UniProt Acce	Protein Name	SWATH Log2 P42/P7	SWATH BH	SILAC Log2 P42/P7
Q03265	ATP synthase subunit alph	1.89	0.000	0.73
Q91VD9	NADH-ubiquinone oxidor	1.46	0.004	0.75
P70404	Isocitrate dehydrogenase	3.09	0.005	1.19
Q9CQ54	NADH dehydrogenase [ub	2.51	0.006	0.84
Q99KI0	Aconitate hydratase, mitc	1.36	0.010	0.98
Q9CRB8	Mitochondrial fission pro	2.13	0.011	1.14
P30275	Creatine kinase U-type, m	1.44	0.011	2.14
P08249	Malate dehydrogenase, m	0.95	0.013	0.80
Q8BMF4	Dihydrolipoyllysine-residu	1.58	0.013	1.26
Q9WTQ8	Mitochondrial import inn	-1.57	0.024	-0.79
Q9D172	ES1 protein homolog, mit	2.25	0.027	1.28
Q91WS0	CDGSH iron-sulfur domai	1.31	0.027	0.86
O08749	Dihydrolipoyl dehydroger	1.35	0.029	0.79
Q9CQC7	NADH dehydrogenase [ub	1.37	0.029	0.85
Q9JLZ3	Methylglutaconyl-CoA hy	1.75	0.029	1.11
Q9D1G1	Ras-related protein Rab-1	1.95	0.029	1.40
P09671	Superoxide dismutase [M	1.01	0.029	1.44
A2ASZ8	Calcium-binding mitochor	3.72	0.029	0.38
Q9CZU6	Citrate synthase, mitocho	-0.59	0.029	0.42
P17710	Hexokinase-1 OS=Mus mu	1.23	0.031	1.51
Q99N89	39S ribosomal protein L4	-1.41	0.034	-0.75
Q9Z0V7	Mitochondrial import inn	-1.80	0.034	-0.90
D3Z7P3	Glutaminase kidney isofo	1.18	0.034	1.13
P97450	ATP synthase-coupling fa	1.39	0.035	0.74
Q9CQ69	Cytochrome b-c1 comple	1.53	0.036	0.81
P52480	Pyruvate kinase PKM OS=	1.51	0.036	1.94
P50516	V-type proton ATPase cat	1.95	0.036	3.97
Q8QZT1	Acetyl-CoA acetyltransfer	-0.86	0.036	-0.34
Q9WUR9	Adenylate kinase 4, mitoc	1.72	0.036	2.44
O08599	Syntaxin-binding protein	1.56	0.040	3.11
Q8K1Z0	Ubiquinone biosynthesis	1.63	0.041	1.29
P55096	ATP-binding cassette sub-	-2.25	0.042	-1.94
Q8K009	Mitochondrial 10-formylt	-1.99	0.042	-1.23
Q9D6U8	Protein FAM162A OS=Mu	1.93	0.042	0.79
Q9CYH2	Redox-regulatory protein	1.36	0.044	0.75
Q9CQ40	39S ribosomal protein L4	-1.47	0.045	-1.09
Q9JHS4	ATP-dependent Clp prote	-1.30	0.045	-0.71
Q791T5	Mitochondrial carrier hon	-2.05	0.045	-0.52
Q61425	Hydroxyacyl-coenzyme A	2.61	0.045	0.33
Q9D6R2	Isocitrate dehydrogenase	0.65	0.049	1.00
Q9DCW4	Electron transfer flavopro	5.48	0.005	0.35

Q9CPQ3	Mitochondrial import rec	-1.67	0.006	-0.11
P99027	60S acidic ribosomal prot	-2.03	0.011	-0.42
Q99LC5	Electron transfer flavopro	3.65	0.013	0.30
Q8BH04	Phosphoenolpyruvate car	2.36	0.013	0.66
Q8BP92	Reticulocalbin-2 OS=Mus	-1.74	0.019	-1.48
O35658	Complement component	-2.01	0.020	0.14
Q9CY16	28S ribosomal protein S2	-1.65	0.029	-0.51
Q9CZR8	Elongation factor Ts, mito	2.21	0.029	0.19
P24369	Peptidyl-prolyl cis-trans is	-2.10	0.029	-0.38
Q80Y14	Glutaredoxin-related prot	-1.28	0.029	-0.18
Q8BLN5	Lanosterol synthase OS=	-2.79	0.030	0.06
P14131	40S ribosomal protein S1	-2.06	0.032	-0.83
Q8CD10	Calcium uptake protein 2,	-1.82	0.036	-4.30
Q99KK9	Probable histidine--tRNA	-1.20	0.036	0.03
P63017	Heat shock cognate 71 k	2.16	0.044	0.72
P58064	28S ribosomal protein S6,	-2.73	0.047	-3.14
Q9Z110	Delta-1-pyrroline-5-carbo	-1.33	0.047	-0.61
Q6PCP5	Mitochondrial fission fact	2.49	0.047	-0.07
Q8BX10	Serine/threonine-protein	-1.22	0.050	-0.62
Q8BWT1	3-ketoacyl-CoA thiolase,	-1.27	0.050	-0.29
Q62425	Cytochrome c oxidase su	1.03	0.050	0.76
Q7TMF3	NADH dehydrogenase [u	1.54	0.050	0.84
P05202	Aspartate aminotransfera	1.28	0.050	1.18
Q9D1I6	39S ribosomal protein L1	-1.52	0.051	-0.92
Q9D855	Cytochrome b-c1 comple	2.23	0.052	0.67
Q91YT0	NADH dehydrogenase [u	1.05	0.052	0.69
Q9CR62	Mitochondrial 2-oxogluta	0.90	0.052	0.85
