

Supplementary Table 1: proteins showing a significant change in abundance vs control in one of the two tested conditions

bold: proteins with a change greater in amplitude at the end of the recovery period compared to the change observed immediately after exposure

italics : proteins showing a significant change by the Mann-Whitney U test but not by the Student T test

when present : ac=acidic form; bas=basic form : med=median form

| code | name | accession | peptide count | percent seq coverage | ratio acute/ctrl | T test acute vs ctrl | ratio recov/ctrl | T test recov vs ctrl |
|-----------------|---|----------------------|------------------|-------------------------|---------------------|-------------------------|---------------------|-------------------------|
| 14-3-3 zeta | 14-3-3 protein zeta/delta | P63101 | 21 | 75% | 0,76290 | 0,02651 | 0,99007 | 0,92966 |
| aars ac | Alanine--tRNA ligase, cytoplasmic | Q8BGQ7 | 39 | 49% | 1,57024 | 0,01813 | 1,18233 | 0,59140 |
| aars bas | Alanine--tRNA ligase, cytoplasmic | Q8BGQ7 | 46 | 55% | 1,49569 | 0,03230 | 1,07151 | 0,81469 |
| aars Σ | Alanine--tRNA ligase, cytoplasmic | Q8BGQ7 | | | 1,53022 | 0,02138 | 1,12284 | 0,70052 |
| acoc | Cytoplasmic aconitate hydratase | P28271 | 5 | 5% | 0,50617 | 0,04263 | 1,03364 | 0,90416 |
| akr1a1 | <i>Alcohol dehydrogenase [NADP(+)]</i> | <i>Q9JII6</i> | 17 | 66% | 1,23212 | 0,38746 | 0,75380 | 0,07708 |
| akr1b1 | Aldose reductase | P45376 | 15 | 50% | 0,90708 | 0,33590 | 0,82794 | 0,03855 |
| amrp | Alpha-2-macroglobulin receptor-associated protein | P55302 | 29 | 61% | 0,61065 | 0,00437 | 0,91219 | 0,62467 |
| anxa2 | Annexin A2 | P07356 | 27 | 66% | 0,64136 | 0,01630 | 0,97415 | 0,76721 |
| anxa5 ac | Annexin A5 | P48036 | 19 | 62% | 0,50928 | 0,04541 | 0,65936 | 0,12303 |
| anxa5 bas | Annexin A5 | P48036 | 29 | 83% | 1,13620 | 0,04198 | 1,14672 | 0,09548 |
| anxa5 med | Annexin A5 | P48036 | 23 | 56% | 0,81264 | 0,26440 | 0,94032 | 0,62948 |
| anxa5 Σ | Annexin A5 | P48036 | | | 0,86677 | 0,22537 | 0,95345 | 0,47953 |
| ap3m1 | AP-3 complex subunit mu-1 | Q9JKC8 | 18 | 67% | 2,23364 | 0,01103 | 0,79387 | 0,64513 |
| arl3 | ADP-ribosylation factor-like protein 3 | Q9WUL7 | 11 | 69% | 2,17187 | 0,01683 | 1,22052 | 0,43727 |
| atpb ac | ATP synthase subunit beta, mitochondrial | P56480 | 16 | 39% | 1,46182 | 0,04489 | 1,22323 | 0,32400 |
| atpb bas | ATP synthase subunit beta, mitochondrial | P56480 | 9 | 27% | 1,61813 | 0,01289 | 1,21226 | 0,28437 |
