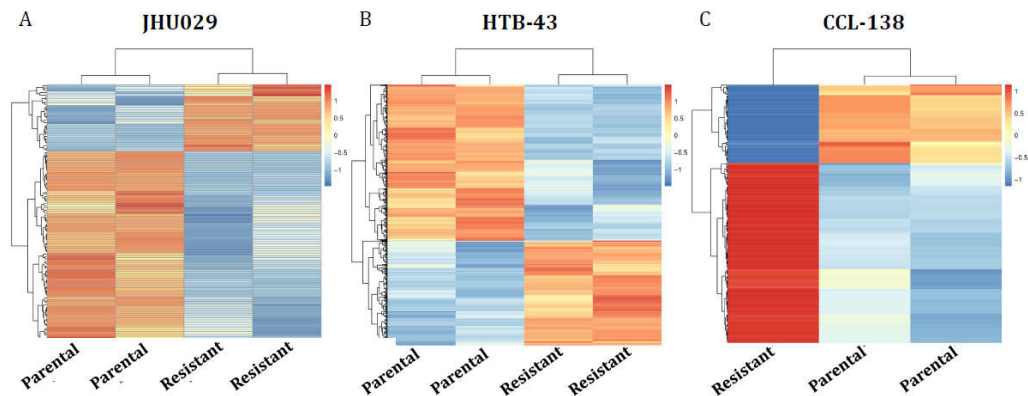
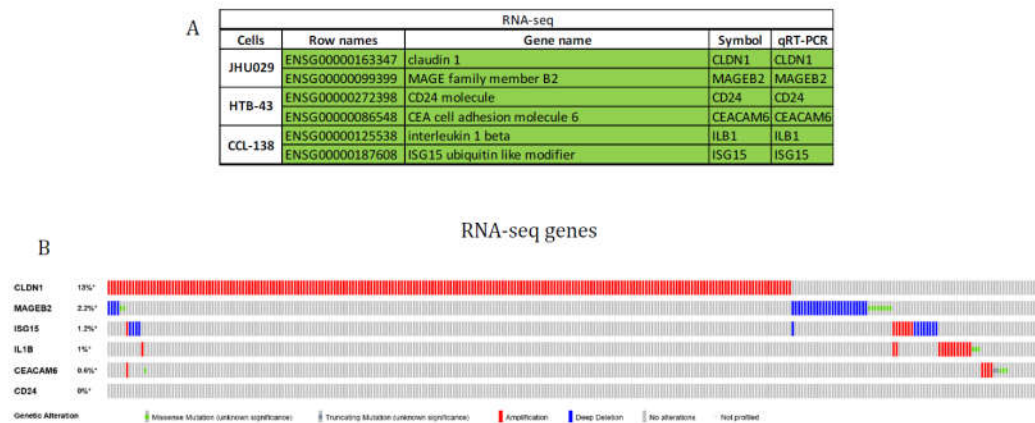


Supplementary Figure legends

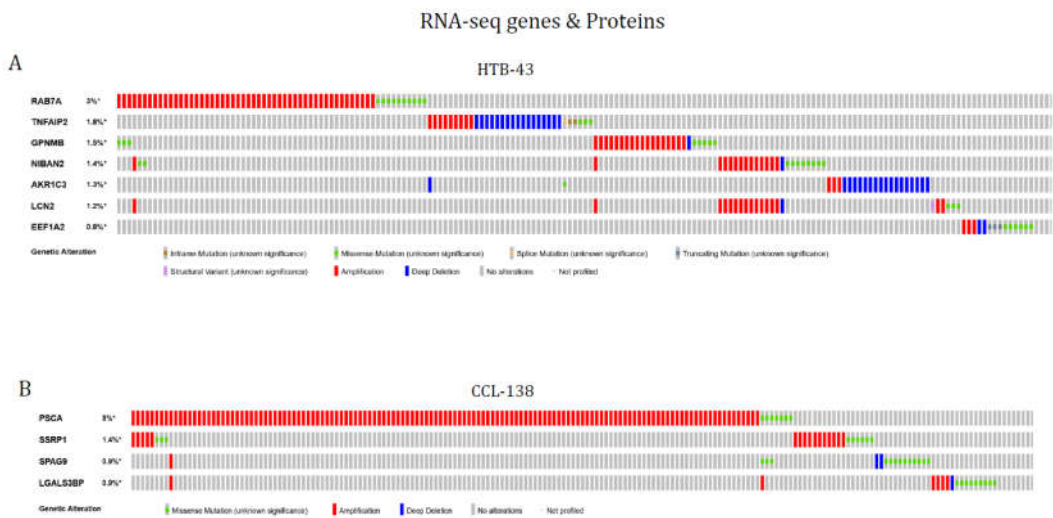


Supplementary Figure S1. Heatmap of the RNA-seq data: **(A)** Heatmap of the JHU029 cells. Note the difference between resistant and parental cells; **(B)** Heatmap of HTB-43 cells. Note the difference between resistant and parental cells; **(C)** Heatmap of the CCL-138 cells. Note the difference between resistant and parental.

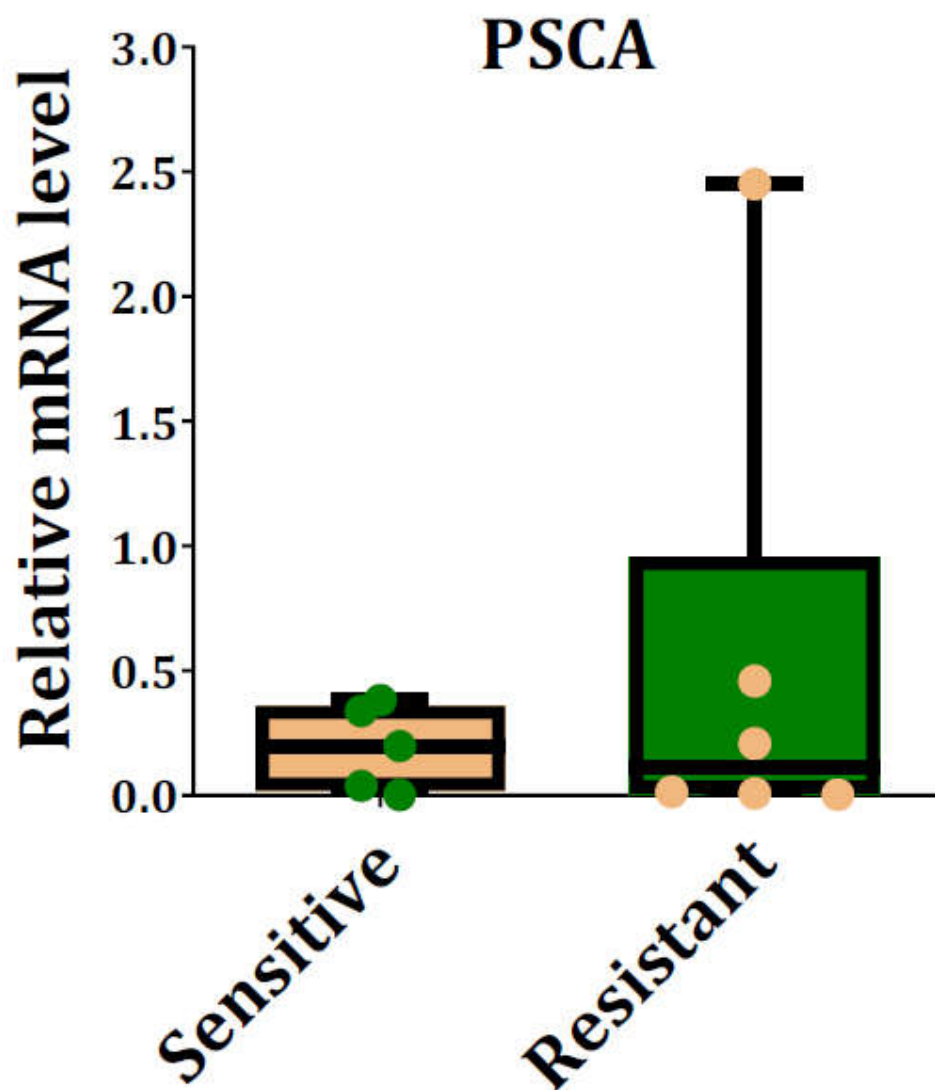


Supplementary Figure S2. *In silico* study of gene status: **(A)** Summary of selected genes for qRT-PCR; **(B)** Genomic alteration of the indicated genes according to the Oncoprint dataset.

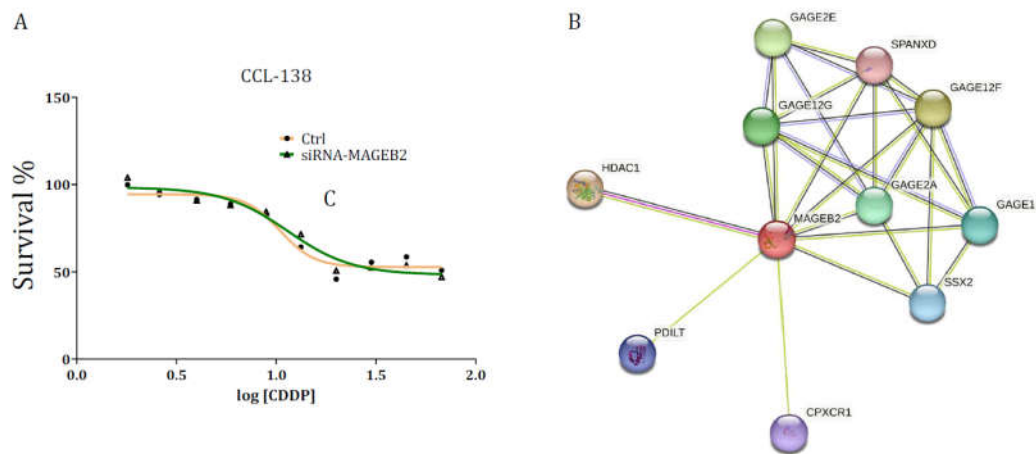
were commonly found to be upregulated; **(B)** A total of 6 proteins were commonly found to be deregulated.



Supplementary Figure S5. *In silico* study of gene status: **(A)** Genomic alteration of the indicated genes according to the Oncoprint dataset found to be deregulated in HTB-43 cells; **(B)** Genomic alteration of the indicated genes according to the Oncoprint dataset found to be deregulated in CCL-138 cells.



Supplementary Figure S6. *PSCA* gene expression shows a trend to significance when resistant *versus* sensitive patients were compared.



Supplementary Figure S7. Characterization of *MAGEB2*: (A) Lack of sensitization in *MAGEB2* depletion conditions in CCL-138; (B) *MAGEB2* protein interactions.

