

Supplemental Table 1 Semiquantitative analysis based on spectral counts of palmitoylated proteins in WT and DHHC7ko mice kidneys.

SPROT accession number	PROTEIN NAME	p-value	FOLD CHANGE
A2ARV4	Low-density lipoprotein receptor-related protein 2	0,0011	0,71
Q60928	Gamma-glutamyltranspeptidase 1	0,0012	2,77
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	0,0068	2,23
P25444	40S ribosomal protein S2	0,0114	1,08
P62242	40S ribosomal protein S8	0,0133	1,14
Q8VIM4	Barttin	0,0150	0,68
O09174	Alpha-methylacyl-CoA racemase	0,0163	2,64
Q91Y97	Fructose-bisphosphate aldolase B	0,0196	0,81
Q8VDD5	Myosin-9	0,0207	2,93
P07759	Serine protease inhibitor A3K	0,0218	1,86
P18760	Cofilin-1	0,0293	2,56
P07724	Serum albumin	0,0299	1,29
P62317	Small nuclear ribonucleoprotein Sm D2	0,0314	1,83
Q9WUB7	Chloride channel protein ClC-Ka	0,0352	2,94
Q91WR5	Aldo-keto reductase family 1 member C21	0,0368	2,46
Q9DCY0	Glycine N-acyltransferase-like protein Keg1	0,0379	1,12
P63260	Actin, cytoplasmic 2	0,0393	1,71
Q8BY89	Choline transporter-like protein 2	0,0481	0,87
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	0,0599	1,60
P11499	Heat shock protein HSP 90-beta	0,0609	2,81
P24270	Catalase	0,0635	1,39
P30275	Creatine kinase U-type, mitochondrial	0,0637	0,84
Q60866	Phosphotriesterase-related protein	0,0639	1,12
Q99KI0	Aconitate hydratase, mitochondrial	0,0661	0,98
Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondrial	0,0668	1,69
P97449	Aminopeptidase N	0,0681	2,05
Q9CPR4	60S ribosomal protein L17	0,0778	2,08
Q8K4Z3	NAD(P)H-hydrate epimerase	0,0792	1,66
P68254	14-3-3 protein theta	0,0798	1,67
Q8CIB5	Fermitin family homolog 2	0,0820	2,12
P28825	Meprin A subunit alpha	0,0834	1,61
P62281	40S ribosomal protein S11	0,0856	1,59
P40142	Transketolase	0,0868	0,34
Q8R2N1	Aquaporin-3	0,0908	1,31
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	0,0983	2,00
O55125	Protein NipSnap homolog 1	0,1083	1,91
Q9Z0S1	3'(2'),5'-bisphosphate nucleotidase 1	0,1121	0,94
Q91XE4	N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming)	0,1125	1,39
O88338	Cadherin-16	0,1152	2,15
P60710	Actin, cytoplasmic 1	0,1189	1,16
Q05920	Pyruvate carboxylase, mitochondrial	0,1214	0,43
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0,1241	2,52
Q9DOM5	Dynein light chain 2, cytoplasmic	0,1250	2,73
B5X0G2	Major urinary protein 17	0,1312	1,71
P02762	Major urinary protein 6	0,1312	1,71
P04939	Major urinary protein 3	0,1312	1,71
P11589	Major urinary protein 2	0,1312	1,71
Q9EQF5	Dihydropyrimidinase	0,1350	2,45
P10649	Glutathione S-transferase Mu 1	0,1371	1,77
Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial	0,1383	1,26
P52196	Thiosulfate sulfurtransferase	0,1472	1,78
Q9WV54	Acid ceramidase	0,1484	0,68
P61922	4-aminobutyrate aminotransferase, mitochondrial	0,1540	0,66
P12970	60S ribosomal protein L7a	0,1573	1,19
P47964	60S ribosomal protein L36	0,1623	1,11
Q9DBM2	Peroxisomal bifunctional enzyme	0,1632	0,47
Q9DCS2	UPF0585 protein C16orf13 homolog	0,1648	0,61
Q8VE95	UPF0598 protein C8orf82 homolog	0,1719	1,63
P47740	Fatty aldehyde dehydrogenase	0,1723	1,51
Q02013	Aquaporin-1	0,1729	1,63
Q6P1B1	Xaa-Pro aminopeptidase 1	0,1738	1,80
P57780	Alpha-actinin-4	0,1750	1,13
P11930	Nucleoside diphosphate-linked moiety X motif 19	0,1761	1,82

P55096	ATP-binding cassette sub-family D member 3	0,1783	1,59
P49312	Heterogeneous nuclear ribonucleoprotein A1	0,1797	2,57
Q8VC30	Triokinase/FMN cyclase	0,1873	1,21
Q8BH61	Coagulation factor XIII A chain	0,1882	0,99
P19536	Cytochrome c oxidase subunit 5B, mitochondrial	0,2002	2,12
P56382	ATP synthase subunit epsilon, mitochondrial	0,2058	1,81
P63158	High mobility group protein B1	0,2091	1,47
Q6NSQ9	Glucose-6-phosphatase 3	0,2112	0,51
Q92111	Serotransferrin	0,2152	0,73
Q8BGC4	Zinc-binding alcohol dehydrogenase domain-containing protein 2	0,2183	1,58
Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	0,2189	0,97
Q9QUM9	Proteasome subunit alpha type-6	0,2259	1,00
P62274	40S ribosomal protein S29	0,2325	1,91
Q9JII6	Alcohol dehydrogenase [NADP(+)]	0,2329	0,61
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	0,2340	1,24
Q8R3L5	Solute carrier organic anion transporter family member 3A1	0,2340	1,31
Q8K0L3	Acyl-coenzyme A synthetase ACSM2, mitochondrial	0,2371	0,30
Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial	0,2395	0,88
P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	0,2430	0,46
Q9ESE1	Lipopolysaccharide-responsive and beige-like anchor protein	0,2486	2,36
Q60692	Proteasome subunit beta type-6	0,2586	1,58
P30999	Catenin delta-1	0,2589	0,52
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	0,2700	1,32
Q922B1	O-acetyl-ADP-ribose deacetylase MACROD1	0,2701	1,32
Q9R1P0	Proteasome subunit alpha type-4	0,2703	1,32
Q01768	Nucleoside diphosphate kinase B	0,2721	0,33
P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	0,2761	0,49
Q99LB7	Sarcosine dehydrogenase, mitochondrial	0,2826	0,65
P63323	40S ribosomal protein S12	0,2886	1,88
P16858	Glyceraldehyde-3-phosphate dehydrogenase	0,2999	0,97
Q8VCR7	Protein ABHD14B	0,3003	0,89
Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	0,3030	0,78
P97351	40S ribosomal protein S3a	0,3149	0,69
Q02053	Ubiquitin-like modifier-activating enzyme 1	0,3176	1,06