| atpb Σ | ATP synthase subunit beta, mitochondrial | P56480 | | | 1,54692 | 0,01159 | 1,21726 | 0,27273 |
| bpnt1 | 3'(2'),5'-bisphosphate nucleotidase 1 | Q9Z0S1 | 12 | 45% | 2,08832 | 0,01616 | 1,18476 | 0,36510 |
| bvra ac | Biliverdin reductase A | Q9CY64 | 13 | 51% | 0,40829 | 0,03776 | 1,00416 | 0,98931 |
| <i>bvra bas</i> | <i>Biliverdin reductase A</i> | <i>Q9CY64</i> | <i>14</i> | <i>59%</i> | <i>0,85976</i> | <i>0,06744</i> | <i>0,92202</i> | <i>0,73954</i> |
| bvra Σ | Biliverdin reductase A | Q9CY64 | | | 0,70094 | 0,02176 | 0,95091 | 0,84054 |
| cah13 | Carbonic anhydrase 13 | Q9D6N1 | 4 | 12% | 0,68610 | 0,04922 | 0,91080 | 0,60251 |

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|----------------|--|---------------|-----------|------------|----------------|----------------|----------------|----------------|
| cap1 | Adenylyl cyclase-associated protein 1 | P40124 | 9 | 22% | 0,68705 | 0,03278 | 1,00948 | 0,96051 |
| capg | Macrophage-capping protein | P24452 | 11 | 34% | 0,80400 | 0,04840 | 0,91501 | 0,43314 |
| capg ac | Macrophage-capping protein | P24452 | 12 | 49% | 0,84106 | 0,06848 | 0,88736 | 0,30541 |
| capg Σ | Macrophage-capping protein | P24452 | | | 0,82039 | 0,04019 | 0,90278 | 0,31255 |
| casp3 | Caspase-3 | P70677 | 12 | 53% | 0,99746 | 0,98635 | 0,68063 | 0,03546 |
| catS | Cathepsin S | O70370 | 6 | 22% | 0,71356 | 0,02330 | 0,91490 | 0,32559 |
| caza2 ac | F-actin-capping protein subunit alpha-2 | P47754 | 11 | 59% | 1,79361 | 0,01906 | 1,11616 | 0,23413 |
| caza2 bas | F-actin-capping protein subunit alpha-2 | P47754 | 6 | 29% | 1,02448 | 0,85172 | 0,86522 | 0,25628 |
| caza2 Σ | F-actin-capping protein subunit alpha-2 | P47754 | | | 1,31082 | 0,02220 | 0,95864 | 0,55954 |
| ccs | Copper chaperone for superoxide dismutase | Q9WU84 | 2 | 8% | 0,94578 | 0,35003 | 1,20553 | 0,03962 |
| cdk6 | Cyclin-dependent kinase 6 | Q64261 | 3 | 11% | 0,69009 | 0,03320 | 0,81637 | 0,31945 |
| chm2a | Charged multivesicular body protein 2a | Q9DB34 | 6 | 26% | 0,94643 | 0,39662 | 0,65042 | 0,00898 |
| cof bas | Cofilin-1 | P18760 | 5 | 42% | 0,51738 | 0,05847 | 0,94789 | 0,88027 |
| cpsn1 ac | Calpain small subunit 1 | O88456 | 5 | 33% | 0,55295 | 0,03978 | 1,16217 | 0,26487 |
| cpsn1 bas | Calpain small subunit 1 | O88456 | 9 | 68% | 1,09112 | 0,71534 | 0,95775 | 0,86606 |
| cpsn1 Σ | Calpain small subunit 1 | O88456 | | | 0,82100 | 0,11007 | 1,06036 | 0,54005 |
| dcup | Uroporphyrinogen decarboxylase | P70697 | 4 | 14,00% | 0,46458 | 0,02995 | 0,89999 | 0,45250 |