P08228	Superoxide dismutase [C	2.83	0.052	1.02
Q9DC71	28S ribosomal protein S1	3.84	0.055	-0.66
Q6P3A8	2-oxoisovalerate dehydro	-1.97	0.055	-0.48
P16858	Glyceraldehyde-3-phosph	2.80	0.056	2.13
Q68FD5	Clathrin heavy chain 1 OS	1.27	0.056	2.94
P63011	Ras-related protein Rab-3	1.74	0.061	2.88
Q9CQE3	28S ribosomal protein S1	-1.10	0.062	-0.73
Q8VE22	28S ribosomal protein S2	-1.26	0.062	-0.61
Q9CQR4	Acyl-coenzyme A thioeste	1.17	0.062	1.67
P17182	Alpha-enolase OS=Mus m	1.61	0.062	1.88
Q9CZS1	Aldehyde dehydrogenase	-0.99	0.064	-0.72
P58059	28S ribosomal protein S2	-1.27	0.065	-0.65
Q9D3D9	ATP synthase subunit delt	1.44	0.066	0.72
Q8BTX9	Inactive hydroxysteroid d	-1.34	0.068	-0.79
Q9DC69	NADH dehydrogenase [u	2.92	0.068	0.82

Q8K3J1	NADH dehydrogenase [ub	3.19	0.070	1.21
P14152	Malate dehydrogenase, c	1.37	0.083	2.66
P09411	Phosphoglycerate kinase	1.26	0.086	2.34
Q9D0S9	Histidine triad nucleotide-	1.09	0.087	0.82
Q9CXZ1	NADH dehydrogenase [ub	1.23	0.087	0.82
Q3UIU2	NADH dehydrogenase [ub	4.53	0.088	0.67
P17751	Triosephosphate isomera	1.26	0.088	2.89
P56480	ATP synthase subunit bet	0.24	0.095	0.72
Q9CQV7	Mitochondrial import inn	-1.12	0.097	-0.71
P99029	Peroxiredoxin-5, mitocho	0.81	0.098	1.28
Q99N96	39S ribosomal protein L1,	-1.23	0.100	-0.89
Q3UUI3	Acyl-coenzyme A thioeste	1.05	0.100	1.14
Q9WUM5	Succinate--CoA ligase [AD	1.16	0.104	1.26
Q9CR68	Cytochrome b-c1 comple	0.77	0.111	0.75
Q99LC3	NADH dehydrogenase [ub	1.14	0.112	0.62
Q9CQE1	Protein NipSnap homolog	-1.26	0.115	-1.15
P12787	Cytochrome c oxidase sub	0.72	0.125	0.64
P56135	ATP synthase subunit f, m	2.76	0.125	0.69
Q9D1B9	39S ribosomal protein L2	-1.13	0.127	-0.58
Q9D0K2	Succinyl-CoA:3-ketoacid c	1.16	0.127	-0.39
P51175	Protoporphyrinogen oxid	-1.35	0.127	0.74
Q922B1	O-acetyl-ADP-ribose deac	1.72	0.127	1.64
Q8CAQ8	MICOS complex subunit M	0.67	0.134	0.41
Q9CWE0	Mitochondrial fission regu	1.43	0.139	0.48
Q9D6K8	FUN14 domain-containin	1.23	0.139	0.91
Q8R164	Valacyclovir hydrolase OS	1.33	0.139	1.38
Q9CQ92	Mitochondrial fission 1 pr	2.04	0.139	0.97
Q9CZ13	Cytochrome b-c1 comple	-1.48	0.144	0.76
Q811U4	Mitofusin-1 OS=Mus mus	-1.30	0.144	-0.67
Q9CQX8	28S ribosomal protein S3	0.93	0.144	0.70
Q9DB77	Cytochrome b-c1 comple	0.55	0.144	0.81
Q91WC3	Long-chain-fatty-acid--Co	2.13	0.144	1.43
Q8BH59	Calcium-binding mitochon	0.59	0.148	0.90
P51660	Peroxisomal multifunctio	-0.77	0.155	-1.03
P56379	6.8 kDa mitochondrial pro	1.20	0.155	0.76
Q6ZWN5	40S ribosomal protein S9	-1.90	0.155	-2.72
Q3UJU9	Regulator of microtubule	0.96	0.156	1.29
Q99J39	Malonyl-CoA decarboxyla	0.90	0.157	0.46
P97807	Fumarate hydratase, mitc	0.96	0.158	0.70
Q9DBG3	AP-2 complex subunit bet	0.89	0.158	2.27
Q8K0Z7	Translational activator of	-0.92	0.165	0.57
Q9CPP6	NADH dehydrogenase [ub	1.47	0.175	0.80

Q9DCS9	NADH dehydrogenase [u	0.76	0.179	0.74
Q921H8	3-ketoacyl-CoA thiolase A	-1.35	0.179	-1.69
Q9Z2Q5	39S ribosomal protein L4	-1.00	0.191	-1.28
O55125	Protein NipSnap homolog	1.48	0.191	0.62
P03921	NADH-ubiquinone oxidor	1.18	0.193	0.82
Q99LY9	NADH dehydrogenase [u	3.59	0.198	0.68
P35486	Pyruvate dehydrogenase	0.54	0.198	0.98
Q9CPQ8	ATP synthase subunit g,	1.84	0.198	1.23
Q9DCX2	ATP synthase subunit d,	0.79	0.202	0.72
Q9CQN7	39S ribosomal protein L4	-0.99	0.210	-0.56
Q9D023	Mitochondrial pyruvate c	1.07	0.210	0.34
Q91WD5	NADH dehydrogenase [u	0.78	0.210	0.72
Q61102	ATP-binding cassette sub-	2.63	0.212	0.82