Q99K67	Alpha-aminoadipic semialdehyde synthase, mitochondrial	0,3229	0,62
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	0,3242	0,60
Q9D854	Oligoribonuclease, mitochondrial	0,3265	1,64
P26041	Moesin	0,3267	1,66
P10126	Elongation factor 1-alpha 1	0,3353	0,87
P63082	V-type proton ATPase 16 kDa proteolipid subunit	0,3373	1,27
P06745	Glucose-6-phosphate isomerase	0,3391	0,70
Q8R242	Di-N-acetylchitinase	0,3565	0,35
Q9WUB6	Chloride channel protein ClC-Kb	0,3634	0,89
P70404	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	0,3648	0,69
P17742	Peptidyl-prolyl cis-trans isomerase A	0,3689	0,79
Q91X52	L-xylulose reductase	0,3703	0,46
P79457	Histone demethylase UTY	0,3710	1,44
Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	0,3783	0,41
P09671	Superoxide dismutase [Mn], mitochondrial	0,3789	1,08
P50285	Dimethylaniline monooxygenase [N-oxide-forming] 1	0,3789	1,08
P26040	Ezrin	0,3831	0,44
Q80W22	Threonine synthase-like 2	0,3933	0,68
P14131	40S ribosomal protein S16	0,3944	1,34
Q93092	Transaldolase	0,3952	0,71
P06797	Cathepsin L1	0,3984	0,97
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0,4118	1,13
Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	0,4131	0,56
Q9DC37	Major facilitator superfamily domain-containing protein 1	0,4157	0,74
P13707	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	0,4163	0,39
Q9DBJ1	Phosphoglycerate mutase 1	0,4173	0,33
Q9D823	60S ribosomal protein L37	0,4193	2,21
Q3TLP5	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	0,4214	1,07
P54116	Erythrocyte band 7 integral membrane protein	0,4243	1,36
P50247	Adenosylhomocysteinase	0,4303	0,58
Q9DCW4	Electron transfer flavoprotein subunit beta	0,4315	1,07
Q32Q92	Acyl-coenzyme A thioesterase 6	0,4318	1,46
Q9DBF1	Alpha-aminoadipic semialdehyde dehydrogenase	0,4350	0,47
Q61147	Ceruloplasmin	0,4368	1,78
Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	0,4441	0,46
P62897	Cytochrome c, somatic	0,4510	0,76

Q791V5	Mitochondrial carrier homolog 2	0,4524	1,28
Q9DCW2	Phospholipid scramblase 2	0,4527	0,61
P45376	Aldose reductase	0,4536	0,67
Q9D8E6	60S ribosomal protein L4	0,4597	0,50
P62830	60S ribosomal protein L23	0,4643	0,44
Q60676	Serine/threonine-protein phosphatase 5	0,4706	1,19
Q3TC72	Fumarylacetoacetate hydrolase domain-containing protein 2A	0,4731	0,44
Q9CR51	V-type proton ATPase subunit G 1	0,4754	1,47
Q9DCT1	1,5-anhydro-D-fructose reductase	0,4755	1,32
P35700	Peroxiredoxin-1	0,4762	1,02
P97494	Glutamate--cysteine ligase catalytic subunit	0,4813	0,59
Q8BP48	Methionine aminopeptidase 1	0,4864	1,16
P60766	Cell division control protein 42 homolog	0,4873	0,82
Q99NB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	0,4915	1,14
P62855	40S ribosomal protein S26	0,4943	0,90
Q91ZD1	Protein odd-skipped-related 2	0,4985	1,11
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	0,4989	0,87
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	0,5091	0,52
O70435	Proteasome subunit alpha type-3	0,5111	0,57
P0C8K7	Small integral membrane protein 1	0,5183	0,78
O09117	Synaptophysin-like protein 1	0,5255	0,56
O55013	Trafficking protein particle complex subunit 3	0,5264	0,77
P62908	40S ribosomal protein S3	0,5273	0,47
P10639	Thioredoxin	0,5306	1,28
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	0,5320	0,37
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	0,5362	1,06
Q3TH56	S-adenosylmethionine synthase isoform type-2	0,5419	0,54
Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	0,5669	0,58
Q9R0P5	Destrin	0,5675	0,58
Q8BGD4	Solute carrier organic anion transporter family member 4C1	0,5678	0,32
P08905	Lysozyme C-2	0,5735	0,91
P05202	Aspartate aminotransferase, mitochondrial	0,5775	0,31
P35979	60S ribosomal protein L12	0,5841	0,39
A2BIM8	Major urinary protein 18	0,5864	0,85
P04938	Major urinary protein 11	0,5864	0,85
P60335	Poly(rC)-binding protein 1	0,6040	0,40
Q68FL4	Putative adenosylhomocysteinase 3	0,6052	0,71
Q923D2	Flavin reductase (NADPH)	0,6075	0,80
Q9R112	Sulfide:quinone oxidoreductase, mitochondrial	0,6076	0,80
O54734	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	0,6076	0,80
O35350	Calpain-1 catalytic subunit	0,6077	0,80
P97314	Cysteine and glycine-rich protein 2	0,6090	0,89
Q9D964	Glycine amidinotransferase, mitochondrial	0,6237	0,26
Q91VM9	Inorganic pyrophosphatase 2, mitochondrial	0,6274	0,65
P56395	Cytochrome b5	0,6291	0,76
Q99JY3	GTPase IMAP family member 4	0,6292	0,76
Q91X17	Uromodulin	0,6292	0,76
P29699	Alpha-2-HS-glycoprotein	0,6414	0,30
P97315	Cysteine and glycine-rich protein 1	0,6421	0,55
Q6PDN3	Myosin light chain kinase, smooth muscle	0,6422	0,32
P28665	Murinoglobulin-1	0,6431	0,53
P70296	Phosphatidylethanolamine-binding protein 1	0,6522	0,32
P99024	Tubulin beta-5 chain	0,6683	0,44
P63276	40S ribosomal protein S17	0,6714	0,30
Q8CD54	Piezo-type mechanosensitive ion channel component 2	0,6736	0,66
Q6P8X1	Sorting nexin-6	0,6740	0,66
Q8CHG5	Apoptosis-resistant E3 ubiquitin protein ligase 1	0,6741	0,66
Q8C129	Leucyl-cystinyl aminopeptidase	0,6741	0,66
Q78J03	Methionine-R-sulfoxide reductase B2, mitochondrial	0,6742	0,66
Q9D565	WD repeat-containing protein 64	0,6744	0,66
Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial	0,6746	0,66
