	11	24.9	0.333	0.095	0.720
SUMO-activating enzyme subunit 1;	Q9R1T2	1	12	13	39.1	0.333	0.026	0.692
	A6H630	1	4	4	9.1	0.333	0.074	0.709
Small ubiquitin-related modifier 2;	P61957	1	2	2	16.9	0.333	0.037	0.694
Integrin beta-5;	O70309	1	4	4	2.1	0.345	0.054	0.687

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Proteasome subunit alpha type-2;	P49722	1	12	16	42.7	0.345	0.076	0.696
GTPase NRas;	P08556	1	4	4	16.9	0.345	0.041	0.690
Sorcin;	Q6P069	1	10	10	36.4	0.345	0.13	0.727
Septin-9;	Q80UG5	1	10	11	15.8	0.345	0.035	0.687
Protein disulfide-isomerase A6;	Q922R8	1	15	18	30.7	0.345	0.062	0.690
Vacuolar protein-sorting-associated protein 25;	Q9CQ80	1	3	3	14.1	0.345	0.046	0.684
Ubiquitin-conjugating enzyme E2 variant 1;	Q9CZY3	1	7	9	38.8	0.345	0.014	0.683
Cullin-3;	Q9JLV5	1	3	3	2.5	0.345	0.098	0.708
Proteasome subunit alpha type-5;	Q9Z2U1	1	14	22	58.9	0.345	0.06	0.695
Nucleosome assembly protein 1-like 1;	P28656	1	5	5	9.9	0.356	0.05	0.679
Junction plakoglobin;	Q02257	1	9	9	16.4	0.356	0.1	0.701
Catenin beta-1;	Q02248	1	5	5	6.9	0.526	0.146	0.567
Heterogeneous nuclear ribonucleoprotein A1;	P49312	1	9	13	15.3	0.367	0.051	0.673
Calcineurin subunit B type 1;	Q63810	1	3	3	12.9	0.367	0.048	0.665
NHL repeat-containing protein 3;	Q8CCH2	1	4	4	11	0.367	0.046	0.665
Eukaryotic translation initiation factor 6;	O55135	1	6	6	29.8	0.367	0.071	0.674
Calpain small subunit 1;	O88456	1	7	7	13.3	0.367	0.034	0.668
C-terminal-binding protein 1;	O88712	1	6	7	15.2	0.367	0.057	0.675
Ubiquitin carboxyl-terminal hydrolase 5;	P56399	1	16	22	18	0.367	0.051	0.673
Mitogen-activated protein kinase 3;	Q63844	1	5	5	18.7	0.367	0.046	0.665
Mitogen-activated protein kinase 1;	P63085	1	4	4	11.2	0.239	0.075	0.803
Programmed cell death protein 10;	Q8VE70	1	3	3	15.6	0.367	0.091	0.690
NADH-cytochrome b5 reductase 3;	Q9DCN2	1	4	4	13	0.367	0.148	0.718
Proteasome subunit alpha type-6;	Q9QUM9	1	17	23	41.9	0.367	0.088	0.682
Histone-arginine methyltransferase CARM1;	Q9WVG6	1	3	3	6.6	0.367	0.185	0.742
Uncharacterized protein;	E9Q9T2	1	14	18	34.9	0.367	0.176	0.738
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	6	11	11.7	-1.286	-0.188	0.135
Twinfilin-2;	Q9Z0P5	1	2	2	10.9	0.367	0.048	0.672
Macrophage migration inhibitory factor;	P34884	1	2	7	7.8	0.379	0.102	0.682
Serpin B5;	P70124	1	43	100	65.6	0.379	0.029	0.655
Proteasome subunit beta type-7;	P70195	1	4	9	7.2	0.379	0.064	0.664
Glutaredoxin-related protein 5, mitochondrial;	Q80Y14	1	2	2	12.5	0.379	0.029	0.654
Alanyl-tRNA synthetase, cytoplasmic;	Q8BGQ7	1	14	16	14.2	0.379	0.093	0.674
Dynamin-1-like protein;	Q8K1M6	1	12	12	16	0.379	0.079	0.665
Threonyl-tRNA synthetase, cytoplasmic;	Q9D0R2	1	7	7	9.1	0.379	0.143	0.705
Gamma-glutamylcyclotransferase;	Q9D7X8	1	4	4	22.9	0.379	0.038	0.650
Coatomer subunit gamma;	Q9QZE5	1	4	4	5.9	0.379	0.16	0.717
Puromycin-sensitive aminopeptidase;	Q11011	1	26	34	24.8	0.379	0.128	0.692
Protein RCC2;	Q8BK67	1	6	6	11.3	0.379	0.157	0.709
5-oxoprolinase;	Q8K010	1	19	22	14.7	0.379	0.16	0.716

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SAR1 gene homolog A (S. cerevisiae); SAR1 gene homolog A (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q99JZ4	1	6	7	25.8	0.379	0.079	0.665
GTP-binding protein SAR1b;	Q9CQC9	1	4	5	39.4	0.433	0.058	0.614
Hypoxanthine-guanine phosphoribosyltransferase;	P00493	1	17	21	50.5	0.39	0.045	0.646
Ras-related protein Rap-1A;	P62835	1	6	6	19.6	0.39	0.188	0.723
Tubulin-specific chaperone D;	Q8BYA0	1	8	8	4.8	0.39	0.176	0.716
MKIAA0079 protein; SEC24 related gene family, member C (S. cerevisiae), isoform CRA_b; Uncharacterized protein;	Q80U83	1	8	8	10.1	0.39	0.086	0.662
Phosphatidylinositol transfer protein alpha isoform;	P53810	1	7	8	27.3	0.39	0.036	0.644
Eukaryotic initiation factor 4A-I;	P60843	1	4	4	30.5	0.39	0.11	0.673
Eukaryotic initiation factor 4A-II;	P10630	1	2	2	20.7	-0.69	-0.111	0.431
SAM domain and HD domain-containing protein 1;	Q60710	1	18	20	27.9	0.39	0.095	0.667
6-phosphogluconolactonase;	Q9CQ60	1	14	16	36.2	0.39	0.06	0.651
MCG21235; Uncharacterized protein;	Q9D1Q5	1	19	34	32	0.39	0.113	0.676
Ribosome-releasing factor 2, mitochondrial;	Q8R2Q4	0.996	2	2	5.1	0.39	0.146	0.694
Tryptophanyl-tRNA synthetase, cytoplasmic;	P32921	1	9	10	15.4	0.401	0.085	0.653
H-2 class I histocompatibility antigen, L-D alpha chain;	P01897	1	9	11	25.4	0.401	0.112	0.662
H-2 class I histocompatibility antigen, Q10 alpha chain;	P01898	1	5	5	18.5	0.651	0.274	0.529
H-2 class I histocompatibility antigen, K-W28 alpha chain;	P03991	1	3	3	11	1.144	0.16	0.182
Cofilin-1;	P18760	1	14	34	45.2	0.401	0.085	0.655
Epidermal growth factor receptor substrate 15;	P42567	1	6	6	9.3	0.401	0.122	0.668
Ubiquitin-conjugating enzyme E2 K;	P61087	1	6	6	20	0.401	0.091	0.651
NudC domain-containing protein 3;	Q8R1N4	1	2	2	3.3	0.401	0.033	0.631
Vasodilator-stimulated phosphoprotein;	P70460	1	2	2	9.9	0.411	0.077	0.639
Costars family protein C6orf115 homolog;	Q4KML4	1	4	4	27.2	0.411	0.059	0.632
CD166 antigen;	Q61490	1	3	3	9.3	0.411	0.108	0.653
Polyadenylate-binding protein 2;	Q8CCS6	1	2	2	7	0.411	0.015	0.623
Protein LSM12 homolog;	Q9D0R8	1	2	2	19	0.411	0.114	0.657
EH domain-binding protein 1;	Q69ZW3	1	2	2	1.1	0.422	0.094	0.634
Sorting nexin-6;	Q6P8X1	1	10	12	18.5	0.422	0.12	0.653