P85094	Isochorismatase domain-	3.41	0.212	1.83
P63101	14-3-3 protein zeta/delta	0.95	0.221	1.36
Q91VA6	Polymerase delta-interac	-0.83	0.231	-0.42
Q3KNM2	E3 ubiquitin-protein ligas	-0.77	0.232	-0.75
Q9EQ20	Methylmalonate-semiald	0.84	0.232	0.61
Q91VR2	ATP synthase subunit ga	0.50	0.232	0.74
O09111	NADH dehydrogenase [u	0.82	0.233	0.87
Q99J99	3-mercaptopyruvate sulf	-0.81	0.239	-0.76
Q9CPQ1	Cytochrome c oxidase su	0.74	0.245	0.76
Q99N92	39S ribosomal protein L2	-0.93	0.245	-0.68
Q8VEM8	Phosphate carrier protein	0.49	0.249	0.74
Q8VDT9	39S ribosomal protein L5	-0.85	0.249	-1.08
P61922	4-aminobutyrate aminotr	0.74	0.249	1.61
Q9D6J5	NADH dehydrogenase [u	0.67	0.250	0.84
Q9D051	Pyruvate dehydrogenase	-0.77	0.252	0.93
Q78IK2	Up-regulated during skel	-0.54	0.259	0.54
Q9DCJ5	NADH dehydrogenase [u	0.69	0.264	0.91
P29758	Ornithine aminotransfera	0.95	0.275	-0.69
Q8BGC4	Prostaglandin reductase-	-0.76	0.279	1.38
Q9DCT2	NADH dehydrogenase [u	0.56	0.288	0.99
Q9Z2I9	Succinate--CoA ligase [AD	0.65	0.293	1.22
Q80VL1	Tudor and KH domain-co	1.64	0.297	-1.27
Q8BU88	39S ribosomal protein L2	-0.69	0.299	-0.69
P62897	Cytochrome c, somatic O	0.81	0.300	0.55
Q9EQI8	39S ribosomal protein L4	-1.50	0.306	-1.04
Q9JIK9	28S ribosomal protein S3	-1.84	0.306	-0.83
Q5HZI9	Solute carrier family 25 m	1.66	0.306	0.62
Q9CQZ6	NADH dehydrogenase [u	0.61	0.306	0.74
O55126	Protein NipSnap homolog	0.70	0.306	0.77

Q8VE33	Ganglioside-induced diffe	0.73	0.317	0.61
Q921G7	Electron transfer flavopro	2.43	0.317	0.39
Q9D338	39S ribosomal protein L1	-1.00	0.318	-0.80
Q91YP2	Neurolysin, mitochondria	-0.84	0.319	-0.86
Q80X85	28S ribosomal protein S7,	-0.64	0.344	-0.55
Q8BGH2	Sorting and assembly ma	2.16	0.344	0.56
Q9D0G0	28S ribosomal protein S3	-1.33	0.347	-0.60
Q8BGX2	Mitochondrial import inn	-0.60	0.351	0.46
Q8JZU2	Tricarboxylate transport	-0.59	0.355	-0.59
Q8R404	MICOS complex subunit	1.49	0.381	0.62
Q9CQ91	NADH dehydrogenase [u	0.63	0.382	1.03
Q9D6M3	Mitochondrial glutamate	0.43	0.386	0.92
Q9ERD7	Tubulin beta-3 chain OS=	-0.74	0.393	0.47
Q9ER88	28S ribosomal protein S2	0.68	0.405	-0.67
P56391	Cytochrome c oxidase su	-0.97	0.407	0.64
O35459	Delta(3,5)-Delta(2,4)-dien	-0.47	0.410	-0.88
P47791	Glutathione reductase, m	0.68	0.410	0.55
O88441	Metaxin-2 OS=Mus muscu	0.97	0.422	0.57
P52196	Thiosulfate sulfurtransfer	-0.45	0.425	0.47
Q9D880	Mitochondrial import inn	-0.49	0.427	-0.53
Q9D2G2	Dihydrolipoyllysine-resid	0.41	0.428	0.53
Q8K4F5	Protein ABHD11 OS=Mus	0.57	0.445	1.44
Q9D0L7	Armadillo repeat-containi	-0.49	0.457	-0.82
P51881	ADP/ATP translocase 2 O	0.52	0.457	0.67
Q9JKL4	NADH dehydrogenase [u	-0.38	0.457	0.74
Q8BJZ4	28S ribosomal protein S3	1.13	0.457	-1.29
P22315	Ferrochelatase, mitochon	0.81	0.468	0.49
Q9D0M3	Cytochrome c1, heme pro	0.29	0.468	0.60
Q99L13	3-hydroxyisobutyrate deh	0.43	0.492	1.04
P53026	60S ribosomal protein L1	0.90	0.494	-3.18
Q9CZP5	Mitochondrial chaperone	0.53	0.497	0.80
Q8BWF0	Succinate-semialdehyde	0.36	0.499	0.71
Q4VAE3	Transmembrane protein	0.27	0.502	0.67
Q14C51	Pentatricopeptide repeat	-0.49	0.504	-0.91
Q9DB20	ATP synthase subunit O,	0.34	0.518	0.71
Q9CQZ5	NADH dehydrogenase [u	0.28	0.518	0.76
P56382	ATP synthase subunit eps	0.47	0.532	0.66
Q9JKC6	Cell cycle exit and neuron	-0.30	0.532	1.25
Q91ZA3	Propionyl-CoA carboxylas	0.38	0.537	0.53
Q99NB1	Acetyl-coenzyme A synth	-0.49	0.540	-2.69
Q60930	Voltage-dependent anion	0.26	0.542	0.85