Q8CG76	Aflatoxin B1 aldehyde reductase member 2	0,6904	0,30
Q9D826	Peroxisomal sarcosine oxidase	0,7024	0,27
P09411	Phosphoglycerate kinase 1	0,7094	0,32
Q99PG0	Arylacetamide deacetylase	0,7243	0,56
P67984	60S ribosomal protein L22	0,7243	0,56
O89106	Bis(5'-adenosyl)-triphosphatase	0,7324	0,50
O70325	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	0,7364	0,33
P19253	60S ribosomal protein L13a	0,7396	0,25
O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	0,7430	0,52

Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	0,7434	0,52
Q8RON6	Hydroxyacid-oxoacid transhydrogenase, mitochondrial	0,7468	0,52
Q61419	Cytidine monophosphate-N-acetylneuraminic acid hydroxylase	0,7469	0,52
Q9WTL7	Acyl-protein thioesterase 2	0,7503	0,74
Q78JN3	Enoyl-CoA delta isomerase 3, peroxisomal	0,7516	0,28
Q8R0F8	Acylpyruvase FAHD1, mitochondrial	0,7648	0,29
Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	0,7704	0,67
Q61233	Plastin-2	0,7880	0,35
P46412	Glutathione peroxidase 3	0,7926	0,60
Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial	0,7930	0,33
Q62261	Spectrin beta chain, non-erythrocytic 1	0,7945	0,42
Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G	0,7948	0,42
Q9D8U8	Sorting nexin-5	0,7950	0,42
P52760	Ribonuclease UK114	0,7982	0,38
Q8R1G2	Carboxymethylenebutenolidase homolog	0,8027	0,30
Q8VHL0	Urea transporter 1	0,8407	0,45
P62320	Small nuclear ribonucleoprotein Sm D3	0,8495	0,28
Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	0,8850	0,25
Q64467	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	0,1398	1,93
P10605	Cathepsin B	0,0436	1,59
P56389	Cytidine deaminase	0,1802	1,53
P52480	Pyruvate kinase PKM	0,0333	2,67
O08709	Peroxioredoxin-6	0,4180	1,60
P26043	Radixin	0,0652	4,75
Q01853	Transitional endoplasmic reticulum ATPase	0,4671	1,58
Q9DC50	Peroxisomal carnitine O-octanoyltransferase	0,0705	1,94
Q9QXD6	Fructose-1,6-bisphosphatase 1	0,3324	1,68
Q6ZVV3	60S ribosomal protein L10	0,1784	1,87
P86048	60S ribosomal protein L10-like	0,1784	1,87
P61079	Ubiquitin-conjugating enzyme E2 D3	0,5964	1,53
P62838	Ubiquitin-conjugating enzyme E2 D2	0,5964	1,53
Q9CPU0	Lactoylglutathione lyase	0,1631	1,64
Q9NYQ2	Hydroxyacid oxidase 2	0,3459	1,74
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	0,0856	1,74
Q9WVJ3	Carboxypeptidase Q	0,1186	1,05
P60764	Ras-related C3 botulinum toxin substrate 3	0,5911	2,56
Q05144	Ras-related C3 botulinum toxin substrate 2	0,7862	1,51
P84096	Rho-related GTP-binding protein RhoG	0,3259	1,61
Q9ER71	Rho-related GTP-binding protein RhoJ	0,0612	3,74
Q61696	Heat shock 70 kDa protein 1A	0,2066	1,97
Q91WU0	Carboxylesterase 1F	0,3664	1,52
Q9D0F3	Protein ERGIC-53	0,3739	3,37
Q8QZY2	Glycerate kinase	0,5695	1,62
Q8BKCS	Importin-5	0,3739	3,03
Q9JLB4	Cubilin	0,1208	2,06
Q9D7I0	Protein shisa-5	0,1707	42,00
P83940	Transcription elongation factor B polypeptide 1	0,3739	29,00
Q3UDE2	Tubulin--tyrosine ligase-like protein 12	0,6308	2,21
P28666	Murinoglobulin-2	0,5811	1,92
Q99L27	GMP reductase 2	0,1910	1,53
O08581	Potassium channel subfamily K member 1	0,3739	28,00
Q61753	D-3-phosphoglycerate dehydrogenase	0,3739	27,33
Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	0,0524	1,77
P61082	NEDD8-conjugating enzyme Ubc12	0,3739	25,67
Q9CWD8	Iron-sulfur protein NUBPL	0,3739	25,67
Q9EQP2	EH domain-containing protein 4	0,3739	25,67
Q8K183	Pyridoxal kinase	0,1285	42,33
Q9D8T7	SRA stem-loop-interacting RNA-binding protein, mitochondrial	0,6110	1,70
Q9EPU0	Regulator of nonsense transcripts 1	0,1371	38,33
Q9Z1W8	Potassium-transporting ATPase alpha chain 2	0,2089	2,57
A2AVZ9	Solute carrier family 43 member 3	0,1297	38,67
Q6P4T0	Autophagy-related protein 2 homolog A	0,3739	23,33
P80315	T-complex protein 1 subunit delta	0,3739	23,00
P04117	Fatty acid-binding protein, adipocyte	0,3739	23,00
Q9CZR2	N-acetylated-alpha-linked acidic dipeptidase 2	0,2826	1,68
Q9DBT9	Dimethylglycine dehydrogenase, mitochondrial	0,3739	22,67
Q99LF4	tRNA-splicing ligase RtcB homolog	0,5000	1,78
Q8R180	ERO1-like protein alpha	0,1162	41,00
P11404	Fatty acid-binding protein, heart	0,3739	21,33
Q9Z130	Heterogeneous nuclear ribonucleoprotein D-like	0,3739	21,33

Q3UMF0	Cordon-bleu protein-like 1	0,1166	39,67
Q9D273	Cob(II)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	0,3739	20,67
Q9D6Y7	Mitochondrial peptide methionine sulfoxide reductase	0,3739	20,67
P62737	Actin, aortic smooth muscle	0,1273	34,67
P63268	Actin, gamma-enteric smooth muscle	0,6839	1,88
Q8R1Q9	Ribokinase	0,3739	20,00
O08756	3-hydroxyacyl-CoA dehydrogenase type-2	0,1346	31,67
Q02248	Catenin beta-1	0,3739	19,00
Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial	0,1274	44,33
P55014	Solute carrier family 12 member 1	0,3739	18,67
Q6A0A9	Constitutive coactivator of PPAR-gamma-like protein 1	0,3739	18,67
Q8BT60	Copine-3	0,3739	17,33
P62307	Small nuclear ribonucleoprotein F	0,1178	31,67
Q9JIY7	N-acetyltransferase 8	0,3739	17,00
Q6ZQI3	Malectin	0,3739	17,00
Q9JIF9	Signal peptide peptidase-like 2A	0,1448	45,00
P63254	Cysteine-rich protein 1	0,3739	17,00
P35564	Calnexin	0,3739	17,00
Q9CR21	Acyl carrier protein, mitochondrial	0,3739	16,67
Q6P9Q6	FK506-binding protein 15	0,3739	16,67
Q3UHK1	Proton myo-inositol cotransporter	0,1220	36,67
Q6PDY2	2-aminoethanethiol dioxygenase	0,3739	16,67
Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2	0,3739	16,33
Q8K0Z7	Translational activator of cytochrome c oxidase 1	0,1525	45,33
O35566	CD151 antigen	0,3739	16,33
Q61496	Probable ATP-dependent RNA helicase DDX4	0,3739	16,00
Q8CFA2	Aminomethyltransferase, mitochondrial	0,3739	16,00
Q8K1R3	Polyrribonucleotide nucleotidyltransferase 1, mitochondrial	0,3739	16,00
P57776	Elongation factor 1-delta	0,3739	16,00
Q61553	Fascin	0,3739	15,67
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	0,3739	15,33
Q80TN5	Palmitoyltransferase ZDHHC17	0,3739	15,33
P48754	Breast cancer type 1 susceptibility protein homolog	0,3739	15,33
P15533	Tripartite motif-containing protein 30A	0,3739	15,33
Q9QZ88	Vacuolar protein sorting-associated protein 29	0,3739	15,33
P48758	Carbonyl reductase [NADPH] 1	0,3739	15,33
P67871	Casein kinase II subunit beta	0,1162	30,00
P29387	Guanine nucleotide-binding protein subunit beta-4	0,1662	22,00
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	0,3739	15,00
Q501J6	Probable ATP-dependent RNA helicase DDX17	0,3739	15,00
Q61656	Probable ATP-dependent RNA helicase DDX5	0,3739	15,00
P11588	Major urinary protein 1	0,1174	30,00
P86049	Probable RNA-binding protein 46	0,3739	14,67
O08638	Myosin-11	0,1210	31,00
Q61879	Myosin-10	0,3739	14,33
O35516	Neurogenic locus notch homolog protein 2	0,5260	1,91
Q8CI51	PDZ and LIM domain protein 5	0,3739	14,33
Q9D8W5	26S proteasome non-ATPase regulatory subunit 12	0,3739	14,00
Q8VC69	Solute carrier family 22 member 6	0,3739	14,00
A2A5R2	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	0,3739	14,00
Q8VDQ1	Prostaglandin reductase 2	0,1363	34,67
Q9DCT8	Cysteine-rich protein 2	0,3739	13,67
P16332	Methylmalonyl-CoA mutase, mitochondrial	0,1525	36,67
O70228	Probable phospholipid-transporting ATPase IIA	0,3739	13,00
P08228	Superoxide dismutase [Cu-Zn]	0,1204	23,33
Q8BWM0	Prostaglandin E synthase 2	0,1677	30,67
P31428	Dipeptidase 1	0,3039	2,16
B2RSH2	Guanine nucleotide-binding protein G(i) subunit alpha-1	0,6707	1,61
Q9D8B4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	0,3739	31,00
Q08857	Platelet glycoprotein 4	0,3739	31,00
P63101	14-3-3 protein zeta/delta	0,1274	48,33
Q9CQY6	Ubiquinol-cytochrome-c reductase complex assembly factor 2	0,1231	6,10
P80313	T-complex protein 1 subunit eta	0,7653	1,57
P14824	Annexin A6	0,3739	26,33
P47856	Glutamine-fructose-6-phosphate aminotransferase [isomerizing] 1	0,3739	26,00
P16045	Galectin-1	0,1192	4,60
O70433	Four and a half LIM domains protein 2	0,3739	24,67
Q8R4N0	Citrate lyase subunit beta-like protein, mitochondrial	0,3739	24,00
Q9Z1Q5	Chloride intracellular channel protein 1	0,3739	23,00
Q922F4	Tubulin beta-6 chain	0,3739	22,33

P26516	26S proteasome non-ATPase regulatory subunit 7	0,3739	22,00
P17710	Hexokinase-1	0,3739	22,00
P00756	Kallikrein 1-related peptidase b3	0,1183	37,00
O35660	Glutathione S-transferase Mu 6	0,3472	2,73
Q61411	GTPase HRas	0,3739	20,00
P03958	Adenosine deaminase	0,3739	19,33
Q9R1Q7	Proteolipid protein 2	0,3739	18,67
Q3UX10	Tubulin alpha chain-like 3	0,1166	37,67
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	0,3739	18,33
Q3UMB9	WASH complex subunit 7	0,3739	17,67
P09055	Integrin beta-1	0,3739	17,67
Q99N95	39S ribosomal protein L3, mitochondrial	0,1179	36,00
Q6ZQ93	Ubiquitin carboxyl-terminal hydrolase 34	0,3739	13,67
Q8BFS6	Serine/threonine-protein phosphatase CPPED1	0,3739	13,00
Q9Z1Q9	Valine--tRNA ligase	0,3739	12,67
Q05860	Formin-1	0,5922	1,72
Q7TNG8	Probable D-lactate dehydrogenase, mitochondrial	0,0061	0,74
P08249	Malate dehydrogenase, mitochondrial	0,2458	1,06
Q91V76	Ester hydrolase C11orf54 homolog	0,7194	0,96
P00329	Alcohol dehydrogenase 1	0,0219	0,76
O09173	Homogentisate 1,2-dioxygenase	0,8619	0,98
Q80X90	Filamin-B	0,4996	1,20
Q8BTM8	Filamin-A	0,4605	1,23
P62889	60S ribosomal protein L30	0,8773	1,03
Q9WUM5	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	0,5421	1,13
Q64442	Sorbitol dehydrogenase	0,3084	1,27
Q60932	Voltage-dependent anion-selective channel protein 1	0,2920	1,28
P99029	Peroxiredoxin-5, mitochondrial	0,5812	0,93
Q3UNX5	Acyl-coenzyme A synthetase ACSM3, mitochondrial	0,1252	1,25
Q8JZV9	3-hydroxybutyrate dehydrogenase type 2	0,8457	1,04
Q9JHW2	Omega-amidase NIT2	0,2662	0,89
Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	0,4157	1,33
Q8BFR5	Elongation factor Tu, mitochondrial	0,5328	0,89
Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	0,0734	1,28
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	0,1380	1,15
P47791	Glutathione reductase, mitochondrial	0,8181	0,97
P35762	CD81 antigen	0,8661	0,95
Q61598	Rab GDP dissociation inhibitor beta	0,7405	0,95
P47962	60S ribosomal protein L5	0,2268	0,81
Q91X72	Hemopexin	0,7404	1,07
P68040	Receptor of activated protein C kinase 1	0,4498	1,13
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	0,9721	0,99
Q9DCZ1	GMP reductase 1	0,9212	1,03
Q9D6F9	Tubulin beta-4A chain	0,5368	1,25
P68372	Tubulin beta-4B chain	0,5368	1,25
Q68FD5	Clathrin heavy chain 1	0,6972	0,93
Q9DCM0	Persulfide dioxygenase ETHE1, mitochondrial	0,2318	1,18
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	0,3164	1,46
P47738	Aldehyde dehydrogenase, mitochondrial	0,1890	1,33