Elongation factor 1-gamma;	Q9D8N0	1	17	26	21.1	0.422	0.088	0.633
Intersectin-1;	Q9Z0R4	1	2	2	1	0.422	0.079	0.628
Polyadenylate-binding protein 1;	P29341	1	24	26	25.6	0.422	0.088	0.637
Ubiquitin-conjugating enzyme E2 N;	P61089	1	10	12	41.4	0.422	0.101	0.642
Inter-alpha-trypsin inhibitor heavy chain H2;	Q61703	1	10	13	12.9	0.422	0.195	0.696
Cullin-associated NEDD8-dissociated protein 1;	Q6ZQ38	1	17	20	13.7	0.422	0.148	0.664
Heterogeneous nuclear ribonucleoprotein Q;	Q7TMK9	1	18	23	22.5	0.422	0.11	0.649
Heterogeneous nuclear ribonucleoprotein R; Uncharacterized protein;	Q8VHM5	1	5	7	9.2	0.766	0.194	0.399
Heterogeneous nuclear ribonucleoprotein H;	O35737	1	12	12	25.8	0.433	0.042	0.610
Nidogen-1;	P10493	1	7	9	5.1	0.433	0.173	0.671
Dual specificity mitogen-activated protein kinase kinase 4;	P47809	1	3	3	10.1	0.433	0.144	0.650
Ribose-5-phosphate isomerase;	P47968	1	2	2	9.6	0.433	0.077	0.616
Trifunctional enzyme subunit alpha, mitochondrial;	Q8BMS1	1	26	34	29.4	0.433	0.199	0.686

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Heat shock 70 kDa protein 12A;	Q8K0U4	1	2	2	1.5	0.433	0.051	0.612
Bifunctional protein NCOAT;	Q9EQQ9	1	2	2	4.4	0.433	0.135	0.650
Ubiquitin-conjugating enzyme E2 L3;	P68037	1	6	9	41.6	0.433	0.055	0.613
T-complex protein 1 subunit gamma;	P80318	1	4	4	9.5	0.433	0.048	0.612
Protein arginine N-methyltransferase 1;	Q9JIF0	1	3	4	7.5	0.433	0.154	0.660
Vigilin;	Q8VDJ3	1	5	5	2.4	0.444	0.176	0.664
Ras GTPase-activating-like protein IQGAP1;	Q9JKF1	1	40	49	20	0.444	0.219	0.684
ADP-ribosylation factor 3;	P61205	1	7	20	42	0.444	0.036	0.597
ADP-ribosylation factor 5;	P84084	1	6	18	43.3	1.17	0.796	0.364
Peptidyl-prolyl cis-trans isomerase FKBP2;	P45878	0.934	2	3	8.6	0.444	0.202	0.676
Pro-interleukin-16;	O54824	1	2	2	0.8	0.454	0.056	0.591
Leukocyte surface antigen CD47;	Q61735	1	3	6	8.9	0.454	0.099	0.607
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1;	Q8R3B1	1	11	12	11.6	0.454	0.109	0.617
Ras-related protein Rap-1b;	Q99JI6	1	2	2	19.6	0.454	0.05	0.590
Tumor protein D54;	Q9CYZ2	1	3	3	18	0.454	0.056	0.591
GTP-binding nuclear protein Ran;	P62827	1	11	25	31	0.454	0.023	0.584
55 kDa erythrocyte membrane protein;	P70290	1	4	4	9.4	0.454	0.04	0.587
Uncharacterized protein;	E9QJY4	1	4	4	2.4	0.454	0.083	0.606
Transitional endoplasmic reticulum ATPase;	Q01853	1	43	60	31	0.465	0.067	0.588
26S proteasome non-ATPase regulatory subunit 3;	P14685	1	19	20	27.5	0.465	0.249	0.681
Catalase;	P24270	1	33	46	43.5	0.465	0.104	0.607
IgG receptor FcRn large subunit p51;	Q61559	1	2	2	6.6	0.475	0.113	0.596
UMP-CMP kinase;	Q9DBP5	1	12	20	40.8	0.475	0.123	0.601
PDZ domain-containing protein GIPC1;	Q9Z0G0	1	2	2	3.9	0.475	0.068	0.578
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform;	Q6P1F6	1	4	5	6.7	0.475	0.144	0.612
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;	P63330	1	9	11	39.2	0.485	0.052	0.563
Proteasome activator complex subunit 1;	P97371	1	15	19	34.1	0.485	0.132	0.600
Glucuronidase, beta; Glucuronidase, beta, isoform CRA_a; Uncharacterized protein;	Q6IR10	1	15	17	15.6	0.485	0.381	0.731
Regulator of nonsense transcripts 1;	Q9EPU0	0.999	2	2	2.6	0.485	0.087	0.579
Ran-specific GTPase-activating protein;	P34022	1	3	3	10.8	0.496	0.084	0.567
Epoxide hydrolase 2;	P34914	1	11	11	17	0.496	0.077	0.564
Hormone-sensitive lipase;	P54310	1	8	10	10.9	0.496	0.088	0.569
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Q8BMF4	1	25	29	30.8	0.496	0.056	0.562
Heterogeneous nuclear ribonucleoprotein A3;	Q8BG05	1	10	20	18.3	0.496	0.091	0.570
Serine/threonine-protein kinase 38;	Q91VJ4	1	4	4	7.7	0.496	0.169	0.607
Uncharacterized protein;	F7DBB3	1	3	9	14.3	0.496	0.067	0.561
Uncharacterized protein;	E9PYB0	1	3	3	23.7	-0.168	-0.034	0.855
Microtubule-associated protein 1B;	P14873	1	2	2	2	0.506	0.15	0.591
ELAV-like protein 1;	P70372	1	8	9	20.2	0.506	0.196	0.616
Acyl-CoA synthetase family member 2, mitochondrial;	Q8VCW8	1	11	11	18.7	0.506	0.189	0.614
Twinfilin-1;	Q91YR1	1	2	3	3.7	0.506	0.071	0.557
COP9 signalosome complex subunit 1;	Q99LD4	1	5	6	10.2	0.506	0.064	0.551

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
Sodium/potassium-transporting ATPase subunit alpha-1;	Q8VDN2	1	11	12	18.3	0.506	0.217	0.624
Sodium/potassium-transporting ATPase subunit alpha-2;	Q6PIE5	1	6	6	15.3	-0.252	-0.015	0.761
Sodium/potassium-transporting ATPase subunit alpha-3;	Q6PIC6	1	3	3	12.4	-0.252	-0.048	0.771
GTP:AMP phosphotransferase, mitochondrial;	Q9WTP7	1	9	9	33.9	0.506	0.078	0.560
Sushi domain-containing protein 2;	Q9DBX3	0.992	2	2	1.1	0.506	0.05	0.552
Nuclear protein localization protein 4 homolog;	P60670	1	2	2	2.5	0.516	0.043	0.540
T-complex protein 1 subunit beta;	P80314	1	11	11	20.7	0.516	0.032	0.538
COP9 signalosome complex subunit 3;	O88543	1	4	4	19.6	0.516	0.159	0.585
Elongation factor 1-alpha 1;	P10126	1	16	94	37.9	0.516	0.188	0.601
Adenylate kinase 2, mitochondrial;	Q9WTP6	1	4	5	27.6	0.516	0.141	0.575
Importin subunit alpha-3;	O35344	0.997	2	2	5.2	0.516	0.04	0.539
Sec1 family domain-containing protein 1;	Q8BRF7	1	4	4	6.7	0.526	0.23	0.613
Coactosin-like protein;	Q9CQI6	1	6	7	46.5	0.526	0.194	0.597
Isoamyl acetate-hydrolyzing esterase 1 homolog;	Q9DB29	1	12	13	28.5	0.526	0.153	0.570
Pleckstrin;	Q9JHK5	1	2	2	4.3	0.526	0.099	0.546