Table S1. Patients in whom the RNA study of the 12 selected genes was carried out. Both patients who received chemotherapy and radiotherapy, these treatments were after surgery. QT, chemotherapy; RT, radiotherapy.

| Patient | Surgery | Cancer type | Resistant | QT | RT |
|---------|---------|-------------|-----------|-----|-----|
| P2 | YES | larynx | YES | NO | YES |
| P7 | YES | larynx | NO | YES | YES |
| P8 | YES | larynx | NO | YES | YES |
| P15 | YES | larynx | YES | YES | YES |
| P17 | YES | larynx | NO | NO | YES |
| P22 | YES | larynx | NO | NO | YES |
| P29 | YES | larynx | NO | NO | YES |
| P32 | YES | larynx | YES | NO | YES |
| P33 | YES | larynx | YES | NO | YES |
| P42 | YES | larynx | YES | YES | YES |
| P70 | YES | larynx | YES | NO | YES |

Table S2. Data counts before and after some processing steps. The raw data is available in the NCBI SRA database under the following accession numbers and the BioProject accession code PRJNA893841.

| Cell Line | Replicates | Number of raw reads | Number of reads after trimming | Mapping percent after filtering | Accession number in NCBI SRA database |
|---|------------|---------------------|--------------------------------|---------------------------------|---------------------------------------|
| HTB-43 (FaDu) | HTB-43P-1 | 23755496 | 9205260 | 99.97% | SRR22028463 |
| Pharynx primary parental HTB-43 (FaDu) | HTB-43P-2 | 23662886 | 9036143 | 99.96% | SRR22028462 |
| Pharynx primary resistant HTB-43 (FaDu) | HTB-43R-1 | 30351858 | 10865117 | 99.92% | SRR22028461 |
| Pharynx primary resistant HTB-43 (FaDu) | HTB-43R-2 | 24438226 | 9050392 | 99.96% | SRR22028460 |
| CCL-138 (Detroit 562) | CCL-138P-1 | 27025306 | 10198441 | 99.96% | SRR22028467 |
| Pharynx metastatic parental CCL-138 (Detroit 562) | CCL-138P-2 | 26819396 | 10136993 | 99.96% | SRR22028466 |
| Pharynx metastatic parental CCL-138 (Detroit 562) | CCL-138R-1 | 25446870 | 9258014 | 99.95% | SRR22028464 |
| Pharynx metastatic resistant JHU029 Larynx primary parental | JHU029P-1 | 32029104 | 9921133 | 99.96% | SRR22028457 |
| JHU029 Larynx primary parental | JHU029P-2 | 25886458 | 12091413 | 99.95% | SRR22028458 |
| JHU029 Larynx primary resistant | JHU029R-1 | 21267200 | 8397834 | 99.87% | SRR22028459 |
| JHU029 Larynx primary resistant | JHU029R-2 | 25049098 | 10108380 | 99.96% | SRR22028465 |

Table S3. Deregulated genes resulting from RNA-seq in the JHU029-R cell line compared to the parental line (JHU029). A total of 85 downregulated genes and 30 upregulated genes were found. Green indicates downregulated genes and orange indicates upregulated genes.

| Sample No. | Gene Code | Gene name | Chromosome |
|------------|-----------------|--|------------|
| 22 | ENSG00000135074 | ADAM metalloproteinase domain 19 | 5 |
| 27 | ENSG00000122644 | ADP ribosylation factor like GTPase 4A | 7 |
| 64 | ENSG00000184254 | aldehyde dehydrogenase 1 family member A3 | 15 |
| 13 | ENSG00000187134 | aldo-keto reductase family 1 member C1 | 10 |
| 14 | ENSG00000151632 | aldo-keto reductase family 1 member C2 | 10 |
| 15 | ENSG00000196139 | aldo-keto reductase family 1 member C3 | 10 |
| 65 | ENSG00000109107 | aldolase, fructose-bisphosphate C | 17 |
| 9 | ENSG00000071073 | alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A | 2 |
| 46 | ENSG00000152766 | ankyrin repeat domain 22 | 10 |
| 40 | ENSG00000165272 | aquaporin 3 (Gill blood group) | 9 |
| 29 | ENSG00000106546 | aryl hydrocarbon receptor | 7 |
| 21 | ENSG00000183876 | arylsulfatase family member I | 5 |
| 41 | ENSG00000165029 | ATP binding cassette subfamily A member 1 | 9 |
| 52 | ENSG00000186318 | beta-secretase 1 | 11 |
| 60 | ENSG00000074410 | carbonic anhydrase 12 | 15 |
| 12 | ENSG00000128510 | carboxypeptidase A4 | 7 |
| 62 | ENSG00000103888 | cell migration inducing hyaluronidase 1 | 15 |
| 5 | ENSG00000143320 | cellular retinoic acid binding protein 2 | 1 |
| 61 | ENSG00000173546 | chondroitin sulfate proteoglycan 4 | 15 |

| | | | |
|----|-----------------|--|-----|
| 26 | ENSG00000166446 | chromodomain Y like 2 | 16 |
| 21 | ENSG00000235162 | chromosome 12 open reading frame 75 | 12 |
| 71 | ENSG00000176659 | chromosome 20 putative open reading frame 197 | 20 |
| 5 | ENSG00000163347 | claudin 1 | 3 |
| 10 | ENSG00000204262 | collagen type V alpha 2 chain | 2 |
| 18 | ENSG00000182326 | complement C1s | 12 |
| 16 | ENSG00000107562 | C-X-C motif chemokine ligand 12 | 10 |
| 8 | ENSG00000145824 | C-X-C motif chemokine ligand 14 | 5 |
| 56 | ENSG00000118971 | cyclin D2 | 12 |
| 32 | ENSG00000173852 | dpy-19 like C-mannosyltransferase 1 | 7 |
| 9 | ENSG00000151914 | dystonin | 6 |
| 14 | ENSG00000182585 | epithelial mitogen | 4 |
| 69 | ENSG00000161671 | ER membrane protein complex subunit 10 | 19 |
| 74 | ENSG00000179083 | family with sequence similarity 133 member A | X |
| 48 | ENSG00000149485 | fatty acid desaturase 1 | 11 |
| 2 | ENSG00000115414 | fibronectin 1 | 2 |
| 33 | ENSG00000132436 | fidgetin like 1 | 7 |
| 3 | ENSG00000168386 | filamin A interacting protein 1 like | 3 |
| 31 | ENSG00000106080 | FKBP prolyl isomerase 14 | 7 |
| 45 | ENSG00000151025 | G protein-coupled receptor 158 | 10 |
| 7 | ENSG00000143891 | galactose mutarotase | 2 |
| | ENSEMBL | GENENAME | CHR |
| | ENSEMBL | GENENAME | CHR |
| 24 | ENSG00000176153 | glutathione peroxidase 2 | 14 |
| 30 | ENSG00000136235 | glycoprotein nmb | 7 |
| 72 | ENSG00000189060 | H1.0 linker histone | 22 |
| 23 | ENSG00000276410 | H2B clustered histone 3 | 6 |
| 25 | ENSG00000274290 | H2B clustered histone 6 | 6 |
| 24 | ENSG00000287080 | H3 clustered histone 3 | 6 |
| 59 | ENSG00000126803 | heat shock protein family A (Hsp70) member 2 | 14 |
| 6 | ENSG00000143341 | hemicentin 1 | 1 |
| 13 | ENSG00000170801 | HtrA serine peptidase 3 | 4 |
| 39 | ENSG00000170961 | hyaluronan synthase 2 | 8 |
| 12 | ENSG00000115457 | insulin like growth factor binding protein 2 | 2 |
| 58 | ENSG00000167779 | insulin like growth factor binding protein 6 | 12 |
| 66 | ENSG00000171401 | keratin 13 | 17 |
| 25 | ENSG00000178573 | MAF bZIP transcription factor | 16 |
| 83 | ENSG00000198681 | MAGE family member A1 | X |
| 81 | ENSG00000213401 | MAGE family member A12 | X |
| 80 | ENSG00000221867 | MAGE family member A3 | X |
| 79 | ENSG00000147381 | MAGE family member A4 | X |
| 29 | ENSG00000099399 | MAGE family member B2 | X |
| 73 | ENSG00000179222 | MAGE family member D1 | X |
| 38 | ENSG00000147676 | mal, T cell differentiation protein 2 | 8 |
| 50 | ENSG00000196611 | matrix metalloproteinase 1 | 11 |
| 54 | ENSG00000076706 | melanoma cell adhesion molecule | 11 |
| 78 | ENSG00000076770 | muscleblind like splicing regulator 3 | X |
| 53 | ENSG00000149573 | myelin protein zero like 2 | 11 |
| 35 | ENSG00000135272 | MyoD family inhibitor domain containing | 7 |
| 11 | ENSG00000228509 | NA | NA |
| 67 | ENSG00000279207 | NA | NA |
| 4 | ENSG00000177551 | nescient helix-loop-helix 2 | 1 |
| 84 | ENSG00000165246 | neuroligin 4 Y-linked | Y |
| 20 | ENSG00000112992 | nicotinamide nucleotide transhydrogenase | 5 |
| 7 | ENSG00000151014 | nocturnin | 4 |
| 22 | ENSG00000074590 | NUAK family kinase 1 | 12 |
| 19 | ENSG00000173391 | oxidized low density lipoprotein receptor 1 | 12 |
| 70 | ENSG00000101417 | peroxisomal membrane protein 4 | 20 |
| 2 | ENSG00000162407 | phospholipid phosphatase 3 | 1 |
| 4 | ENSG00000188313 | phospholipid scramblase 1 | 3 |
| 37 | ENSG00000076641 | phosphoprotein membrane anchor with glycosphingolipid microdomains 1 | 8 |
| 57 | ENSG00000139629 | polypeptide N-acetylgalactosaminyltransferase 6 | 12 |
| 44 | ENSG00000148344 | prostaglandin E synthase | 9 |

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|----|-----------------|---|----|
| 19 | ENSG00000132356 | protein kinase AMP-activated catalytic subunit alpha 1 | 5 |
| 3 | ENSG00000142875 | protein kinase cAMP-activated catalytic subunit beta | 1 |
| 51 | ENSG00000178202 | protein O-glucosyltransferase 3 | 11 |
| 49 | ENSG00000123892 | RAB38, member RAS oncogene family | 11 |
| 17 | ENSG00000039560 | retinoic acid induced 14 | 5 |
| 77 | ENSG00000133135 | ring finger protein 128 | X |
| 23 | ENSG00000278771 | RNA component of signal recognition particle 7SL3 | 14 |
| 1 | ENSG00000143546 | S100 calcium binding protein A8 | 1 |
| 16 | ENSG00000112902 | semaphorin 5A | 5 |
| 17 | ENSG00000150687 | serine protease 23 | 11 |
| 18 | ENSG00000079215 | solute carrier family 1 member 3 | 5 |
| 47 | ENSG00000134802 | solute carrier family 43 member 3 | 11 |
| 6 | ENSG00000151012 | solute carrier family 7 member 11 | 4 |
| 55 | ENSG00000137642 | sortilin related receptor 1 | 11 |
| 34 | ENSG00000157214 | STEAP2 metalloredutase | 7 |
| 15 | ENSG00000145545 | steroid 5 alpha-reductase 1 | 5 |
| 63 | ENSG00000182253 | synemin | 15 |
| 28 | ENSG00000106537 | tetraspanin 13 | 7 |
| 75 | ENSG00000000003 | tetraspanin 6 | X |
| 8 | ENSG00000144115 | threonine synthase like 2 | 2 |
| 1 | ENSG00000186891 | TNF receptor superfamily member 18 | 1 |
| 42 | ENSG00000181634 | TNF superfamily member 15 | 9 |
| 43 | ENSG00000136869 | toll like receptor 4 | 9 |
| 76 | ENSG00000180964 | transcription elongation factor A like 8 | X |
| 26 | ENSG00000106460 | transmembrane protein 106B | 7 |
| 20 | ENSG00000167552 | tubulin alpha 1a | 12 |
| 28 | ENSG00000128294 | tyrosylprotein sulfotransferase 2 | 22 |
| 68 | ENSG00000179913 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3 | 19 |
| 82 | ENSG00000147394 | zinc finger protein 185 with LIM domain | X |
| 27 | ENSG00000197013 | zinc finger protein 429 | 19 |
| 36 | ENSG00000164684 | zinc finger protein 704 | 8 |
| 10 | ENSG00000214652 | zinc finger protein 727 | 7 |
| 11 | ENSG00000234444 | zinc finger protein 736 | 7 |

Table S4. Deregulated genes resulting from RNA-seq in the HTB-43-R cell line compared to the parental line (HTB-43). A total of 392 downregulated genes and 263 upregulated genes were found. Green indicates downregulated genes and orange indicates upregulated genes.