| dcxr | L-xylulose reductase | Q91X52 | 8 | 42% | 0,30716 | 0,04586 | 0,99983 | 0,99949 |
| ddx39b | Spliceosome RNA helicase Ddx39b | Q9Z1N5 | 16 | 46% | 1,33840 | 0,04630 | 0,99179 | 0,96254 |
| dhb8 | Estradiol 17-beta-dehydrogenase 8 | P50171 | 8 | 49% | 1,43632 | 0,00789 | 0,77165 | 0,19337 |
| dj1 ac | Protein deglycase DJ-1 | Q99LX0 | 9 | 69% | 0,60700 | 0,15160 | 1,00820 | 0,96792 |
| dj1 bas | Protein deglycase DJ-1 | Q99LX0 | 11 | 83% | 1,64818 | 0,09085 | 0,92780 | 0,77092 |
| dj1 Σ | Protein deglycase DJ-1 | Q99LX0 | | | 1,11572 | 0,45086 | 0,96892 | 0,84485 |
| dnja2 | DnaJ homolog subfamily A member 2 | Q9QYJ0 | 4 | 9% | 0,95942 | 0,68473 | 0,69231 | 0,02057 |
| dpp3 ac | Dipeptidyl peptidase 3 | Q99KK7 | 11 | 22% | 1,45965 | 0,09187 | 1,35807 | 0,37938 |
| dpp3 bas | Dipeptidyl peptidase 3 | Q99KK7 | 9 | 19% | 1,76586 | 0,01153 | 1,37127 | 0,34811 |
| dpp3 Σ | Dipeptidyl peptidase 3 | Q99KK7 | | | 1,63796 | 0,01459 | 1,36576 | 0,35615 |
| ef1d | Elongation factor 1-delta | P57776 | 5 | 21% | 1,40944 | 0,00230 | 1,07337 | 0,39758 |
| esd | S-formylglutathione hydrolase | Q9R0P3 | 14 | 73% | 1,25939 | 0,02840 | 0,85967 | 0,09616 |
| fkbp4 ac | Peptidyl-prolyl cis-trans isomerase FKBP4 | P30416 | 13 | 27,00% | 1,17122 | 0,38770 | 0,85906 | 0,46634 |
| fkbp4 bas | Peptidyl-prolyl cis-trans isomerase FKBP4 | P30416 | 23 | 50% | 1,52073 | 0,18928 | 0,99570 | 0,98926 |

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|---------------------|---|---------------|-----------|------------|----------------|----------------|----------------|----------------|
| <i>fkbp4 med</i> | Peptidyl-prolyl cis-trans isomerase FKBP4 | P30416 | 20 | 43% | 1,56506 | 0,10775 | 0,90989 | 0,72179 |
| <i>fkbp4</i> ∑ | Peptidyl-prolyl cis-trans isomerase FKBP4 | P30416 | | | 1,44136 | 0,16404 | 0,92684 | 0,76864 |
| <i>fpys ac</i> | Farnesyl pyrophosphate synthase | Q920E5 | 17 | 63% | 1,02992 | 0,75642 | 1,13639 | 0,22162 |
| <i>fpys bas</i> | Farnesyl pyrophosphate synthase | Q920E5 | 10 | 31% | 1,40391 | 0,04292 | 1,24951 | 0,35046 |
| <i>fpys</i> ∑ | Farnesyl pyrophosphate synthase | Q920E5 | | | 1,14425 | 0,12395 | 1,17097 | 0,27736 |
| <i>gapdh</i> | Glyceraldehyde-3-phosphate dehydrogenase | P16858 | 22 | 59% | 0,56124 | 0,01185 | 1,02877 | 0,84796 |
| gars | Glycine--tRNA ligase | Q9CZD3 | 22 | 36% | 1,11067 | 0,72866 | 0,58764 | 0,01867 |
| | Guanine nucleotide-binding protein G(I)/G(S)/G(T) | | | | | | | |
| <i>gbb1</i> | subunit beta-1 | P62874 | 7 | 24% | 1,89777 | 0,01888 | 0,92893 | 0,41875 |