Carbonyl reductase 3; Uncharacterized protein;	Q8K354	1	18	27	48	0.526	0.026	0.532
Sodium/potassium-transporting ATPase subunit beta-3;	P97370	1	5	6	19.1	0.526	0.168	0.578
26S proteasome non-ATPase regulatory subunit 14;	O35593	1	3	4	5.3	0.536	0.174	0.575
40S ribosomal protein S3a;	P97351	1	2	2	4.9	0.536	0.092	0.539
Transgelin-2;	Q9WVA4	1	13	19	46.7	0.536	0.081	0.535
General vesicular transport factor p115;	Q9Z1Z0	1	6	8	6.2	0.536	0.44	0.712
Calpain-2 catalytic subunit;	O08529	1	18	24	20.1	0.536	0.17	0.574
N-acetylgalactosamine kinase;	Q68FH4	1	6	7	18.5	0.536	0.296	0.643
Smoothelin-like protein 1;	Q99LM3	1	4	4	10	0.536	0.085	0.536
Band 4.1-like protein 1;	Q9Z2H5	1	3	3	5.6	0.536	0.203	0.587
Long-chain-fatty-acid--CoA ligase 1;	P41216	1	4	4	5.4	0.536	0.104	0.542
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;	P31230	1	6	8	25.5	0.546	0.086	0.531
Stress-induced-phosphoprotein 1;	Q60864	1	23	30	24.1	0.546	0.101	0.536
Thimet oligopeptidase;	Q8C1A5	1	19	24	24	0.546	0.127	0.547
Phospholysine phosphohistidine inorganic pyrophosphate phosphatase;	Q9D7I5	1	5	5	13	0.546	0.15	0.557
Phosphoglycerate mutase 1;	Q9DBJ1	1	23	75	52.8	0.546	0.056	0.522
Serine/threonine-protein kinase WNK1;	P83741	1	4	5	1.9	0.546	0.105	0.537
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial;	Q8BH04	1	4	5	5.6	0.546	0.217	0.588
Coronin-7;	Q9D2V7	1	9	9	14.2	0.546	0.108	0.539
Lysosomal alpha-mannosidase;	O09159	1	8	8	5.7	0.556	0.208	0.573
Copper transport protein ATOX1;	O08997	1	7	12	57.4	0.566	0.283	0.608
Cytosol aminopeptidase;	Q9CPY7	1	31	43	45.7	0.566	0.115	0.521
3-ketoacyl-CoA thiolase A, peroxisomal;	Q921H8	1	16	20	42	0.566	0.184	0.556
26S proteasome non-ATPase regulatory subunit 13;	Q9WVJ2	1	11	11	25.5	0.566	0.275	0.602
Cyclin-dependent kinase 6;	Q64261	1	2	2	10.1	0.566	0.122	0.524
Dipeptidase 1;	P31428	1	6	7	17.3	0.575	0.32	0.616
UV excision repair protein RAD23 homolog B;	P54728	1	5	5	12.5	0.575	0.131	0.523
Peflin;	Q8BFY6	1	5	5	11.6	0.575	0.062	0.495

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
Erythrocyte band 7 integral membrane protein;	P54116	1	4	4	11.3	0.575	0.166	0.537
14-3-3 protein epsilon;	P62259	1	14	23	45.9	0.575	0.297	0.604
Acyl-CoA dehydrogenase family member 9, mitochondrial;	Q8JZN5	1	17	20	30.6	0.575	0.208	0.556
Anamorsin;	Q8WTY4	1	4	4	16.8	0.575	0.324	0.620
CAP-Gly domain-containing linker protein 1;	Q922J3	1	9	9	5.1	0.575	0.216	0.561
Dual specificity protein phosphatase 23;	Q6NT99	1	3	3	26	0.585	0.14	0.521
DAZ-associated protein 1;	Q9JII5	1	6	9	28.1	0.585	0.129	0.512
V-type proton ATPase subunit E 1;	P50518	1	4	5	9.3	0.585	0.152	0.519
Tubulin--tyrosine ligase-like protein 12;	Q3UDE2	1	12	16	17.5	0.585	0.23	0.561
WD repeat-containing protein 82;	Q8BFQ4	0.997	2	2	4.5	0.585	0.094	0.499
Syntaxin 17; Syntaxin 17, isoform CRA_b; Uncharacterized protein;	Q9D614	0.981	2	3	3.3	0.585	0.066	0.491
Cathepsin B;	P10605	1	21	33	41.6	0.595	0.154	0.514
Programmed cell death protein 6;	P12815	1	5	6	17.8	0.595	0.11	0.501
Farnesyl pyrophosphate synthase;	Q920E5	1	14	21	27.5	0.595	0.193	0.536
Synaptobrevin homolog YKT6;	Q9CQW1	1	10	12	36.4	0.595	0.256	0.564
AH receptor-interacting protein;	O08915	1	3	4	13.9	0.595	0.252	0.563
Acyl-coenzyme A thioesterase 1;	O55137	1	11	14	24.8	0.595	0.213	0.546
Acyl-coenzyme A thioesterase 2, mitochondrial;	Q9QYR9	1	2	3	12.8	-0.136	-0.022	0.880
Vesicular integral-membrane protein VIP36;	Q9DBH5	1	3	3	13.1	0.595	0.051	0.483
Protein canopy homolog 3;	Q9DAU1	0.994	2	2	9.4	0.595	0.169	0.519
Calpastatin;	P51125	1	4	6	8.5	0.604	0.052	0.471
Heat shock protein HSP 90-beta;	P11499	1	36	64	37.6	0.604	0.187	0.520
Endoplasmin;	P08113	1	24	30	26.4	0.084	0.053	0.947
Heat shock protein HSP 90-alpha;	P07901	1	23	38	27.7	0.263	0.085	0.780
Inorganic pyrophosphatase;	Q9D819	1	18	31	45.7	0.604	0.207	0.529
Zinc finger CCCH domain-containing protein 15;	Q3TIV5	1	3	3	3.3	0.614	0.084	0.473
Far upstream element-binding protein 2;	Q3U0V1	1	13	15	15.4	0.614	0.157	0.499
Activator of 90 kDa heat shock protein ATPase homolog 1;	Q8BK64	1	7	9	18.9	0.614	0.209	0.526
Bleomycin hydrolase;	Q8R016	1	14	18	30.1	0.614	0.084	0.472
T-complex protein 1 subunit theta;	P42932	1	12	14	17.3	0.623	0.21	0.520
Vitamin K-dependent protein S;	Q08761	1	2	2	2.7	0.623	0.109	0.471
Src substrate cortactin;	Q60598	1	2	2	8.6	0.623	0.134	0.481
Hsp90 co-chaperone Cdc37;	Q61081	1	6	7	20.1	0.623	0.138	0.486
COP9 signalosome complex subunit 8;	Q8VBV7	1	4	4	23.4	0.623	0.121	0.476
Ubiquitin carboxyl-terminal hydrolase isozyme L5;	Q9WUP7	1	4	4	17	0.623	0.312	0.569
H-2 class II histocompatibility antigen, A-Q beta chain;	P06342	1	10	12	32.8	0.623	0.55	0.681
COP9 signalosome complex subunit 2;	P61202	1	8	9	15.8	0.623	0.243	0.537
Tubulin alpha-1A chain;	P68369	1	12	21	43.7	0.623	0.235	0.533
Tubulin alpha-4A chain;	P68368	1	7	8	37.5	0.832	0.276	0.384
C-Jun-amino-terminal kinase-interacting protein 4;	Q58A65	1	11	15	7	0.623	0.198	0.514
Prefoldin subunit 5;	Q9WU28	1	3	3	31.2	0.623	0.202	0.514
Fibrillin 1; Uncharacterized protein;	A2AQ53	1	7	7	3.7	0.623	0.182	0.502
Protein MEMO1;	Q91VH6	1	2	3	5.1	0.632	0.236	0.524

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15 kDa selenoprotein;	Q9ERR7	1	4	5	17.9	0.632	0.204	0.507
Alpha-enolase;	P17182	1	33	106	71.9	0.632	0.106	0.466