Q60597	2-oxoglutarate dehydrog	0.37	0.549	0.45

Q9DCZ4	MICOS complex subunit	-0.26	0.553	0.75
Q91YP0	L-2-hydroxyglutarate deh	0.37	0.553	0.76
Q91VC9	Growth hormone-inducib	-0.83	0.572	0.76
Q8QZS1	3-hydroxyisobutyryl-CoA	-0.34	0.575	0.97
P07901	Heat shock protein HSP 9	0.45	0.586	0.85
Q8BWM0	Prostaglandin E synthase	0.66	0.602	-0.33
Q9CZW5	Mitochondrial import rec	0.82	0.602	0.49
Q91VT4	Carbonyl reductase famil	-0.39	0.603	0.46
Q9CR61	NADH dehydrogenase [ub	0.28	0.603	1.51
O88967	ATP-dependent zinc meta	0.32	0.604	-0.67
Q99MN9	Propionyl-CoA carboxylas	-0.29	0.608	0.55
P00405	Cytochrome c oxidase sub	-0.11	0.614	0.60
P48962	ADP/ATP translocase 1 O	-0.46	0.625	0.88
Q9CPR5	39S ribosomal protein L1	-0.38	0.625	-1.20
Q9CQH3	NADH dehydrogenase [ub	0.31	0.625	0.89
Q8JZQ2	AFG3-like protein 2 OS=	0.31	0.642	0.62
Q9D6K5	Synaptojanin-2-binding p	0.35	0.642	1.06
Q9EP89	Serine beta-lactamase-lik	-0.36	0.697	0.40
Q9D6J6	NADH dehydrogenase [ub	0.21	0.705	0.69
P48771	Cytochrome c oxidase sub	0.18	0.717	0.60
Q9QZD8	Mitochondrial dicarboxyl	-0.31	0.720	1.19
P59017	Bcl-2-like protein 13 OS=	-0.52	0.724	-0.55
Q8BGT5	Alanine aminotransferase	-0.38	0.730	-1.81
Q9D3P8	Plasminogen receptor (KT	-0.32	0.730	-1.35
Q8BHF7	CDP-diacylglycerol--glyce	-0.18	0.730	0.96
Q9CQA3	Succinate dehydrogenase	-0.25	0.732	0.37
Q8BKZ9	Pyruvate dehydrogenase	0.23	0.732	0.98
Q9CRB9	MICOS complex subunit	-0.20	0.754	0.41
Q9CPV4	Glyoxalase domain-conta	0.34	0.757	1.44
Q5M8N4	Epimerase family protein	0.43	0.759	-0.80
Q922H2	[Pyruvate dehydrogenase	0.39	0.759	0.65
Q99JR1	Sideroflexin-1 OS=Mus m	-0.16	0.760	-0.42
Q9CQJ8	NADH dehydrogenase [ub	0.20	0.765	0.92
Q9DC70	NADH dehydrogenase [ub	0.11	0.793	0.71
Q8CI78	Required for meiotic nucl	0.19	0.802	0.66
Q06185	ATP synthase subunit e,	0.14	0.802	0.68
P58281	Dynamin-like 120 kDa pro	0.18	0.805	0.53
P32020	Non-specific lipid-transfe	-0.36	0.814	-1.25
Q64521	Glycerol-3-phosphate deh	0.17	0.815	0.70
Q9CZN8	Glutamyl-tRNA(Gln) amid	-0.31	0.820	0.81
Q60931	Voltage-dependent anion	0.11	0.839	0.37
P03930	ATP synthase protein 8 O	-0.09	0.845	0.56

Q8BK72	28S ribosomal protein S2	0.22	0.847	-0.67
Q8R4N0	Citrate lyase subunit beta	0.11	0.865	1.12
Q80U63	Mitofusin-2 OS=Mus mus	0.13	0.868	0.34
Q9CQQ7	ATP synthase F(0) comple	0.09	0.880	0.77
P68254	14-3-3 protein theta OS=	-0.16	0.888	3.84
P62259	14-3-3 protein epsilon OS	0.11	0.890	1.06
Q3UV70	[Pyruvate dehydrogenase	0.10	0.893	0.89
Q9CPX8	Cytochrome b-c1 comple	-0.25	0.893	0.95
Q6PB66	Leucine-rich PPR motif-co	-0.15	0.896	-0.79
P62075	Mitochondrial import inn	-0.12	0.897	0.63
Q8BIJ6	Isoleucine--tRNA ligase,	-0.09	0.899	0.64
Q8C163	Nuclease EXOG, mitochor	-0.09	0.901	0.37
Q8K2B3	Succinate dehydrogenase	0.15	0.903	0.29
Q9D1N9	39S ribosomal protein L2	-0.12	0.913	-0.76
Q60932	Voltage-dependent anion	-0.06	0.917	0.91
Q99KB8	Hydroxyacylglutathione h	0.11	0.926	1.77
Q3TC33	Coiled-coil domain-contai	0.15	0.932	0.73
Q9WV84	Nucleoside diphosphate	0.15	0.940	-0.94
Q2TPA8	Hydroxysteroid dehydrog	0.17	0.948	-0.50
Q9Z2I0	Mitochondrial proton/ca	0.06	0.948	0.48
Q791V5	Mitochondrial carrier hon	0.06	0.948	0.57
Q9CQ75	NADH dehydrogenase [u	0.05	0.948	0.75
P35700	Peroxiredoxin-1 OS=Mus	0.11	0.948	1.08
Q3ULF4	Paraplegin OS=Mus musc	0.11	0.948	2.19
Q5ND52	rRNA methyltransferase	0.10	0.949	-1.54
Q9QXX4	Calcium-binding mitochor	0.09	0.951	0.72
P42125	Enoyl-CoA delta isomeras	0.04	0.958	0.51