| Sample No. | Gene Code | Gene name | Chromosome |
|------------|-----------------|---|------------|
| 91 | ENSG00000116133 | 24-dehydrocholesterol reductase | 1 |
| 188 | ENSG00000089127 | 2'-5'-oligoadenylate synthetase 1 | 12 |
| 189 | ENSG00000111335 | 2'-5'-oligoadenylate synthetase 2 | 12 |
| 297 | ENSG00000135114 | 2'-5'-oligoadenylate synthetase like | 12 |
| 194 | ENSG00000112972 | 3-hydroxy-3-methylglutaryl-CoA synthase 1 | 5 |
| 66 | ENSG00000186603 | 4-hydroxyphenylpyruvate dioxygenase like | 1 |
| 29 | ENSG00000123836 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1 |
| 21 | ENSG00000143322 | ABL proto-oncogene 2, non-receptor tyrosine kinase | 1 |
| 210 | ENSG00000075624 | actin beta | 7 |
| 261 | ENSG00000169129 | actin filament associated protein 1 like 2 | 10 |
| 22 | ENSG00000162704 | actin related protein 2/3 complex subunit 5 | 1 |
| 348 | ENSG00000072778 | acyl-CoA dehydrogenase very long chain | 17 |
| 86 | ENSG00000151726 | acyl-CoA synthetase long chain family member 1 | 4 |
| 58 | ENSG00000163638 | ADAM metalloproteinase with thrombospondin type 1 motif 9 | 3 |
| 139 | ENSG00000168710 | adenosylhomocysteinase like 1 | 1 |

| | | | |
|-----|-----------------|--|----|
| 99 | ENSG00000162433 | adenylate kinase 4 | 1 |
| 114 | ENSG00000153292 | adhesion G protein-coupled receptor F1 | 6 |
| 206 | ENSG00000112414 | adhesion G protein-coupled receptor G6 | 6 |
| 25 | ENSG00000143862 | ADP ribosylation factor like GTPase 8A | 1 |
| 55 | ENSG00000134108 | ADP ribosylation factor like GTPase 8B | 3 |
| 196 | ENSG00000169252 | adrenoceptor beta 2 | 5 |
| 2 | ENSG00000188157 | agrin | 1 |
| 226 | ENSG00000127914 | A-kinase anchoring protein 9 | 7 |
| 48 | ENSG00000174574 | akirin 1 | 1 |
| 69 | ENSG00000117448 | aldo-keto reductase family 1 member A1 | 1 |
| 166 | ENSG00000151632 | aldo-keto reductase family 1 member C2 | 10 |
| 167 | ENSG00000196139 | aldo-keto reductase family 1 member C3 | 10 |
| 96 | ENSG00000088035 | ALG6 alpha-1,3-glucosyltransferase | 1 |
| 79 | ENSG00000109321 | amphiregulin | 4 |
| 125 | ENSG00000162688 | amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase | 1 |
| 126 | ENSG00000146416 | androgen induced 1 | 6 |
| 45 | ENSG00000174501 | ankyrin repeat domain 36C | 2 |
| 245 | ENSG00000165272 | aquaporin 3 (Gill blood group) | 9 |
| 217 | ENSG00000172379 | aryl hydrocarbon receptor nuclear translocator 2 | 15 |
| 197 | ENSG00000183876 | arylsulfatase family member I | 5 |
| 184 | ENSG00000180801 | arylsulfatase family member J | 4 |
| 159 | ENSG00000165029 | ATP binding cassette subfamily A member 1 | 9 |
| 51 | ENSG00000144452 | ATP binding cassette subfamily A member 12 | 2 |
| 164 | ENSG00000107331 | ATP binding cassette subfamily A member 2 | 9 |
| 36 | ENSG00000130770 | ATP synthase inhibitory factor subunit 1 | 1 |
| 78 | ENSG00000123472 | ATP synthase mitochondrial F1 complex assembly factor 1 | 1 |
| 141 | ENSG00000116459 | ATP synthase peripheral stalk-membrane subunit b | 1 |
| 4 | ENSG00000160072 | ATPase family AAA domain containing 3B | 1 |
| 60 | ENSG00000114573 | ATPase H+ transporting V1 subunit A | 3 |
| 141 | ENSG00000147416 | ATPase H+ transporting V1 subunit B2 | 8 |
| 149 | ENSG00000155097 | ATPase H+ transporting V1 subunit C1 | 8 |
| 3 | ENSG00000175756 | aurora kinase A interacting protein 1 | 1 |
| 332 | ENSG00000066739 | autophagy related 2B | 14 |
| 382 | ENSG00000167601 | AXL receptor tyrosine kinase | 19 |
| 179 | ENSG00000043039 | BARX homeobox 2 | 11 |
| 175 | ENSG00000082153 | basic leucine zipper and W2 domains 1 | 2 |
| 374 | ENSG00000172270 | basigin (Ok blood group) | 19 |
| 337 | ENSG00000169594 | basonuclin 1 | 15 |
| 114 | ENSG00000142867 | BCL10 immune signaling adaptor | 1 |
| 212 | ENSG00000166710 | beta-2-microglobulin | 15 |
| 80 | ENSG00000174808 | betacellulin | 4 |
| 248 | ENSG00000182240 | beta-secretase 2 | 21 |
| 379 | ENSG00000130303 | bone marrow stromal cell antigen 2 | 19 |
| 81 | ENSG00000152785 | bone morphogenetic protein 3 | 4 |
| 188 | ENSG00000176788 | brain abundant membrane attached signal protein 1 | 5 |
| 245 | ENSG00000064787 | brain enriched myelin associated protein 1 | 20 |
| 261 | ENSG00000184515 | brain expressed X-linked 5 | X |
| 131 | ENSG00000164713 | brain protein I3 | 7 |
| 184 | ENSG00000060982 | branched chain amino acid transaminase 1 | 12 |
| 336 | ENSG00000064726 | BTB domain containing 1 | 15 |
| 328 | ENSG00000011114 | BTB domain containing 7 | 14 |
| 136 | ENSG00000143126 | cadherin EGF LAG seven-pass G-type receptor 2 | 1 |
| 220 | ENSG00000103381 | calcineurin like phosphoesterase domain containing 1 | 16 |
| 320 | ENSG00000198668 | calmodulin 1 | 14 |
| 123 | ENSG00000117519 | calponin 3 | 1 |
| 223 | ENSG00000180917 | cap methyltransferase 2 | 16 |
| 142 | ENSG00000116489 | capping actin protein of muscle Z-line subunit alpha 1 | 1 |
| 216 | ENSG00000103811 | cathepsin H | 15 |
| 5 | ENSG00000163131 | cathepsin S | 1 |
| 367 | ENSG00000177469 | caveolae associated protein 1 | 17 |
| 120 | ENSG00000272398 | CD24 molecule | 6 |
| 237 | ENSG00000120217 | CD274 molecule | 9 |
| 30 | ENSG00000196352 | CD55 molecule (Cromer blood group) | 1 |

| | | | |
|-----|-----------------|--|----|
| 241 | ENSG00000086548 | CEA cell adhesion molecule 6 | 19 |
| 58 | ENSG00000117399 | cell division cycle 20 | 1 |
| 18 | ENSG00000070831 | cell division cycle 42 | 1 |
| 116 | ENSG00000142871 | cellular communication network factor 1 | 1 |
| 205 | ENSG00000118523 | cellular communication network factor 2 | 6 |
| 151 | ENSG00000136999 | cellular communication network factor 3 | 8 |
| 244 | ENSG00000044459 | centlein | 9 |
| 62 | ENSG00000047457 | ceruloplasmin | 3 |
| 284 | ENSG00000166226 | chaperonin containing TCP1 subunit 2 | 12 |
| 222 | ENSG00000146731 | chaperonin containing TCP1 subunit 6A | 7 |
| 133 | ENSG00000121940 | chloride channel CLIC like 1 | 1 |
| 29 | ENSG00000169504 | chloride intracellular channel 4 | 1 |
| 258 | ENSG00000171365 | chloride voltage-gated channel 5 | X |
| 103 | ENSG00000153046 | chromodomain Y like | 6 |
| 224 | ENSG00000166446 | chromodomain Y like 2 | 16 |
| 113 | ENSG00000162642 | chromosome 1 open reading frame 52 | 1 |
| 204 | ENSG00000227051 | chromosome 14 open reading frame 132 | 14 |
| 76 | ENSG00000154274 | chromosome 4 open reading frame 19 | 4 |
| 189 | ENSG00000082213 | chromosome 5 open reading frame 22 | 5 |
| 213 | ENSG00000128849 | cingulin like 1 | 15 |
| 323 | ENSG00000165934 | cleavage and polyadenylation specific factor 2 | 14 |
| 314 | ENSG00000198894 | CLOCK interacting pacemaker | 14 |
| 149 | ENSG00000009307 | cold shock domain containing E1 | 1 |
| 373 | ENSG00000183287 | collagen and calcium binding EGF domains 1 | 18 |
| 203 | ENSG00000111799 | collagen type XII alpha 1 chain | 6 |
| 345 | ENSG00000108561 | complement C1q binding protein | 17 |
| 234 | ENSG00000125730 | complement C3 | 19 |
| 358 | ENSG00000141030 | COP9 signalosome subunit 3 | 17 |
| 279 | ENSG00000111481 | COPI coat complex subunit zeta 1 | 12 |
| 386 | ENSG00000214078 | copine 1 | 20 |
| 158 | ENSG00000106789 | coronin 2A | 9 |
| 77 | ENSG00000163739 | C-X-C motif chemokine ligand 1 | 4 |
| 50 | ENSG00000131236 | cyclase associated actin cytoskeleton regulatory protein 1 | 1 |
| 227 | ENSG00000105810 | cyclin dependent kinase 6 | 7 |
| 156 | ENSG00000147883 | cyclin dependent kinase inhibitor 2B | 9 |
| 256 | ENSG00000008086 | cyclin dependent kinase like 5 | X |
| 86 | ENSG00000162377 | cytochrome c oxidase assembly factor 7 (putative) | 1 |
| 293 | ENSG00000136026 | cytoskeleton associated protein 4 | 12 |
| 329 | ENSG00000089737 | DEAD-box helicase 24 | 14 |
| 219 | ENSG00000136271 | DEAD-box helicase 56 | 7 |
| 135 | ENSG00000257093 | DENN domain containing 11 | 7 |
| 102 | ENSG00000024526 | DEP domain containing 1 | 1 |
| 252 | ENSG00000165732 | DExD-box helicase 21 | 10 |
| 330 | ENSG00000100697 | dicer 1, ribonuclease III | 14 |
| 310 | ENSG00000119689 | dihydrolipoamide S-succinyltransferase | 14 |
| 115 | ENSG00000153904 | dimethylarginine dimethylaminohydrolase 1 | 1 |
| 61 | ENSG00000132768 | diphthamide biosynthesis 2 | 1 |
| 129 | ENSG00000117543 | diphthamide biosynthesis 5 | 1 |
| 59 | ENSG00000057019 | discoidin, CUB and LCCL domain containing 2 | 3 |
| 241 | ENSG00000137038 | distal membrane arm assembly complex 1 | 9 |
| 80 | ENSG00000142700 | DMRT like family A2 | 1 |
| 146 | ENSG00000118655 | DNA cross-link repair 1B | 1 |
| 187 | ENSG00000136048 | DNA damage regulated autophagy modulator 1 | 12 |
| 10 | ENSG00000160049 | DNA fragmentation factor subunit alpha | 1 |
| 120 | ENSG00000117505 | down-regulator of transcription 1 | 1 |
| 198 | ENSG00000113758 | drebrin 1 | 5 |
| 36 | ENSG00000143507 | dual specificity phosphatase 10 | 1 |
| 227 | ENSG00000108861 | dual specificity phosphatase 3 | 17 |
| 142 | ENSG00000120875 | dual specificity phosphatase 4 | 8 |
| 307 | ENSG00000119661 | dynein axonemal light chain 1 | 14 |
| 207 | ENSG00000197102 | dynein cytoplasmic 1 heavy chain 1 | 14 |
| 202 | ENSG00000151914 | dystonin | 6 |
| 57 | ENSG00000117395 | EBNA1 binding protein 2 | 1 |