Beta-enolase;	P21550	1	29	346	51.4	-0.916	-0.086	0.277
Gamma-enolase;	P17183	1	2	3	23.3	-0.029	-0.009	0.971
Tyrosyl-tRNA synthetase, cytoplasmic;	Q91WQ3	1	3	3	5.5	0.632	0.053	0.453
SEC14-like protein 2;	Q99J08	1	4	4	8.4	0.642	0.111	0.459
Arginyl-tRNA synthetase, cytoplasmic;	Q9D0I9	1	19	21	23.9	0.642	0.173	0.483
Phosphoribosylformylglycinamidine synthase;	Q5SUR0	1	11	11	11.5	0.642	0.045	0.443
Complement C1s-A subcomponent;	Q8CG14	1	6	6	7.8	0.642	0.074	0.450
Hydroxymethylglutaryl-CoA synthase, mitochondrial;	P54869	1	3	4	8.7	0.651	0.124	0.459
Epidermal growth factor receptor substrate 15-like 1;	Q60902	1	4	4	8.6	0.651	0.182	0.484
Phospholipase B-like 1;	Q8VCI0	1	9	11	15.3	0.651	0.124	0.460
Uncharacterized protein;	Q9CX86	1	8	12	29.2	0.651	0.058	0.437
14-3-3 protein zeta/delta;	P63101	1	15	28	41.6	0.651	0.133	0.457
Plastin-2;	Q61233	1	57	86	52.8	0.651	0.207	0.490
Proteasome-associated protein ECM29 homolog;	Q6PDI5	1	6	6	4	0.651	0.075	0.444
EGF-containing fibulin-like extracellular matrix protein 1;	Q8BPB5	1	12	14	31	0.651	0.145	0.464
Chloride intracellular channel protein 4;	Q9QYB1	1	6	6	24.5	0.66	0.267	0.515
Phenylalanyl-tRNA synthetase beta chain;	Q9WUA2	1	4	5	8.6	0.669	0.038	0.426
26S protease regulatory subunit 6A;	O88685	1	17	18	34.2	0.669	0.261	0.504
Aldehyde dehydrogenase family 1 member A3;	Q9JHW9	1	4	4	7.4	0.669	0.614	0.666
Low affinity immunoglobulin gamma Fc region receptor II;	P08101	1	2	3	3.8	0.678	0.076	0.424
V-type proton ATPase catalytic subunit A;	P50516	1	15	18	18.2	0.678	0.225	0.480
Serine/threonine-protein phosphatase 6 regulatory subunit 3;	Q922D4	1	2	2	2.8	0.687	0.418	0.568
Ribosome-binding protein 1;	Q99PL5	1	19	24	11	0.687	0.132	0.436
WD repeat-containing protein 61;	Q9ERF3	1	2	2	13.3	0.687	0.081	0.422
Glycerol-3-phosphate dehydrogenase 1-like protein;	Q3ULJ0	1	12	16	21.9	0.687	0.333	0.525
Retinoid-inducible serine carboxypeptidase;	Q920A5	1	13	15	13.9	0.687	0.235	0.481
Phosphomannomutase 2;	Q9Z2M7	1	7	7	22.3	0.687	0.367	0.544
Protein prune homolog;	Q8BIW1	1	7	9	13.2	0.696	0.236	0.472
Palmitoyl-protein thioesterase 1;	O88531	1	5	5	17.9	0.696	0.172	0.443
GMP synthase [glutamine-hydrolyzing];	Q3THK7	1	9	11	14.3	0.705	0.203	0.449
Ubiquitin-like modifier-activating enzyme 6;	Q8C7R4	1	15	15	12.9	0.705	0.177	0.437
Haloacid dehalogenase-like hydrolase domain-containing protein 3;	Q9CYW4	1	3	3	10.8	0.705	0.35	0.524
Tubulin-folding cofactor B;	Q9D1E6	1	3	3	8.6	0.705	0.117	0.416
COP9 signalosome complex subunit 7a;	Q9CZ04	1	2	3	13.6	0.705	0.074	0.404
14-3-3 protein theta;	P68254	1	8	8	38.4	0.714	0.135	0.417
Cold shock domain-containing protein E1;	Q91W50	1	3	3	4.8	0.714	0.17	0.429
Eosinophil cationic-type ribonuclease 3;	O35290	1	2	2	14.7	0.714	0.122	0.409
Rho GDP-dissociation inhibitor 2;	Q61599	1	9	14	35	0.714	0.044	0.392
26S proteasome non-ATPase regulatory subunit 12;	Q9D8W5	1	9	11	12.3	0.714	0.257	0.465
ADP-sugar pyrophosphatase;	Q9JKX6	1	4	5	17.9	0.714	0.091	0.400
5'(3')-deoxyribonucleotidase, cytosolic type;	Q9JM14	1	5	5	20	0.714	0.087	0.400

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Ribosomal protein S6 kinase alpha-3;	P18654	1	6	6	10.2	0.722	0.328	0.495
Interleukin-1 receptor antagonist protein;	P25085	1	6	8	29.4	0.722	0.074	0.393
GrpE protein homolog 1, mitochondrial;	Q99LP6	1	3	3	10.1	0.722	0.083	0.395
Macrophage colony-stimulating factor 1 receptor;	P09581	1	3	3	3.9	0.731	0.185	0.423
Glutamate--cysteine ligase regulatory subunit;	O09172	1	3	3	16.4	0.731	0.432	0.541
Clathrin heavy chain 1;	Q68FD5	1	43	53	24.5	0.74	0.372	0.504
Nuclease-sensitive element-binding protein 1;	P62960	1	3	4	17.1	0.748	0.125	0.387
Nucleophosmin;	Q61937	1	2	2	13.2	0.748	0.116	0.388
Uncharacterized protein;	E9Q912	1	14	16	21.6	0.748	0.183	0.407
CD63 antigen;	P41731	0.998	2	2	4.6	0.748	0.045	0.374
Gbp6 protein; Guanylate binding protein 7; MCG141961, isoform CRA_a; Uncharacterized protein;	Q91Z40	1	4	4	7.8	0.757	0.273	0.439
Heterogeneous nuclear ribonucleoprotein F;	Q9Z2X1	1	11	11	28.4	0.766	0.302	0.447
Ezrin;	P26040	1	11	12	23.2	0.766	0.144	0.385
Moesin;	P26041	1	11	11	19.8	-1.434	-1.163	0.319
Radixin;	P26043	1	4	4	12.9	-0.943	-0.091	0.268
Protein S100-A11;	P50543	1	8	21	27.6	0.766	0.117	0.374
Mitogen-activated protein kinase kinase kinase MLT;	Q9ESL4	1	6	6	5.7	0.766	0.342	0.466
Coronin-1B;	Q9WUM3	1	5	5	13.6	0.766	0.27	0.433
Proteasome subunit beta type-10;	O35955	1	4	4	11	0.774	0.43	0.505
Nardilysin;	Q8BHG1	1	8	8	8.5	0.774	0.145	0.380
Pantothenate kinase 4;	Q80YV4	1	2	2	2.9	0.774	0.104	0.368
60 kDa heat shock protein, mitochondrial;	P63038	1	25	55	39.8	0.782	0.114	0.362
Carbonyl reductase [NADPH] 1;	P48758	1	15	24	52.7	0.791	0.146	0.368
6-phosphogluconate dehydrogenase, decarboxylating;	Q9DCD0	1	16	27	26.5	0.791	0.187	0.382
Uncharacterized protein;	E9Q2Z8	1	3	3	3.6	0.791	0.128	0.363
Tyrosine-protein kinase CSK;	P41241	1	3	3	5.1	0.791	0.169	0.376
Stromal membrane-associated protein 1;	Q91VZ6	1	3	3	7.3	0.791	0.11	0.358
mRNA cap guanine-N7 methyltransferase;	Q9D0L8	1	2	2	8.8	0.791	0.169	0.375
Heterogeneous nuclear ribonucleoprotein M;	Q9D0E1	0.998	2	2	2.7	0.799	0.156	0.362
Pirin;	Q9D711	1	3	4	11.1	0.807	0.143	0.354
Cytoplasmic dynein 1 intermediate chain 2;	O88487	1	4	4	3.8	0.807	0.078	0.338
Polyubiquitin-B;	P0CG49	1	5	6	32.8	0.807	0.138	0.355