Q8C5H8	NAD kinase 2, mitochond	-0.04	0.961	0.32
P20108	Thioredoxin-dependent p	-0.02	0.962	0.51
P19783	Cytochrome c oxidase su	0.02	0.962	0.69
P19536	Cytochrome c oxidase su	0.02	0.983	0.70
P45952	Medium-chain specific ac	0.02	0.983	-0.45
Q91V61	Sideroflexin-3 OS=Mus m	-0.02	0.983	0.75
Q9D8T7	SRA stem-loop-interactin	0.02	0.986	-0.74
Q8BFR5	Elongation factor Tu, mit	-0.01	0.986	0.29
Q9CXJ4	ATP-binding cassette sub-	-0.02	0.986	0.55
Q8K215	LYR motif-containing prot	0.02	0.986	0.60
Q9ERS2	NADH dehydrogenase [u	0.01	0.986	0.78
Q91VM9	Inorganic pyrophosphata	0.02	0.986	0.84
Q9Z1P6	NADH dehydrogenase [u	-0.01	0.986	0.85
Q505D7	Optic atrophy 3 protein h	-0.01	0.987	0.66
Q91VN4	MICOS complex subunit	-0.01	0.987	0.52

O08734	Bcl-2 homologous antago	-1.15	0.050	-1.73
P50431	Serine hydroxymethyltrar	-2.21	0.050	-0.97
Q8BMS1	Trifunctional enzyme subu	1.60	0.050	0.30
Q9D8E6	60S ribosomal protein L4	-1.83	0.052	-0.66
O88986	2-amino-3-ketobutyrate c	-1.94	0.057	-0.32
Q61578	NADPH:adrenodoxin oxid	-1.00	0.061	-0.13
P14869	60S acidic ribosomal prot	-1.37	0.062	-1.58
Q99JB2	Stomatin-like protein 2, m	2.17	0.062	-0.02
P14148	60S ribosomal protein L7	-0.99	0.068	-0.67
P54071	Isocitrate dehydrogenase	-1.06	0.068	-0.10
Q91V92	ATP-citrate synthase OS=	-1.58	0.071	-3.25
Q3UHB1	5'-nucleotidase domain-c	1.93	0.071	-0.17
Q8C5Q4	G-rich sequence factor 1	-1.46	0.071	1.03
Q9CTY5	Calcium uptake protein 3,	1.42	0.072	0.39
Q8K2Y7	39S ribosomal protein L4	1.59	0.075	-0.28
Q99LB2	Dehydrogenase/reductas	1.22	0.077	0.71
Q9DCU6	39S ribosomal protein L4,	-1.24	0.083	-0.53
P14211	Calreticulin OS=Mus musc	-1.52	0.086	-0.50
Q9CR88	28S ribosomal protein S1	-1.18	0.088	-3.35
Q9QZH6	Evolutionarily conserved	-1.24	0.088	-0.21
Q60714	Long-chain fatty acid tran	-0.96	0.088	0.15
P67778	Prohibitin OS=Mus muscu	-0.64	0.100	-0.02
O08756	3-hydroxyacyl-CoA dehyd	-0.91	0.112	-0.23
Q9CQU0	Thioredoxin domain-cont	-2.11	0.126	-0.22
P09925	Surfeit locus protein 1 OS	1.85	0.127	0.10
Q9CQN1	Heat shock protein 75 kD	-0.89	0.127	-0.36
Q8VCL2	Protein SCO2 homolog, m	-1.18	0.127	0.08
Q99JY0	Trifunctional enzyme subu	2.83	0.127	0.28
Q91WM2	Haloacid dehalogenase-lik	1.80	0.129	-0.20
Q9JKF7	39S ribosomal protein L3	-1.13	0.131	-0.46
Q91YM4	Protein TBRG4 OS=Mus m	-1.25	0.132	0.29
P38647	Stress-70 protein, mitoch	0.73	0.139	-0.08
Q99JT1	Glutamyl-tRNA(Gln) amid	-1.00	0.142	3.05
Q8BMF3	NADP-dependent malic e	1.25	0.142	-0.74
Q9DCC8	Mitochondrial import rec	-1.02	0.144	0.00
Q9CRD0	OCIA domain-containing	2.80	0.144	0.06
Q8K4Z3	NAD(P)H-hydrate epimer	1.76	0.144	0.17
Q9Z2I8	Succinate--CoA ligase [GD	-0.82	0.144	0.29
Q8BUY5	Complex I assembly facto	-0.75	0.145	-0.55
Q91YJ5	Translation initiation fact	-0.90	0.158	-0.33
Q9CQS4	Solute carrier family 25 m	1.14	0.159	-0.21
Q9WTP6	Adenylate kinase 2, mitoc	3.00	0.161	-0.36

Q3U186	Probable arginine--tRNA l	-1.46	0.165	0.12
O35435	Dihydroorotate dehydrog	-0.71	0.166	-0.13
Q3ULD5	Methylcrotonoyl-CoA carl	-0.81	0.175	-0.19
Q3TUH1	Phosphatidate cytidylyltra	-1.89	0.193	-1.07
Q8CHT0	Delta-1-pyrroline-5-carbo	-0.73	0.206	-0.20
P50544	Very long-chain specific a	-0.83	0.209	-0.04
Q9QYF1	Retinol dehydrogenase 1	-1.62	0.210	-0.99
Q8BYL4	Tyrosine--tRNA ligase, mit	1.38	0.211	-0.13
O88696	ATP-dependent Clp prote	-0.61	0.216	-0.15
Q91WK1	SPRY domain-containing p	-0.83	0.221	-0.09
Q99J25	rRNA methyltransferase 1	-0.98	0.222	-0.91
Q99MR8	Methylcrotonoyl-CoA carl	3.01	0.228	0.04