| <i>glrx3 ac</i> | Glutaredoxin-3 | Q9CQM9 | 2 | 9% | 1,23829 | 0,17960 | 0,97262 | 0,66012 |
| <i>glrx3 bas</i> | Glutaredoxin-3 | Q9CQM9 | 11 | 41% | 1,45099 | 0,04340 | 0,98694 | 0,88249 |
| <i>glrx3</i> ∑ | Glutaredoxin-3 | Q9CQM9 | | | 1,35547 | 0,07363 | 0,98051 | 0,79051 |
| <i>gmfb</i> | Glia maturation factor beta | Q9CQI3 | 8 | 44% | 0,75495 | 0,02699 | 1,22229 | 0,29340 |
| <i>grp75</i> | Stress-70 protein, mitochondrial | O35501 | 25 | 43% | 1,93665 | 0,00736 | 1,02408 | 0,88684 |
| <i>hmgcl</i> | Hydroxymethylglutaryl-CoA lyase, mitochondrial | P38060 | 7 | 34% | 1,60154 | 0,12343 | 0,52947 | 0,07353 |
| | Heterogeneous nuclear ribonucleoprotein U-like | | | | | | | |
| <i>hnrl2</i> | protein 2 | Q00PI9 | 13 | 19,00% | 0,58894 | 0,01850 | 1,07315 | 0,88827 |
| hook3 | Protein Hook homolog 3 | Q8BUK6 | 4 | 5% | 1,07412 | 0,65045 | 0,45019 | 0,00519 |
| <i>iF3M</i> | Eukaryotic translation initiation factor 3 subunit M | Q99JX4 | 20 | 64% | 1,49603 | 0,02779 | 1,03209 | 0,81144 |
| <i>ima7</i> | Importin subunit alpha-7 | O35345 | 18 | 41% | 2,11765 | 0,01582 | 0,84029 | 0,61907 |
| <i>imdH2</i> | Inosine-5'-monophosphate dehydrogenase 2 | P24547 | 11 | 21% | 1,30452 | 0,04136 | 1,33870 | 0,30872 |
| <i>ipyr</i> | Inorganic pyrophosphatase | Q9D819 | 5 | 14% | 1,89687 | 0,02540 | 0,98832 | 0,93752 |
| <i>kcy</i> | UMP-CMP kinase | Q9DBP5 | 10 | 59% | 0,42646 | 0,03794 | 1,06299 | 0,80275 |
| <i>kpym ac</i> | Pyruvate kinase PKM | P52480 | 19 | 42% | 0,65913 | 0,04843 | 0,98415 | 0,88103 |
| <i>kpym bas</i> | Pyruvate kinase PKM | P52480 | 27 | 61% | 0,72140 | 0,05389 | 0,78313 | 0,10077 |
| <i>kpym</i> ∑ | Pyruvate kinase PKM | P52480 | | | 0,68433 | 0,04725 | 0,90280 | 0,37449 |
| <i>ldha</i> | L-lactate dehydrogenase A chain | P06151 | 20 | 44% | 0,60178 | 0,00675 | 0,91651 | 0,63780 |
| <i>lypa1</i> | Acyl-protein thioesterase 1 | P97823 | 4 | 20% | 1,40416 | 0,04461 | 0,89530 | 0,54447 |

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|--------------------|--|----------------------|-----------|------------|----------------|----------------|----------------|----------------|
| maom | NAD-dependent malic enzyme, mitochondrial | Q99KE1 | 22 | 57% | 0,86697 | 0,28223 | 0,79794 | 0,02883 |
| mapk1 | Mitogen-activated protein kinase 1 | P63085 | 7 | 16% | 0,82515 | 0,02731 | 0,66086 | 0,01112 |
| mk14 | Mitogen-activated protein kinase 14 | P47811 | 13 | 57% | 1,76129 | 0,03954 | 1,74841 | 0,03047 |