O35658	Complement component 1 Q subcomponent-binding protein, mitochondrial	0,4712	1,13
P63038	60 kDa heat shock protein, mitochondrial	0,8019	1,07
P50396	Rab GDP dissociation inhibitor alpha	0,6659	0,81
Q9JLJ2	4-trimethylaminobutyraldehyde dehydrogenase	0,8780	1,07
P05064	Fructose-bisphosphate aldolase A	0,7235	0,92
P14206	40S ribosomal protein SA	0,1197	0,75
Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	0,2334	0,75
Q91VA0	Acyl-coenzyme A synthetase ACSM1, mitochondrial	0,6195	0,91
Q9CPY7	Cytosol aminopeptidase	0,5987	1,09
Q64516	Glycerol kinase	0,6952	1,10
P40124	Adenylyl cyclase-associated protein 1	0,8136	1,06
P00493	Hypoxanthine-guanine phosphoribosyltransferase	0,3267	1,24
P28271	Cytoplasmic aconitate hydratase	0,3998	1,41
P28474	Alcohol dehydrogenase class-3	0,2329	0,84
Q62468	Villin-1	0,8334	1,05
Q92317	Sodium/glucose cotransporter 2	0,3528	0,72
P51855	Glutathione synthetase	0,8499	1,03
O35488	Very long-chain acyl-CoA synthetase	0,4246	1,23
P51660	Peroxisomal multifunctional enzyme type 2	0,1531	1,30
P14152	Malate dehydrogenase, cytoplasmic	0,1929	0,72
Q9D404	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	0,2238	0,63

P27659	60S ribosomal protein L3	0,7554	1,09
P16125	L-lactate dehydrogenase B chain	0,9876	1,00
Q11136	Xaa-Pro dipeptidase	0,3138	0,81
Q9D1A2	Cytosolic non-specific dipeptidase	0,7647	1,14
O89017	Legumain	0,8267	1,16
P63001	Ras-related C3 botulinum toxin substrate 1	0,3053	1,34
P14869	60S acidic ribosomal protein P0	0,7269	1,18
O88428	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	0,5860	1,17
Q7TMS5	ATP-binding cassette sub-family G member 2	0,9860	1,00
Q99KC8	von Willebrand factor A domain-containing protein 5A	0,4445	1,47
Q99JW2	Aminoacylase-1	0,0656	0,93
P68373	Tubulin alpha-1C chain	0,2550	1,34
P58252	Elongation factor 2	0,3977	1,26
Q61838	Pregnancy zone protein	0,3041	0,71
P35505	Fumarylacetoacetase	0,6339	1,18
Q99LX0	Protein deglycase DJ-1	0,7793	1,07
P62911	60S ribosomal protein L32	0,0730	1,33
Q8BMF4	Dihydrolypoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	0,1570	1,28
P36552	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	0,0121	0,68
Q3TNA1	Xylulose kinase	0,6434	0,89
P15105	Glutamine synthetase	0,8412	1,14
P97461	40S ribosomal protein S5	0,5592	0,89
Q8R527	Rho-related GTP-binding protein RhoQ	0,8384	0,89
P05063	Fructose-bisphosphate aldolase C	1,0000	1,00
P98197	Probable phospholipid-transporting ATPase IH	0,4847	0,86
P01837	Ig kappa chain C region	0,9729	1,02
Q61990	Poly(rC)-binding protein 2	0,3752	1,17
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	0,4420	1,16
P97447	Four and a half LIM domains protein 1	0,6386	0,86
Q8R164	Valacyclovir hydrolase	0,7157	1,11
Q8BMK4	Cytoskeleton-associated protein 4	0,2833	1,25
Q03734	Serine protease inhibitor A3M	0,9850	0,98
Q8C3K6	Sodium/glucose cotransporter 1	0,3546	1,38
Q8BWF0	Succinate-semialdehyde dehydrogenase, mitochondrial	0,9080	1,07
Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	0,6511	0,84
P06151	L-lactate dehydrogenase A chain	0,2012	0,69
Q8BH00	Aldehyde dehydrogenase family 8 member A1	0,8297	1,08
Q99KR3	Endoribonuclease LACTB2	0,6900	1,10
Q9JIL4	Na(+)/H(+) exchange regulatory cofactor NHE-RF3	0,4678	0,83
P55264	Adenosine kinase	0,7995	0,97
P11352	Glutathione peroxidase 1	0,3453	0,82
Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochondrial	0,7126	0,67
Q91VI7	Ribonuclease inhibitor	0,5858	0,72
P06801	NADP-dependent malic enzyme	0,8861	1,05
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	0,7136	1,14
Q9JIZ9	Phospholipid scramblase 3	0,8590	1,15
O08553	Dihydropyrimidinase-related protein 2	0,7997	0,88
Q64462	Cytochrome P450 4B1	0,6487	0,88
P62264	40S ribosomal protein S14	0,1034	1,26
P62858	40S ribosomal protein S28	0,4193	1,28
P26443	Glutamate dehydrogenase 1, mitochondrial	0,8695	1,05
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	0,6703	0,86
P26039	Talin-1	0,7050	0,67
Q8VHX6	Filamin-C	1,0000	1,00
Q9Z2J0	Solute carrier family 23 member 1	0,3110	0,78
P14094	Sodium/potassium-transporting ATPase subunit beta-1	0,7219	1,11
Q9D172	ES1 protein homolog, mitochondrial	0,7218	0,90
Q99JY9	Actin-related protein 3	0,9190	1,08
Q99LB2	Dehydrogenase/reductase SDR family member 4	0,4674	1,42
Q3UNZ8	Quinone oxidoreductase-like protein 2	0,8974	0,98
Q9DD20	Methyltransferase-like protein 7B	0,5799	1,12
Q8R086	Sulfite oxidase, mitochondrial	0,4687	0,79
P09470	Angiotensin-converting enzyme	0,8513	0,96
Q99KB8	Hydroxyacylglutathione hydrolase, mitochondrial	0,6913	0,87
O88575	Sodium- and chloride-dependent transporter XTRP3B	0,4285	0,90
Q9QUI0	Transforming protein RhoA	0,3269	0,73
Q62159	Rho-related GTP-binding protein RhoC	0,3269	0,73
Q9CR57	60S ribosomal protein L14	0,5029	1,15
P27773	Protein disulfide-isomerase A3	0,7231	0,88

Q9DBE0	Cysteine sulfinic acid decarboxylase	0,0586	0,67
Q9ES97	Reticulon-3	0,9620	1,03
P16627	Heat shock 70 kDa protein 1-like	0,3330	1,31
Q5U5V2	Hydroxylysine kinase	0,0561	0,72
P48722	Heat shock 70 kDa protein 4L	0,0191	0,75
P34914	Bifunctional epoxide hydrolase 2	0,9244	0,97
O35643	AP-1 complex subunit beta-1	0,6526	0,91
P16675	Lysosomal protective protein	0,2582	0,97
P51410	60S ribosomal protein L9	0,5308	0,74
Q8BH95	Enoyl-CoA hydratase, mitochondrial	0,4943	1,20