14-3-3 protein eta;	P68510	1	9	10	42.7	0.807	0.286	0.408
Rho-related GTP-binding protein RhoC;	Q62159	1	5	5	36.8	0.807	0.148	0.354
Programmed cell death 6-interacting protein;	Q9WU78	1	20	26	24.6	0.807	0.203	0.376
Peptidyl-prolyl cis-trans isomerase-like 1;	Q9D0W5	1	2	2	10.2	0.807	0.161	0.359
Alanine aminotransferase 2;	Q8BGT5	0.994	2	2	4.2	0.807	0.719	0.600
Caspase-1;	P29452	1	5	5	11.2	0.816	0.408	0.460
26S protease regulatory subunit 6B;	P54775	1	11	12	22.5	0.816	0.399	0.452
Lon protease homolog, mitochondrial;	Q8CGK3	1	5	6	5.7	0.816	0.134	0.345
NEDD8-conjugating enzyme Ubc12;	P61082	1	9	11	25.7	0.816	0.209	0.369
Transportin-3;	Q6P2B1	1	4	4	4.4	0.816	0.417	0.464

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Acetyl-coenzyme A synthetase, cytoplasmic;	Q9QXG4	1	2	2	4.9	0.824	0.093	0.333
26S protease regulatory subunit 10B;	P62334	1	14	20	39.6	0.832	0.739	0.584
Carbamoyl-phosphate synthase [ammonia], mitochondrial;	Q8C196	1	22	23	15.8	0.832	0.594	0.531
Protein SEC13 homolog;	Q9D1M0	1	6	6	15.2	0.832	0.224	0.364
Cathepsin Z;	Q9WUU7	1	4	4	11.8	0.832	0.065	0.324
Clusterin;	Q06890	1	4	4	9.6	0.832	0.182	0.348
Elongation factor 1-beta;	O70251	1	5	10	34.7	0.84	0.117	0.328
Synergin gamma;	Q5SV85	1	2	2	1.7	0.84	0.239	0.367
Glutathione S-transferase omega-1;	O09131	1	2	2	7.1	0.84	0.174	0.343
Nuclear migration protein nudC;	O35685	1	9	10	23.8	0.848	0.188	0.341
Alpha-soluble NSF attachment protein;	Q9DB05	1	5	5	14.6	0.848	0.236	0.358
COP9 signalosome complex subunit 4;	O88544	1	12	12	28.8	0.848	0.207	0.348
Selenoprotein O;	Q9DBC0	1	3	3	9.1	0.848	0.155	0.334
Oxysterol-binding protein;	E9QPD4	1	2	3	5.2	0.848	0.118	0.321
Probable E3 ubiquitin-protein ligase HERC4;	Q6PAV2	1	6	6	8.4	0.856	0.307	0.381
S-adenosylmethionine synthase;	F8WJ09	1	5	6	15.2	0.856	0.359	0.404
AP-3 complex subunit beta-1;	Q9Z1T1	1	3	3	3.8	0.864	0.456	0.445
14-3-3 protein beta/alpha;	Q9CQV8	1	10	15	41.1	0.864	0.161	0.323
Protein CREG1;	O88668	1	4	4	13.2	0.872	0.143	0.316
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1;	Q60967	1	4	6	6.9	0.872	0.152	0.315
Uncharacterized protein;	E9PUF0	1	4	4	9.6	0.872	0.129	0.312
Proteasomal ubiquitin receptor ADRM1;	Q9JKV1	1	2	2	2.2	0.872	0.052	0.297
Peroxisomal biogenesis factor 19;	Q8VCI5	0.999	2	2	11	0.872	0.172	0.320
Stromal membrane-associated protein 2;	Q7TN29	0.998	3	3	7.5	0.872	0.143	0.312
Dihydrofolate reductase;	P00375	1	2	2	8.6	0.88	0.12	0.304
Ribonucleoprotein PTB-binding 1;	Q9CW46	1	3	3	8.2	0.888	0.552	0.471
Glycolipid transfer protein;	Q9JL62	1	4	5	10	0.888	0.13	0.304
Protein phosphatase 1B;	P36993	1	5	5	10	0.895	0.212	0.317
Carnitine O-palmitoyltransferase 2, mitochondrial;	P52825	1	3	5	3.2	0.895	0.101	0.293
Flotillin-2;	Q60634	1	3	3	8.4	0.895	0.563	0.467
Polypyrimidine tract-binding protein 1;	P17225	1	9	14	24.9	0.895	0.375	0.383
Calcium/calmodulin-dependent protein kinase type 1D;	Q8BW96	1	7	7	16.9	0.903	0.222	0.318
Heterogeneous nuclear ribonucleoprotein U-like protein 1;	Q8VDM6	1	4	4	4.2	0.903	0.367	0.375
Receptor-type tyrosine-protein phosphatase C;	P06800	1	6	6	6.9	0.903	0.169	0.301
E3 ubiquitin-protein ligase HUWE1;	Q7TMY8	1	13	15	3.6	0.903	0.681	0.508
Retinol-binding protein 1;	Q00915	1	5	6	27.4	0.911	0.174	0.301
Protein transport protein Sec31A;	Q3UPL0	1	26	30	22.5	0.911	0.615	0.479
Epidermal growth factor receptor kinase substrate 8-like protein 1;	Q8R5F8	1	7	7	8.4	0.911	0.572	0.460
Uncharacterized protein;	F6RPJ9	1	31	35	25.5	0.911	0.16	0.294
Glutaredoxin-1;	Q9QUH0	1	2	4	29.9	0.918	0.117	0.281
Uncharacterized protein;	E9Q1Y3	1	6	9	1.4	0.918	0.194	0.301
Inactive tyrosine-protein kinase 7;	Q8BKG3	1	2	2	1.5	0.918	0.165	0.293
Cathepsin S;	O70370	1	9	11	29.1	0.926	0.112	0.276

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Peroxisomal acyl-coenzyme A oxidase 2;	Q9QXD1	1	2	3	1.6	0.926	0.132	0.280
Importin subunit alpha-4;	O35343	1	2	3	5.2	0.926	0.117	0.279
Keratin, type II cytoskeletal 79;	Q8VED5	1	14	17	23.4	0.934	0.416	0.374
Ribose-phosphate pyrophosphokinase 1;	Q9D7G0	1	8	13	21.4	0.934	0.059	0.266
D-3-phosphoglycerate dehydrogenase;	Q61753	1	14	17	21.6	0.934	0.528	0.425
3-ketoacyl-CoA thiolase, mitochondrial;	Q8BWT1	1	20	27	42.6	0.941	0.603	0.449
Myosin-Ic;	Q9WTI7	1	5	7	4.9	0.941	0.446	0.383
26S protease regulatory subunit 8;	P62196	1	7	7	17.2	0.941	0.127	0.271
Ribose-phosphate pyrophosphokinase 2;	Q9CS42	0.999	2	2	15.7	0.941	0.196	0.290
Tryptase beta-2;	P21845	0.998	2	2	6.5	0.941	0.191	0.285
Caspase-3;	P70677	1	6	6	26	0.949	0.118	0.266
Nicotinate phosphoribosyltransferase;	Q8CC86	1	3	3	5.2	0.949	0.211	0.287
Striatin-3;	Q9ERG2	1	3	3	3.7	0.956	0.557	0.419
Sialoadhesin;	Q62230	0.998	2	2	1.6	0.956	0.271	0.303
Epithelial splicing regulatory protein 1;	Q3US41	1	3	4	7.1	0.963	0.568	0.421
CDKN2A-interacting protein;	Q8BI72	1	3	3	5.7	0.971	0.218	0.277
40S ribosomal protein S3;	P62908	1	5	5	17.3	0.971	0.53	0.396
Tripeptidyl-peptidase 1;	O89023	1	4	5	6.2	0.978	0.204	0.269
Tyrosine-protein phosphatase non-receptor type 23;	Q6PB44	1	3	3	2.8	0.978	0.293	0.300
H-2 class II histocompatibility antigen, A-Q alpha chain;	P04227	1	3	3	6.8	0.986	0.085	0.243
Non-specific lipid-transfer protein;	P32020	1	12	19	10.8	0.986	0.393	0.329
FAS-associated factor 1;	P54731	1	2	2	1.7	0.986	0.174	0.256