| mvp bas | Major vault protein | Q9EQK5 | 7 | 10% | 1,74152 | 0,00741 | 1,30534 | 0,60262 |
| mvp med | Major vault protein | Q9EQK5 | 14 | 18% | 1,68139 | 0,00736 | 1,21356 | 0,63499 |
| mvp Σ | Major vault protein | Q9EQK5 | | | 1,70938 | 0,00982 | 1,25629 | 0,61698 |
| naa20 | N-alpha-acetyltransferase 20 | ,P6160 | 5 | 35% | 1,92416 | 0,00790 | 1,26842 | 0,07015 |
| naga ac | N-acetylglucosamine-6-phosphate deacetylase | Q8JZV7 | 9 | 31% | 1,26353 | 0,02255 | 0,93615 | 0,72583 |
| ndus3 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial | Q9DCT2 | 5 | 23% | 1,76446 | 0,00980 | 1,06141 | 0,71227 |
| nit1 | Nitrilase homolog 1 | Q8VDK1 | 13 | 55% | 0,53363 | 0,00972 | 0,82315 | 0,10447 |
| nsflc | NSFL1 cofactor p47 | Q9CZ44 | 8 | 28% | 0,75149 | 0,03603 | 1,23871 | 0,16724 |
| odb2 | Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial | P53395 | 18 | 42,00% | 1,33892 | 0,03519 | 1,18731 | 0,24036 |
| odo2 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial | Q9D2G2 | 9 | 24% | 1,33185 | 0,01980 | 0,94383 | 0,79661 |
| pcbp1 | Poly(rC)-binding protein 1 | P60335 | 14 | 75% | 0,67657 | 0,04239 | 0,98541 | 0,92459 |
| pdcd6 | Programmed cell death protein 6 | P12815 | 9 | 58% | 1,32354 | 0,03975 | 1,05803 | 0,52904 |
| pdcd1 | Parkinson disease 7 domain-containing protein 1 | Q8BFQ8 | 3 | 19% | 0,69947 | 0,20457 | 0,76998 | 0,01039 |
| pdia1 ac | Protein disulfide-isomerase | P09103 | 20 | 42,00% | 1,34229 | 0,13581 | 0,96016 | 0,84230 |
| pdia1 med | Protein disulfide-isomerase | P09103 | 33 | 70,00% | 1,60723 | 0,02123 | 1,02115 | 0,82547 |
| pdia1 Σ | Protein disulfide-isomerase | P09103 | | | 1,46574 | 0,04547 | 0,93445 | 0,56375 |
| <i>pdxk</i> | <i>Pyridoxal kinase</i> | <i>Q8K183</i> | 7 | 24% | 1,46207 | 0,07857 | 0,58608 | 0,02273 |
| pgk1 ac | Phosphoglycerate kinase 1 | P09411 | 20 | 62% | 0,62818 | 0,02486 | 0,93025 | 0,41128 |
| pgk1 bas | Phosphoglycerate kinase 1 | P09411 | 25 | 69,00% | 0,79014 | 0,04707 | 0,97776 | 0,75765 |
| pgk1 sum | Phosphoglycerate kinase 1 | P09411 | | | 0,69633 | 0,02968 | 0,95024 | 0,49578 |
| pgls | 6-phosphogluconolactonase | Q9CQ60 | 9 | 51% | 1,48915 | 0,02618 | 0,94561 | 0,64183 |
| phb | Prohibitin | P67778 | 12 | 53% | 1,27375 | 0,00183 | 0,98638 | 0,78453 |

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|----------------|---|---------------|-----------|------------|----------------|----------------|----------------|----------------|
| pipna | Phosphatidylinositol transfer protein alpha isoform | P53810 | 23 | 76% | 0,70142 | 0,02782 | 0,87336 | 0,22829 |
