Supplimentary Table 1: List of all identified proteins and their relative quantitation (sorted by protein name)

Identified Proteins (582)	Acc. No.	Mol. W.	Seq. coverage	No. of unique peptides	Tag_114	Tag_115	Tag_116	Tag_117	Ratio (KO/Ctrl)	T-test
10 kDa heat shock protein, mitochondrial OS=Mus musculus GN	Q64433	11 kDa	61.00%	8	1	1.0	1.0	1.1	1.1	0.42
14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 S	Q9CQV8 (+1)	28 kDa	46.00%	5	1	0.9	1.2	1.2	1.3	0.04
14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	P62259	29 kDa	51.00%	10	1	0.9	1.0	1.1	1.1	0.29
14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	P68510	28 kDa	27.00%	2	1	0.6	0.8	0.8	1.0	0.98
14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	P61982	28 kDa	58.00%	13	1	1.0	1.0	1.1	1.1	0.42
14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV	P63101	28 kDa	44.00%	5	1	0.9	1.1	1.1	1.2	0.03
2,4-dienoyl-CoA reductase, mitochondrial OS=Mus musculus GN	Q9CQ62	36 kDa	35.00%	9	1	1.0	1.0	1.1	1.0	0.42
26S protease regulatory subunit 6A OS=Mus musculus GN=Psm	A2AGN7 (+2)	45 kDa	6.80%	2	1	#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!
26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2	P46471 (+1)	49 kDa	6.00%	2	1	2.0	1.9	0.9	0.9	0.90
26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5	Q8K1K2	39 kDa	9.20%	2	1	2.3	2.3	2.8	1.6	0.32
26S proteasome non-ATPase regulatory subunit 11 OS=Mus mu	Q8BG32	47 kDa	8.30%	3	1	0.9	1.0	0.9	1.0	0.71
26S proteasome non-ATPase regulatory subunit 13 OS=Mus mu	E9Q5I9 (+1)	40 kDa	6.00%	2	1	0.9	1.0	1.5	1.3	0.35
26S proteasome non-ATPase regulatory subunit 2 OS=Mus mus	Q8VDM4	100 kDa	3.40%	3	1	1.1	1.3	1.1	1.1	0.49
26S proteasome non-ATPase regulatory subunit 6 OS=Mus mus	Q99JI4	46 kDa	6.20%	2	1	0.8	1.1	1.0	1.2	0.34
28S ribosomal protein S36, mitochondrial OS=Mus musculus GN	Q9CQX8 (+1)	11 kDa	46.00%	3	1	1.1	1.0	1.1	1.0	1.00
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochond	Q9CXI0	37 kDa	6.10%	2	1	1.1	1.1	1.1	1.1	0.42
2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculu	Q60597	116 kDa	43.00%	38	1	1.1	1.1	1.3	1.1	0.29
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial O	P50136 (+1)	50 kDa	9.30%	3	1	1.0	1.3	1.3	1.3	0.00
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS	Q6P3A8	43 kDa	14.00%	4	1	1.1	1.0	1.1	1.0	0.69
39S ribosomal protein L28, mitochondrial OS=Mus musculus GN	Q9D1B9	30 kDa	8.20%	2	1	1.3	1.6	1.5	1.4	0.14
3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN	A2AFQ2 (+2)	28 kDa	20.00%	4	1	0.7	0.8	0.9	1.0	0.94
3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Mus m	Q99L13	35 kDa	18.00%	5	1	1.6	1.5	1.7	1.2	0.44
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Mus mus	Q8QZS1	43 kDa	14.00%	5	1	1.1	1.1	1.2	1.1	0.32
3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=A	Q8BWT1	42 kDa	56.00%	14	1	1.2	1.1	1.3	1.1	0.68
40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV	P63325	19 kDa	28.00%	4	1	0.9	1.1	1.1	1.2	0.03

40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV	P63323 (+1)	15 kDa	13.00%	2	1	0.8	1.1	1.2	1.3	0.11
40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV	P14131	16 kDa	17.00%	3	1	0.9	1.0	1.0	1.1	0.42
40S ribosomal protein S19 (Fragment) OS=Mus musculus GN=Rp	D3YUG3 (+5)	15 kDa	16.00%	2	1	0.8	0.9	1.1	1.2	0.42
40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=	D3YV43 (+1)	21 kDa	14.00%	2	1	1.1	0.9	1.3	1.1	0.69
40S ribosomal protein S3a OS=Mus musculus GN=Rps3a2 PE=3 S	D3Z6C3 (+2)	30 kDa	11.00%	3	1	1.0	1.1	1.2	1.2	0.20
40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=	P62754	29 kDa	8.80%	2	1	0.7	1.0	1.1	1.2	0.35
40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=	P62242	24 kDa	9.60%	2	1	0.8	0.9	1.1	1.1	0.50
40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=1 SV=	Q6ZWN5	23 kDa	9.80%	2	1	1.1	1.1	1.1	1.1	0.29
40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=	P14206	33 kDa	9.50%	2	1	1.0	0.9	0.9	0.9	0.00
60 kDa heat shock protein, mitochondrial OS=Mus musculus GN	P63038	61 kDa	35.00%	16	1	0.9	0.9	1.1	1.0	0.69
60S acidic ribosomal protein P0 (Fragment) OS=Mus musculus G	D3YVM5 (+2)	16 kDa	14.00%	2	1	1.0	0.9	1.1	1.0	0.98
60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1	P19253 (+1)	23 kDa	8.40%	2	1	0.7	0.9	1.0	1.1	0.53
60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1	P62717	21 kDa	12.00%	2	1	0.9	1.5	1.2	1.4	0.11
60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=1 SV	Q8BP67	18 kDa	11.00%	2	1	0.9	1.1	1.0	1.1	0.31
60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	Q9D8E6	47 kDa	5.50%	2	1	1.0	0.9	1.1	1.0	0.95
60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	P47962	34 kDa	5.10%	2	1	0.8	1.3	1.2	1.4	0.07
60S ribosomal protein L6 OS=Mus musculus GN=Gm5428 PE=3 S	E9PUX4 (+1)	34 kDa	13.00%	4	1	1.0	1.0	1.1	1.1	0.42
60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2	P14148	31 kDa	10.00%	3	1	1.1	1.2	1.2	1.1	0.17
6-phosphofructokinase OS=Mus musculus GN=Pfkp PE=1 SV=1	Q8C605 (+1)	86 kDa	5.20%	2	1	0.7	0.8	1.0	1.1	0.84
78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5	P20029	72 kDa	31.00%	13	1	0.9	0.9	1.1	1.1	0.55
Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus	Q8QZT1	45 kDa	41.00%	13	1	1.1	1.0	1.1	1.0	0.69
Acetyl-coenzyme A synthetase 2-like, mitochondrial OS=Mus mu	Q99NB1	75 kDa	15.00%	8	1	1.0	1.1	1.2	1.2	0.20
Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2	Q99KI0	85 kDa	51.00%	34	1	1.1	1.1	1.2	1.1	0.32
Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1	P68033	42 kDa	47.00%	17	1	1.2	0.9	1.1	0.9	0.49
Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	P60710 (+1)	42 kDa	41.00%	4	1	1.2	1.1	1.0	0.9	0.58
Actin-related protein 2/3 complex subunit 2 OS=Mus musculus	Q9CVB6	34 kDa	8.30%	3	1	0.9	1.1	1.1	1.2	0.03
Actin-related protein 2/3 complex subunit 4 OS=Mus musculus	P59999	20 kDa	15.00%	3	1	0.9	1.0	0.9	1.0	1.00
Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3	Q99JY9	47 kDa	5.70%	2	1	0.9	0.8	0.9	0.8	0.15

Acyl carrier protein (Fragment) OS=Mus musculus GN=Ndufab1	F6ZFT1 (+2)	14 kDa	17.00%	3	1	0.9	1.1	1.1	1.1	0.09
Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2	P31786	10 kDa	47.00%	3	1	0.9	0.9	1.1	1.1	0.55
Acyl-coenzyme A thioesterase 13 OS=Mus musculus GN=Acot13	Q9CQR4	15 kDa	16.00%	2	1	1.1	1.1	1.1	1.1	0.29
Acyl-coenzyme A thioesterase 2, mitochondrial OS=Mus muscul	Q9QYR9	50 kDa	23.00%	9	1	0.9	0.9	1.1	1.1	0.58
Acylphosphatase-2 OS=Mus musculus GN=Acyp2 PE=2 SV=2	P56375	12 kDa	34.00%	4	1	1.1	1.1	1.2	1.1	0.11
Acylpyruvase FAHD1, mitochondrial OS=Mus musculus GN=Fah	Q8R0F8	25 kDa	9.30%	2	1	1.1	1.4	1.3	1.3	0.03
Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2	P55264 (+1)	40 kDa	5.30%	2	1	1.1	1.3	1.2	1.2	0.15
Adenylate kinase isoenzyme 1 OS=Mus musculus GN=Ak1 PE=1	Q9R0Y5 (+1)	22 kDa	49.00%	10	1	1.0	1.0	1.1	1.1	0.42
Adenylosuccinate synthetase isozyme 1 OS=Mus musculus GN=	J3QN31 (+2)	53 kDa	11.00%	4	1	1.1	1.1	1.2	1.1	0.55
Adiponectin OS=Mus musculus GN=Adipoq PE=1 SV=2	Q60994	27 kDa	11.00%	2	1	1.2	1.0	1.1	1.0	0.79
ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=	P48962	33 kDa	52.00%	18	1	1.1	1.0	1.1	1.0	0.69
ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=	P51881	33 kDa	43.00%	6	1	1.0	0.9	1.1	1.0	0.98
ADP-ribosylation factor 3 OS=Mus musculus GN=Arf3 PE=2 SV=2	P61205 (+1)	21 kDa	13.00%	2	1	0.9	0.9	1.1	1.1	0.58
AFG3-like protein 2 OS=Mus musculus GN=Afg3l2 PE=1 SV=1	Q8JZQ2	90 kDa	7.90%	6	1	1.0	0.9	1.1	1.0	0.98
Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus G	Q8CG76	41 kDa	7.10%	2	1	1.1	0.9	1.2	1.0	0.97
A-kinase anchor protein 12 OS=Mus musculus GN=Akap12 PE=1	Q9WTQ5 (+1)	181 kDa	2.10%	2	1	0.8	0.9	1.1	1.1	0.50
Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=	P47738	57 kDa	30.00%	11	1	1.1	1.1	1.2	1.1	0.11
Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3	P45376	36 kDa	32.00%	9	1	1.0	1.1	1.2	1.2	0.20
Alpha-1-antitrypsin 1-3 OS=Mus musculus GN=Serpina1c PE=1 S	Q00896	46 kDa	24.00%	8	1	1.1	0.9	0.9	0.9	0.10
Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1	P29699	37 kDa	7.00%	2	1	2.1	1.9	3.2	1.6	0.39
Alpha-2-macroglobulin OS=Mus musculus GN=Pzp PE=4 SV=1	D3YW52 (+1)	167 kDa	3.60%	4	1	1.1	1.0	1.0	1.0	0.42
Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=2	Q9JI91	104 kDa	47.00%	34	1	1.1	0.9	1.0	0.9	0.32
Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2	P23927	20 kDa	55.00%	8	1	0.9	1.0	1.1	1.1	0.29
Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	P17182	47 kDa	24.00%	5	1	1.0	1.0	1.2	1.1	0.42
Aminoacyl tRNA synthase complex-interacting multifunctional p	P31230 (+1)	34 kDa	12.00%	2	1	0.9	0.9	1.0	1.0	1.00
Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	P07356	39 kDa	25.00%	8	1	0.9	0.9	1.0	1.0	0.71
Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	P48036	36 kDa	35.00%	9	1	0.9	1.1	1.1	1.1	0.11
Annexin OS=Mus musculus GN=Anxa6 PE=1 SV=1	F8WIT2 (+1)	75 kDa	10.00%	6	1	1.0	1.0	1.1	1.0	0.42

AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=	O35643 (+2)	104 kDa	2.20%	2	1	0.8	0.8	1.0	1.0	1.00
Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=2	Q00623	31 kDa	34.00%	9	1	1.2	1.1	1.0	0.9	0.58
Apolipoprotein A-IV OS=Mus musculus GN=Apoa4 PE=1 SV=3	P06728	45 kDa	6.60%	3	1	1.1	1.2	0.9	1.0	0.97
Apolipoprotein O OS=Mus musculus GN=Apoo PE=4 SV=1	B1ASQ2 (+2)	23 kDa	39.00%	6	1	1.0	1.0	1.1	1.0	0.42
Apolipoprotein O-like OS=Mus musculus GN=Apool PE=2 SV=1	Q78IK4	29 kDa	19.00%	4	1	1.1	1.1	1.0	1.0	1.00
Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus G	B1AU25 (+1)	66 kDa	23.00%	11	1	1.1	1.1	1.1	1.0	0.71
Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN	P05201	46 kDa	46.00%	15	1	0.9	1.0	1.1	1.1	0.29
Aspartate aminotransferase, mitochondrial OS=Mus musculus G	P05202	47 kDa	37.00%	18	1	1.1	1.1	1.3	1.2	0.17
Aspartyl aminopeptidase OS=Mus musculus GN=Dnpep PE=2 SV	Q9Z2W0	52 kDa	5.30%	2	1	1.1	0.9	1.1	0.9	0.61
Aspartyl/asparaginyl beta-hydroxylase OS=Mus musculus GN=A	A2AL85 (+2)	81 kDa	4.40%	2	1	1.1	1.0	1.1	1.0	1.00
ATP synthase F(0) complex subunit B1, mitochondrial OS=Mus m	Q9CQQ7	29 kDa	31.00%	12	1	1.1	1.0	1.1	1.0	0.69
ATP synthase protein 8 OS=Mus musculus GN=Mtatp8 PE=1 SV=	P03930 (+1)	8 kDa	43.00%	3	1	1.1	1.0	1.1	1.0	1.00
ATP synthase subunit alpha, mitochondrial OS=Mus musculus G	Q03265	60 kDa	48.00%	24	1	1.0	1.0	1.1	1.0	0.42
ATP synthase subunit beta, mitochondrial OS=Mus musculus GN	P56480	56 kDa	50.00%	19	1	1.0	0.9	1.1	1.0	0.98
ATP synthase subunit delta, mitochondrial OS=Mus musculus GI	Q9D3D9	18 kDa	17.00%	3	1	1.1	0.9	1.1	1.0	0.97
ATP synthase subunit e, mitochondrial OS=Mus musculus GN=A	Q06185	8 kDa	52.00%	4	1	1.0	0.9	1.0	1.0	0.42
ATP synthase subunit epsilon, mitochondrial OS=Mus musculus	P56382	6 kDa	29.00%	2	1	0.9	1.1	1.1	1.1	0.09
ATP synthase subunit f, mitochondrial OS=Mus musculus GN=At	P56135	10 kDa	26.00%	2	1	1.1	0.9	1.1	1.0	0.82
ATP synthase subunit g, mitochondrial OS=Mus musculus GN=A	Q9CPQ8	11 kDa	34.00%	4	1	0.9	1.0	1.0	1.1	0.42
ATP synthase subunit gamma OS=Mus musculus GN=Atp5c1 PE=	A2AKU9 (+2)	33 kDa	21.00%	6	1	0.9	0.9	1.1	1.0	0.69
ATP synthase subunit O, mitochondrial OS=Mus musculus GN=A	Q9DB20	23 kDa	42.00%	8	1	1.1	1.1	1.1	1.1	0.29
ATP synthase-coupling factor 6, mitochondrial OS=Mus musculu	P97450	12 kDa	35.00%	3	1	1.0	1.0	1.1	1.0	0.42
ATPase family AAA domain-containing protein 3 OS=Mus muscu	Q925I1 (+1)	67 kDa	6.60%	3	1	1.2	0.9	1.1	0.9	0.68
ATPase inhibitor, mitochondrial OS=Mus musculus GN=Atpif1 PE	E9PV44 (+1)	9 kDa	24.00%	2	1	1.2	1.1	1.3	1.1	0.68
ATP-binding cassette sub-family B member 8, mitochondrial OS=	Q9CXJ4	78 kDa	3.50%	2	1	1.1	1.0	1.3	1.1	0.68
ATP-dependent 6-phosphofructokinase, liver type OS=Mus mus	P12382	85 kDa	5.90%	2	1	0.9	1.1	1.2	1.2	0.17
ATP-dependent 6-phosphofructokinase, muscle type OS=Mus m	P47857	85 kDa	21.00%	13	1	1.1	1.1	1.2	1.1	0.11
ATP-dependent Clp protease proteolytic subunit, mitochondrial	O88696	30 kDa	12.00%	2	1	1.4	1.2	1.5	1.1	0.58

BAG family molecular chaperone regulator 3 OS=Mus musculus	Q9JLV1	62 kDa	8.80%	5	1	0.8	0.8	0.9	0.9	0.58
Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	P21550	47 kDa	49.00%	17	1	1.2	1.2	1.2	1.1	0.42
Bifunctional epoxide hydrolase 2 OS=Mus musculus GN=Ephx2	P34914	63 kDa	16.00%	7	1	1.1	1.1	1.3	1.1	0.49
Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus	Q8CGC7	170 kDa	3.00%	4	1	0.9	1.1	1.2	1.2	0.17
Branched-chain-amino-acid aminotransferase OS=Mus musculu	D3Z7C8 (+2)	43 kDa	9.00%	3	1	1.0	1.1	1.2	1.2	0.20
Cadherin-2 OS=Mus musculus GN=Cdh2 PE=3 SV=1	D3YYT0 (+1)	94 kDa	8.40%	5	1	1.0	0.9	1.0	1.0	0.42
Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus	Q8BH59	75 kDa	26.00%	15	1	1.1	1.1	1.2	1.1	0.55
Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus	Q9QXX4	74 kDa	18.00%	6	1	1.0	0.9	1.0	1.0	0.42
Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2	P62204	17 kDa	20.00%	4	1	0.9	1.0	1.0	1.0	0.42
Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	P35564	67 kDa	7.60%	4	1	1.0	1.1	1.2	1.2	0.20
Calpastatin OS=Mus musculus GN=Cast PE=1 SV=2	P51125 (+5)	85 kDa	3.60%	2	1	2.0	2.1	1.9	1.3	0.43
Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	P14211	48 kDa	20.00%	5	1	0.7	0.8	0.9	1.0	0.94
Calsequestrin OS=Mus musculus GN=Casq2 PE=3 SV=1	F6QYE1 (+1)	48 kDa	14.00%	7	1	1.0	1.1	1.1	1.1	0.10
Calumenin (Fragment) OS=Mus musculus GN=Calu PE=1 SV=1	G3UXA8 (+3)	20 kDa	19.00%	2	1	0.9	#VALUE!	#VALUE!	#VALUE!	#VALUE!
CAP-Gly domain-containing linker protein 1 OS=Mus musculus	D3Z2Z1 (+4)	160 kDa	2.90%	3	1	0.9	0.8	1.0	0.9	0.72
Carboxylesterase 1C OS=Mus musculus GN=Ces1c PE=1 SV=4	P23953	61 kDa	9.70%	5	1	1.9	1.9	1.3	1.1	0.78
Carnitine O-acetyltransferase OS=Mus musculus GN=Crat PE=1	H7BX88 (+1)	69 kDa	29.00%	16	1	1.1	1.1	1.2	1.1	0.11
Carnitine O-palmitoyltransferase 1, muscle isoform OS=Mus mu	Q924X2	88 kDa	19.00%	16	1	1.0	1.0	1.1	1.0	0.42
Carnitine O-palmitoyltransferase 2, mitochondrial OS=Mus musc	P52825	74 kDa	19.00%	10	1	0.9	0.9	1.1	1.0	0.79
Catalase OS=Mus musculus GN=Cat PE=1 SV=4	P24270	60 kDa	6.50%	3	1	0.9	0.8	1.1	1.0	0.83
Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1	P26231	100 kDa	3.90%	3	1	0.8	0.8	1.0	1.0	0.88
Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	P10605	37 kDa	8.80%	2	1	1.1	1.1	1.1	1.1	0.09
Cathepsin D (Fragment) OS=Mus musculus GN=Ctsd PE=3 SV=1	F6Y6L6 (+1)	30 kDa	23.00%	5	1	1.6	1.9	2.1	1.5	0.18
Caveolin-1 OS=Mus musculus GN=Cav1 PE=1 SV=1	P49817	21 kDa	21.00%	4	1	0.9	0.9	1.0	1.0	1.00
CDGSH iron-sulfur domain-containing protein 1 OS=Mus muscul	Q91WS0	12 kDa	34.00%	3	1	0.9	0.9	0.9	1.0	0.42
Cell division control protein 42 homolog OS=Mus musculus GN=	P60766	21 kDa	15.00%	2	1	1.1	1.1	1.1	1.0	0.42
Ceruloplasmin OS=Mus musculus GN=Cp PE=4 SV=1	E9PZD8 (+3)	124 kDa	4.40%	4	1	0.9	0.7	1.2	1.0	0.91
Chaperone activity of bc1 complex-like, mitochondrial (Fragmen	F7B1B6 (+2)	45 kDa	6.20%	2	1	1.1	0.8	1.0	0.9	0.33