Protein KIAA1967 homolog;	Q8VDP4	1	3	3	3.1	0.993	0.259	0.277
Gamma-interferon-inducible lysosomal thiol reductase;	Q9ESY9	1	2	2	5.2	0.993	0.105	0.241
Histone deacetylase 1;	O09106	1	3	3	10.4	0.993	0.419	0.335
Inosine triphosphate pyrophosphatase;	Q9D892	1	8	9	28.3	1	0.1	0.238
RuvB-like 1;	P60122	1	2	2	4.6	1	0.15	0.247
Ubiquitin-like-conjugating enzyme ATG3;	Q9CPX6	1	2	2	4.1	1.007	0.095	0.233
Fatty acid synthase;	P19096	1	116	176	37.7	1.014	0.909	0.511
Talin-1;	P26039	1	79	89	31.3	1.014	0.909	0.511
Talin-2;	Q71LX4	1	6	7	6.1	-0.136	-0.03	0.884
Far upstream element (FUSE) binding protein 3; MCG130458; Uncharacterized protein;	A2AJ72	1	4	4	10.9	1.014	0.141	0.236
Ferric-chelate reductase 1;	Q8K385	1	2	2	3.5	1.014	0.11	0.231
Tyrosine-protein phosphatase non-receptor type 6;	P29351	1	12	12	17.6	1.021	0.282	0.266
Fascin;	Q61553	1	6	7	13.6	1.021	0.096	0.226
Phosphoribosyl pyrophosphate synthase-associated protein 2;	Q8R574	1	2	2	10.6	1.021	0.121	0.230
Sulfotransferase family cytosolic 2B member 1;	O35400	1	4	5	11.2	1.021	0.05	0.220
Small ubiquitin-related modifier 1;	P63166	1	2	3	11.9	1.029	0.383	0.298
Peptidyl-prolyl cis-trans isomerase FKBP4;	P30416	1	15	15	27.7	1.05	0.259	0.248
Leucyl-tRNA synthetase, cytoplasmic;	Q8BMJ2	1	5	5	5.9	1.057	0.224	0.232
Signal transducer and activator of transcription 1;	P42225	1	4	4	7.1	1.057	0.274	0.248
Ras-related protein Rab-21;	P35282	1	9	12	33.3	1.064	0.972	0.495

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Tubulin beta-5 chain;	P99024	1	6	12	52	1.064	0.249	0.238
Tubulin beta-2A chain;	Q7TMM9	1	4	6	42.5	0.978	0.109	0.250
Tubulin beta-4B chain;	P68372	1	3	4	52.4	1.084	0.097	0.199
Ubiquitin-associated protein 2-like;	Q80X50	1	6	6	5.7	1.064	0.122	0.212
Interferon-induced guanylate-binding protein 2;	Q9Z0E6	1	13	15	17	1.064	0.265	0.243
SUMO-activating enzyme subunit 2;	Q9Z1F9	1	15	18	16.5	1.064	0.173	0.221
CD44 antigen;	P15379	0.998	2	2	4.5	1.064	0.214	0.229
Phosphoserine aminotransferase;	Q99K85	1	21	23	41.9	1.07	0.214	0.226
26S proteasome non-ATPase regulatory subunit 7;	P26516	1	8	9	31.5	1.077	0.107	0.204
Cytosolic acyl coenzyme A thioester hydrolase;	Q91V12	1	5	6	16.3	1.077	0.398	0.275
Inositol monophosphatase 2;	Q91UZ5	1	4	6	11	1.084	0.153	0.207
Calmodulin-4;	Q9JM83	1	12	25	41.2	1.084	0.138	0.205
Coronin-1A;	O89053	1	8	10	10.8	1.084	0.225	0.219
Dynamin-2;	P39054	1	2	2	7	1.084	0.169	0.208
Transportin-1;	Q8BFY9	1	5	5	9.4	1.091	0.246	0.223
Transportin-2;	Q99LG2	1	3	3	7	1.163	0.421	0.236
Calponin-2;	Q08093	1	5	5	16.1	1.098	0.072	0.190
Dermokine;	Q6P253	1	5	6	10.4	1.098	0.113	0.195
Serine/threonine-protein kinase 24;	Q99KH8	1	6	8	10.7	1.104	0.462	0.281
Lysosome-associated membrane glycoprotein 2;	P17047	1	5	6	6.5	1.118	0.577	0.316
Ganglioside GM2 activator;	Q60648	1	4	4	20.7	1.118	0.129	0.187
Poly(rC)-binding protein 1;	P60335	1	11	19	40.7	1.118	0.345	0.238
Poly(rC)-binding protein 2;	Q61990	1	10	15	26	0.856	0.17	0.332
Aldo-keto reductase family 1 member C18;	Q8K023	1	4	4	14.6	1.118	0.144	0.191
Aspartyl-tRNA synthetase, cytoplasmic;	Q922B2	1	11	11	16	1.118	0.649	0.345
Cation-dependent mannose-6-phosphate receptor;	P24668	1	2	2	9.7	1.118	0.252	0.210
Dipeptidyl peptidase 1;	P97821	1	10	11	15.4	1.124	0.093	0.182
26S proteasome non-ATPase regulatory subunit 2;	Q8VDM4	1	17	25	18.7	1.124	0.294	0.220
Amidophosphoribosyltransferase;	Q8CIH9	1	3	3	6	1.131	0.356	0.235
Uncharacterized protein;	E9Q4K7	1	6	7	3	1.138	0.316	0.219
F-actin-capping protein subunit alpha-1;	P47753	1	11	19	32.9	1.144	0.326	0.219
Glutaminyl-tRNA synthetase; Uncharacterized protein;	Q8BML9	1	13	14	20.3	1.144	0.595	0.306
Sorting nexin-3;	O70492	0.908	2	2	9.3	1.151	0.404	0.239
Cellular nucleic acid-binding protein;	P53996	1	2	2	7.3	1.17	0.203	0.179
Protein FAM49B;	Q921M7	1	8	10	33.6	1.17	0.598	0.293
Coatomer subunit beta';	O55029	1	2	2	4.5	1.176	0.369	0.217
N-acetylneuraminate lyase;	Q9DCJ9	1	18	21	55.3	1.176	0.541	0.269
Adenylyl cyclase-associated protein 1;	P40124	1	22	32	35	1.183	0.240	0.180
Protein phosphatase 1A;	P49443	1	4	4	13	1.189	0.271	0.184
T-complex protein 1 subunit eta;	P80313	1	5	5	11.6	1.189	0.302	0.191
Bcl-2-like protein 13;	P59017	1	4	4	12	1.208	0.173	0.160
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Q76MZ3	1	22	27	30.4	1.208	0.758	0.325
Adenosine deaminase;	P03958	1	5	5	17	1.214	0.434	0.213

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26S proteasome non-ATPase regulatory subunit 6;	Q99JI4	1	9	10	19.5	1.214	0.570	0.257
Periostin;	Q62009	1	12	12	12.1	1.214	0.141	0.152
Nucleoside diphosphate-linked moiety X motif 17;	Q9CWD3	1	2	2	11.8	1.227	0.288	0.172
Ubiquitin carboxyl-terminal hydrolase 4;	P35123	1	5	5	5.2	1.227	0.593	0.258
Histone-binding protein RBBP7;	Q60973	1	2	2	4.7	1.227	0.220	0.159
14-3-3 protein sigma;	O70456	1	13	46	37.5	1.239	0.341	0.181
T-complex protein 1 subunit delta;	P80315	1	9	9	15	1.239	0.578	0.246
Asparagine synthetase [glutamine-hydrolyzing];	Q61024	1	3	3	3.6	1.239	0.089	0.141
Phosphatidylinositol-binding clathrin assembly protein;	Q7M6Y3	1	3	3	5.3	1.239	0.362	0.184
Uncharacterized protein;	F7BJK1	1	2	2	0.8	1.239	0.184	0.151
Proliferating cell nuclear antigen;	P17918	1	8	9	27.2	1.239	0.284	0.167
Elongation factor 1-delta;	P57776	1	2	2	38.8	1.239	0.562	0.244