P97328	Ketohexokinase	0,9040	1,05
P19096	Fatty acid synthase	0,7863	1,23
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	0,5297	0,72
O08917	Flotillin-1	0,4743	1,14
Q8BFZ3	Beta-actin-like protein 2	0,2868	0,86
Q9Z1N5	Spliceosome RNA helicase Ddx39b	0,1556	1,36
Q9JJZ2	Tubulin alpha-8 chain	0,7360	1,18
P62814	V-type proton ATPase subunit B, brain isoform	0,8476	1,10
Q60759	Glutaryl-CoA dehydrogenase, mitochondrial	0,6959	0,71
Q5SWY8	Sodium/glucose cotransporter 5	0,6159	0,67
Q9QXD1	Peroxisomal acyl-coenzyme A oxidase 2	0,6897	0,83
Q922Q1	Mitochondrial amidoxime reducing component 2	0,8506	1,07
Q8QZY6	Tetraspanin-14	0,5856	0,77
Q9CPV4	Glyoxalase domain-containing protein 4	0,8313	0,82
Q6ZWY3	40S ribosomal protein S27-like	0,4290	1,11
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4	0,9231	1,03
Q8CAY6	Acetyl-CoA acetyltransferase, cytosolic	0,3573	0,74
Q8VCH0	3-ketoacyl-CoA thiolase B, peroxisomal	0,7097	0,75
Q7TPR4	Alpha-actinin-1	0,7979	0,93
Q64737	Trifunctional purine biosynthetic protein adenosine-3	0,8981	1,10
Q9DCM2	Glutathione S-transferase kappa 1	0,8223	0,84
P62827	GTP-binding nuclear protein Ran	0,2888	0,81
Q64105	Sepiapterin reductase	0,4058	0,84
P62717	60S ribosomal protein L18a	0,7849	0,95
P70349	Histidine triad nucleotide-binding protein 1	0,6606	0,89
Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	0,6895	0,87
P70290	55 kDa erythrocyte membrane protein	0,8267	0,92
Q91XR9	Phospholipid hydroperoxide glutathione peroxidase, nuclear	0,8775	1,12
Q8BWN8	Acyl-coenzyme A thioesterase 4	0,7033	1,34
P21981	Protein-glutamine gamma-glutamyltransferase 2	0,7887	0,80
O88398	Advillin	0,1289	0,81
O88990	Alpha-actinin-3	0,4298	0,70
Q9JI91	Alpha-actinin-2	0,9517	1,05
Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial	0,9197	1,11
A3KMP2	Tetratricopeptide repeat protein 38	0,3249	0,60
Q9D1R9	60S ribosomal protein L34	0,8852	0,97
Q68FL6	Methionine--tRNA ligase, cytoplasmic	0,9122	1,17
Q64331	Unconventional myosin-VI	0,6560	0,70
Q64514	Tripeptidyl-peptidase 2	0,0842	0,61
P16406	Glutamyl aminopeptidase	0,6591	1,10
Q8BVQ5	Protein phosphatase methylesterase 1	0,9932	0,99
Q78PY7	Staphylococcal nuclease domain-containing protein 1	0,8911	0,90
Q8CGK3	Lon protease homolog, mitochondrial	0,4517	1,47
Q8BTY1	Kynurenine--oxoglutarate transaminase 1	0,5791	0,76
Q9DCG6	Phenazine biosynthesis-like domain-containing protein 1	0,4847	0,75
P62754	40S ribosomal protein S6	0,9155	1,06
Q8C7R4	Ubiquitin-like modifier-activating enzyme 6	0,9673	0,98
Q6ZQM8	UDP-glucuronosyltransferase 1-7C	0,9855	1,01
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial	0,8014	1,45
Q60864	Stress-induced-phosphoprotein 1	0,8859	1,11
Q61792	LIM and SH3 domain protein 1	0,6583	0,71
Q9DC07	LIM zinc-binding domain-containing Nebulette	0,1406	0,51
O35226	26S proteasome non-ATPase regulatory subunit 4	0,7700	0,84
P82343	N-acetylglucosamine 2-epimerase	0,4700	0,55
Q60972	Histone-binding protein RBBP4	0,4291	0,90
P40936	Indolethylamine N-methyltransferase	0,4517	0,85
Q9ZON1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	0,9380	1,06
Q9WU84	Copper chaperone for superoxide dismutase	0,7463	1,11
Q9Z219	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	0,8943	0,96
P02104	Hemoglobin subunit epsilon-Y2	0,7512	1,01

Q9CYN2	Signal peptidase complex subunit 2	0,7260	0,67
Q9WTP6	Adenylate kinase 2, mitochondrial	0,3864	1,50
P62245	40S ribosomal protein S15a	0,6127	0,97
Q9CXW4	60S ribosomal protein L11	0,7049	1,10
P83882	60S ribosomal protein L36a	0,1018	0,76
Q8KOD5	Elongation factor G, mitochondrial	0,8853	1,11
P14211	Calreticulin	0,0951	0,76
O08677	Kininogen-1	0,4013	1,34
Q9DBG3	AP-2 complex subunit beta	0,8004	0,83
Q9JK81	UPF0160 protein MYG1, mitochondrial	0,4088	0,68
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	0,9108	1,06
Q99K51	Plastin-3	0,8875	1,23
P05201	Aspartate aminotransferase, cytoplasmic	0,8501	1,02
Q8BH86	UPF0317 protein C14orf159 homolog, mitochondrial	0,7480	0,88
P68134	Actin, alpha skeletal muscle	0,8813	0,85
P41216	Long-chain-fatty-acid-CoA ligase 1	0,6941	1,35
P13020	Gelsolin	0,8467	0,87
P38647	Stress-70 protein, mitochondrial	0,8771	1,11
O88342	WD repeat-containing protein 1	0,5322	0,87
Q8VEM8	Phosphate carrier protein, mitochondrial	0,8536	1,03
P14115	60S ribosomal protein L27a	0,5349	0,74
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	0,9856	1,01
POC1Q2	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11A	0,7868	0,96
Q9ROQ7	Prostaglandin E synthase 3	0,7841	0,95
Q9Z2V4	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	0,3361	0,63
Q9R1P1	Proteasome subunit beta type-3	0,6709	0,70
P62821	Ras-related protein Rab-1A	0,8510	1,15
A2AS89	Agmatinase, mitochondrial	0,5769	0,77
Q8VDK1	Nitrilase homolog 1	0,5778	0,62
Q60825	Sodium-dependent phosphate transport protein 2A	0,2962	0,92
Q9R1P3	Proteasome subunit beta type-2	1,0000	1,00
O55222	Integrin-linked protein kinase	0,1169	0,75
P49222	Erythrocyte membrane protein band 4,2	0,5360	0,53
Q9CYR6	Phosphoacetylglucosamine mutase	0,3248	0,64
Q9DOK2	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	0,1125	1,17
P50516	V-type proton ATPase catalytic subunit A	0,0654	1,35
Q9D8I3	Glyoxalase domain-containing protein 5	0,0877	0,58