| | | | |
|-----|-----------------|---|-----|
| 79 | ENSG00000159658 | EF-hand calcium binding domain 14 | 1 |
| 13 | ENSG00000142634 | EF-hand domain family member D2 | 1 |
| 165 | ENSG00000115380 | EGF containing fibulin extracellular matrix protein 1 | 2 |
| 24 | ENSG00000011007 | elongin A | 1 |
| 59 | ENSG00000066322 | ELOVL fatty acid elongase 1 | 1 |
| 9 | ENSG00000074800 | enolase 1 | 1 |
| 19 | ENSG00000133216 | EPH receptor B2 | 1 |
| 221 | ENSG00000146648 | epidermal growth factor receptor | 7 |
| 82 | ENSG00000085832 | epidermal growth factor receptor pathway substrate 15 | 1 |
| 78 | ENSG00000124882 | epiregulin | 4 |
| 56 | ENSG00000134109 | ER degradation enhancing alpha-mannosidase like protein 1 | 3 |
| 34 | ENSG00000196482 | estrogen related receptor gamma | 1 |
| 69 | ENSG00000244405 | ETS variant transcription factor 5 | 3 |
| 246 | ENSG00000101210 | eukaryotic translation elongation factor 1 alpha 2 | 20 |
| 46 | ENSG00000084623 | eukaryotic translation initiation factor 3 subunit I | 1 |
| 277 | ENSG00000063046 | eukaryotic translation initiation factor 4B | 12 |
| 349 | ENSG00000132507 | eukaryotic translation initiation factor 5A | 17 |
| 385 | ENSG00000242372 | eukaryotic translation initiation factor 6 | 20 |
| 127 | ENSG00000162694 | exostosin like glycosyltransferase 2 | 1 |
| 20 | ENSG00000116199 | FAM20B glycosaminoglycan xylosylkinase | 1 |
| 208 | ENSG00000177706 | FAM20C golgi associated secretory pathway kinase | 7 |
| 133 | ENSG00000196937 | FAM3 metabolism regulating signaling molecule C | 7 |
| 214 | ENSG00000157470 | family with sequence similarity 81 member A | 15 |
| 152 | ENSG00000147689 | family with sequence similarity 83 member A | 8 |
| 234 | ENSG00000168522 | farnesyltransferase, CAAX box, alpha | 8 |
| 211 | ENSG00000075618 | fascin actin-bundling protein 1 | 7 |
| 265 | ENSG00000149485 | fatty acid desaturase 1 | 11 |
| 309 | ENSG00000119616 | FCF1 rRNA-processing protein | 14 |
| 303 | ENSG00000139926 | FERM domain containing 6 | 14 |
| 124 | ENSG00000156869 | ferric chelate reductase 1 | 1 |
| 267 | ENSG00000172500 | FGF1 intracellular binding protein | 11 |
| 269 | ENSG00000075388 | fibroblast growth factor 4 | 11 |
| 182 | ENSG00000137440 | fibroblast growth factor binding protein 1 | 4 |
| 264 | ENSG00000066468 | fibroblast growth factor receptor 2 | 10 |
| 72 | ENSG00000068078 | fibroblast growth factor receptor 3 | 4 |
| 52 | ENSG00000115414 | fibronectin 1 | 2 |
| 366 | ENSG00000141756 | FKBP prolyl isomerase 10 | 17 |
| 216 | ENSG00000106080 | FKBP prolyl isomerase 14 | 7 |
| 94 | ENSG00000217128 | folliculin interacting protein 1 | 5 |
| 85 | ENSG00000052795 | folliculin interacting protein 2 | 4 |
| 52 | ENSG00000198815 | forkhead box J3 | 1 |
| 100 | ENSG00000164379 | forkhead box Q1 | 6 |
| 211 | ENSG00000248905 | formin 1 | 15 |
| 121 | ENSG00000137942 | formin binding protein 1 like | 1 |
| 313 | ENSG00000170345 | Fos proto-oncogene, AP-1 transcription factor subunit | 14 |
| 253 | ENSG00000196968 | fucosyltransferase 11 | 10 |
| 89 | ENSG00000082074 | FYN binding protein 1 | 5 |
| 122 | ENSG00000111816 | fyn related Src family tyrosine kinase | 6 |
| 132 | ENSG00000121957 | G protein signaling modulator 2 | 1 |
| 138 | ENSG00000065135 | G protein subunit alpha i3 | 1 |
| 41 | ENSG00000116977 | galectin 8 | 1 |
| 154 | ENSG00000196505 | ganglioside induced differentiation associated protein 2 | 1 |
| 204 | ENSG00000152661 | gap junction protein alpha 1 | 6 |
| 1 | ENSG00000189433 | gap junction protein beta 4 | 1 |
| 368 | ENSG00000182963 | gap junction protein gamma 1 | 17 |
| 71 | ENSG00000159592 | GC-rich promoter binding protein 1 like 1 | 1 |
| | ENSEMBL | GENENAME | CHR |
| | ENSEMBL | GENENAME | CHR |
| 231 | ENSG00000147536 | GIN5 complex subunit 4 | 8 |
| 96 | ENSG00000113552 | glucosamine-6-phosphate deaminase 1 | 5 |
| 104 | ENSG00000111846 | glucosaminyl (N-acetyl) transferase 2 (I blood group) | 6 |
| 215 | ENSG00000140297 | glucosaminyl (N-acetyl) transferase 3, mucin type | 15 |
| 11 | ENSG00000177628 | glucosylceramidase beta | 1 |

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| 255 | ENSG00000148672 | glutamate dehydrogenase 1 | 10 |
| 173 | ENSG00000115419 | glutaminase | 2 |
| 296 | ENSG00000257218 | glutamyl-tRNA amidotransferase subunit C | 12 |
| 331 | ENSG00000182512 | glutaredoxin 5 | 14 |
| 143 | ENSG00000104687 | glutathione-disulfide reductase | 8 |
| 82 | ENSG00000138678 | glycerol-3-phosphate acyltransferase 3 | 4 |
| 302 | ENSG00000100504 | glycogen phosphorylase L | 14 |
| 129 | ENSG00000136235 | glycoprotein nmb | 7 |
| 13 | ENSG00000198715 | glycosylated lysosomal membrane protein | 1 |
| 179 | ENSG00000063660 | glypican 1 | 2 |
| 325 | ENSG00000066455 | golgin A5 | 14 |
| 326 | ENSG00000170270 | GON7 subunit of KEOPS complex | 14 |
| 101 | ENSG00000116717 | growth arrest and DNA damage inducible alpha | 1 |
| 238 | ENSG00000130513 | growth differentiation factor 15 | 19 |
| 224 | ENSG00000105793 | GTP binding protein 10 | 7 |
| 157 | ENSG00000119125 | guanine deaminase | 9 |
| 3 | ENSG00000183347 | guanylate binding protein family member 6 | 1 |
| 48 | ENSG00000144366 | GULP PTB domain containing engulfment adaptor 1 | 2 |
| 201 | ENSG00000273703 | H2B clustered histone 14 | 6 |
| 199 | ENSG00000276410 | H2B clustered histone 3 | 6 |
| 200 | ENSG00000276180 | H4 clustered histone 9 | 6 |
| 190 | ENSG00000135116 | harakiri, BCL2 interacting protein | 12 |
| 42 | ENSG00000118960 | HCLS1 binding protein 3 | 2 |
| 192 | ENSG00000152137 | heat shock protein family B (small) member 8 | 12 |
| 174 | ENSG00000144381 | heat shock protein family D (Hsp60) member 1 | 2 |
| 64 | ENSG00000126107 | HECT domain E3 ubiquitin protein ligase 3 | 1 |
| 95 | ENSG00000113070 | heparin binding EGF like growth factor | 5 |
| 17 | ENSG00000127483 | heterochromatin protein 1 binding protein 3 | 1 |
| 22 | ENSG00000125944 | heterogeneous nuclear ribonucleoprotein R | 1 |
| 92 | ENSG00000049860 | hexosaminidase subunit beta | 5 |
| 31 | ENSG00000198830 | high mobility group nucleosomal binding domain 2 | 1 |
| 106 | ENSG00000095951 | HIVEP zinc finger 1 | 6 |
| 125 | ENSG00000010818 | HIVEP zinc finger 2 | 6 |
| 111 | ENSG00000206337 | HLA complex P5 | 6 |
| 97 | ENSG00000113716 | HMG-box containing 3 | 5 |
| 201 | ENSG00000215271 | homeobox and leucine zipper encoding | 14 |
| 233 | ENSG00000168172 | hook microtubule tethering protein 3 | 8 |
| 203 | ENSG00000100644 | hypoxia inducible factor 1 subunit alpha | 14 |
| 50 | ENSG00000030419 | IKAROS family zinc finger 2 | 2 |
| 291 | ENSG00000166130 | IKBKB interacting protein | 12 |
| 151 | ENSG00000143061 | immunoglobulin superfamily member 3 | 1 |
| 23 | ENSG00000117318 | inhibitor of DNA binding 3, HLH protein | 1 |
| 181 | ENSG00000178035 | inosine monophosphate dehydrogenase 2 | 3 |
| 84 | ENSG00000109452 | inositol polyphosphate-4-phosphatase type II B | 4 |
| 369 | ENSG00000159217 | insulin like growth factor 2 mRNA binding protein 1 | 17 |
| 215 | ENSG00000136231 | insulin like growth factor 2 mRNA binding protein 3 | 7 |
| 278 | ENSG00000167779 | insulin like growth factor binding protein 6 | 12 |
| 235 | ENSG00000171105 | insulin receptor | 19 |
| 90 | ENSG00000164171 | integrin subunit alpha 2 | 5 |
| 172 | ENSG00000091409 | integrin subunit alpha 6 | 2 |
| 212 | ENSG00000105855 | integrin subunit beta 8 | 7 |
| 236 | ENSG00000090339 | intercellular adhesion molecule 1 | 19 |
| 111 | ENSG00000137965 | interferon induced protein 44 | 1 |
| 169 | ENSG00000125538 | interleukin 1 beta | 2 |
| 164 | ENSG00000162892 | interleukin 24 | 1 |
| 10 | ENSG00000160712 | interleukin 6 receptor | 1 |
| 73 | ENSG00000197429 | intracisternal A particle-promoted polypeptide | 1 |
| 185 | ENSG00000170561 | iroquois homeobox 2 | 5 |
| 1 | ENSG00000187608 | ISG15 ubiquitin like modifier | 1 |
| 98 | ENSG00000162434 | Janus kinase 1 | 1 |
| 236 | ENSG00000096968 | Janus kinase 2 | 9 |
| 94 | ENSG00000177606 | Jun proto-oncogene, AP-1 transcription factor subunit | 1 |
| 383 | ENSG00000167754 | kallikrein related peptidase 5 | 19 |