| prps1 | Ribose-phosphate pyrophosphokinase 1 | ,Q9D7G | 10 | 39% | 1,09710 | 0,56441 | 0,66283 | 0,01079 |
| prx3 | Thioredoxin-dependent peroxide reductase, mitochondrial | P20108 | 3 | 11% | 1,83406 | 0,02181 | 0,82291 | 0,37112 |
| prx6 | Peroxiredoxin-6 | O08709 | 17 | 80% | 1,01587 | 0,82669 | 0,79438 | 0,00237 |
| psa1 | Proteasome subunit alpha type-1 | Q9R1P4 | 17 | 76% | 1,34609 | 0,03449 | 0,86170 | 0,06202 |
| psb10 | Proteasome subunit beta type-10 | O35955 | 8 | 38% | 1,45026 | 0,03400 | 0,64042 | 0,06162 |
| psb4 ac | Proteasome subunit beta type-4 | P99026 | 3 | 16% | 2,90441 | 0,03758 | 1,01946 | 0,93154 |
| psb4 bas | Proteasome subunit beta type-4 | P99026 | 8 | 49% | 1,48629 | 0,14464 | 1,07429 | 0,32620 |
| psb4 Σ | Proteasome subunit beta type-4 | P99026 | | | 2,04997 | 0,07086 | 1,05250 | 0,49369 |
| psmd2 ac | 26S proteasome non-ATPase regulatory subunit 2 | Q8VDM4 | 11 | 14% | 1,56132 | 0,13670 | 1,05633 | 0,78149 |
| psmd2 bas | 26S proteasome non-ATPase regulatory subunit 2 | Q8VDM4 | 13 | 16% | 1,68826 | 0,03615 | 1,04733 | 0,79279 |
| psmd2 Σ | 26S proteasome non-ATPase regulatory subunit 2 | Q8VDM4 | | | 1,63196 | 0,04585 | 1,05132 | 0,75403 |
| <i>psmd8</i> | 26S proteasome non-ATPase regulatory subunit 8 | Q9CX56 | 7 | 18% | 1,26859 | 0,14314 | 0,69290 | 0,06247 |
| psmd14 | 26S proteasome non-ATPase regulatory subunit 14 | O35593 | 5 | 18% | 1,51073 | 0,04974 | 0,90995 | 0,61498 |
| <i>pth2</i> | Peptidyl-tRNA hydrolase 2, mitochondrial | Q8R2Y8 | 4 | 32% | 1,58200 | 0,07167 | 1,02366 | 0,91501 |
| ran b3/1 | Ran-binding protein 3 | Q9CT10 | 8 | 20% | 2,21322 | 0,04081 | 3,38495 | 0,06131 |
| ranb3/2 | Ran-binding protein 3 | Q9CT10 | 10 | 24% | 0,42471 | 0,05814 | 0,44310 | 0,00779 |
| rap1a | Ras-related protein Rap-1A | P62835 | 3 | 21,00% | 4,47577 | 0,03998 | 1,51363 | 0,35884 |
| rbm8a | RNA-binding protein 8A | Q9CWZ3 | 5 | 51% | 1,52292 | 0,07422 | 1,29914 | 0,19575 |
| rm46 | 39S ribosomal protein L46, mitochondrial | Q9EQI8 | 5 | 22% | 2,06179 | 0,01680 | 0,77167 | 0,15948 |
| rssa | 40S ribosomal protein SA | P14206 | 18 | 60% | 1,40236 | 0,02817 | 0,97659 | 0,85186 |
| sarnp | SAP domain-containing ribonucleoprotein | Q9D1J3 | 5 | 28% | 0,94784 | 0,44484 | 0,74430 | 0,00535 |
| sdcbl | Syntenin-1 | O08992 | 3 | 26% | 1,71727 | 0,02408 | 0,70053 | 0,05999 |
| sera | D-3-phosphoglycerate dehydrogenase | Q61753 | 3 | 7% | 0,74962 | 0,05766 | 0,46038 | 0,02610 |
| sias | Sialic acid synthase OS=Homo sapiens | 9 | 9 | 32% | 0,52749 | 0,03753 | 0,91001 | 0,52460 |