Q8R3P0	Aspartoacylase	0,2681	0,61
Q8BP40	Lysophosphatidic acid phosphatase type 6	0,9586	1,01
Q9CR09	Ubiquitin-fold modifier-conjugating enzyme 1	0,9086	0,92
Q9CZU6	Citrate synthase, mitochondrial	0,5068	1,11
O55142	60S ribosomal protein L35a	0,2857	1,10
Q9DCQ2	Putative L-aspartate dehydrogenase	0,8267	0,96
Q9QYJ0	DnaJ homolog subfamily A member 2	0,2305	0,58
Q8VI36	Paxillin	0,6559	0,78
P60867	40S ribosomal protein S20	0,8140	0,97
Q64727	Vinculin	0,9888	0,98
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	0,1312	1,24
Q3UEG6	Alanine-glyoxylate aminotransferase 2, mitochondrial	0,8111	1,10
O35459	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	0,0560	0,70
Q9QX96	Sal-like protein 2	0,9658	0,94
P11862	Growth arrest-specific protein 2	0,3754	1,18
P16381	Putative ATP-dependent RNA helicase PI10	0,8353	0,74
Q5PT54	Sodium/bile acid cotransporter 5	0,9635	1,07
Q78KK3	Solute carrier family 22 member 18	0,9891	1,01
Q61543	Golgi apparatus protein 1	0,7900	1,47
Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	0,8687	1,08
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	0,9635	0,94
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	0,9635	0,94
P63087	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	0,9635	0,94
P35802	Neuronal membrane glycoprotein M6-a	0,6072	0,59
P35803	Neuronal membrane glycoprotein M6-b	0,6072	0,59
Q81110	ATP synthase mitochondrial F1 complex assembly factor 1	0,9608	1,07
O54749	Cytochrome P450 2J5	0,9608	1,07
Q91WT9	Cystathionine beta-synthase	0,7525	1,39
Q91ZN5	Adenosine 3'-phospho 5'-phosphosulfate transporter 1	0,1058	0,77
O09061	Proteasome subunit beta type-1	0,3224	0,82
Q9WUU7	Cathepsin Z	0,9506	0,97
Q8BK29	Pyruvate dehydrogenase protein X component, mitochondrial	1,0000	1,00
P23116	Eukaryotic translation initiation factor 3 subunit A	0,8998	0,84

P62984	Ubiquitin-60S ribosomal protein L40	0,3941	0,93
Q8BZN6	Dedicator of cytokinesis protein 10	0,8203	0,98
Q78JT3	3-hydroxyanthranilate 3,4-dioxygenase	0,5501	0,89
Q9QXB9	Developmentally-regulated GTP-binding protein 2	0,5490	0,54
O35286	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	0,9697	0,95
Q9D939	Sulfotransferase 1C2	0,3854	0,59
P28843	Dipeptidyl peptidase 4	0,5855	1,34
Q9DB29	Isoamyl acetate-hydrolyzing esterase 1 homolog	0,3184	0,72
Q8BXX2	Zinc finger and BTB domain-containing protein 49	0,9317	0,94
Q9ERD7	Tubulin beta-3 chain	0,9572	0,94
P58044	Isopentenyl-diphosphate Delta-isomerase 1	0,9541	1,04
P24527	Leukotriene A-4 hydrolase	0,4873	0,70
P45377	Aldose reductase-related protein 2	0,7421	0,69
P16331	Phenylalanine-4-hydroxylase	0,6347	0,76
Q8C0M9	Isoaspartyl peptidase/L-asparaginase	0,8179	1,23
Q6ZWU9	40S ribosomal protein S27	0,5861	0,76
P97823	Acyl-protein thioesterase 1	0,9795	0,98
Q8BVI4	Dihydropteridine reductase	0,7111	0,67
Q9D8X1	Copper homeostasis protein cutC homolog	0,7540	0,77
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form,	0,8533	0,82
Q62167	ATP-dependent RNA helicase DDX3X	0,8748	0,79
Q8VHQ9	Acyl-coenzyme A thioesterase 11	0,7288	0,69
A2AJL3	FGGY carbohydrate kinase domain-containing protein	0,6313	0,74
Q9JLZ3	Methylglutaconyl-CoA hydratase, mitochondrial	0,7742	0,80
P31254	Ubiquitin-like modifier-activating enzyme 1 Y	0,7148	1,32
Q9CZR8	Elongation factor Ts, mitochondrial	0,7308	0,75
Q7TMR0	Lysosomal Pro-X carboxypeptidase	0,9576	0,93
Q8KOH1	Multidrug and toxin extrusion protein 1	0,1919	0,55
P15947	Kallikrein-1	0,9477	0,93
Q80W21	Glutathione S-transferase Mu 7	0,7984	0,76
P15626	Glutathione S-transferase Mu 2	0,7873	1,49
P19639	Glutathione S-transferase Mu 3	0,5979	0,56
Q99JW4	LIM and senescent cell antigen-like-containing domain protein 1	0,8712	0,79
P62196	26S protease regulatory subunit 8	0,8655	1,28
Q3UFF7	Lysophospholipase-like protein 1	0,4086	0,69
Q8BP67	60S ribosomal protein L24	1,0000	1,00
Q9QXW9	Large neutral amino acids transporter small subunit 2	0,8716	1,13
Q61165	Sodium/hydrogen exchanger 1	0,9649	1,03
Q9D819	Inorganic pyrophosphatase	0,9881	1,02
Q60648	Ganglioside GM2 activator	0,5804	0,55
P11103	Poly [ADP-ribose] polymerase 1	1,0000	1,00
Q9QUR7	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	1,0000	1,00
O35961	Submaxillary gland androgen-regulated protein 2, isoform epsilon	0,9359	1,12
O35982	Submaxillary gland androgen-regulated protein 2, isoform beta	0,9359	1,12
Q0VBB0	PRELI domain-containing protein 2	0,9359	1,12
Q05922	Dual specificity protein phosphatase 2	1,0000	1,00
Q8CDN6	Thioredoxin-like protein 1	0,7247	0,76
P61080	Ubiquitin-conjugating enzyme E2 D1	0,5330	0,58
O55137	Acyl-coenzyme A thioesterase 1	0,5768	0,62
P49282	Natural resistance-associated macrophage protein 2	0,9063	0,84
P48774	Glutathione S-transferase Mu 5	0,9939	1,01
P63037	DnaJ homolog subfamily A member 1	0,9605	0,95
P17879	Heat shock 70 kDa protein 1B	0,9829	1,03
Q91WU5	Arsenite methyltransferase	0,8341	0,73
Q99L04	Dehydrogenase/reductase SDR family member 1	0,9555	1,08
P62835	Ras-related protein Rap-1A	0,8693	1,27
Q9QYC0	Alpha-adducin	0,9466	1,10
P61161	Actin-related protein 2	0,8546	1,30
Q9CQ88	Tetraspanin-31	0,6979	0,54
Q8VHF2	Cadherin-related family member 5	0,6608	0,64
P68033	Actin, alpha cardiac muscle 1	0,6396	0,62
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	0,8026	0,69