Q9D8Y1	Transmembrane protein 1	-0.81	0.232	-0.18
Q99LB7	Sarcosine dehydrogenase	2.41	0.232	0.39
Q9CQV5	28S ribosomal protein S2	-1.43	0.234	-0.51
Q02053	Ubiquitin-like modifier-ac	2.11	0.234	2.69
Q61879	Myosin-10 OS=Mus musc	-1.59	0.235	-0.25
Q80ZS3	28S ribosomal protein S2	-1.08	0.238	0.12
Q925I1	ATPase family AAA domai	0.85	0.242	0.20
P97478	5-demethoxyubiquinone	-0.83	0.243	2.74
Q78IK4	MICOS complex subunit M	1.26	0.246	-0.27
Q9CZU4	GTPase Era, mitochondria	-1.54	0.249	0.09
Q61387	Cytochrome c oxidase sub	-0.77	0.253	-0.05
Q7TSQ8	Pyruvate dehydrogenase	-0.72	0.253	0.27
Q14CH7	Alanine--tRNA ligase, mito	-1.01	0.266	-0.02
P62242	40S ribosomal protein S8	-1.31	0.267	-1.96
P52503	NADH dehydrogenase [ub	2.47	0.269	0.50
P50171	Estradiol 17-beta-dehydro	-0.85	0.270	0.12
Q91YQ5	Dolichyl-diphosphooligosa	-0.79	0.271	-0.53
B7ZMP1	Probable Xaa-Pro aminop	-2.07	0.271	-0.18
P40630	Transcription factor A, mi	-0.71	0.271	0.12
Q9CQF0	39S ribosomal protein L1	-1.19	0.280	-0.57
Q922Q1	Mitochondrial amidoxime	-1.27	0.281	0.37
P47911	60S ribosomal protein L6	-0.95	0.282	-0.60
Q9D2R6	Cytochrome c oxidase ass	-0.73	0.282	0.26
P35980	60S ribosomal protein L1	1.19	0.287	-1.52
Q9CZ42	ATP-dependent (S)-NAD(	0.84	0.287	0.21
Q8VCW8	Acyl-CoA synthetase fami	2.06	0.288	-0.07
Q64133	Amine oxidase [flavin-con	-0.56	0.288	-0.01
P47738	Aldehyde dehydrogenase	0.92	0.289	-0.25
Q9CWG8	Protein arginine methyltr	-0.76	0.292	0.14
Q9CQB5	CDGSH iron-sulfur domai	-1.49	0.301	-0.35

P47963	60S ribosomal protein L1	-0.80	0.303	-0.43
Q9D1D4	Transmembrane emp24 c	1.51	0.305	-0.80
P62889	60S ribosomal protein L3	-0.93	0.305	-0.33
Q9CR98	Protein FAM136A OS=Mu	0.87	0.305	-0.01
Q9D0L4	Uncharacterized aarF don	-0.68	0.306	0.05
Q9CQV1	Mitochondrial import inn	1.34	0.306	0.14
Q3UQ84	Threonine--tRNA ligase,	-1.13	0.306	0.32
Q9DB73	NADH-cytochrome b5 red	2.11	0.306	0.91
P61027	Ras-related protein Rab-1	1.56	0.309	0.66
P26443	Glutamate dehydrogenas	-0.45	0.314	0.09
Q9WVA2	Mitochondrial import inn	0.92	0.317	0.27
Q924L1	LETM1 domain-containin	-0.63	0.318	0.00
Q9JLJ2	4-trimethylaminobutyral	0.77	0.318	0.28
Q8R127	Saccharopine dehydroger	1.96	0.329	0.08
P36552	Oxygen-dependent copro	-1.07	0.330	-0.14
Q91WK5	Glycine cleavage system	-0.91	0.335	5.22
Q9DBG6	Dolichyl-diphosphooligos	1.94	0.339	-0.27
Q9QZ23	NFU1 iron-sulfur cluster s	-0.62	0.339	-0.26
Q99N93	39S ribosomal protein L1	1.49	0.340	-0.35
O88741	Ganglioside-induced diffe	-0.43	0.340	0.39
P62908	40S ribosomal protein S3	-0.90	0.344	-1.96
Q5U458	DnaJ homolog subfamily	-0.71	0.344	0.34
Q9QYR9	Acyl-coenzyme A thioeste	1.14	0.353	0.15
P45878	Peptidyl-prolyl cis-trans is	-0.64	0.355	-2.71
Q920A7	AFG3-like protein 1 OS=	1.29	0.355	0.14
Q8R3Q6	Coiled-coil domain-contai	-0.56	0.357	1.85
P52825	Carnitine O-palmitoyltran	-0.70	0.368	0.24
Q9ESW4	Acylglycerol kinase, mitoc	-0.43	0.371	-0.18
Q8BYM8	Probable cysteine--tRNA l	0.78	0.376	0.49
Q99JI6	Ras-related protein Rap-1	-1.26	0.381	1.82
P97493	Thioredoxin, mitochondri	-0.57	0.398	-4.68
Q9DBL1	Short/branched chain spe	-0.51	0.398	-0.17
Q9WTP7	GTP:AMP phosphotransfe	-0.48	0.398	0.18
Q9D1H8	39S ribosomal protein L5	-0.87	0.406	-0.17
P35564	Calnexin OS=Mus muscul	-0.51	0.407	-0.46
P38060	Hydroxymethylglutaryl-C	0.61	0.407	-0.12
Q8BG51	Mitochondrial Rho GTPas	0.45	0.407	0.17
Q9CQL5	39S ribosomal protein L1	-1.07	0.410	-0.36
Q99L04	Dehydrogenase/reductas	-0.95	0.422	0.26