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| 384 | ENSG00000167755 | kallikrein related peptidase 6 | 19 |
| 44 | ENSG00000025800 | karyopherin subunit alpha 6 | 1 |
| 167 | ENSG00000114982 | KAT8 regulatory NSL complex subunit 3 | 2 |
| 68 | ENSG00000114796 | kelch like family member 24 | 3 |
| 138 | ENSG00000176595 | kelch repeat and BTB domain containing 11 | 8 |
| 365 | ENSG00000186847 | keratin 14 | 17 |
| 364 | ENSG00000171345 | keratin 19 | 17 |
| 185 | ENSG00000170477 | keratin 4 | 12 |
| 276 | ENSG00000205420 | keratin 6A | 12 |
| 19 | ENSG00000235750 | KIAA0040 | 1 |
| 218 | ENSG00000164542 | KIAA0895 | 7 |
| 11 | ENSG00000116685 | KIAA2013 | 1 |
| 305 | ENSG00000126777 | kinectin 1 | 14 |
| 62 | ENSG00000142945 | kinesin family member 2C | 1 |
| 287 | ENSG00000049130 | KIT ligand | 12 |
| 24 | ENSG00000159166 | ladinin 1 | 1 |
| 250 | ENSG00000133424 | LARGE xylosyl- and glucuronyltransferase 1 | 22 |
| 43 | ENSG00000213626 | LBH regulator of WNT signaling pathway | 2 |
| 324 | ENSG00000100600 | legumain | 14 |
| 103 | ENSG00000066557 | leucine rich repeat containing 40 | 1 |
| 74 | ENSG00000132128 | leucine rich repeat containing 41 | 1 |
| 88 | ENSG00000116212 | leucine rich repeat containing 42 | 1 |
| 21 | ENSG00000169641 | leucine zipper protein 1 | 1 |
| 249 | ENSG00000128342 | LIF interleukin 6 family cytokine | 22 |
| 274 | ENSG00000050405 | LIM domain and actin binding 1 | 12 |
| 70 | ENSG00000145012 | LIM domain containing preferred translocation partner in lipoma | 3 |
| 161 | ENSG00000148346 | lipocalin 2 | 9 |
| 219 | ENSG00000189067 | lipopolysaccharide induced TNF factor | 16 |
| 359 | ENSG00000131899 | LLGL scribble cell polarity complex component 1 | 17 |
| 117 | ENSG00000233237 | long intergenic non-protein coding RNA 472 | 6 |
| 370 | ENSG00000227036 | long intergenic non-protein coding RNA 511 | 17 |
| 380 | ENSG00000261824 | long intergenic non-protein coding RNA 662 | 19 |
| 371 | ENSG00000227036 | long intergenic non-protein coding RNA 673 | 17 |
| 67 | ENSG00000240024 | long intergenic non-protein coding RNA 888 | 3 |
| 153 | ENSG00000168672 | LRAT domain containing 2 | 8 |
| 154 | ENSG00000160932 | lymphocyte antigen 6 family member E | 8 |
| 193 | ENSG00000136167 | lymphocyte cytosolic protein 1 | 13 |
| 20 | ENSG00000004487 | lysine demethylase 1A | 1 |
| 44 | ENSG00000172086 | lysine rich coiled-coil 1 | 2 |
| 32 | ENSG00000123684 | lysophosphatidylglycerol acyltransferase 1 | 1 |
| 26 | ENSG00000011009 | lysophospholipase 2 | 1 |
| 199 | ENSG00000185896 | lysosomal associated membrane protein 1 | 13 |
| 262 | ENSG00000005893 | lysosomal associated membrane protein 2 | X |
| 40 | ENSG00000143669 | lysosomal trafficking regulator | 1 |
| 258 | ENSG00000138131 | lysyl oxidase like 4 | 10 |
| 230 | ENSG00000197063 | MAF bZIP transcription factor G | 17 |
| 110 | ENSG00000234745 | major histocompatibility complex, class I, B | 6 |
| 108 | ENSG00000204642 | major histocompatibility complex, class I, F | 6 |
| 150 | ENSG00000147676 | mal, T cell differentiation protein 2 | 8 |
| 181 | ENSG00000003056 | mannose-6-phosphate receptor, cation dependent | 12 |
| 77 | ENSG00000079277 | MAPK interacting serine/threonine kinase 1 | 1 |
| 177 | ENSG00000196611 | matrix metalloproteinase 1 | 11 |
| 197 | ENSG00000126217 | MCF.2 cell line derived transforming sequence like | 13 |
| 60 | ENSG00000159479 | mediator complex subunit 8 | 1 |
| 144 | ENSG00000081026 | membrane associated guanylate kinase, WW and PDZ domain containing 3 | 1 |
| 132 | ENSG00000105976 | MET proto-oncogene, receptor tyrosine kinase | 7 |
| 340 | ENSG00000169715 | metallothionein 1E | 16 |
| 378 | ENSG00000071655 | methyl-CpG binding domain protein 3 | 19 |
| 37 | ENSG00000154305 | MIA SH3 domain ER export factor 3 | 1 |
| 139 | ENSG00000129422 | microtubule associated scaffold protein 1 | 8 |
| 91 | ENSG00000069020 | microtubule associated serine/threonine kinase family member 4 | 5 |
| 14 | ENSG00000125462 | MIR9-1 host gene | 1 |
| 346 | ENSG00000167842 | MIS12 kinetochore complex component | 17 |

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| 90 | ENSG00000116221 | mitochondrial ribosomal protein L37 | 1 |
| 259 | ENSG00000055950 | mitochondrial ribosomal protein L43 | 10 |
| 12 | ENSG00000116688 | mitofusin 2 | 1 |
| 304 | ENSG00000168175 | mitogen-activated protein kinase 1 interacting protein 1 like | 14 |
| 308 | ENSG00000156030 | mitotic deacetylase associated SANT domain protein | 14 |
| 375 | ENSG00000099812 | mitotic spindle positioning | 19 |
| 208 | ENSG00000080823 | MOK protein kinase | 14 |
| 16 | ENSG00000053372 | MRT4 homolog, ribosome maturation factor | 1 |
| 2 | ENSG00000055732 | mucolipin 3 | 1 |
| 93 | ENSG00000162601 | Myb like, SWIRM and MPN domains 1 | 1 |
| 47 | ENSG00000214114 | MYC binding protein | 1 |
| 361 | ENSG00000278259 | myosin XIX | 17 |
| 102 | ENSG00000260604 | NA | NA |
| 88 | ENSG00000248370 | NA | NA |
| 195 | ENSG00000275989 | NA | NA |
| 196 | ENSG00000225760 | NA | NA |
| 198 | ENSG00000235280 | NA | NA |
| 225 | ENSG00000263934 | NA | NA |
| 56 | ENSG00000228192 | NA | NA |
| 162 | ENSG00000275131 | NA | NA |
| 249 | ENSG00000273760 | NA | NA |
| 355 | ENSG00000179277 | NA | NA |
| 356 | ENSG00000276855 | NA | NA |
| 388 | ENSG00000198618 | NA | NA |
| 392 | ENSG00000210196 | NA | NA |
| 140 | ENSG00000104763 | N-acylsphingosine amidohydrolase 1 | 8 |
| 83 | ENSG00000078618 | nardilysin convertase | 1 |
| 282 | ENSG00000196531 | nascent polypeptide associated complex subunit alpha | 12 |
| 87 | ENSG00000058804 | NDC1 transmembrane nucleoporin | 1 |
| 16 | ENSG00000143217 | nectin cell adhesion molecule 4 | 1 |
| 98 | ENSG00000145911 | NEDD4 binding protein 3 | 5 |
| 352 | ENSG00000065320 | netrin 1 | 17 |
| 105 | ENSG00000111859 | neural precursor cell expressed, developmentally down-regulated 9 | 6 |
| 112 | ENSG00000204386 | neuraminidase 1 | 6 |
| 163 | ENSG00000107130 | neuronal calcium sensor 1 | 9 |
| 163 | ENSG00000135842 | niban apoptosis regulator 1 | 1 |
| 160 | ENSG00000136830 | niban apoptosis regulator 2 | 9 |
| 311 | ENSG00000119638 | NIMA related kinase 9 | 14 |
| 148 | ENSG00000104361 | NIPA like domain containing 2 | 8 |
| 136 | ENSG00000164867 | nitric oxide synthase 3 | 7 |
| 169 | ENSG00000229544 | NK1 homeobox 2 | 10 |
| 221 | ENSG00000140853 | NLR family CARD domain containing 5 | 16 |
| 347 | ENSG00000091592 | NLR family pyrin domain containing 1 | 17 |
| 218 | ENSG00000103202 | NME/NM23 nucleoside diphosphate kinase 4 | 16 |
| 186 | ENSG00000037474 | NOP2/Sun RNA methyltransferase 2 | 5 |
| 76 | ENSG00000117481 | NOP2/Sun RNA methyltransferase 4 | 1 |
| 160 | ENSG00000134250 | notch receptor 2 | 1 |
| 148 | ENSG00000213281 | NRAS proto-oncogene, GTPase | 1 |
| 319 | ENSG00000119720 | NRDE-2, necessary for RNA interference, domain containing | 14 |
| 70 | ENSG00000132780 | nuclear autoantigenic sperm protein | 1 |
| 243 | ENSG00000124151 | nuclear receptor coactivator 3 | 20 |
| 123 | ENSG00000111912 | nuclear receptor coactivator 7 | 6 |
| 93 | ENSG00000175745 | nuclear receptor subfamily 2 group F member 1 | 5 |
| 281 | ENSG00000139579 | nucleic acid binding protein 2 | 12 |
| 260 | ENSG00000166197 | nucleolar and coiled-body phosphoprotein 1 | 10 |
| 7 | ENSG00000162408 | nucleolar protein 9 | 1 |
| 260 | ENSG00000186462 | nucleosome assembly protein 1 like 2 | X |
| 251 | ENSG00000226328 | NUP50 divergent transcript | 22 |
| 178 | ENSG00000124006 | obscurin like cytoskeletal adaptor 1 | 2 |
| 84 | ENSG00000085840 | origin recognition complex subunit 1 | 1 |
| 176 | ENSG00000115942 | origin recognition complex subunit 2 | 2 |
| 121 | ENSG00000081087 | osteoclastogenesis associated transmembrane protein 1 | 6 |
| 146 | ENSG00000164823 | oxidative stress induced growth inhibitor family member 2 | 8 |