Chloride channel calcium activated 2; Endothelial chloride channel; MCG120735; Uncharacterized protein;	Q9EQR4	1	17	19	23.5	1.239	0.409	0.198
Uncharacterized protein;	E9PUF7	0.984	2	2	4.2	1.239	0.163	0.148
Protein Niban;	Q3UW53	1	10	10	15.4	1.245	0.636	0.263
Ras-related C3 botulinum toxin substrate 1;	P63001	1	10	15	34.4	1.251	0.279	0.162
Cell division control protein 42 homolog;	P60766	1	8	11	32.5	0.714	0.078	0.402
Mevalonate kinase;	Q9R008	1	5	6	23.3	1.257	0.289	0.160
Cadherin-1;	P09803	1	3	4	4.9	1.263	0.232	0.149
Cellular retinoic acid-binding protein 2;	P22935	1	7	7	41.3	1.263	0.126	0.135
tRNA (cytosine(34)-C(5))-methyltransferase;	Q1HFZ0	1	3	3	5.7	1.263	0.837	0.319
Alcohol dehydrogenase 1;	P00329	1	2	2	8	1.263	0.089	0.132
Ras-related protein Rab-18;	P35293	1	2	2	6.8	1.269	0.242	0.147
SEC14-like protein 4;	Q8R0F9	1	11	15	32.3	1.269	0.379	0.175
26S proteasome non-ATPase regulatory subunit 8;	Q9CX56	1	3	6	11.3	1.275	0.448	0.191
Uncharacterized protein;	E9PYU6	1	6	6	1.7	1.275	0.300	0.156
Oxysterol-binding protein-related protein 9;	A2A8Z1	0.998	2	2	4.9	1.275	0.738	0.280
Isoleucyl-tRNA synthetase, cytoplasmic;	Q8BU30	0.997	3	3	3.3	1.275	0.443	0.191
Vacuolar protein sorting-associated protein 4B;	P46467	1	3	3	12.6	1.281	0.648	0.249
Cystatin-B;	Q62426	1	3	6	32.7	1.281	0.084	0.127
Importin-7;	Q9EPL8	1	6	7	7.2	1.281	0.643	0.245
Rho-associated protein kinase 2;	P70336	1	3	3	3.3	1.287	0.733	0.273
Protein Hook homolog 3;	Q8BUK6	1	2	2	4.2	1.287	0.274	0.146
Diphosphomevalonate decarboxylase;	Q99JF5	1	6	10	14.5	1.287	0.158	0.131
Lysosomal protective protein;	P16675	1	19	25	19.8	1.287	0.095	0.125
Transcription intermediary factor 1-beta;	Q62318	1	7	7	5.4	1.293	0.654	0.243
Pantetheinase;	Q9Z0K8	1	4	5	10.2	1.293	0.670	0.247
Lysosomal Pro-X carboxypeptidase;	Q7TMR0	1	2	2	9.6	1.293	0.391	0.169
Signal transducer and activator of transcription 5A;	P42230	1	2	2	2.4	1.299	0.169	0.129
Large proline-rich protein BAG6;	Q9Z1R2	1	3	4	4.7	1.299	0.216	0.134
Uncharacterized protein;	E9Q7G0	1	7	8	8.3	1.305	1.025	0.353
Lymphocyte-specific protein 1;	P19973	1	3	4	13.7	1.316	0.270	0.136

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Fibulin-5;	Q9WVH9	1	11	12	23.7	1.316	0.159	0.121
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);	Q8VC30	1	6	9	9.5	1.316	0.359	0.152
26S proteasome non-ATPase regulatory subunit 1;	Q3TXS7	1	21	28	23	1.328	0.450	0.169
Leucyl-cystinyl aminopeptidase;	Q8C129	1	2	2	3.1	1.328	0.497	0.180
T-complex protein 1 subunit alpha;	P11983	1	5	5	9	1.339	0.376	0.148
Latexin;	P70202	1	5	6	17.6	1.350	0.122	0.110
Heparan N-sulfatase; N-sulfoglucosamine sulfohydrolase (Sulfamidase); N-sulfoglucosamine sulfohydrolase (Sulfamidase), isoform CRA_b; Uncharacterized protein;	Q9EQ08	1	2	2	3.2	1.350	0.365	0.143
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-2;	Q8CIH5	1	2	2	2.1	1.356	0.260	0.123
Tax1-binding protein 3;	Q9DBG9	1	4	5	13.7	1.356	0.900	0.285
PDZ and LIM domain protein 1;	O70400	1	6	8	29.4	1.362	0.334	0.133
Perilipin-4;	O88492	1	43	74	42.9	1.367	0.736	0.230
26S protease regulatory subunit 7;	P46471	1	9	9	19.2	1.367	0.466	0.157
Ectonucleoside triphosphate diphosphohydrolase 1;	P55772	1	3	3	5.9	1.367	0.334	0.131
Arfip1 protein; Uncharacterized protein;	A2RSX9	1	2	2	11.7	1.367	0.286	0.122
Ly6/PLAUR domain-containing protein 3;	Q91YK8	1	2	2	5.2	1.373	0.398	0.141
Alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB); Uncharacterized protein;	A2BFA6	1	2	2	4.1	1.373	0.355	0.133
Secretory carrier-associated membrane protein 2;	Q9ERN0	1	2	2	3.6	1.384	0.159	0.103
T-complex protein 1 subunit epsilon;	P80316	1	6	6	11.3	1.384	0.361	0.130
Uncharacterized protein;	E9Q9C6	1	9	9	4.2	1.384	0.334	0.126
Guanylate-binding protein 4;	Q61107	1	3	3	5.3	1.390	0.605	0.183
Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2;	Q6ZQK5	1	3	4	3.8	1.395	0.827	0.244
MOB kinase activator 1B;	Q8BPB0	1	3	3	10.6	1.395	0.149	0.099
BRO1 domain-containing protein BROX;	Q8K2Q7	1	3	3	11.9	1.401	0.287	0.114
CD 81 antigen, isoform CRA_c; CD81 antigen; Tapa-1 protein; Uncharacterized protein;	Q91V78	1	2	2	19.1	1.406	0.276	0.111
Lipopolysaccharide-responsive and beige-like anchor protein;	Q9ESE1	1	5	5	2.6	1.417	0.265	0.106
Alcohol dehydrogenase class 4 mu/sigma chain;	Q64437	1	14	22	43.3	1.428	1.109	0.307
Acetyl-CoA acetyltransferase, cytosolic;	Q8CAY6	1	7	8	38.5	1.433	0.494	0.140
Bifunctional aminoacyl-tRNA synthetase;	Q8CGC7	1	16	16	11.4	1.438	0.499	0.139
F-box only protein 6;	Q9QZN4	1	2	2	7.1	1.438	0.801	0.214
Acid ceramidase;	Q9WV54	1	8	9	18.8	1.449	0.276	0.098
Epidermal growth factor receptor kinase substrate 8-like protein 2;	Q99K30	0.998	2	2	3.7	1.449	0.393	0.116
Phosphoserine phosphatase;	Q99LS3	1	4	8	16.4	1.454	0.196	0.089
Nuclear autoantigenic sperm protein;	Q99MD9	1	3	4	9.8	1.459	0.170	0.086
Early endosome antigen 1;	Q8BL66	1	9	10	8.2	1.459	0.451	0.123
26S protease regulatory subunit 4;	P62192	1	12	13	22.7	1.480	0.371	0.104
Ubiquitin-conjugating enzyme E2 D3;	P61079	1	2	3	19.7	1.485	0.154	0.079
Uncharacterized protein;	Q8BVL6	1	2	3	5.6	1.485	0.122	0.078
Uncharacterized protein;	E9PZ00	1	14	31	16.7	1.496	0.647	0.151
V-type proton ATPase subunit H;	Q8BVE3	1	8	8	16.6	1.511	0.392	0.098
6-phosphofructokinase type C;	Q9WUA3	1	13	15	24.9	1.521	0.996	0.228