Chloride intracellular channel protein 4 OS=Mus musculus GN=C	Q9QYB1	29 kDa	14.00%	2	1	1.9	1.7	2.0	1.3	0.44
Citrate lyase subunit beta-like protein, mitochondrial OS=Mus m	Q8R4N0	38 kDa	11.00%	3	1	1.0	1.0	1.4	1.2	0.42
Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 S	Q9CZU6	52 kDa	20.00%	9	1	1.1	1.2	1.3	1.2	0.15
Clathrin heavy chain OS=Mus musculus GN=Cltc PE=1 SV=1	Q5SXR6 (+1)	192 kDa	15.00%	19	1	0.9	1.0	1.1	1.1	0.31
Clustered mitochondria protein homolog OS=Mus musculus GN	Q5SW19 (+2)	148 kDa	2.30%	2	1	1.1	0.9	0.7	0.8	0.23
Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=1	F8WGL3 (+1)	25 kDa	22.00%	3	1	0.9	1.1	0.9	1.1	0.55
Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1	P45591	19 kDa	38.00%	5	1	0.8	0.9	1.1	1.1	0.50
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, n	Q9CRB9	26 kDa	27.00%	5	1	1.1	1.0	1.1	1.0	0.69
Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3	P01027	186 kDa	7.90%	10	1	0.7	0.7	1.1	1.1	0.76
Complement component 1 Q subcomponent-binding protein, m	Q8R5L1	31 kDa	16.00%	3	1	1.1	1.1	1.1	1.0	0.98
Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	Q04447	43 kDa	19.00%	4	1	0.8	1.0	0.9	1.0	0.82
Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1	P07310	43 kDa	48.00%	15	1	1.0	1.1	1.1	1.1	0.10
Creatine kinase S-type, mitochondrial OS=Mus musculus GN=Ck	Q6P8J7	47 kDa	54.00%	19	1	1.1	1.0	1.1	1.0	0.69
Cysteine and glycine-rich protein 3 OS=Mus musculus GN=Csrp3	P50462	21 kDa	41.00%	8	1	0.9	1.0	1.1	1.1	0.29
Cysteine-rich protein 2 OS=Mus musculus GN=Crip2 PE=1 SV=1	Q9DCT8	23 kDa	32.00%	4	1	0.9	1.0	1.1	1.1	0.32
Cytochrome b OS=Mus musculus GN=Mt-Cyb PE=2 SV=1	P00158 (+1)	43 kDa	3.90%	2	1	1.2	1.1	1.1	1.0	0.80
Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus mu	Q9CZ13	53 kDa	33.00%	12	1	1.1	1.0	1.1	1.0	0.69
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus mu	Q9DB77	48 kDa	43.00%	15	1	1.1	1.0	1.1	1.0	1.00
Cytochrome b-c1 complex subunit 6, mitochondrial OS=Mus mu	P99028	10 kDa	62.00%	5	1	1.1	1.2	1.3	1.2	0.05
Cytochrome b-c1 complex subunit 7 OS=Mus musculus GN=Uqc	Q9CQB4 (+1)	14 kDa	44.00%	6	1	1.1	1.0	1.1	1.0	0.69
Cytochrome b-c1 complex subunit 8 OS=Mus musculus GN=Uqc	Q9CQ69	10 kDa	39.00%	5	1	1.1	1.0	1.1	1.0	1.00
Cytochrome b-c1 complex subunit 9 OS=Mus musculus GN=Uqc	Q8R1I1	7 kDa	38.00%	2	1	0.9	1.0	1.0	1.1	0.42
Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mu	Q9CR68	29 kDa	25.00%	5	1	1.1	1.1	1.1	1.1	0.29
Cytochrome c oxidase assembly factor 3 homolog, mitochondria	E9Q6W2 (+1)	10 kDa	23.00%	2	1	1.0	1.1	1.0	1.0	0.42
Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 P	P00405 (+1)	26 kDa	25.00%	4	1	1.0	0.9	1.0	1.0	0.42
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=M	P19783	20 kDa	51.00%	8	1	1.1	1.0	1.1	1.0	1.00
Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus muscu	P12787	16 kDa	21.00%	3	1	1.0	0.9	1.1	1.0	0.80
Cytochrome c oxidase subunit 5B, mitochondrial OS=Mus muscu	P19536 (+1)	14 kDa	53.00%	6	1	1.1	1.1	1.1	1.1	0.29

Cytochrome c oxidase subunit 6B1 OS=Mus musculus GN=Cox6	P56391	10 kDa	62.00%	5	1	1.0	1.0	1.1	1.0	0.42
Cytochrome c oxidase subunit 6C OS=Mus musculus GN=Cox6c	Q9CPQ1	8 kDa	38.00%	5	1	1.1	0.9	1.1	1.0	0.71
Cytochrome c oxidase subunit 7A1, mitochondrial OS=Mus mus	P56392	9 kDa	29.00%	2	1	1.2	0.9	1.0	0.9	0.34
Cytochrome c oxidase subunit 7A2, mitochondrial OS=Mus mus	P48771	9 kDa	28.00%	2	1	1.1	1.1	1.1	1.1	0.29
Cytochrome c oxidase subunit 7C, mitochondrial OS=Mus muscu	P17665	7 kDa	29.00%	2	1	1.1	1.0	1.1	1.0	0.69
Cytochrome c1, heme protein, mitochondrial OS=Mus musculus	Q9D0M3 (+1)	35 kDa	23.00%	5	1	0.9	1.1	1.1	1.2	0.15
Cytochrome c-type heme lyase OS=Mus musculus GN=Hccs PE=	P53702	31 kDa	6.60%	2	1	0.9	1.2	1.0	1.2	0.34
Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dyn	Q9JHU4	532 kDa	2.10%	8	1	0.9	1.0	0.9	1.0	0.71
Cytoplasmic dynein 1 intermediate chain 2 OS=Mus musculus G	A2BFF5 (+4)	71 kDa	6.40%	3	1	0.8	0.7	0.8	0.8	0.36
Cytosolic 5'-nucleotidase 3A OS=Mus musculus GN=Nt5c3a PE=	Q9D020 (+1)	37 kDa	7.30%	2	1	1.1	1.2	1.3	1.2	0.05
D3YXL0-R	D3YXL0-R (+1)	?	0.00%	2	1	1.1	0.9	1.2	1.0	0.79
D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus	Q80XN0	38 kDa	19.00%	6	1	1.1	1.1	1.0	1.0	1.00
Dehydrogenase/reductase SDR family member 4 OS=Mus muscu	Q99LB2	30 kDa	14.00%	4	1	0.8	0.9	1.1	1.1	0.45
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=	O35459	36 kDa	31.00%	9	1	0.8	0.9	1.1	1.1	0.68
Delta-aminolevulinic acid dehydratase OS=Mus musculus GN=A	P10518	36 kDa	8.80%	2	1	1.1	1.0	1.1	1.0	1.00
Desmin OS=Mus musculus GN=Des PE=1 SV=3	P31001	53 kDa	54.00%	23	1	0.7	0.8	0.9	1.0	0.92
Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	E9PZW0 (+1)	261 kDa	0.70%	2	1	1.1	1.1	0.9	0.9	0.55
Destrin OS=Mus musculus GN=Dstn PE=1 SV=3	Q9R0P5	19 kDa	15.00%	2	1	0.9	1.0	1.1	1.1	0.29
Diablo homolog, mitochondrial OS=Mus musculus GN=Diablo P	Q9JIQ3	27 kDa	8.40%	2	1	#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!
Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus	O08749	54 kDa	23.00%	11	1	1.1	1.1	1.1	1.1	0.29
Dihydrolipoyllysine-residue acetyltransferase component of pyr	Q8BMF4	68 kDa	25.00%	13	1	1.0	1.1	1.1	1.1	0.10
Dihydrolipoyllysine-residue succinyltransferase component of 2-	Q9D2G2	49 kDa	25.00%	10	1	1.2	1.2	1.4	1.2	0.30
Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=D	O08553	62 kDa	5.40%	2	1	1.0	1.0	1.1	1.1	0.42
DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dn	Q9QYJ0	46 kDa	8.50%	3	1	0.9	1.1	1.1	1.1	0.11
DnaJ homolog subfamily A member 3, mitochondrial OS=Mus m	Q99M87 (+2)	52 kDa	9.60%	3	1	0.9	0.9	1.1	1.0	0.69
DnaJ homolog subfamily A member 4 OS=Mus musculus GN=Dn	Q9JMC3	45 kDa	8.80%	3	1	0.9	1.1	1.1	1.2	0.08
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	Q91YQ5	69 kDa	4.10%	2	1	0.9	0.9	1.0	1.0	0.71
Dysferlin OS=Mus musculus GN=Dysf PE=4 SV=1	E9PXU9 (+5)	237 kDa	1.60%	3	1	1.1	1.1	1.1	1.1	0.42

Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=3	P11531	426 kDa	0.87%	3	1	1.7	1.3	1.5	1.0	0.91
Echinoderm microtubule-associated protein-like 2 OS=Mus mus	D3YWS2 (+3)	67 kDa	3.60%	2	1	2.5	2.5	3.2	1.6	0.31
EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE	Q9WVK4	61 kDa	6.40%	3	1	0.7	0.8	0.8	1.0	0.80
EH domain-containing protein 2 OS=Mus musculus GN=Ehd2 PE	Q8BH64	61 kDa	9.20%	3	1	1.2	1.1	1.3	1.1	0.68
EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE	Q9EQP2	61 kDa	17.00%	8	1	0.8	0.9	1.0	1.1	0.56
Electron transfer flavoprotein subunit alpha, mitochondrial OS=	Q99LC5	35 kDa	49.00%	12	1	1.1	1.1	1.2	1.1	0.31
Electron transfer flavoprotein subunit beta OS=Mus musculus G	Q9DCW4	28 kDa	46.00%	11	1	1.1	1.1	1.2	1.1	0.32
Electron transfer flavoprotein-ubiquinone oxidoreductase, mito	Q921G7	68 kDa	37.00%	20	1	1.0	0.9	1.1	1.0	0.98
Elongation factor 1-alpha 2 OS=Mus musculus GN=Eef1a2 PE=1	P62631	50 kDa	16.00%	8	1	0.9	1.1	1.1	1.1	0.11
Elongation factor 1-delta (Fragment) OS=Mus musculus GN=Eef	D3YUQ9 (+9)	21 kDa	17.00%	3	1	1.0	1.0	1.1	1.0	0.42
Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 S	Q9D8N0	50 kDa	18.00%	6	1	0.9	1.0	1.2	1.2	0.34
Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	P58252	95 kDa	15.00%	13	1	0.9	1.1	1.2	1.2	0.05
Elongation factor G, mitochondrial OS=Mus musculus GN=Gfm1	Q8K0D5	84 kDa	2.90%	2	1	0.9	0.8	1.1	1.0	0.87
Elongation factor Tu OS=Mus musculus GN=Gm9755 PE=3 SV=1	D3YVN7 (+1)	50 kDa	28.00%	10	1	1.1	1.1	1.1	1.0	0.98
Endonuclease G, mitochondrial OS=Mus musculus GN=Endog PE	O08600	32 kDa	9.20%	2	1	0.8	0.9	1.2	1.2	0.40
Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	P08113	92 kDa	6.10%	4	1	0.8	0.9	1.1	1.1	0.50
Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculus	P42125	32 kDa	36.00%	10	1	1.0	1.0	1.1	1.1	0.42
Enoyl-CoA delta isomerase 2, mitochondrial OS=Mus musculus	Q3TCD4 (+2)	42 kDa	9.30%	3	1	1.0	1.0	1.0	1.0	0.00
Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Echs	Q8BH95	31 kDa	27.00%	7	1	1.1	1.1	1.1	1.1	0.29
Epimerase family protein SDR39U1 OS=Mus musculus GN=Sdr39	Q5M8N4 (+1)	33 kDa	8.80%	2	1	1.1	1.2	1.1	1.1	0.32
ES1 protein homolog, mitochondrial OS=Mus musculus GN=D10	Q9D172	28 kDa	46.00%	9	1	1.1	1.1	1.1	1.1	0.29
Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Eif4a2 P	P10630 (+2)	46 kDa	9.80%	4	1	1.0	1.5	1.4	1.5	0.01
Eukaryotic translation initiation factor 3 subunit B OS=Mus mus	Q8JZQ9	91 kDa	8.60%	4	1	1.1	1.4	1.4	1.4	0.01
Fatty acid-binding protein, adipocyte OS=Mus musculus GN=Fab	P04117	15 kDa	42.00%	5	1	0.9	1.0	1.2	1.2	0.34
Fatty acid-binding protein, epidermal OS=Mus musculus GN=Fab	Q05816	15 kDa	22.00%	3	1	0.8	1.2	1.1	1.3	0.18
Fatty acid-binding protein, heart OS=Mus musculus GN=Fabp3 P	P11404	15 kDa	59.00%	9	1	1.1	1.1	1.1	1.1	0.29
Fibrinogen beta chain OS=Mus musculus GN=Fgb PE=2 SV=1	Q8K0E8	55 kDa	9.80%	3	1	0.8	0.5	1.2	1.0	0.99
Fibrinogen gamma chain OS=Mus musculus GN=Fgg PE=2 SV=1	Q8VCM7	49 kDa	7.60%	3	1	0.6	0.5	1.1	1.0	0.97

Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=1	D3YW87 (+3)	289 kDa	8.70%	14	1	0.9	1.1	1.0	1.1	0.31
Fission 1 (Mitochondrial outer membrane) homolog (Yeast), iso	G3X9U9 (+1)	16 kDa	25.00%	3	1	1.0	0.9	1.1	1.0	0.98
Four and a half LIM domains protein 1 OS=Mus musculus GN=F	A2AEX6 (+2)	35 kDa	15.00%	4	1	0.6	1.0	1.1	1.3	0.37
Four and a half LIM domains protein 2 OS=Mus musculus GN=F	O70433	32 kDa	12.00%	3	1	1.0	1.4	1.2	1.3	0.07
Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa	P05064	39 kDa	60.00%	18	1	0.9	1.0	1.1	1.1	0.29
Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh P	P97807 (+1)	54 kDa	30.00%	12	1	1.0	1.1	1.2	1.2	0.20
FUN14 domain-containing protein 2 OS=Mus musculus GN=Fun	Q9D6K8	17 kDa	15.00%	2	1	0.9	0.8	1.0	0.9	0.56
Galectin-1 OS=Mus musculus GN=Lgals1 PE=1 SV=3	P16045	15 kDa	39.00%	4	1	1.1	1.1	1.2	1.1	0.31
Gamma-sarcoglycan OS=Mus musculus GN=Sgcg PE=1 SV=2	P82348	32 kDa	7.20%	2	1	1.0	1.0	1.0	1.0	0.00
Gap junction alpha-1 protein OS=Mus musculus GN=Gja1 PE=1	P23242	43 kDa	6.30%	2	1	0.9	1.1	1.1	1.1	0.11
Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=	P06745	63 kDa	20.00%	10	1	0.9	0.9	1.1	1.1	0.58
Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus	P26443	61 kDa	17.00%	8	1	0.9	0.8	1.0	1.0	0.82
Glutaredoxin-1 OS=Mus musculus GN=Glrx PE=1 SV=3	Q9QUH0	12 kDa	18.00%	2	1	0.9	0.9	1.1	1.0	0.79
Glutaredoxin-related protein 5, mitochondrial OS=Mus musculu	Q80Y14	16 kDa	22.00%	2	1	0.9	0.8	0.8	0.8	0.04
Glutathione S-transferase A4 OS=Mus musculus GN=Gsta4 PE=1	P24472	26 kDa	14.00%	3	1	1.0	1.0	1.1	1.1	0.42
Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gstk1	Q9DCM2	26 kDa	27.00%	5	1	1.1	1.1	1.2	1.1	0.32
Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1 P	P10649	26 kDa	50.00%	11	1	1.1	1.0	1.2	1.1	0.58
Glutathione S-transferase Mu 2 OS=Mus musculus GN=Gstm2 P	P15626	26 kDa	37.00%	5	1	0.9	0.9	1.1	1.1	0.58
Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto	O09131	27 kDa	21.00%	5	1	0.9	1.1	1.1	1.2	0.03
Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=	P19157	24 kDa	30.00%	4	1	1.2	1.4	1.4	1.3	0.12
Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus	P16858	36 kDa	44.00%	13	1	1.1	1.2	1.3	1.2	0.15
Glycerol kinase OS=Mus musculus GN=Gyk PE=3 SV=1	B1ASZ3 (+3)	60 kDa	3.60%	2	1	1.1	1.0	1.3	1.1	0.53
Glycerol-3-phosphate dehydrogenase 1-like protein OS=Mus mu	Q3ULJ0 (+1)	38 kDa	7.40%	2	1	0.9	0.8	1.1	1.0	0.87
Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1	Q9CZD3	82 kDa	7.10%	4	1	1.0	1.0	1.1	1.1	0.42
Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1	D3Z0Q6 (+1)	77 kDa	9.20%	3	1	0.7	0.7	1.1	1.0	0.97
Glycogen phosphorylase, brain form OS=Mus musculus GN=Pyg	Q8CI94	97 kDa	22.00%	11	1	0.9	0.9	1.1	1.1	0.55
Glycogen phosphorylase, muscle form OS=Mus musculus GN=Py	Q9WUB3	97 kDa	26.00%	19	1	0.9	1.0	1.1	1.1	0.29
Glyoxalase domain-containing protein 4 OS=Mus musculus GN=	E9Q197 (+4)	31 kDa	15.00%	3	1	1.1	1.1	1.2	1.1	0.32

GrpE protein homolog 1, mitochondrial OS=Mus musculus GN=	Q99LP6	24 kDa	18.00%	3	1	1.0	0.9	1.1	1.0	0.98
GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=	P62827	24 kDa	15.00%	3	1	0.9	1.0	1.1	1.1	0.32
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mu	P08752	40 kDa	9.00%	2	1	0.8	0.7	0.8	0.8	0.31
Guanine nucleotide-binding protein G(s) subunit alpha isoforms	Q6R0H7 (+1)	122 kDa	1.70%	2	1	1.1	1.1	1.1	1.0	0.98
Guanine nucleotide-binding protein subunit beta-2-like 1 OS=M	P68040	35 kDa	5.00%	2	1	0.8	1.1	1.2	1.3	0.20
Haptoglobin OS=Mus musculus GN=Hp PE=1 SV=1	Q61646	39 kDa	16.00%	6	1	0.3	0.2	1.4	1.3	0.83
Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1	Q3U2G2	94 kDa	21.00%	11	1	1.0	1.1	1.2	1.2	0.20
Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa	P63017	71 kDa	48.00%	25	1	0.9	1.1	1.1	1.1	0.11
Heat shock protein 75 kDa, mitochondrial OS=Mus musculus GN	Q9CQN1	80 kDa	6.50%	2	1	0.8	1.0	1.1	1.2	0.30
Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 S	P14602 (+1)	23 kDa	43.00%	8	1	0.8	0.9	1.1	1.1	0.60
Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=2 S	Q5EBG6	18 kDa	22.00%	3	1	0.7	1.1	1.1	1.3	0.29
Heat shock protein beta-7 OS=Mus musculus GN=Hspb7 PE=1 S	P35385	19 kDa	24.00%	3	1	1.0	1.1	1.1	1.1	0.00
Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90a	P07901	85 kDa	20.00%	3	1	0.8	1.0	1.2	1.3	0.29
Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab	P11499	83 kDa	36.00%	22	1	0.9	1.0	1.1	1.1	0.29
Heme oxygenase 2 (Fragment) OS=Mus musculus GN=Hmox2 PE	D3YX62 (+1)	26 kDa	12.00%	2	1	1.1	1.2	1.3	1.2	0.15
Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=	P01942 (+1)	15 kDa	46.00%	6	1	1.1	1.0	1.1	1.0	0.69
Hemoglobin subunit beta-1 OS=Mus musculus GN=Hbb-b1 PE=1	P02088	16 kDa	83.00%	5	1	1.1	1.1	1.1	1.1	0.42
Hemoglobin subunit beta-2 OS=Mus musculus GN=Hbb-b2 PE=1	P02089	16 kDa	90.00%	12	1	1.1	1.1	1.1	1.0	0.42
Hemopexin OS=Mus musculus GN=Hpx PE=1 SV=2	Q91X72	51 kDa	34.00%	14	1	0.5	0.4	1.1	1.0	0.96
Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculu	Q20BD0 (+2)	36 kDa	11.00%	3	1	1.0	1.1	1.1	1.1	0.00
Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus	A2AL12 (+5)	34 kDa	12.00%	2	1	0.9	1.0	1.1	1.1	0.29
Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus	O35737 (+1)	49 kDa	7.60%	2	1	0.9	1.2	1.3	1.4	0.05
Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus	B2M1R6 (+6)	49 kDa	16.00%	5	1	0.7	0.9	0.8	1.0	0.92
Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus	G3UXJ6 (+4)	50 kDa	8.00%	3	1	0.8	0.9	1.1	1.1	0.47
Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus	G3XA10 (+1)	87 kDa	4.20%	2	1	1.3	1.9	1.4	1.4	0.22
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus mus	O88569 (+2)	37 kDa	29.00%	9	1	1.2	1.2	1.3	1.1	0.33
Hexaprenyldihydroxybenzoate methyltransferase, mitochondria	Q8BMS4	41 kDa	7.80%	2	1	0.9	1.1	0.9	1.1	0.58
Hexokinase 1, isoform CRA_f OS=Mus musculus GN=Hk1 PE=3 S	G3UVV4 (+4)	102 kDa	4.90%	3	1	1.0	0.8	1.2	1.0	0.93