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| 182 | ENSG00000173391 | oxidized low density lipoprotein receptor 1 | 12 |
| 228 | ENSG00000242265 | paternally expressed 10 | 7 |
| 243 | ENSG00000164985 | PC4 and SFRS1 interacting protein 1 | 9 |
| 257 | ENSG00000107438 | PDZ and LIM domain 1 | 10 |
| 43 | ENSG00000162517 | penta-EF-hand domain containing 1 | 1 |
| 220 | ENSG00000196262 | peptidylprolyl isomerase A | 7 |
| 68 | ENSG00000117450 | peroxiredoxin 1 | 1 |
| 263 | ENSG00000165672 | peroxiredoxin 3 | 10 |
| 252 | ENSG00000186951 | peroxisome proliferator activated receptor alpha | 22 |
| 299 | ENSG00000247077 | PGAM family member 5, mitochondrial serine/threonine protein phosphatase | 12 |
| 391 | ENSG00000177096 | PH domain containing endocytic trafficking adaptor 2 | 22 |
| 108 | ENSG00000142892 | phosphatidylinositol glycan anchor biosynthesis class K | 1 |
| 362 | ENSG00000276293 | phosphatidylinositol-5-phosphate 4-kinase type 2 beta | 17 |
| 210 | ENSG00000179364 | phosphofurin acidic cluster sorting protein 2 | 14 |
| 97 | ENSG00000079739 | phosphoglucosyltransferase 1 | 1 |
| 159 | ENSG00000092621 | phosphoglycerate dehydrogenase | 1 |
| 53 | ENSG00000127125 | phosphopantotheneoylcysteine synthetase | 1 |
| 253 | ENSG00000198355 | Pim-3 proto-oncogene, serine/threonine kinase | 22 |
| 25 | ENSG00000057757 | PITH domain containing 1 | 1 |
| 207 | ENSG00000118495 | PLAG1 like zinc finger 1 | 6 |
| 209 | ENSG00000197461 | platelet derived growth factor subunit A | 7 |
| 240 | ENSG00000166289 | pleckstrin homology and FYVE domain containing 1 | 19 |
| 306 | ENSG00000126822 | pleckstrin homology and RhoGEF domain containing G3 | 14 |
| 186 | ENSG00000139289 | pleckstrin homology like domain family A member 1 | 12 |
| 17 | ENSG00000143157 | pogo transposable element derived with KRAB domain | 1 |
| 333 | ENSG00000090060 | poly(A) polymerase alpha | 14 |
| 28 | ENSG00000162896 | polymeric immunoglobulin receptor | 1 |
| 47 | ENSG00000136542 | polypeptide N-acetylgalactosaminyltransferase 5 | 2 |
| 275 | ENSG00000139629 | polypeptide N-acetylgalactosaminyltransferase 6 | 12 |
| 390 | ENSG00000157551 | potassium inwardly rectifying channel subfamily J member 15 | 21 |
| 85 | ENSG00000134748 | pre-mRNA processing factor 38A | 1 |
| 131 | ENSG00000134186 | pre-mRNA processing factor 38B | 1 |
| 285 | ENSG00000177425 | pro-apoptotic WT1 regulator | 12 |
| 344 | ENSG00000108518 | profilin 1 | 17 |
| 15 | ENSG00000162734 | proliferation and apoptosis adaptor protein 15 | 1 |
| 137 | ENSG00000134222 | proline and serine rich coiled-coil 1 | 1 |
| 27 | ENSG00000189266 | proline rich nuclear receptor coactivator 2 | 1 |
| 55 | ENSG00000117385 | prolyl 3-hydroxylase 1 | 1 |
| 92 | ENSG00000169174 | proprotein convertase subtilisin/kexin type 9 | 1 |
| 162 | ENSG00000148344 | prostaglandin E synthase | 9 |
| 152 | ENSG00000134247 | prostaglandin F2 receptor inhibitor | 1 |
| 247 | ENSG00000095303 | prostaglandin-endoperoxide synthase 1 | 9 |
| 343 | ENSG00000142507 | proteasome 20S subunit beta 6 | 17 |
| 318 | ENSG00000100764 | proteasome 26S subunit, ATPase 1 | 14 |
| 112 | ENSG00000142875 | protein kinase cAMP-activated catalytic subunit beta | 1 |
| 180 | ENSG00000114302 | protein kinase cAMP-dependent type II regulatory subunit alpha | 3 |
| 235 | ENSG00000185900 | protein O-mannose kinase | 8 |
| 26 | ENSG00000077157 | protein phosphatase 1 regulatory subunit 12B | 1 |
| 256 | ENSG00000119938 | protein phosphatase 1 regulatory subunit 3C | 10 |
| 34 | ENSG00000117751 | protein phosphatase 1 regulatory subunit 8 | 1 |
| 33 | ENSG00000066027 | protein phosphatase 2 regulatory subunit B'alpha | 1 |
| 206 | ENSG00000078304 | protein phosphatase 2 regulatory subunit B'gamma | 14 |
| 321 | ENSG00000100796 | protein phosphatase 4 regulatory subunit 3A | 14 |
| 124 | ENSG00000152894 | protein tyrosine phosphatase receptor type K | 6 |
| 271 | ENSG00000129317 | pseudouridine synthase 7 like | 12 |
| 257 | ENSG00000067992 | pyruvate dehydrogenase kinase 3 | X |
| 147 | ENSG00000164951 | pyruvate dehydrogenase phosphatase catalytic subunit 1 | 8 |
| 107 | ENSG00000137955 | Rab geranylgeranyltransferase subunit beta | 1 |
| 27 | ENSG00000117280 | RAB29, member RAS oncogene family | 1 |
| 372 | ENSG00000168461 | RAB31, member RAS oncogene family | 18 |
| 61 | ENSG00000075785 | RAB7A, member RAS oncogene family | 3 |
| 255 | ENSG00000123595 | RAB9A, member RAS oncogene family | X |
| 18 | ENSG00000227373 | RABGAP1L divergent transcript | 1 |

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| 239 | ENSG00000137040 | RAN binding protein 6 | 9 |
| 298 | ENSG00000132341 | RAN, member RAS oncogene family | 12 |
| 268 | ENSG00000173156 | ras homolog family member D | 11 |
| 137 | ENSG00000106615 | Ras homolog, mTORC1 binding | 7 |
| 170 | ENSG00000144118 | RAS like proto-oncogene B | 2 |
| 12 | ENSG00000143622 | Ras like without CAAX 1 | 1 |
| 119 | ENSG00000025039 | Ras related GTP binding D | 6 |
| 118 | ENSG00000213516 | RBMX like 1 | 1 |
| 194 | ENSG00000136144 | RCC1 and BTB domain containing protein 1 | 13 |
| 341 | ENSG00000183688 | refilin B | 17 |
| 37 | ENSG00000180198 | regulator of chromosome condensation 1 | 1 |
| 15 | ENSG00000179051 | regulator of chromosome condensation 2 | 1 |
| 73 | ENSG00000159788 | regulator of G protein signaling 12 | 4 |
| 35 | ENSG00000117748 | replication protein A2 | 1 |
| 5 | ENSG00000157916 | retention in endoplasmic reticulum sorting receptor 1 | 1 |
| 65 | ENSG00000118849 | retinoic acid receptor responder 1 | 3 |
| 122 | ENSG00000137962 | Rho GTPase activating protein 29 | 1 |
| 166 | ENSG00000114993 | rhotekin | 2 |
| 200 | ENSG00000165799 | ribonuclease A family member 7 | 14 |
| 363 | ENSG00000108298 | ribosomal protein L19 | 17 |
| 6 | ENSG00000116251 | ribosomal protein L22 | 1 |
| 193 | ENSG00000145592 | ribosomal protein L37 | 5 |
| 280 | ENSG00000229117 | ribosomal protein L41 | 12 |
| 295 | ENSG000000089157 | ribosomal protein lateral stalk subunit P0 | 12 |
| 377 | ENSG00000115268 | ribosomal protein S15 | 19 |
| 63 | ENSG00000142937 | ribosomal protein S8 | 1 |
| 238 | ENSG00000107036 | RIC1 homolog, RAB6A GEF complex partner 1 | 9 |
| 81 | ENSG00000123091 | ring finger protein 11 | 1 |
| 171 | ENSG00000153250 | RNA binding motif single stranded interacting protein 1 | 2 |
| 350 | ENSG00000181222 | RNA polymerase II subunit A | 17 |
| 145 | ENSG000000081019 | round spermatid basic protein 1 | 1 |
| 9 | ENSG00000197956 | S100 calcium binding protein A6 | 1 |
| 8 | ENSG00000163220 | S100 calcium binding protein A9 | 1 |
| 74 | ENSG00000163993 | S100 calcium binding protein P | 4 |
| 161 | ENSG00000265808 | SEC22 homolog B, vesicle trafficking protein | 1 |
| 242 | ENSG00000124107 | secretory leukocyte peptidase inhibitor | 20 |
| 75 | ENSG000000091490 | SEL1L family member 3 | 4 |
| 223 | ENSG000000075213 | semaphorin 3A | 7 |
| 217 | ENSG00000122545 | septin 7 | 7 |
| 99 | ENSG00000161011 | sequestosome 1 | 5 |
| 28 | ENSG00000188529 | serine and arginine rich splicing factor 10 | 1 |
| 104 | ENSG00000116754 | serine and arginine rich splicing factor 11 | 1 |
| 40 | ENSG00000116350 | serine and arginine rich splicing factor 4 | 1 |
| 270 | ENSG00000150687 | serine protease 23 | 11 |
| 376 | ENSG00000118046 | serine/threonine kinase 11 | 19 |
| 101 | ENSG00000170542 | serpin family B member 9 | 6 |
| 100 | ENSG00000142864 | SERPINE1 mRNA binding protein 1 | 1 |
| 31 | ENSG000000082497 | SERTA domain containing 4 | 1 |
| 135 | ENSG000000031698 | seryl-tRNA synthetase 1 | 1 |
| 205 | ENSG00000183576 | SET domain containing 3, actin histidine methyltransferase | 14 |
| 262 | ENSG00000187164 | shootin 1 | 10 |
| 283 | ENSG00000166888 | signal transducer and activator of transcription 6 | 12 |
| 266 | ENSG00000213445 | signal-induced proliferation-associated 1 | 11 |
| 113 | ENSG00000186577 | small integral membrane protein 29 | 6 |
| 41 | ENSG000000060688 | small nuclear ribonucleoprotein U5 subunit 40 | 1 |
| 242 | ENSG00000164975 | small nuclear RNA activating complex polypeptide 3 | 9 |
| 214 | ENSG00000228649 | small nucleolar RNA host gene 26 | 7 |
| 357 | ENSG00000175061 | small nucleolar RNA host gene 29 | 17 |
| 38 | ENSG00000242125 | small nucleolar RNA host gene 3 | 1 |
| 39 | ENSG00000200087 | small nucleolar RNA, H/ACA box 73B | 1 |
| 192 | ENSG00000079215 | solute carrier family 1 member 3 | 5 |
| 143 | ENSG00000155380 | solute carrier family 16 member 1 | 1 |
| 180 | ENSG000000059804 | solute carrier family 2 member 3 | 12 |

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| 202 | ENSG00000183032 | solute carrier family 25 member 21 | 14 |
| 290 | ENSG00000075415 | solute carrier family 25 member 3 | 12 |
| 128 | ENSG00000162695 | solute carrier family 30 member 7 | 1 |
| 126 | ENSG00000117620 | solute carrier family 35 member A3 | 1 |
| 106 | ENSG00000137968 | solute carrier family 44 member 5 | 1 |
| 389 | ENSG00000198743 | solute carrier family 5 member 3 | 21 |
| 57 | ENSG00000131389 | solute carrier family 6 member 6 | 3 |
| 83 | ENSG00000151012 | solute carrier family 7 member 11 | 4 |
| 230 | ENSG00000120896 | sorbin and SH3 domain containing 3 | 8 |
| 168 | ENSG00000198142 | sosondowah ankyrin repeat domain family member C | 2 |
| 229 | ENSG00000008294 | sperm associated antigen 9 | 17 |
| 191 | ENSG00000145604 | S-phase kinase associated protein 2 | 5 |
| 232 | ENSG00000134278 | spire type actin nucleation factor 1 | 18 |
| 30 | ENSG00000117632 | stathmin 1 | 1 |
| 247 | ENSG00000197457 | stathmin 3 | 20 |
| 130 | ENSG00000127954 | STEAP4 metalloredutase | 7 |
| 187 | ENSG00000145545 | steroid 5 alpha-reductase 1 | 5 |
| 246 | ENSG00000148175 | stomatin | 9 |
| 315 | ENSG00000140022 | stonin 2 | 14 |
| 32 | ENSG00000175793 | stratifin | 1 |
| 190 | ENSG00000113387 | SUB1 regulator of transcription | 5 |
| 387 | ENSG00000196562 | sulfatase 2 | 20 |
| 53 | ENSG00000144455 | sulfatase modifying factor 1 | 3 |
| 288 | ENSG00000120833 | suppressor of cytokine signaling 2 | 12 |
| 14 | ENSG00000055070 | SUZ RNA binding domain containing 1 | 1 |
| 176 | ENSG00000137501 | synaptotagmin like 2 | 11 |
| 171 | ENSG00000166900 | syntaxin 3 | 11 |
| 353 | ENSG00000133028 | synthesis of cytochrome C oxidase 1 | 17 |
| 67 | ENSG00000132773 | target of EGR1, exonuclease | 1 |
| 134 | ENSG00000197780 | TATA-box binding protein associated factor 13 | 1 |
| 45 | ENSG00000084652 | taxilin alpha | 1 |
| 66 | ENSG00000177565 | TBL1X receptor 1 | 3 |
| 254 | ENSG00000108219 | tetraspanin 14 | 10 |
| 183 | ENSG00000168785 | tetraspanin 5 | 4 |
| 316 | ENSG00000165533 | tetratricopeptide repeat domain 8 | 14 |
| 231 | ENSG00000177426 | TGFB induced factor homeobox 1 | 18 |
| 175 | ENSG00000137492 | THAP domain containing 12 | 11 |
| 4 | ENSG000000265972 | thioredoxin interacting protein | 1 |
| 335 | ENSG00000137801 | thrombospondin 1 | 15 |
| 128 | ENSG00000005108 | thrombospondin type 1 domain containing 7A | 7 |
| 292 | ENSG00000139372 | thymine DNA glycosylase | 12 |
| 254 | ENSG00000205542 | thymosin beta 4 X-linked | X |
| 322 | ENSG00000100815 | thyroid hormone receptor interactor 11 | 14 |
| 233 | ENSG00000223573 | TINCR ubiquitin domain containing | 19 |
| 209 | ENSG00000185215 | TNF alpha induced protein 2 | 14 |
| 115 | ENSG00000146072 | TNF receptor superfamily member 21 | 6 |
| 170 | ENSG00000078902 | toll interacting protein | 11 |
| 89 | ENSG00000116205 | transcription elongation factor A N-terminal and central domain containing 2 | 1 |
| 251 | ENSG00000108064 | transcription factor A, mitochondrial | 10 |
| 153 | ENSG00000116830 | transcription termination factor 2 | 1 |
| 228 | ENSG00000141232 | transducer of ERBB2, 1 | 17 |
| 35 | ENSG00000092969 | transforming growth factor beta 2 | 1 |
| 195 | ENSG00000120708 | transforming growth factor beta induced | 5 |
| 360 | ENSG00000171928 | trans-golgi network vesicle protein 23 homolog B | 17 |
| 39 | ENSG00000173726 | translocase of outer mitochondrial membrane 20 | 1 |
| 213 | ENSG00000196683 | translocase of outer mitochondrial membrane 7 | 7 |
| 63 | ENSG00000169908 | transmembrane 4 L six family member 1 | 3 |
| 289 | ENSG00000057704 | transmembrane and coiled-coil domain family 3 | 12 |
| 286 | ENSG00000139324 | transmembrane O-mannosyltransferase targeting cadherins 3 | 12 |
| 312 | ENSG00000170348 | transmembrane p24 trafficking protein 10 | 14 |
| 71 | ENSG00000168936 | transmembrane protein 129, E3 ubiquitin ligase | 4 |
| 172 | ENSG00000006118 | transmembrane protein 132A | 11 |
| 173 | ENSG00000179292 | transmembrane protein 151A | 11 |