Q8BV79	TPR and ankyrin repeat-containing protein 1	0,9635	0,94
O70305	Ataxin-2	0,6779	0,52
Q9ROM5	Thiamin pyrophosphokinase 1	0,6642	0,51
Q9QZD9	Eukaryotic translation initiation factor 3 subunit I	0,7859	0,67
Q8BQ33	Treslin	1,0000	1,00
Q7TMA4	Free fatty acid receptor 4	0,9378	0,90
Q64028	Polyhomeotic-like protein 1	1,0000	1,00
Q9WVP9	Interferon-induced GTP-binding protein Mx2	1,0000	1,00

P16460	Argininosuccinate synthase	0,5821	1,15
O35215	D-dopachrome decarboxylase	0,8093	0,96
P47199	Quinone oxidoreductase	0,6442	1,09
Q9R0P3	S-formylglutathione hydrolase	0,2617	0,81
P17182	Alpha-enolase	0,1581	0,80
Q61171	Peroxiredoxin-2	0,2616	0,73
P17563	Selenium-binding protein 1	0,0867	1,22
Q63836	Selenium-binding protein 2	0,8796	1,26
P68368	Tubulin alpha-4A chain	0,2177	1,24
P68369	Tubulin alpha-1A chain	0,1456	1,90
P17751	Triosephosphate isomerase	0,1272	1,69
Q6PIE5	Sodium/potassium-transporting ATPase subunit alpha-2	0,0295	1,71
Q8VCT3	Aminopeptidase B	0,0747	0,29
Q91YR9	Prostaglandin reductase 1	0,4066	0,41
Q9D1Q6	Endoplasmic reticulum resident protein 44	0,4520	0,45
Q9CXN7	Phenazine biosynthesis-like domain-containing protein 2	0,0814	0,35
Q8BGA8	Acyl-coenzyme A synthetase ACSM5, mitochondrial	0,5011	0,44
Q62470	Integrin alpha-3	0,3615	0,35
Q49B93	Sodium-coupled monocarboxylate transporter 2	0,1316	0,34
P16546	Spectrin alpha chain, non-erythrocytic 1	0,1084	0,34
Q61699	Heat shock protein 105 kDa	0,0389	0,49
Q9D8N0	Elongation factor 1-gamma	0,2217	0,22
Q8VCM7	Fibrinogen gamma chain	0,2750	0,29
Q9R0N0	Galactokinase	0,3404	0,33
P20918	Plasminogen	0,2208	0,40
Q8CIE6	Coatomer subunit alpha	0,0140	0,39
Q62433	Protein NDRG1	0,6368	0,49
Q9DC51	Guanine nucleotide-binding protein G(k) subunit alpha	0,4915	0,48
P01942	Hemoglobin subunit alpha	0,0255	0,23
P17156	Heat shock-related 70 kDa protein 2	0,1615	0,38
Q8VCN5	Cystathionine gamma-lyase	0,0880	0,32
P63168	Dynein light chain 1, cytoplasmic	0,3552	0,35
Q9D1G1	Ras-related protein Rab-1B	0,1228	0,35
Q91VC4	Plasmalemma vesicle-associated protein	0,2285	0,21
P62878	E3 ubiquitin-protein ligase RBX1	0,3137	0,33
Q99PL5	Ribosome-binding protein 1	0,0234	0,18
Q8VDM6	Heterogeneous nuclear ribonucleoprotein U-like protein 1	0,0429	0,23
P00342	L-lactate dehydrogenase C chain	0,1969	0,38
Q9DCU9	4-hydroxy-2-oxoglutarate aldolase, mitochondrial	0,1860	0,39
Q9QZD8	Mitochondrial dicarboxylate carrier	0,2499	0,44
P61759	Prefoldin subunit 3	0,4554	0,46
P80316	T-complex protein 1 subunit epsilon	0,3552	0,37
Q8K010	5-oxoprolinase	0,0275	0,20
O70456	14-3-3 protein sigma	0,3768	0,39
P35276	Ras-related protein Rab-3D	0,0940	0,33
Q9WTI7	Unconventional myosin-Ic	0,5994	0,41
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	0,1907	1,44
P62631	Elongation factor 1-alpha 2	0,8276	1,38
P63017	Heat shock cognate 71 kDa protein	0,2978	1,15
P05214	Tubulin alpha-3 chain	0,6506	0,62
P21550	Beta-enolase	0,0660	0,75
P17183	Gamma-enolase	0,6711	0,71
Q6PIC6	Sodium/potassium-transporting ATPase subunit alpha-3	0,1404	2,11
E9Q5G7	Oogenesis-1	0,4962	0,50
Q9Z1F9	SUMO-activating enzyme subunit 2	0,2690	0,29
P20060	Beta-hexosaminidase subunit beta	0,0256	0,22
Q80V42	Carboxypeptidase M	0,4211	0,44
Q64337	Sequestosome-1	0,0478	0,22
P62880	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	0,4514	0,18
P01738	T-cell receptor alpha chain V region PHDSS8	0,1307	0,37
Q9JJ00	Phospholipid scramblase 1	0,3882	0,35
Q9EPE9	Manganese-transporting ATPase 13A1	0,3560	0,38
P02089	Hemoglobin subunit beta-2	0,0024	0,00
Q8CHR6	Dihydropyrimidine dehydrogenase [NADP(+)]	0,0037	0,00
Q9EQ06	Estradiol 17-beta-dehydrogenase 11	0,1853	0,02
Q8VDZ4	Palmitoyltransferase ZDHHC5	0,0031	0,01
Q5SW19	Clustered mitochondria protein homolog	0,3739	0,04
O89013	Leptin receptor gene-related protein	0,0001	0,01
P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	0,2259	0,03
Q924M7	Mannose-6-phosphate isomerase	0,3739	0,04

P15532	Nucleoside diphosphate kinase A	0,3739	0,04
Q6P3A8	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	0,1161	0,02
Q9D7G0	Ribose-phosphate pyrophosphokinase 1	0,1221	0,03
Q62095	ATP-dependent RNA helicase DDX3Y	0,3739	0,05
Q91V92	ATP-citrate synthase	0,1264	0,03
Q91VH6	Protein MEMO1	0,3739	0,05
P52825	Carnitine O-palmitoyltransferase 2, mitochondrial	0,3739	0,05
P01029	Complement C4-B	0,1202	0,03
Q9DCL9	Multifunctional protein ADE2	0,3739	0,05
P27601	Guanine nucleotide-binding protein subunit alpha-13	0,0159	0,01
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	0,1161	0,03
P04186	Complement factor B	0,3739	0,06
Q9ET30	Transmembrane 9 superfamily member 3	0,3739	0,06
Q9DC04	Regulator of G-protein signaling 3	0,1161	0,03
Q3V3R1	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	0,3739	0,06
Q6IRU5	Clathrin light chain B	0,3739	0,06
O08585	Clathrin light chain A	0,3739	0,06
P01027	Complement C3	0,1180	0,03
Q99LM2	CDK5 regulatory subunit-associated protein 3	0,3739	0,06
P61514	60S ribosomal protein L37a	0,0001	0,02
Q9CZM2	60S ribosomal protein L15	0,1161	0,04
Q6DYE8	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3	0,0120	0,03
Q9DCN1	Peroxisomal NADH pyrophosphatase NUDT12	0,1360	0,05
P62267	40S ribosomal protein S23	0,0509	0,03
Q9CWF2	Tubulin beta-2B chain	0,1242	0,00