Hexokinase-2 OS=Mus musculus GN=Hk2 PE=3 SV=1	E9Q5B5 (+1)	99 kDa	8.90%	6	1	1.0	1.4	1.5	1.5	0.01
Histidine rich calcium binding protein, isoform CRA_a OS=Mus m	G5E8J6	85 kDa	27.00%	11	1	0.8	0.8	1.0	1.0	0.88
Histidine triad nucleotide-binding protein 2, mitochondrial OS=M	Q9D0S9	17 kDa	21.00%	2	1	26.0	27.9	27.9	2.1	0.37
Histone H1.0 OS=Mus musculus GN=H1f0 PE=2 SV=4	P10922	21 kDa	12.00%	2	1	1.0	0.9	1.1	1.0	0.98
Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	P15864	21 kDa	23.00%	4	1	1.1	1.1	1.1	1.1	0.42
Histone H2A OS=Mus musculus GN=Hist1h2al PE=3 SV=1	F8WIX8 (+9)	14 kDa	28.00%	3	1	1.0	1.0	1.0	1.0	0.00
Histone H2B type 1-F/J/L OS=Mus musculus GN=Hist1h2bf PE=1	P10853 (+9)	14 kDa	23.00%	3	1	1.1	1.1	0.9	1.0	0.71
Histone H3 OS=Mus musculus GN=H3f3a PE=3 SV=1	F8WI35 (+4)	15 kDa	9.60%	2	1	1.4	1.1	1.1	0.9	0.69
Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	P62806	11 kDa	46.00%	5	1	1.0	0.9	0.9	0.9	0.00
Histone-lysine N-methyltransferase Smyd1 OS=Mus musculus G	P97443 (+1)	56 kDa	13.00%	4	1	1.1	1.2	1.2	1.2	0.03
Hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Mus	Q8R0N6 (+1)	50 kDa	9.90%	3	1	1.1	1.1	1.3	1.1	0.49
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Mu	Q61425	34 kDa	13.00%	5	1	0.9	0.9	1.1	1.1	0.58
Hydroxysteroid dehydrogenase-like protein 2 OS=Mus musculus	Q2TPA8	54 kDa	4.50%	2	1	1.0	1.1	1.0	1.0	0.42
Inorganic pyrophosphatase 2, mitochondrial OS=Mus musculus	Q91VM9 (+1)	38 kDa	10.00%	3	1	1.6	1.7	1.9	1.4	0.26
Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 S\	Q9D819	33 kDa	8.70%	2	1	0.9	0.9	1.1	1.1	0.58
Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	P09055 (+1)	88 kDa	2.60%	2	1	0.8	0.8	0.9	1.0	0.79
Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GI	A6X935 (+3)	105 kDa	1.90%	2	1	0.5	0.3	1.0	0.9	0.87
Isobutyryl-CoA dehydrogenase, mitochondrial OS=Mus musculu	D3YTT4 (+1)	45 kDa	11.00%	4	1	1.1	1.1	1.2	1.1	0.32
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial O	Q9D6R2	40 kDa	32.00%	11	1	1.0	1.0	1.1	1.1	0.42
Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondria	P70404	43 kDa	30.00%	6	1	1.4	1.2	1.5	1.1	0.58
Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculu	O88844	47 kDa	13.00%	5	1	1.1	1.1	1.2	1.1	0.55
Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus muscu	P54071	51 kDa	48.00%	20	1	1.1	1.1	1.3	1.2	0.34
Isocitrate dehydrogenase 3 (NAD+) beta OS=Mus musculus GN=	Q91VA7	42 kDa	28.00%	9	1	1.0	1.1	1.1	1.1	0.00
Isoform 2 of Dynamin-like 120 kDa protein, mitochondrial OS=M	P58281-2	116 kDa	10.00%	9	1	1.2	0.9	1.1	0.9	0.49
Isoform 2 of Myomesin-1 OS=Mus musculus GN=Myom1	Q62234-2	175 kDa	26.00%	34	1	1.1	1.1	1.1	1.1	0.29
Isoform 2 of Probable hydrolase PNKD OS=Mus musculus GN=Pr	Q69ZP3-2	16 kDa	20.00%	2	1	0.7	1.2	1.0	1.3	0.30
Isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPa	O55143-2	110 kDa	39.00%	37	1	1.1	1.1	1.1	1.0	0.71
Isoform 2 of Sorbin and SH3 domain-containing protein 2 OS=M	Q3UTJ2-2	145 kDa	11.00%	11	1	0.8	0.9	0.9	1.0	0.74

Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Mus mu	Q62261-2	251 kDa	5.80%	9	1	1.1	1.0	1.0	1.0	0.42
Isoform 3 of Sarcolemmal membrane-associated protein OS=Mu	Q3URD3-3 (+1)	42 kDa	16.00%	5	1	0.9	0.9	1.1	1.1	0.49
Isoform M1 of Pyruvate kinase PKM OS=Mus musculus GN=Pkm	P52480-2	58 kDa	54.00%	25	1	1.0	1.1	1.2	1.2	0.04
Isoform Mt-VDAC1 of Voltage-dependent anion-selective chann	Q60932-2	31 kDa	65.00%	13	1	1.1	1.0	1.1	1.0	1.00
Isoform Short of Thymosin beta-4 OS=Mus musculus GN=Tmsb4	P20065-2	5 kDa	41.00%	2	1	1.0	1.4	1.1	1.3	0.17
Isovaleryl-CoA dehydrogenase, mitochondrial OS=Mus musculus	Q9JHI5	46 kDa	15.00%	6	1	1.0	0.9	1.2	1.1	0.64
Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	Q02257	82 kDa	6.70%	3	1	1.1	1.1	1.2	1.1	0.55
Junctophilin-2 OS=Mus musculus GN=Jph2 PE=2 SV=2	Q9ET78	75 kDa	11.00%	4	1	1.1	0.9	1.1	1.0	0.97
Kelch-like protein 41 OS=Mus musculus GN=Klhl41 PE=1 SV=1	A2AUC9	68 kDa	7.10%	4	1	0.8	1.1	1.1	1.3	0.12
Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=3	A2A513 (+3)	57 kDa	3.70%	2	1	0.9	0.7	0.5	0.6	0.13
Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 S	P04104	66 kDa	4.90%	3	1	0.5	0.4	0.4	0.5	0.26
Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=3	Q61768	110 kDa	2.80%	2	1	0.9	1.0	1.1	1.1	0.29
Kininogen-1 OS=Mus musculus GN=Kng1 PE=4 SV=1	D3YTY9 (+3)	53 kDa	7.30%	3	1	0.8	0.7	1.0	0.9	0.79
Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3	Q9CPU0	21 kDa	10.00%	2	1	0.9	1.1	1.2	1.2	0.17
Laminin subunit alpha-2 OS=Mus musculus GN=Lama2 PE=1 SV=	Q60675	344 kDa	2.00%	5	1	1.0	0.9	0.9	0.9	0.00
Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=4 SV	F8VQJ3 (+1)	177 kDa	2.50%	3	1	1.0	1.0	1.0	1.0	0.00
LETM1 and EF-hand domain-containing protein 1, mitochondria	Q9Z2I0	83 kDa	5.80%	4	1	1.1	1.0	1.1	1.0	0.69
Leucine-rich PPR motif-containing protein, mitochondrial OS=M	Q6PB66	157 kDa	4.90%	6	1	0.9	1.0	1.0	1.0	0.42
Leucyl-cystinyl aminopeptidase OS=Mus musculus GN=Lnpep PE	Q8C129	117 kDa	2.60%	2	1	0.8	0.8	1.1	1.0	0.84
LIM domain-binding protein 3 OS=Mus musculus GN=Ldb3 PE=1	Q9JKS4 (+1)	76 kDa	30.00%	15	1	1.1	1.1	1.2	1.1	0.32
L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE	P16125	37 kDa	35.00%	10	1	1.1	1.0	1.1	1.0	0.69
L-lactate dehydrogenase OS=Mus musculus GN=Ldha PE=1 SV=1	G5E8N5 (+1)	40 kDa	30.00%	11	1	0.9	1.0	1.1	1.1	0.29
Lon protease homolog, mitochondrial OS=Mus musculus GN=Lo	Q8CGK3	106 kDa	5.30%	4	1	1.0	1.1	1.1	1.1	0.00
Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=	P51174	48 kDa	42.00%	16	1	1.0	1.1	1.2	1.2	0.20
Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=Acsl1	D3Z041 (+1)	78 kDa	41.00%	26	1	1.0	0.9	1.1	1.0	0.98
m7GpppX diphosphatase OS=Mus musculus GN=Dcps PE=1 SV=	Q9DAR7	39 kDa	7.70%	2	1	1.1	1.4	1.1	1.2	0.46
Macrophage migration inhibitory factor OS=Mus musculus GN=	P34884	13 kDa	17.00%	2	1	0.7	0.9	1.1	1.2	0.45
Major vault protein OS=Mus musculus GN=Mvp PE=4 SV=1	E9Q3X0 (+1)	97 kDa	3.30%	2	1	1.4	1.4	1.7	1.3	0.30

Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Md	P14152	37 kDa	34.00%	10	1	1.1	1.1	1.3	1.1	0.29
Malate dehydrogenase, mitochondrial OS=Mus musculus GN=M	P08249	36 kDa	63.00%	19	1	1.1	1.2	1.3	1.2	0.15
Mannose-6-phosphate isomerase OS=Mus musculus GN=Mpi P	Q924M7	47 kDa	11.00%	3	1	0.9	0.9	1.2	1.1	0.53
MCG10343, isoform CRA_b OS=Mus musculus GN=Slc25a3 PE=1	G5E902 (+1)	40 kDa	29.00%	11	1	1.1	1.1	1.1	1.0	0.42
MCG115977 OS=Mus musculus GN=Gm10108 PE=3 SV=1	G3UWG1 (+1)	12 kDa	54.00%	5	1	0.9	0.9	1.0	1.0	0.71
MCG130675 OS=Mus musculus GN=Zbed5 PE=2 SV=1	B2RPU8 (+2)	84 kDa	4.90%	3	1	0.8	0.9	0.8	1.0	0.79
MCG142036 OS=Mus musculus GN=Acad12 PE=1 SV=1	D3Z7X0	61 kDa	7.90%	4	1	1.1	1.0	1.2	1.1	0.58
MCG55033 OS=Mus musculus GN=Gm10250 PE=4 SV=1	G3X9L6 (+1)	19 kDa	72.00%	11	1	1.1	1.0	1.1	1.0	1.00
MCG5603 OS=Mus musculus GN=Ndufa11 PE=4 SV=1	G5E814 (+1)	15 kDa	35.00%	3	1	1.0	0.9	1.0	1.0	0.42
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	P45952	46 kDa	42.00%	17	1	1.0	1.1	1.1	1.1	0.10
Metaxin-2 OS=Mus musculus GN=Mtx2 PE=1 SV=1	O88441	30 kDa	8.40%	2	1	0.9	0.7	0.9	0.8	0.34
Methylglutaconyl-CoA hydratase, mitochondrial (Fragment) OS=	F6RT60 (+1)	25 kDa	19.00%	3	1	1.1	0.9	1.1	1.0	0.97
Methylmalonate-semialdehyde dehydrogenase [acylating], mito	Q9EQ20	58 kDa	22.00%	9	1	1.1	1.2	1.4	1.2	0.17
Methylmalonyl-CoA mutase, mitochondrial OS=Mus musculus G	P16332	83 kDa	6.60%	3	1	2.3	2.6	2.8	1.7	0.24
Microtubule-associated protein OS=Mus musculus GN=Map4 P	E9QPW8 (+3)	114 kDa	2.50%	2	1	#VALUE!	1.2	1.2	#VALUE!	#VALUE!
Mimitin, mitochondrial OS=Mus musculus GN=Ndufaf2 PE=2 SV	Q59J78	20 kDa	18.00%	2	1	1.0	1.0	0.8	0.9	0.42
Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus m	Q9CR62	34 kDa	31.00%	9	1	1.0	0.9	1.1	1.0	0.98
Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus m	Q9Z2Z6	33 kDa	16.00%	4	1	1.0	0.9	1.1	1.0	0.80
Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2	A2AFW6 (+2)	32 kDa	4.80%	2	1	1.0	0.9	1.1	1.0	0.74
Mitochondrial fission process protein 1 OS=Mus musculus GN=M	Q9CRB8	18 kDa	13.00%	2	1	1.0	1.0	1.0	1.0	0.00
Mitochondrial import inner membrane translocase subunit Tim1	P62075	10 kDa	28.00%	2	1	1.1	1.1	1.1	1.1	0.42
Mitochondrial import receptor subunit TOM22 homolog OS=Mu	Q9CPQ3	16 kDa	37.00%	3	1	1.0	0.9	0.8	0.9	0.17
Mitochondrial import receptor subunit TOM70 OS=Mus muscul	Q9CZW5	68 kDa	2.80%	2	1	1.0	1.1	0.9	1.0	0.98
Mitochondrial inner membrane protein OS=Mus musculus GN=	E9Q800	76 kDa	37.00%	21	1	1.1	0.9	1.1	1.0	0.71
Mitochondrial pyruvate carrier 1 OS=Mus musculus GN=Mpc1 P	D3YWY6 (+3)	10 kDa	20.00%	2	1	1.1	1.1	1.1	1.0	0.42
Mitochondrial pyruvate carrier 2 OS=Mus musculus GN=Mpc2 P	Q9D023	14 kDa	18.00%	3	1	1.1	1.0	1.1	1.0	1.00
Moesin OS=Mus musculus GN=Msn PE=1 SV=3	P26041	68 kDa	17.00%	10	1	0.9	1.1	1.1	1.1	0.11
Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1	P53986	53 kDa	7.10%	3	1	1.0	1.0	1.1	1.0	0.42

Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3	P28665	165 kDa	1.90%	2	1	1.3	1.1	1.1	0.9	0.64
Muscle-related coiled-coil protein OS=Mus musculus GN=Murc	A2AMM0	41 kDa	7.50%	2	1	1.2	1.2	1.5	1.2	0.29
Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3	P04247	17 kDa	66.00%	11	1	1.1	1.1	1.2	1.1	0.11
Myomesin 2 OS=Mus musculus GN=Myom2 PE=2 SV=1	Q14BI5	165 kDa	31.00%	36	1	1.2	1.0	1.2	1.0	1.00
Myosin light chain 1/3, skeletal muscle isoform OS=Mus muscul	E9PWG4	18 kDa	35.00%	3	1	0.7	0.7	1.0	1.0	0.93
Myosin light chain 3 OS=Mus musculus GN=Myl3 PE=1 SV=4	P09542	22 kDa	75.00%	12	1	1.1	0.9	1.0	0.9	0.32
Myosin regulatory light chain 2, ventricular/cardiac muscle isofo	P51667	19 kDa	72.00%	12	1	1.0	1.0	1.1	1.0	0.42
Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	Q02566	224 kDa	53.00%	95	1	1.1	0.7	0.7	0.7	0.01
Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1	Q91Z83	223 kDa	44.00%	13	1	0.7	0.7	0.9	1.0	0.85
Myosin-binding protein C, cardiac-type OS=Mus musculus GN=	E9Q9T8 (+1)	141 kDa	41.00%	43	1	1.0	0.9	0.9	0.9	0.00
Myotilin OS=Mus musculus GN=Myot PE=1 SV=1	Q9JIF9	55 kDa	4.60%	2	1	0.8	0.9	1.0	1.1	0.72
Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1	Q9JJW5	30 kDa	51.00%	9	1	1.0	0.9	1.1	1.0	0.95
Myristoylated alanine-rich C-kinase substrate OS=Mus musculus	P26645	30 kDa	26.00%	4	1	1.1	1.3	1.1	1.2	0.34
NAD(P) transhydrogenase, mitochondrial OS=Mus musculus GN	Q61941	114 kDa	27.00%	28	1	1.1	1.0	1.1	1.0	0.69
NAD(P)H-hydrate epimerase OS=Mus musculus GN=Apoa1bp PE	Q8K4Z3	31 kDa	9.90%	2	1	0.8	0.9	0.9	1.0	0.74
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q99LC3	41 kDa	32.00%	12	1	1.1	1.1	1.2	1.1	0.31
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q7TMF3	17 kDa	57.00%	8	1	1.0	1.1	1.1	1.1	0.00
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9ERS2	17 kDa	32.00%	4	1	1.0	1.0	1.1	1.0	0.42
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9CQ75	11 kDa	23.00%	3	1	1.1	1.1	1.1	1.0	0.98
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9CQ91	9 kDa	49.00%	3	1	1.2	1.1	1.1	1.0	0.97
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q62425	9 kDa	56.00%	6	1	1.0	0.9	1.1	1.0	0.98
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9CPP6	13 kDa	59.00%	5	1	1.0	1.0	1.0	1.0	0.00
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9CQZ5	15 kDa	37.00%	5	1	1.1	1.1	1.1	1.1	0.29
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9Z1P6	13 kDa	60.00%	7	1	1.1	1.1	1.1	1.0	0.42
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9DCJ5	20 kDa	43.00%	7	1	0.9	1.0	1.0	1.1	0.42
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	Q9DC69	43 kDa	33.00%	12	1	1.0	1.0	1.1	1.0	0.42
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	Q9DCS9	21 kDa	51.00%	8	1	1.0	1.1	1.1	1.1	0.10
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	O09111	17 kDa	44.00%	4	1	1.1	1.0	0.9	0.9	0.29

NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	Q9CQC7	15 kDa	33.00%	3	1	1.1	1.7	1.5	1.6	0.04
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	Q9CQH3	22 kDa	28.00%	5	1	1.1	1.0	1.1	1.0	1.00
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	A2AP32 (+1)	12 kDa	41.00%	4	1	1.1	1.0	1.1	1.0	1.00
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	Q9CR61	16 kDa	64.00%	6	1	1.3	1.1	1.3	1.1	0.72
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	Q9D6J5	22 kDa	38.00%	5	1	0.9	0.9	0.9	1.0	0.42
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	Q9CQJ8	22 kDa	39.00%	7	1	1.1	1.1	1.1	1.0	0.42
NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Mus muscu	Q9CQ54	14 kDa	24.00%	3	1	1.1	1.1	1.1	1.1	0.29
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondri	D3YUM1 (+1)	50 kDa	33.00%	13	1	1.1	1.0	1.1	1.0	1.00
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondri	Q9D6J6	27 kDa	40.00%	7	1	1.1	1.1	1.1	1.0	0.98
NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondri	Q8BK30	12 kDa	17.00%	2	1	0.9	0.9	0.8	0.9	0.31
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitoch	Q91WD5	53 kDa	31.00%	12	1	1.1	1.0	1.1	1.0	1.00
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitoch	Q9DCT2	30 kDa	25.00%	7	1	1.1	1.0	1.1	1.0	1.00
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitoch	E9QPX3 (+1)	20 kDa	31.00%	5	1	1.0	1.0	1.1	1.0	0.42
NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Mu	Q99LY9	13 kDa	38.00%	4	1	1.2	1.1	1.1	1.0	0.97
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitoch	P52503	13 kDa	34.00%	3	1	1.1	1.1	1.1	1.0	0.42
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitoch	Q9DC70	25 kDa	17.00%	4	1	1.0	0.9	1.1	1.0	0.98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitoch	Q8K3J1	24 kDa	17.00%	4	1	1.0	1.0	0.9	1.0	0.42
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondri	Q91VD9	80 kDa	39.00%	23	1	1.1	1.1	1.1	1.0	0.71
NADH-ubiquinone oxidoreductase chain 1 OS=Mus musculus GN	P03888	36 kDa	5.70%	2	1	1.1	1.1	1.1	1.1	0.29
NADH-ubiquinone oxidoreductase chain 3 OS=Mus musculus GN	P03899 (+1)	13 kDa	18.00%	2	1	0.7	0.8	1.1	1.1	0.75
NADH-ubiquinone oxidoreductase chain 4 OS=Mus musculus GN	P03911 (+1)	52 kDa	6.30%	3	1	1.1	1.2	1.1	1.1	0.31
NADP-dependent malic enzyme, mitochondrial OS=Mus muscul	Q8BMF3	67 kDa	6.10%	3	1	1.0	0.9	1.3	1.1	0.71
Nascent polypeptide-associated complex subunit alpha, muscle-	P70670	220 kDa	6.60%	8	1	0.8	0.9	0.9	1.1	0.70
Nebulette OS=Mus musculus GN=Nebl PE=4 SV=1	B7ZCI2	116 kDa	9.30%	7	1	1.1	1.1	1.2	1.1	0.31
Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap	E9PZF4 (+3)	192 kDa	2.00%	3	1	0.6	1.0	1.0	1.2	0.42
NEDD8-conjugating enzyme Ubc12 (Fragment) OS=Mus musculu	F6WMC0 (+2)	20 kDa	13.00%	2	1	0.9	1.1	1.1	1.2	0.15
Neutral cholesterol ester hydrolase 1 OS=Mus musculus GN=Nc	Q8BLF1	46 kDa	16.00%	6	1	0.9	0.9	1.1	1.0	0.69
Nicotinamide phosphoribosyltransferase OS=Mus musculus GN=	Q99KQ4	55 kDa	10.00%	4	1	1.2	1.1	1.5	1.2	0.42

Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=2	P10493	137 kDa	5.10%	6	1	1.0	0.8	1.0	0.9	0.42
Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 P	P32020 (+1)	59 kDa	5.50%	3	1	0.9	0.8	1.1	1.0	0.94
NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1	Q9CZ44 (+2)	41 kDa	8.40%	2	1	1.3	1.1	1.0	0.9	0.53
Nuclease-sensitive element-binding protein 1 OS=Mus musculus	P62960	36 kDa	34.00%	7	1	0.8	0.9	1.1	1.1	0.50
Nucleolar protein 3 OS=Mus musculus GN=Nol3 PE=1 SV=1	Q9D1X0	25 kDa	17.00%	2	1	0.5	0.5	0.4	0.7	0.46
Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	Q5SQB0 (+3)	30 kDa	6.40%	2	1	0.9	1.1	1.1	1.2	0.03
Nucleoside diphosphate kinase OS=Mus musculus GN=Gm2039	E9PZF0 (+1)	30 kDa	31.00%	8	1	0.9	1.1	1.1	1.1	0.09
O-acetyl-ADP-ribose deacetylase MACROD1 OS=Mus musculus	Q922B1	35 kDa	9.30%	2	1	0.9	0.9	1.1	1.0	0.69
Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2	A2AAJ9 (+4)	966 kDa	1.20%	7	1	0.9	1.1	1.1	1.1	0.11
OCIA domain-containing protein 1 OS=Mus musculus GN=Ociad	Q9CRD0 (+2)	28 kDa	14.00%	2	1	1.1	1.1	0.9	0.9	0.61
Omega-amidase NIT2 OS=Mus musculus GN=Nit2 PE=1 SV=1	Q9JHW2	31 kDa	9.40%	2	1	1.2	1.2	1.4	1.2	0.30
Ornithine aminotransferase, mitochondrial OS=Mus musculus G	P29758	48 kDa	12.00%	5	1	0.9	0.9	1.1	1.0	0.79
Parathymosin OS=Mus musculus GN=Ptms PE=1 SV=3	Q9D0J8	11 kDa	12.00%	2	1	#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!
PDZ and LIM domain protein 1 OS=Mus musculus GN=Pdlim1 PE	O70400	36 kDa	8.60%	3	1	1.0	1.3	1.6	1.5	0.09
PDZ and LIM domain protein 5 OS=Mus musculus GN=Pdlim5 PE	E9Q8P5 (+2)	26 kDa	46.00%	7	1	1.1	1.0	1.1	1.0	1.00
Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia	P17742	18 kDa	35.00%	5	1	1.1	1.3	1.2	1.2	0.15
Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Mus mu	Q99KR7	22 kDa	20.00%	3	1	1.1	1.0	1.0	0.9	0.42
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus G	P26883	12 kDa	25.00%	2	1	1.0	1.1	1.2	1.2	0.04
Perilipin-3 OS=Mus musculus GN=Plin3 PE=1 SV=1	Q9DBG5	47 kDa	5.90%	2	1	0.9	0.7	0.9	0.8	0.35
Peroxiredoxin-1 (Fragment) OS=Mus musculus GN=Prdx1 PE=1 S	B1AXW5 (+2)	19 kDa	44.00%	8	1	1.1	1.1	1.2	1.1	0.11
Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	Q61171	22 kDa	40.00%	8	1	1.2	1.3	1.3	1.2	0.22
Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE	P99029 (+1)	22 kDa	45.00%	9	1	1.1	1.1	1.2	1.1	0.11
Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3	O08709 (+1)	25 kDa	36.00%	6	1	1.2	1.2	1.3	1.1	0.33
Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus GN=	Q9R0H0 (+1)	75 kDa	5.40%	2	1	0.8	0.9	1.4	1.3	0.39
Phosphatidylethanolamine-binding protein 1 OS=Mus musculus	P70296	21 kDa	37.00%	4	1	1.1	1.1	1.4	1.2	0.46
Phosphoglucomutase-1 OS=Mus musculus GN=Pgm1 PE=1 SV=4	Q9D0F9	61 kDa	30.00%	14	1	1.0	1.0	1.1	1.1	0.42
Phosphoglucomutase-like protein 5 OS=Mus musculus GN=Pgm	Q8BZF8	62 kDa	6.00%	2	1	1.1	0.8	0.9	0.8	0.18
Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV	P09411	45 kDa	30.00%	11	1	1.1	1.1	1.1	1.1	0.29

Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1	Q9DBJ1	29 kDa	22.00%	2	1	0.9	1.1	0.9	1.0	0.79
Phosphoglycerate mutase 2 OS=Mus musculus GN=Pgam2 PE=1	O70250	29 kDa	35.00%	8	1	1.0	1.1	1.1	1.1	0.10
Phospholipid hydroperoxide glutathione peroxidase, mitochond	O70325 (+3)	22 kDa	12.00%	2	1	0.9	0.9	0.9	1.0	0.42
Platelet glycoprotein 4 OS=Mus musculus GN=Cd36 PE=1 SV=2	Q08857	53 kDa	12.00%	6	1	1.0	0.9	1.1	1.0	0.74
Plectin OS=Mus musculus GN=Plec PE=1 SV=1	E9Q3W4 (+16)	499 kDa	1.50%	4	1	1.0	1.1	1.1	1.1	0.00
Polymerase delta-interacting protein 2 (Fragment) OS=Mus mus	F6SQH7 (+1)	33 kDa	6.70%	2	1	0.9	1.1	1.0	1.1	0.32
Polymerase I and transcript release factor OS=Mus musculus GN	O54724	44 kDa	20.00%	5	1	1.1	0.9	1.1	1.0	0.97
Polyubiquitin-C (Fragment) OS=Mus musculus GN=Ubc PE=4 SV=	E9Q5F6 (+6)	23 kDa	24.00%	5	1	1.3	1.4	1.5	1.3	0.21
Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	P48678 (+2)	74 kDa	2.90%	2	1	1.0	1.0	1.2	1.1	0.42
Probable C->U-editing enzyme APOBEC-2 OS=Mus musculus GN	Q9WV35	26 kDa	14.00%	2	1	1.3	1.1	1.2	1.0	0.97
Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	P62962 (+1)	15 kDa	31.00%	3	1	1.4	1.6	1.7	1.4	0.16
Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	P67778	30 kDa	33.00%	8	1	1.1	1.0	1.1	1.0	1.00
Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	O35129	33 kDa	29.00%	8	1	1.1	0.9	1.1	1.0	0.71
Prolyl endopeptidase OS=Mus musculus GN=Prep PE=2 SV=1	Q9QUR6	81 kDa	3.50%	2	1	0.8	1.0	1.1	1.2	0.30
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus	Q91ZA3	80 kDa	13.00%	7	1	1.0	1.1	1.1	1.1	0.10
Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus m	Q99MN9	58 kDa	21.00%	8	1	1.0	1.1	1.1	1.1	0.10
Prostaglandin E synthase 2 OS=Mus musculus GN=Ptges2 PE=1 S	Q8BWM0	43 kDa	6.00%	2	1	0.9	1.0	0.9	1.0	1.00
Proteasome activator complex subunit 1 OS=Mus musculus GN=	G3UXY0 (+3)	26 kDa	11.00%	2	1	0.7	1.1	1.1	1.3	0.27
Proteasome subunit alpha type-1 OS=Mus musculus GN=Psma1	Q9R1P4	30 kDa	13.00%	3	1	0.9	1.0	1.1	1.1	0.32
Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3	O70435	28 kDa	11.00%	2	1	0.9	0.9	1.1	1.0	0.79
Proteasome subunit alpha type-6 OS=Mus musculus GN=Psma6	Q9QUM9	27 kDa	8.50%	2	1	1.3	1.4	1.4	1.2	0.25
Protein 5430421N21Rik OS=Mus musculus GN=5430421N21Rik	E9Q1Y9 (+2)	53 kDa	4.00%	2	1	0.2	0.1	0.1	0.2	0.38
Protein ADP-ribosylarginine] hydrolase-like protein 1 OS=Mus m	Q8BGK2	40 kDa	20.00%	6	1	1.2	1.1	1.4	1.1	0.45
Protein Agl OS=Mus musculus GN=Agl PE=4 SV=1	F8VPN4	174 kDa	6.00%	8	1	0.8	0.9	1.1	1.1	0.45
Protein Ahnak OS=Mus musculus GN=Ahnak PE=1 SV=1	E9Q616	604 kDa	0.51%	2	1	1.0	0.9	0.8	0.9	0.17
Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=	P27773	57 kDa	6.50%	3	1	0.9	1.1	1.0	1.1	0.31
Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 S	P09103	57 kDa	6.10%	2	1	0.8	0.8	0.9	0.9	0.49
Protein FAM162A OS=Mus musculus GN=Fam162a PE=2 SV=1	Q9D6U8	18 kDa	24.00%	3	1	1.1	1.0	1.1	1.0	0.69

Protein Fga OS=Mus musculus GN=Fga PE=4 SV=1	E9PV24 (+1)	87 kDa	9.80%	6	1	0.8	0.8	1.1	1.1	0.78
Protein kinase C and casein kinase substrate in neurons protein	Q9WVE8	56 kDa	6.80%	3	1	0.9	0.9	0.8	0.9	0.11
Protein kinase, cAMP dependent regulatory, type II alpha OS=M	Q8K1M3	46 kDa	7.00%	2	1	1.1	1.2	1.3	1.2	0.15
Protein Lmo7 OS=Mus musculus GN=Lmo7 PE=1 SV=1	E9PYF4 (+3)	193 kDa	2.00%	2	1	1.0	1.0	1.1	1.1	0.42
Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1	Q9QYG0 (+1)	41 kDa	19.00%	5	1	1.1	1.1	1.2	1.1	0.31
Protein NipSnap homolog 2 OS=Mus musculus GN=Gbas PE=2 S	O55126 (+1)	33 kDa	22.00%	7	1	1.1	1.1	1.2	1.1	0.32
Protein Ogdhl OS=Mus musculus GN=Ogdhl PE=4 SV=1	E9Q7L0	117 kDa	21.00%	11	1	1.2	1.1	1.4	1.1	0.45
Protein Prob1 (Fragment) OS=Mus musculus GN=Prob1 PE=1 SV	Q3UKG2	106 kDa	2.40%	2	1	2.1	2.5	2.3	1.5	0.30
Protein QIL1 OS=Mus musculus GN=Qil1 PE=2 SV=1	Q8R404	13 kDa	24.00%	2	1	1.1	0.9	1.1	1.0	0.97
Protein S100-A1 OS=Mus musculus GN=S100a1 PE=1 SV=2	P56565 (+1)	11 kDa	30.00%	2	1	1.1	1.0	1.2	1.1	0.58
Protein Tns1 OS=Mus musculus GN=Tns1 PE=1 SV=1	E9Q0S6	201 kDa	1.70%	2	1	0.9	1.0	1.0	1.1	0.42
Protein transport protein Sec23A OS=Mus musculus GN=Sec23a	E9Q1S3 (+1)	83 kDa	2.60%	2	1	1.0	1.0	1.1	1.1	0.42
Protein-cysteine N-palmitoyltransferase HHAT-like protein OS=M	Q9D1G3	56 kDa	3.20%	2	1	1.1	1.1	1.1	1.0	0.71
Protein-glutamine gamma-glutamyltransferase 2 OS=Mus muscu	P21981	77 kDa	7.60%	4	1	1.2	1.3	1.5	1.3	0.18
Puromycin-sensitive aminopeptidase OS=Mus musculus GN=Np	E9Q039 (+2)	100 kDa	2.40%	2	1	1.1	1.1	1.2	1.1	0.31
Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1,	Q8BFP9	49 kDa	15.00%	5	1	1.1	1.2	1.3	1.2	0.05
Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2,	Q9JK42	46 kDa	6.40%	2	1	1.1	0.9	1.1	1.0	0.97
Pyruvate dehydrogenase E1 component subunit alpha, somatic	P35486	43 kDa	27.00%	12	1	1.1	1.0	1.1	1.0	0.69
Pyruvate dehydrogenase E1 component subunit beta, mitochon	Q9D051	39 kDa	28.00%	9	1	1.0	1.0	1.1	1.0	0.42
Pyruvate dehydrogenase protein X component, mitochondrial O	Q8BKZ9	54 kDa	22.00%	7	1	1.1	1.1	1.3	1.1	0.49
Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2	Q61598 (+1)	51 kDa	16.00%	5	1	0.9	1.0	1.1	1.1	0.32
Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 S	Q91V41	24 kDa	23.00%	2	1	1.1	1.2	1.1	1.1	0.31
Ras-related protein Rab-1A OS=Mus musculus GN=Rab1 PE=3 S	Q5SW88	22 kDa	26.00%	5	1	1.0	1.0	1.0	1.0	0.00
Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 S	P51150	23 kDa	23.00%	4	1	0.8	0.9	1.1	1.2	0.42
Reticulon-4-interacting protein 1, mitochondrial OS=Mus muscu	Q924D0	43 kDa	6.30%	3	1	1.1	1.1	1.1	1.1	0.09
Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia	Q99PT1	23 kDa	15.00%	2	1	#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!
Ryanodine receptor 2 OS=Mus musculus GN=Ryr2 PE=1 SV=1	E9Q401 (+1)	565 kDa	4.00%	16	1	1.1	1.0	1.0	1.0	0.42
Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1	Q7TQ48	99 kDa	28.00%	20	1	1.1	1.1	1.2	1.1	0.11

Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE	P17563	53 kDa	13.00%	5	1	1.1	1.1	1.2	1.1	0.31
Sepiapterin reductase OS=Mus musculus GN=Spr PE=4 SV=1	G3UXX3 (+3)	23 kDa	12.00%	2	1	1.2	0.9	1.4	1.0	0.94
Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=2	E9Q1G8 (+2)	51 kDa	8.90%	3	1	0.8	0.8	1.0	1.0	1.00
Serine protease inhibitor A3K OS=Mus musculus GN=Serpina3k	P07759	47 kDa	30.00%	9	1	2.0	1.7	1.3	1.0	0.96
Serine/threonine-protein phosphatase 2A catalytic subunit beta	P62715 (+1)	36 kDa	10.00%	2	1	#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!
Serine/threonine-protein phosphatase PP1-alpha catalytic subu	P62137 (+3)	38 kDa	9.70%	3	1	0.9	0.9	1.0	1.0	1.00
Serotransferrin OS=Mus musculus GN=Tf PE=1 SV=1	Q921I1	77 kDa	43.00%	27	1	0.8	0.8	1.1	1.1	0.74
Serpin B6 OS=Mus musculus GN=Serpinb6a PE=1 SV=1	F8WIV2 (+1)	45 kDa	17.00%	6	1	1.0	1.1	1.3	1.2	0.11
Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	P07724	69 kDa	50.00%	30	1	1.3	1.4	1.0	1.0	0.87
Serum deprivation-response protein OS=Mus musculus GN=Sdp	Q63918	47 kDa	13.00%	3	1	1.1	1.1	1.1	1.1	0.29
SH3 domain-binding glutamic acid-rich protein (Fragment) OS=	F7CKA6 (+1)	10 kDa	42.00%	4	1	1.1	1.1	1.2	1.1	0.11
Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS	Q07417	45 kDa	32.00%	10	1	1.0	1.1	1.2	1.2	0.04
Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=	P62320	14 kDa	15.00%	2	1	0.9	1.1	1.1	1.1	0.09
Sodium/calcium exchanger 1 OS=Mus musculus GN=Slc8a1 PE=	G3X9J1 (+1)	108 kDa	7.30%	5	1	0.9	0.9	0.9	1.0	0.42
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mu	Q8VDN2	113 kDa	24.00%	20	1	1.1	0.9	1.1	1.0	0.71
Sodium/potassium-transporting ATPase subunit beta-1 OS=Mus	P14094	35 kDa	18.00%	4	1	1.1	1.0	0.9	0.9	0.29
Sorbin and SH3 domain-containing protein 1 OS=Mus musculus	E9QNA7 (+2)	83 kDa	21.00%	10	1	0.9	1.1	1.0	1.1	0.29
Sorting and assembly machinery component 50 homolog OS=M	Q8BGH2	52 kDa	27.00%	10	1	1.0	0.9	1.1	1.0	0.98
Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=	A3KGU5 (+4)	283 kDa	9.80%	20	1	0.9	1.0	1.1	1.1	0.29
S-phase kinase-associated protein 1 OS=Mus musculus GN=Skp1	Q9WTX5	19 kDa	22.00%	3	1	0.9	1.1	1.2	1.2	0.17
Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9	P38647	73 kDa	33.00%	19	1	1.0	1.0	1.1	1.1	0.42
Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1	Q60864	63 kDa	4.80%	2	1	0.9	0.9	0.9	1.0	0.69
Striated muscle-specific serine/threonine-protein kinase OS=Mu	E9QQ25 (+1)	354 kDa	0.95%	2	1	#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mi	Q8K2B3	73 kDa	37.00%	18	1	1.1	1.0	1.1	1.0	0.69
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mito	Q9CQA3	32 kDa	32.00%	10	1	1.0	0.9	1.1	1.0	0.98
Succinate dehydrogenase cytochrome b560 subunit, mitochond	Q9CZB0	18 kDa	17.00%	2	1	1.1	1.0	1.0	1.0	0.42
Succinate-semialdehyde dehydrogenase, mitochondrial OS=Mu	Q8BWF0	56 kDa	3.40%	2	1	1.0	1.0	0.9	0.9	0.42
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochon	Q9WUM5	36 kDa	25.00%	7	1	1.1	1.1	1.3	1.1	0.49

Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial C	Q9Z2I9	50 kDa	43.00%	18	1	1.1	1.1	1.2	1.1	0.11
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial C	Q9Z2I8 (+1)	47 kDa	17.00%	7	1	1.0	1.0	1.1	1.1	0.42
Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondri	Q9D0K2	56 kDa	21.00%	8	1	1.4	1.5	1.5	1.3	0.27
Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1	P08228	16 kDa	14.00%	2	1	1.2	1.1	1.2	1.1	0.61
Superoxide dismutase [Mn], mitochondrial OS=Mus musculus G	P09671	25 kDa	38.00%	7	1	1.0	1.0	1.4	1.2	0.42
Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=	B2RQK7 (+2)	103 kDa	6.90%	4	1	0.9	1.1	1.2	1.2	0.05
T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 I	P11983 (+1)	60 kDa	7.90%	4	1	0.9	1.0	1.1	1.1	0.29
T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3	P80318 (+1)	61 kDa	3.90%	2	1	0.8	0.9	0.9	1.0	0.80
Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	P10639	12 kDa	30.00%	3	1	1.0	1.4	1.4	1.4	0.00
Thioredoxin-dependent peroxide reductase, mitochondrial OS=I	P20108	28 kDa	25.00%	4	1	1.2	1.3	1.4	1.2	0.18
Thioredoxin-like protein 1 OS=Mus musculus GN=Txnl1 PE=2 SV	Q8CDN6	32 kDa	17.00%	3	1	0.8	1.1	1.1	1.2	0.22
Titin OS=Mus musculus GN=Ttn PE=1 SV=1	A2ASS6	3906 kDa	13.00%	374	1	1.1	1.1	1.2	1.1	0.31
Transaldolase OS=Mus musculus GN=Taldo1 PE=1 SV=2	Q93092	37 kDa	7.10%	2	1	1.5	1.4	1.5	1.2	0.51
Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=1 SV	Q9QUI0	22 kDa	14.00%	2	1	0.9	0.9	1.1	1.1	0.58
Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4	Q9WVA4	22 kDa	25.00%	4	1	1.1	1.1	1.1	1.1	0.29
Transitional endoplasmic reticulum ATPase OS=Mus musculus G	Q01853	89 kDa	20.00%	11	1	1.0	1.1	0.9	1.0	0.98
Translational activator of cytochrome c oxidase 1 OS=Mus musc	Q8K0Z7	32 kDa	9.90%	2	1	2.8	2.6	2.6	1.4	0.51
Translationally-controlled tumor protein OS=Mus musculus GN=	P63028	19 kDa	22.00%	3	1	0.9	1.1	1.1	1.1	0.17
Trifunctional enzyme subunit alpha, mitochondrial OS=Mus mus	Q8BMS1	83 kDa	41.00%	26	1	1.1	1.1	1.1	1.1	0.29
Trifunctional enzyme subunit beta, mitochondrial OS=Mus musc	Q99JY0	51 kDa	33.00%	13	1	1.1	1.0	1.2	1.1	0.58
Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV	P17751	32 kDa	38.00%	11	1	1.0	1.1	1.2	1.2	0.20
Tripartite motif-containing protein 72 OS=Mus musculus GN=Tri	Q1XH17	53 kDa	33.00%	11	1	0.9	1.0	1.0	1.1	0.42
Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 S	P58771	33 kDa	57.00%	17	1	1.1	1.0	1.0	1.0	0.42
Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 S	Q6IRU2	28 kDa	17.00%	2	1	0.7	1.0	1.1	1.2	0.35
Troponin C, slow skeletal and cardiac muscles OS=Mus musculus	P19123	18 kDa	24.00%	5	1	1.1	0.9	1.1	0.9	0.55
Troponin I, cardiac muscle OS=Mus musculus GN=Tnni3 PE=1 SV	P48787	24 kDa	46.00%	10	1	1.0	0.9	0.9	0.9	0.09
Troponin T, cardiac muscle OS=Mus musculus GN=Tnnt2 PE=4 S	J3QQ13 (+7)	36 kDa	33.00%	10	1	1.1	0.9	1.0	0.9	0.29
Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=	P05213	50 kDa	29.00%	3	1	0.9	1.1	1.1	1.1	0.09

Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=	P68368	50 kDa	29.00%	11	1	0.9	1.1	1.1	1.2	0.03
Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	Q7TMM9	50 kDa	31.00%	2	1	0.9	1.1	1.1	1.2	0.15
Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1	P68372	50 kDa	37.00%	12	1	1.0	1.1	1.1	1.1	0.00
Ubiquinone biosynthesis protein COQ7 homolog OS=Mus muscu	P97478	24 kDa	29.00%	5	1	1.3	1.2	1.3	1.1	0.56
Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Mus	Q8K1Z0	35 kDa	19.00%	4	1	1.1	1.1	1.2	1.1	0.32
Ubiquitin carboxyl-terminal hydrolase 5 OS=Mus musculus GN=	P56399 (+1)	96 kDa	6.50%	4	1	1.0	1.0	1.1	1.0	0.42
Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=	D3YWF6 (+1)	28 kDa	11.00%	2	1	1.1	1.2	1.2	1.1	0.17
Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2	P61089	17 kDa	14.00%	2	1	0.9	1.1	1.4	1.3	0.25
Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus G	Q02053	118 kDa	9.20%	7	1	1.1	1.1	1.2	1.1	0.32
Uncharacterized protein OS=Mus musculus GN=Gm10260 PE=3	F6YVP7 (+2)	18 kDa	11.00%	2	1	1.1	1.1	1.2	1.1	0.11
Uncharacterized protein OS=Mus musculus GN=Gm6576 PE=3 S	F6YTZ4 (+4)	30 kDa	8.40%	2	1	0.9	1.2	1.0	1.2	0.34
Uncharacterized protein OS=Mus musculus GN=Gm7729 PE=4 S	J3QK72 (+2)	34 kDa	10.00%	2	1	1.4	1.3	1.3	1.1	0.64
UPF0598 protein C8orf82 homolog OS=Mus musculus PE=2 SV=	Q8VE95	24 kDa	14.00%	2	1	1.3	1.2	1.4	1.1	0.47
Up-regulated during skeletal muscle growth protein 5 OS=Mus	Q78IK2	6 kDa	43.00%	2	1	1.1	1.0	1.1	1.0	1.00
UTP--glucose-1-phosphate uridylyltransferase OS=Mus musculu	Q91ZJ5 (+1)	57 kDa	14.00%	6	1	0.8	0.8	0.9	1.0	0.79
Vacuolar protein sorting-associated protein 35 OS=Mus musculu	Q9EQH3	92 kDa	2.80%	2	1	1.0	1.0	1.3	1.2	0.42
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	P50544	71 kDa	53.00%	26	1	1.0	0.9	1.1	1.0	0.74
Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	P20152	54 kDa	33.00%	11	1	0.9	1.3	1.1	1.3	0.10
Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	Q64727	117 kDa	16.00%	13	1	1.1	1.0	1.1	1.0	1.00
Voltage-dependent anion-selective channel protein 2 (Fragment	G3UX26 (+1)	30 kDa	36.00%	8	1	1.1	0.9	1.0	0.9	0.29
Voltage-dependent anion-selective channel protein 3 OS=Mus	J3QMG3 (+1)	31 kDa	49.00%	10	1	1.1	1.1	1.1	1.1	0.29
von Willebrand factor A domain-containing protein 8 OS=Mus	Q8CC88 (+1)	213 kDa	1.60%	2	1	1.1	1.1	1.1	1.0	0.42
WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 PE	O88342	66 kDa	20.00%	7	1	1.0	1.2	1.1	1.2	0.04
Wolframin OS=Mus musculus GN=Wfs1 PE=1 SV=1	P56695 (+1)	101 kDa	2.20%	2	1	0.8	0.9	1.0	1.0	0.82
Xin actin-binding repeat-containing protein 1 OS=Mus musculus	E9QQ93 (+1)	124 kDa	19.00%	14	1	0.7	1.0	1.0	1.2	0.42