Q9DBL7	Bifunctional coenzyme A	1.14	0.425	4.06
Q99M87	DnaJ homolog subfamily	-0.46	0.427	0.13
P62270	40S ribosomal protein S1	-0.91	0.432	-0.96

Q9CXW2	28S ribosomal protein S2	-0.56	0.434	-0.40
Q80YD1	ATP-dependent RNA helic	-0.55	0.434	0.29
Q8K1J6	CCA tRNA nucleotidyltran	-0.95	0.440	0.05
P63038	60 kDa heat shock protei	0.44	0.442	0.16
Q9CPY7	Cytosol aminopeptidase	0.54	0.462	-0.12
Q9D7N3	28S ribosomal protein S9,	-0.42	0.463	-0.39
Q9CYR0	Single-stranded DNA-binc	1.05	0.463	-0.35
Q8VDP6	CDP-diacylglycerol--inosit	0.51	0.468	-2.43
Q60649	Caseinolytic peptidase B	-0.58	0.468	-0.24
Q8VCF0	Mitochondrial antiviral-si	1.07	0.468	-0.16
Q8K2M0	39S ribosomal protein L3	-0.57	0.468	-0.13
P46638	Ras-related protein Rab-1	-0.45	0.473	-0.41
P50136	2-oxoisovalerate dehydro	-0.51	0.473	0.10
Q66GT5	Phosphatidylglycerophos	1.05	0.473	0.54
O35857	Mitochondrial import inn	-0.43	0.474	0.01
P62874	Guanine nucleotide-bindi	0.56	0.477	-0.70
P62830	60S ribosomal protein L2	-1.02	0.487	0.59
P97742	Carnitine O-palmitoyltran	0.98	0.487	0.02
Q8K411	Presequence protease, m	-0.43	0.492	-0.21
Q8BFP9	[Pyruvate dehydrogenase	0.41	0.493	-0.13
Q8R3F5	Malonyl-CoA-acyl carrier	-0.87	0.499	-0.48
Q3U2A8	Valine--tRNA ligase, mito	-0.39	0.513	-0.43
Q61207	Prosaposin OS=Mus musc	-0.71	0.518	-0.78
Q91W43	Glycine dehydrogenase (	0.67	0.518	-0.43
Q8JZN5	Acyl-CoA dehydrogenase	-0.39	0.518	-0.06
P51150	Ras-related protein Rab-7	0.56	0.526	0.04
Q924T2	28S ribosomal protein S2,	-0.51	0.530	-0.43
Q9QYA2	Mitochondrial import rec	-0.37	0.532	-0.25
O35129	Prohibitin-2 OS=Mus mus	-0.38	0.532	-0.06
Q3TIU4	2',5'-phosphodiesterase 1	-0.62	0.532	0.24
Q9CZX8	40S ribosomal protein S1	-0.71	0.540	1.34
Q9D1P0	39S ribosomal protein L1	-0.64	0.553	-4.48
Q9JHI5	Isovaleryl-CoA dehydroge	0.57	0.553	0.09
P09103	Protein disulfide-isomera	-0.51	0.564	-0.72
Q9D6S7	Ribosome-recycling facto	-0.40	0.570	0.02
Q99N94	39S ribosomal protein L9,	0.41	0.571	-0.54
P47740	Fatty aldehyde dehydroge	0.33	0.575	2.26
Q924D0	Reticulon-4-interacting pr	-0.57	0.585	0.19
Q6PE15	Mycophenolic acid acyl-gl	-0.30	0.602	-0.99
Q9DCB8	Iron-sulfur cluster assem	-0.33	0.602	0.20
P63037	DnaJ homolog subfamily	0.63	0.602	0.33
Q9JJL8	Serine--tRNA ligase, mito	-0.34	0.603	0.14

Q9CQX2	Cytochrome b5 type B OS	0.33	0.605	0.50
Q8CC88	von Willebrand factor A d	-0.47	0.608	0.31
Q3TBW2	39S ribosomal protein L1	-0.69	0.609	-0.98
Q922Q4	Pyrroline-5-carboxylate re	-0.34	0.611	-0.49
Q8VEG4	Exonuclease 3'-5' domain	0.46	0.612	0.00
Q9R0X4	Acyl-coenzyme A thioeste	0.38	0.623	-0.11
P58252	Elongation factor 2 OS=M	-0.48	0.627	-0.19
Q8CGK3	Lon protease homolog, m	-0.31	0.640	-0.07
Q8BSF4	Phosphatidylserine decar	0.59	0.640	0.63
P20029	78 kDa glucose-regulated	-0.36	0.641	-0.38
Q8R3K3	Pentatricopeptide repeat-	-0.51	0.656	-0.64
Q3UMR5	Calcium uniporter protei	-0.31	0.661	0.10
Q64433	10 kDa heat shock protei	0.16	0.679	0.11
Q8BK08	Transmembrane protein	0.39	0.680	-0.10
Q8K0D5	Elongation factor G, mito	0.40	0.685	-0.22
Q80UU9	Membrane-associated pr	-0.38	0.687	-0.13
P35278	Ras-related protein Rab-5	-0.24	0.704	0.22
Q921S7	39S ribosomal protein L3	-0.29	0.708	-0.24
P16332	Methylmalonyl-CoA muta	-0.29	0.710	0.03
Q80XN0	D-beta-hydroxybutyrate	-0.22	0.717	-0.37
Q59J78	Mimitin, mitochondrial O	0.40	0.717	-0.09
P47802	Metaxin-1 OS=Mus musc	-0.44	0.717	0.44
Q8BH95	Enoyl-CoA hydratase, mit	-0.23	0.726	0.01