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|-----|-----------------|---|----|
| 294 | ENSG00000151135 | transmembrane protein 263 | 12 |
| 183 | ENSG00000165685 | transmembrane protein 52B | 12 |
| 72 | ENSG00000159596 | transmembrane protein 69 | 1 |
| 178 | ENSG00000137648 | transmembrane serine protease 4 | 11 |
| 7 | ENSG00000182898 | trichohyalin like 1 | 1 |
| 354 | ENSG00000221926 | tripartite motif containing 16 | 17 |
| 109 | ENSG00000204616 | tripartite motif containing 31 | 6 |
| 147 | ENSG00000197323 | tripartite motif containing 33 | 1 |
| 87 | ENSG00000179046 | tripartite motif family like 2 | 4 |
| 49 | ENSG00000043514 | tRNA isopentenyltransferase 1 | 1 |
| 23 | ENSG00000198860 | tRNA splicing endonuclease subunit 15 | 1 |
| 105 | ENSG00000162623 | tRNA-yW synthesizing protein 3 homolog | 1 |
| 156 | ENSG00000116874 | tryptophanyl tRNA synthetase 2, mitochondrial | 1 |
| 301 | ENSG00000102804 | TSC22 domain family member 1 | 13 |
| 127 | ENSG00000130338 | TUB like protein 4 | 6 |
| 273 | ENSG00000123416 | tubulin alpha 1b | 12 |
| 42 | ENSG00000142910 | tubulointerstitial nephritis antigen like 1 | 1 |
| 351 | ENSG00000141510 | tumor protein p53 | 17 |
| 272 | ENSG00000151239 | twinfilin actin binding protein 1 | 12 |
| 317 | ENSG00000042088 | tyrosyl-DNA phosphodiesterase 1 | 14 |
| 75 | ENSG00000173660 | ubiquinol-cytochrome c reductase hinge protein | 1 |
| 342 | ENSG00000132388 | ubiquitin conjugating enzyme E2 G1 | 17 |
| 339 | ENSG00000103353 | ubiquitin family domain containing 1 | 16 |
| 240 | ENSG00000147854 | ubiquitin like with PHD and ring finger domains 2 | 9 |
| 327 | ENSG00000012963 | ubiquitin protein ligase E3 component n-recognin 7 | 14 |
| 95 | ENSG00000162607 | ubiquitin specific peptidase 1 | 1 |
| 110 | ENSG00000077254 | ubiquitin specific peptidase 33 | 1 |
| 237 | ENSG00000179913 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3 | 19 |
| 165 | ENSG00000197355 | UDP-N-acetylglucosamine pyrophosphorylase 1 like 1 | 9 |
| 338 | ENSG00000140553 | unc-45 myosin chaperone A | 15 |
| 54 | ENSG00000144455 | uncharacterized LOC100130207 | 3 |
| 144 | ENSG00000237807 | uncharacterized LOC100507516 | 8 |
| 116 | ENSG00000231683 | uncharacterized LOC101927136 | 6 |
| 381 | ENSG00000267575 | uncharacterized LOC101927151 | 19 |
| 225 | ENSG00000105793 | uncharacterized LOC101927446 | 7 |
| 46 | ENSG00000286081 | uncharacterized LOC105373682 | 2 |
| 49 | ENSG00000233654 | uncharacterized LOC105376748 | 2 |
| 65 | ENSG00000126088 | uroporphyrinogen decarboxylase | 1 |
| 174 | ENSG00000198382 | UV radiation resistance associated | 11 |
| 150 | ENSG00000173218 | VANGL planar cell polarity protein 1 | 1 |
| 130 | ENSG00000134215 | vav guanine nucleotide exchange factor 3 | 1 |
| 64 | ENSG00000197415 | ventricular zone expressed PH domain containing 1 | 3 |
| 226 | ENSG00000108828 | vesicle amine transport 1 | 17 |
| 8 | ENSG00000049245 | vesicle associated membrane protein 3 | 1 |
| 263 | ENSG00000102243 | vestigial like family member 1 | X |
| 232 | ENSG00000078668 | voltage dependent anion channel 3 | 8 |
| 334 | ENSG00000100749 | VRK serine/threonine kinase 1 | 14 |
| 157 | ENSG00000231365 | WARS2 antisense RNA 1 | 1 |
| 33 | ENSG00000158195 | WASP family member 2 | 1 |
| 191 | ENSG00000176871 | WD repeat and SOCS box containing 2 | 12 |
| 177 | ENSG00000138442 | WD repeat domain 12 | 2 |
| 155 | ENSG00000065183 | WD repeat domain 3 | 1 |
| 140 | ENSG00000116455 | WD repeat domain 77 | 1 |
| 38 | ENSG00000143816 | Wnt family member 9A | 1 |
| 54 | ENSG00000065978 | Y-box binding protein 1 | 1 |
| 259 | ENSG00000181704 | Yip1 domain family member 6 | X |
| 222 | ENSG00000184939 | ZFP90 zinc finger protein | 16 |
| 229 | ENSG00000105939 | zinc finger CCCH-type containing, antiviral 1 | 7 |
| 117 | ENSG00000117174 | zinc finger HIT-type containing 6 | 1 |
| 107 | ENSG00000197279 | zinc finger protein 165 | 6 |
| 244 | ENSG00000171940 | zinc finger protein 217 | 20 |
| 155 | ENSG00000196922 | zinc finger protein 252, pseudogene | 8 |
| 300 | ENSG00000090612 | zinc finger protein 268 | 12 |

| | | | |
|----------------|-----------------|--------------------------------------|----|
| 118 | ENSG00000188994 | zinc finger protein 292 | 6 |
| 248 | ENSG00000265763 | zinc finger protein 488 | 10 |
| 119 | ENSG00000122482 | zinc finger protein 644 | 1 |
| 6 | ENSG00000143373 | zinc finger protein 687 | 1 |
| 158 | ENSG00000143067 | zinc finger protein 697 | 1 |
| 145 | ENSG00000164684 | zinc finger protein 704 | 8 |
| 134 | ENSG00000048405 | zinc finger protein 800 | 7 |
| 168 | ENSG00000215146 | zinc finger protein 91 pseudogene | 10 |
| 239 | ENSG00000184635 | zinc finger protein 93 | 19 |
| 109 | ENSG00000036549 | zinc finger ZZ-type containing 3 | 1 |
| 51 | ENSG00000084073 | zinc metalloproteinase STE24 | 1 |
| 250 | ENSG00000122952 | ZW10 interacting kinetochore protein | 10 |
| Upregulated | | | |
| Downregulated: | | | |

Table S5. Deregulated genes resulting from RNA-seq in the CCL-138-R cell line compared to the parental line (CCL-138). A total of 68 downregulated genes and 154 upregulated genes were found. Green indicates downregulated genes and orange indicates upregulated genes.

| Sample No. | Gene Code | Gene name | Chromosome |
|------------|-----------------|--|------------|
| 102 | ENSG00000089127 | 2'-5'-oligoadenylate synthetase 1 | 12 |
| 104 | ENSG00000111335 | 2'-5'-oligoadenylate synthetase 2 | 12 |
| 103 | ENSG00000111331 | 2'-5'-oligoadenylate synthetase 3 | 12 |
| 105 | ENSG00000135114 | 2'-5'-oligoadenylate synthetase like | 12 |
| 63 | ENSG00000140350 | acidic nuclear phosphoprotein 32 family member A | 15 |
| 42 | ENSG00000169067 | actin beta like 2 | 5 |
| 58 | ENSG00000153294 | adhesion G protein-coupled receptor F4 | 6 |
| 18 | ENSG00000071073 | alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A | 2 |
| 125 | ENSG00000141279 | aminopeptidase puromycin sensitive | 17 |
| 92 | ENSG00000166016 | ankyrin repeat and BTB domain containing 2 | 11 |
| 135 | ENSG00000130203 | apolipoprotein E | 19 |
| 149 | ENSG00000100342 | apolipoprotein L1 | 22 |
| 12 | ENSG00000180801 | arylsulfatase family member J | 4 |
| 4 | ENSG00000066279 | assembly factor for spindle microtubules | 1 |
| 66 | ENSG00000152234 | ATP synthase F1 subunit alpha | 18 |
| 24 | ENSG00000144476 | atypical chemokine receptor 3 | 2 |
| 97 | ENSG00000023445 | baculoviral IAP repeat containing 3 | 11 |
| 95 | ENSG00000168062 | basic leucine zipper ATF-like transcription factor 2 | 11 |
| 71 | ENSG00000172331 | bisphosphoglycerate mutase | 7 |
| 134 | ENSG00000130303 | bone marrow stromal cell antigen 2 | 19 |
| 136 | ENSG00000125845 | bone morphogenetic protein 2 | 20 |
| 141 | ENSG00000064787 | brain enriched myelin associated protein 1 | 20 |
| 56 | ENSG00000060982 | branched chain amino acid transaminase 1 | 12 |
| 16 | ENSG00000113361 | cadherin 6 | 5 |
| 41 | ENSG00000151882 | C-C motif chemokine ligand 28 | 5 |
| 60 | ENSG00000272398 | CD24 molecule | 6 |
| 45 | ENSG00000019582 | CD74 molecule | 5 |
| 1 | ENSG00000117399 | cell division cycle 20 | 1 |
| 5 | ENSG00000117724 | centromere protein F | 1 |
| 58 | ENSG00000151849 | centromere protein J | 13 |
| 15 | ENSG00000150753 | chaperonin containing TCP1 subunit 5 | 5 |
| 154 | ENSG00000155962 | chloride intracellular channel 2 | X |
| 57 | ENSG00000112782 | chloride intracellular channel 5 | 6 |
| 54 | ENSG00000243649 | complement factor B | 6 |