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Acetoacetyl-CoA synthetase;	Q9D2R0	1	8	9	12.9	1.526	0.477	0.107
Clathrin interactor 1; MCG22297, isoform CRA_b; Uncharacterized protein;	Q5SUH6	1	4	4	8.8	1.531	0.238	0.077
Protein diaphanous homolog 1;	O08808	1	9	9	8.5	1.536	0.461	0.101
Importin-5;	Q8BKC5	1	15	17	17.6	1.536	0.916	0.198
Alpha-galactosidase A;	P51569	1	4	4	8.1	1.546	0.418	0.092
Neutrophil cytosol factor 4;	P97369	1	3	3	7.4	1.546	0.259	0.074
StAR-related lipid transfer protein 5;	Q9EPQ7	1	3	3	24.4	1.551	0.307	0.078
Uncharacterized protein;	E9PZZ3	1	5	5	2.6	1.570	0.539	0.106
RNA-binding protein 14;	Q8C2Q3	1	2	2	6.5	1.570	0.322	0.076
1-acylglycerol-3-phosphate O-acyltransferase ABHD5;	Q9DBL9	1	2	2	4.8	1.580	0.233	0.066
Serine hydroxymethyltransferase, cytosolic;	P50431	1	3	3	7.3	1.585	0.317	0.073
Poly(U)-binding-splicing factor PUF60;	Q3UEB3	1	6	7	13.3	1.590	0.576	0.107
Angio-associated migratory protein; Uncharacterized protein;	Q3TJ22	1	3	3	3	1.590	0.275	0.067
Sphingomyelin phosphodiesterase;	Q04519	1	2	2	4	1.595	0.227	0.064
Heat shock protein 75 kDa, mitochondrial;	Q9CQN1	1	6	7	13.9	1.599	0.290	0.067
Proactivator polypeptide-like 1;	Q8C1C1	1	2	2	5.4	1.609	0.559	0.098
T-cell specific GTPase; Uncharacterized protein;	Q5SVP4	1	2	2	14.4	1.614	0.237	0.060
Dehydrogenase/reductase SDR family member 1;	Q99L04	1	4	5	10.5	1.642	0.258	0.057
Carboxypeptidase E;	Q00493	1	5	6	17	1.646	0.663	0.105
Ribosomal protein S6 kinase alpha-1;	P18653	1	3	3	5	1.651	0.237	0.054
Uroporphyrinogen decarboxylase;	P70697	1	7	7	16.1	1.674	0.561	0.082
Deoxyribonuclease-2-alpha;	P56542	1	7	9	22.3	1.678	1.573	0.291
Apolipoprotein C-III;	P33622	1	3	4	19.2	1.687	0.110	0.044
Treacle protein;	O08784	1	2	2	1.8	1.692	0.278	0.051
Fatty acid-binding protein, epidermal;	Q05816	1	17	81	65.2	1.696	0.230	0.047
Pleckstrin homology domain-containing family O member 2;	Q8K124	1	2	2	10.3	1.705	0.664	0.090
Cytoplasmic dynein 1 heavy chain 1;	Q9JHU4	1	18	18	5.4	1.709	0.408	0.058
Chitotriosidase-1;	Q9D7Q1	0.977	2	2	4.5	1.722	0.204	0.043
Uncharacterized protein;	E9Q4Z2	1	7	7	3.8	1.731	0.480	0.061
Exportin-1;	Q6P5F9	1	6	6	6.6	1.748	0.411	0.052
Apoptosis-associated speck-like protein containing a CARD;	Q9EPB4	1	9	13	35.2	1.757	0.639	0.075
Putative phospholipase B-like 2;	Q3TCN2	1	10	13	13.6	1.770	0.618	0.069
SEC23-interacting protein;	Q6NZC7	1	3	3	5.4	1.778	0.259	0.038
Uncharacterized protein;	D3Z4B0	1	2	2	13	1.778	0.187	0.036
ATP-citrate synthase;	Q91V92	1	35	43	29.5	1.803	0.568	0.058
Isopentenyl-diphosphate Delta-isomerase 1;	P58044	1	3	4	18.9	1.828	0.896	0.094
Latent-transforming growth factor beta-binding protein 4;	Q8K4G1	1	4	4	3.9	1.856	0.795	0.073
Tumor necrosis factor receptor type 1-associated DEATH domain protein;	Q3U0V2	1	6	6	17.1	1.860	0.272	0.030
General transcription factor II-I;	Q9ESZ8	1	2	2	1.7	1.876	0.434	0.037
Importin subunit beta-1;	P70168	1	12	14	12	1.899	0.524	0.040
Aldehyde dehydrogenase;	E9Q3E1	1	7	7	16.5	1.899	0.545	0.041
Cathepsin D;	P18242	1	26	56	37.6	1.930	0.350	0.027
Methylthioribose-1-phosphate isomerase;	Q9CQT1	1	4	4	9.2	1.963	0.327	0.024

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-glutamine gamma-glutamyltransferase E;	Q08189	1	5	5	9.2	1.993	0.481	0.027
Short-chain dehydrogenase/reductase family 16C member 6;	Q05A13	1	3	3	10.1	1.996	1.086	0.082
Cystatin E/M; Cystatin M/E; Uncharacterized protein;	Q9D1B1	1	7	12	49	1.996	0.460	0.026
Retroviral-like aspartic protease 1;	Q09PK2	1	10	21	28	2.046	0.530	0.025
Protein S100-A14;	Q9D2Q8	1	2	3	33.7	2.053	0.143	0.015
Hydroxymethylglutaryl-CoA synthase, cytoplasmic;	Q8JZK9	1	14	18	25	2.070	0.789	0.038
Gamma-glutamyl hydrolase;	Q9Z0L8	1	3	3	12	2.091	0.358	0.016
Uridine 5'-monophosphate synthase;	P13439	1	4	4	11.4	2.094	1.103	0.063
Exportin-2;	Q9ERK4	1	3	3	8.2	2.118	0.332	0.014
Long-chain-fatty-acid--CoA ligase 4;	Q9QUJ7	1	2	2	2.7	2.121	0.395	0.016
Leucine-rich PPR motif-containing protein, mitochondrial;	Q6PB66	0.997	2	2	2.7	2.121	0.536	0.020
Glucocorticoid receptor;	P06537	1	4	4	7.8	2.170	0.473	0.015
Interleukin-36 alpha;	Q9JLA2	1	2	2	8.8	2.186	0.480	0.014
Lymphocyte antigen 6D;	P35459	1	3	4	48	2.239	0.934	0.029
Eosinophil cationic-type ribonuclease 5;	O35292	1	2	3	9.7	2.310	0.410	0.008
Desmoglein-1-gamma;	Q7TSF0	0.991	2	2	2.6	2.319	0.785	0.016
Carboxypeptidase A4;	Q6P8K8	1	6	7	12.1	2.348	0.438	0.007
Uncharacterized protein;	F8VQ05	1	2	2	1.1	2.370	0.601	0.009
Caspase-14;	O89094	1	8	10	26.1	2.480	0.707	0.008
Lymphocyte antigen 6 complex locus protein G6c;	Q9Z1Q4	1	2	2	14.3	2.485	0.821	0.010
Metastasis-associated protein MTA1;	Q8K4B0	1	2	2	3.6	2.524	0.465	0.004
Monoglyceride lipase;	O35678	1	8	10	33	2.568	0.896	0.008
Gasdermin-A;	Q9EST1	1	7	9	17.3	2.816	1.408	0.011
Tumor suppressor p53-binding protein 1;	P70399	1	2	2	3.8	3.155	0.928	0.001
Junctional adhesion molecule A;	O88792	1	3	3	11.3	3.259	0.531	0.000
Perilipin-2;	P43883	1	14	20	31.3	3.458	2.218	0.005
Thrombospondin-1;	P35441	1	3	3	3.1	3.597	0.389	0.000
Cornifin-A;	Q62266	1	2	3	27.8	4.328	0.606	0.000
Afadin;	Q9QZQ1	0.991	2	2	1.7	4.655	1.175	0.000
Uncharacterized protein;	D3YTN4	1	3	3	8.2	6.141	1.664	0
Bifunctional coenzyme A synthase;	Q9DBL7	1	2	2	1.6	9.298	0.15	0
CD2-associated protein;	Q9JLQ0	1	3	3	4.4	9.298	0.15	0