Q9WV98	Mitochondrial import inn	-0.24	0.727	0.21
Q9D773	39S ribosomal protein L2,	-0.34	0.732	-3.26
Q9JIY5	Serine protease HTRA2, m	-0.24	0.732	-0.08
Q5IRJ6	Zinc transporter 9 OS=Mu	-0.20	0.732	0.05
Q9QUJ7	Long-chain-fatty-acid--Co	-0.74	0.734	0.22
O35114	Lysosome membrane pro	-0.50	0.736	0.15
Q9Z0X1	Apoptosis-inducing factor	0.23	0.739	0.29
Q9CQ62	2,4-dienoyl-CoA reductas	-0.27	0.741	-0.22
Q99KE1	NAD-dependent malic en	-0.25	0.741	-0.09
Q810S1	Calcium uniporter regulat	-0.41	0.752	-0.61
Q61941	NAD(P) transhydrogenase	0.21	0.752	0.50
Q3URS9	Coiled-coil domain-contai	-0.33	0.754	0.17
Q9D7B6	Isobutyryl-CoA dehydroge	-0.24	0.757	0.32
Q9WV54	Acid ceramidase OS=Mus	-0.39	0.757	2.87
Q99J47	Dehydrogenase/reductas	0.33	0.765	-0.58
Q9CXT8	Mitochondrial-processing	0.30	0.765	-0.34
Q9WTM5	RuvB-like 2 OS=Mus musc	0.18	0.781	0.78
Q8BH55	Threonine synthase-like 1	0.18	0.785	0.00
Q8VDC0	Probable leucine--tRNA li	-0.34	0.788	0.01

P18572	Basigin OS=Mus musculus	-0.43	0.788	0.19
Q9CQ06	39S ribosomal protein L2	0.31	0.790	-0.47
Q9DB25	Dolichyl-phosphate beta-	-0.26	0.791	-0.61
Q9DB41	Mitochondrial glutamate	-0.20	0.802	0.51
P51174	Long-chain specific acyl-C	-0.16	0.823	-0.15
P99024	Tubulin beta-5 chain OS=	-0.22	0.836	-0.18
Q9D5T0	ATPase family AAA domai	-0.24	0.836	-0.10
Q8VDD5	Myosin-9 OS=Mus muscu	0.42	0.839	-0.41
Q9CRD2	ER membrane protein co	-0.28	0.839	-0.37
Q9D1E8	1-acyl-sn-glycerol-3-phos	0.39	0.842	0.69
Q5SUC9	Protein SCO1 homolog, m	-0.18	0.859	0.18
Q9CWU6	Ubiquinol-cytochrome-c	-0.14	0.865	0.36
P80313	T-complex protein 1 subu	-0.25	0.867	-1.40
Q9DCN2	NADH-cytochrome b5 red	0.15	0.867	-0.64
P62245	40S ribosomal protein S1	-0.24	0.878	0.08
Q62186	Translocon-associated pr	0.22	0.890	-0.38
O08807	Peroxiredoxin-4 OS=Mus	-0.19	0.890	-0.35
Q8K1R3	Polyribonucleotide nucle	-0.22	0.890	0.31
Q9WUR2	Enoyl-CoA delta isomeras	-0.15	0.897	0.00
Q9JLT4	Thioredoxin reductase 2,	-0.21	0.898	-0.07
Q9CPU4	Microsomal glutathione S	0.22	0.903	-1.16
O54734	Dolichyl-diphosphooligos	0.15	0.913	-1.63
P47934	Carnitine O-acetyltransfe	0.10	0.914	0.19
Q3V3R1	Monofunctional C1-tetra	-0.08	0.917	0.45
Q6ZQI3	Malectin OS=Mus muscul	0.17	0.918	-0.71
Q9CZD3	Glycine--tRNA ligase OS=	-0.07	0.930	0.39
Q9DCS3	Enoyl-[acyl-carrier-protei	-0.12	0.940	0.09
Q8R2Y8	Peptidyl-tRNA hydrolase	0.08	0.948	-0.59
P08113	Endoplasmin OS=Mus mu	0.12	0.948	-0.50
Q99LP6	GrpE protein homolog 1,	-0.09	0.948	-0.28
Q9Z2Z6	Mitochondrial carnitine/a	-0.12	0.948	-0.22
P11499	Heat shock protein HSP 9	-0.12	0.948	0.24
Q9CZB0	Succinate dehydrogenase	0.11	0.948	0.26
Q925N0	Sideroflexin-5 OS=Mus m	-0.06	0.948	0.32
P63276	40S ribosomal protein S1	0.13	0.948	0.33
Q91V12	Cytosolic acyl coenzyme	0.06	0.948	1.53
P63321	Ras-related protein Ral-A	-0.09	0.948	4.05
Q8VBT0	Thioredoxin-related trans	-0.09	0.949	-0.05
Q9DC61	Mitochondrial-processing	-0.08	0.949	-0.02
Q99N95	39S ribosomal protein L3,	-0.09	0.951	-1.22
O35465	Peptidyl-prolyl cis-trans is	0.06	0.958	-0.35
Q8VCX5	Calcium uptake protein 1,	-0.05	0.958	-0.18

Q8BHE8	m-AAA protease-interacti	0.04	0.958	0.44
Q9D710	Thioredoxin-related trans	0.06	0.961	-0.12
Q9DCM0	Persulfide dioxygenase ET	0.03	0.969	0.07
Q60759	Glutaryl-CoA dehydrogen	0.04	0.983	0.08
Q99M04	Lipoyl synthase, mitochor	-0.04	0.986	0.02
Q9D8S9	BolA-like protein 1 OS=M	-0.02	0.987	-0.18
Q8BHN3	Neutral alpha-glucosidase	0.01	0.996	-0.71

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