| snaa | Alpha-soluble NSF attachment protein | Q9DB05 | 13 | 49% | 1,70178 | 0,03251 | 1,03238 | 0,86345 |

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|-----------------|--|---------------|-----------|------------|----------------|----------------|----------------|----------------|
| snd1 | Staphylococcal nuclease domain-containing protein 1 | Q78PY7 | 17 | 28% | 1,09108 | 0,66107 | 1,44869 | 0,00084 |
| snx6 ac | Sorting nexin-6 | Q6P8X1 | 9 | 25% | 1,06397 | 0,79998 | 1,22126 | 0,03157 |
| snx6 bas | Sorting nexin-6 | Q6P8X1 | 18 | 44% | 0,87703 | 0,41676 | 0,58176 | 0,00085 |
| snx6 Σ | Sorting nexin-6 | Q6P8X1 | | | 0,96481 | 0,53074 | 0,88205 | 0,00774 |
| spb6 ac | Serpin B6 | Q60854 | 13 | 39% | 0,82831 | 0,11344 | 1,22955 | 0,02473 |
| spb6 bas | Serpin B6 | Q60854 | 8 | 23% | 1,56173 | 0,10652 | 1,07268 | 0,76891 |
| spb6 med | Serpin B6 | Q60854 | 9 | 26% | 1,10774 | 0,59650 | 1,12246 | 0,48335 |
| spb6 Σ | Serpin B6 | Q60854 | | | 1,15245 | 0,42503 | 1,13442 | 0,39370 |
| spee | Spermidine synthase | Q64674 | 2 | 7% | 1,79253 | 0,04341 | 0,91716 | 0,44984 |
| spre | Sepiapterin reductase | Q64105 | 13 | 63% | 0,76223 | 0,03202 | 1,21136 | 0,39068 |
| ssrd | Translocon-associated protein subunit delta | Q62186 | 4 | 31% | 1,88099 | 0,01196 | 1,21136 | 0,39068 |
| tmem11 | Transmembrane protein 11, mitochondrial | Q8BK08 | 6 | 35% | 1,50361 | 0,01978 | 1,20958 | 0,55435 |
| tpm4 | Tropomyosin alpha-4 chain | Q6IRU2 | 17 | 53% | 0,38978 | 0,01036 | 0,50005 | 0,00116 |
| twf2 | Twinfilin-2 | Q9Z0P5 | 10 | 38% | 0,67903 | 0,02618 | 0,92104 | 0,64849 |
| uba1 | Ubiquitin-like modifier-activating enzyme 1 | Q02053 | 25 | 34% | 1,31969 | 0,02355 | 1,06249 | 0,79115 |
| ubql1h | Ubiquilin-1 | Q8R317 | 2 | 3% | 0,89348 | 0,16595 | 0,69245 | 0,01325 |
| ubql4 | Ubiquilin-4 OS=Homo sapiens | Q9NRR5 | 2 | 3% | 0,52405 | 0,02103 | 1,16653 | 0,71920 |
| uchl5 | Ubiquitin carboxyl-terminal hydrolase isozyme L5 | Q9WUP7 | 7 | 21% | 1,35660 | 0,00756 | 1,00065 | 0,99354 |
| vata ac | V-type proton ATPase catalytic subunit A | P50516 | 6 | 12,80% | 1,55768 | 0,03123 | 0,96678 | 0,86184 |
| vata bas | V-type proton ATPase catalytic subunit A | P50516 | 23 | 42% | 1,76854 | 0,01711 | 1,06525 | 0,74919 |
| vata Σ | V-type proton ATPase catalytic subunit A | P50516 | | | 1,65676 | 0,01117 | 1,01305 | 0,94648 |
| vps29 | Vacuolar protein sorting-associated protein 29 | Q9QZ88 | 4 | 21% | 0,99265 | 0,98566 | 0,67061 | 0,02975 |