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|-----|-----------------|--|-----|
| 80 | ENSG00000048740 | CUGBP Elav-like family member 2 | 10 |
| 34 | ENSG00000169245 | C-X-C motif chemokine ligand 10 | 4 |
| 35 | ENSG00000169248 | C-X-C motif chemokine ligand 11 | 4 |
| 18 | ENSG00000134057 | cyclin B1 | 5 |
| 13 | ENSG00000134326 | cytidine/uridine monophosphate kinase 2 | 2 |
| 52 | ENSG00000006634 | DBF4 zinc finger | 7 |
| 39 | ENSG00000181381 | DExD/H-box 60 like | 4 |
| 38 | ENSG00000137628 | DExD/H-box helicase 60 | 4 |
| 37 | ENSG00000070190 | dual adaptor of phosphotyrosine and 3-phosphoinositides 1 | 4 |
| 12 | ENSG00000143507 | dual specificity phosphatase 10 | 1 |
| 7 | ENSG00000115380 | EGF containing fibulin extracellular matrix protein 1 | 2 |
| 111 | ENSG00000129521 | egl-9 family hypoxia inducible factor 3 | 14 |
| 47 | ENSG00000078401 | endothelin 1 | 6 |
| 16 | ENSG00000055332 | eukaryotic translation initiation factor 2 alpha kinase 2 | 2 |
| 23 | ENSG00000115414 | fibronectin 1 | 2 |
| 113 | ENSG00000185070 | fibronectin leucine rich transmembrane protein 2 | 14 |
| 137 | ENSG00000125848 | fibronectin leucine rich transmembrane protein 3 | 20 |
| 40 | ENSG00000082074 | FYN binding protein 1 | 5 |
| 130 | ENSG00000108679 | galectin 3 binding protein | 17 |
| | ENSEMBL | GENENAME | CHR |
| | ENSEMBL | GENENAME | CHR |
| 54 | ENSG00000148672 | glutamate dehydrogenase 1 | 10 |
| 43 | ENSG00000173221 | glutaredoxin | 5 |
| 65 | ENSG00000136235 | glycoprotein nmb | 7 |
| 124 | ENSG00000030582 | granulin precursor | 17 |
| 8 | ENSG00000117228 | guanylate binding protein 1 | 1 |
| 26 | ENSG00000187837 | H1.2 linker histone, cluster member | 6 |
| 32 | ENSG00000124575 | H1.3 linker histone, cluster member | 6 |
| 28 | ENSG00000168298 | H1.4 linker histone, cluster member | 6 |
| 48 | ENSG00000184357 | H1.5 linker histone, cluster member | 6 |
| 38 | ENSG00000196787 | H2A clustered histone 11 | 6 |
| 40 | ENSG00000274997 | H2A clustered histone 12 | 6 |
| 42 | ENSG00000196747 | H2A clustered histone 13 | 6 |
| 44 | ENSG00000276368 | H2A clustered histone 14 | 6 |
| 23 | ENSG00000278463 | H2A clustered histone 4 | 6 |
| 31 | ENSG00000277075 | H2A clustered histone 8 | 6 |
| 36 | ENSG00000278588 | H2B clustered histone 10 | 6 |
| 37 | ENSG00000124635 | H2B clustered histone 11 | 6 |
| 41 | ENSG00000185130 | H2B clustered histone 13 | 6 |
| 45 | ENSG00000273703 | H2B clustered histone 14 | 6 |
| 3 | ENSG00000203814 | H2B clustered histone 18 | 1 |
| 24 | ENSG00000276410 | H2B clustered histone 3 | 6 |
| 29 | ENSG00000274290 | H2B clustered histone 6 | 6 |
| 34 | ENSG00000275713 | H2B clustered histone 9 | 6 |
| 19 | ENSG00000275714 | H3 clustered histone 1 | 6 |
| 43 | ENSG00000278828 | H3 clustered histone 10 | 6 |
| 49 | ENSG00000275379 | H3 clustered histone 11 | 6 |
| 50 | ENSG00000197153 | H3 clustered histone 12 | 6 |
| 22 | ENSG00000286522 | H3 clustered histone 2 | 6 |
| 25 | ENSG00000287080 | H3 clustered histone 3 | 6 |
| 33 | ENSG00000277775 | H3 clustered histone 7 | 6 |
| 35 | ENSG00000273983 | H3 clustered histone 8 | 6 |
| 20 | ENSG00000278637 | H4 clustered histone 1 | 6 |
| 46 | ENSG00000197238 | H4 clustered histone 11 | 6 |
| 47 | ENSG00000273542 | H4 clustered histone 12 | 6 |
| 21 | ENSG00000278705 | H4 clustered histone 2 | 6 |
| 27 | ENSG00000197061 | H4 clustered histone 3 | 6 |
| 30 | ENSG00000277157 | H4 clustered histone 4 | 6 |
| 39 | ENSG00000276180 | H4 clustered histone 9 | 6 |
| 36 | ENSG00000138642 | HECT and RLD domain containing E3 ubiquitin protein ligase family member 6 | 4 |
| 143 | ENSG00000130589 | helicase with zinc finger 2 | 20 |
| 133 | ENSG00000196684 | hematopoietic SH2 domain containing | 19 |
| 60 | ENSG00000189403 | high mobility group box 1 | 13 |

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|-----|-----------------|---|----|
| 53 | ENSG00000206337 | HLA complex P5 | 6 |
| 119 | ENSG00000086696 | hydroxysteroid 17-beta dehydrogenase 2 | 16 |
| 66 | ENSG00000146674 | insulin like growth factor binding protein 3 | 7 |
| 132 | ENSG00000090339 | intercellular adhesion molecule 1 | 19 |
| 114 | ENSG00000165949 | interferon alpha inducible protein 27 | 14 |
| 2 | ENSG00000126709 | interferon alpha inducible protein 6 | 1 |
| 62 | ENSG00000027697 | interferon gamma receptor 1 | 6 |
| 123 | ENSG00000068079 | interferon induced protein 35 | 17 |
| 7 | ENSG00000137965 | interferon induced protein 44 | 1 |
| 6 | ENSG00000137959 | interferon induced protein 44 like | 1 |
| 84 | ENSG00000185745 | interferon induced protein with tetratricopeptide repeats 1 | 10 |
| 82 | ENSG00000119922 | interferon induced protein with tetratricopeptide repeats 2 | 10 |
| 83 | ENSG00000119917 | interferon induced protein with tetratricopeptide repeats 3 | 10 |
| 85 | ENSG00000152778 | interferon induced protein with tetratricopeptide repeats 5 | 10 |
| 86 | ENSG00000185885 | interferon induced transmembrane protein 1 | 11 |
| 87 | ENSG00000142089 | interferon induced transmembrane protein 3 | 11 |
| 21 | ENSG00000115267 | interferon induced with helicase C domain 1 | 2 |
| 88 | ENSG00000185507 | interferon regulatory factor 7 | 11 |
| 115 | ENSG00000172183 | interferon stimulated exonuclease gene 20 | 15 |
| 19 | ENSG00000125538 | interleukin 1 beta | 2 |
| 30 | ENSG00000174564 | interleukin 20 receptor subunit beta | 3 |
| 1 | ENSG00000187608 | ISG15 ubiquitin like modifier | 1 |
| 151 | ENSG00000130487 | kelch domain containing 7B | 22 |
| 122 | ENSG00000186832 | keratin 16 | 17 |
| 121 | ENSG00000108244 | keratin 23 | 17 |
| 57 | ENSG00000186081 | keratin 5 | 12 |
| 79 | ENSG00000067082 | Kruppel like factor 6 | 10 |
| 147 | ENSG00000128342 | LIF interleukin 6 family cytokine | 22 |
| 6 | ENSG00000118961 | lipid droplet associated hydrolase | 2 |
| 32 | ENSG00000078081 | lysosomal associated membrane protein 3 | 3 |
| 52 | ENSG00000234745 | major histocompatibility complex, class I, B | 6 |
| 51 | ENSG00000204525 | major histocompatibility complex, class I, C | 6 |
| 50 | ENSG00000204592 | major histocompatibility complex, class I, E | 6 |
| 49 | ENSG00000204642 | major histocompatibility complex, class I, F | 6 |
| 56 | ENSG00000231389 | major histocompatibility complex, class II, DP alpha 1 | 6 |
| 98 | ENSG00000137673 | matrix metalloproteinase 7 | 11 |
| 144 | ENSG00000157601 | MX dynamin like GTPase 1 | 21 |
| 96 | ENSG00000172927 | myeloma overexpressed | 11 |
| 46 | ENSG00000260604 | NA | NA |
| 62 | ENSG00000224078 | NA | NA |
| 64 | ENSG00000259781 | NA | NA |
| 108 | ENSG00000165795 | NDRG family member 2 | 14 |
| 17 | ENSG00000163121 | neuralized E3 ubiquitin protein ligase 3 | 2 |
| 25 | ENSG00000204099 | neuraminidase 4 | 2 |
| 118 | ENSG00000140853 | NLR family CARD domain containing 5 | 16 |
| 150 | ENSG00000177989 | outer dense fiber of sperm tails 3B | 22 |
| 5 | ENSG00000162366 | PDZK1 interacting protein 1 | 1 |
| 93 | ENSG00000149090 | peptidase domain containing associated with muscle regeneration 1 | 11 |
| 139 | ENSG00000124102 | peptidase inhibitor 3 | 20 |
| 31 | ENSG00000188313 | phospholipid scramblase 1 | 3 |
| 81 | ENSG00000122861 | plasminogen activator, urokinase | 10 |
| 72 | ENSG00000059378 | poly(ADP-ribose) polymerase family member 12 | 7 |
| 29 | ENSG00000173193 | poly(ADP-ribose) polymerase family member 14 | 3 |
| 28 | ENSG00000138496 | poly(ADP-ribose) polymerase family member 9 | 3 |
| 107 | ENSG00000178695 | potassium channel tetramerization domain containing 12 | 13 |
| 127 | ENSG00000167183 | proline rich 15 like | 17 |
| 78 | ENSG00000148344 | prostaglandin E synthase | 9 |
| 74 | ENSG00000167653 | prostate stem cell antigen | 8 |
| 53 | ENSG00000106278 | protein tyrosine phosphatase receptor type Z1 | 7 |
| 106 | ENSG00000184226 | protocadherin 9 | 13 |
| 117 | ENSG00000103485 | quinolinate phosphoribosyltransferase | 16 |
| 14 | ENSG00000134321 | radical S-adenosyl methionine domain containing 2 | 2 |
| 15 | ENSG00000152689 | RAS guanyl releasing protein 3 | 2 |

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|-----|-----------------|---|----|
| 33 | ENSG00000136514 | receptor transporter protein 4 | 3 |
| 69 | ENSG00000189056 | reelin | 7 |
| 101 | ENSG00000139547 | retinol dehydrogenase 16 | 12 |
| 109 | ENSG00000165799 | ribonuclease A family member 7 | 14 |
| 59 | ENSG00000122026 | ribosomal protein L21 | 13 |
| 9 | ENSG00000168028 | ribosomal protein SA | 3 |
| 11 | ENSG00000143556 | S100 calcium binding protein A7 | 1 |
| 138 | ENSG00000101347 | SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1 | 20 |
| 65 | ENSG00000172123 | schlafen family member 12 | 17 |
| 51 | ENSG00000170381 | semaphorin 3E | 7 |
| 112 | ENSG00000165389 | serine palmitoyltransferase small subunit A | 14 |
| 131 | ENSG00000197632 | serpin family B member 2 | 18 |
| 91 | ENSG00000173432 | serum amyloid A1 | 11 |
| 90 | ENSG00000134339 | serum amyloid A2 | 11 |
| 61 | ENSG00000118515 | serum/glucocorticoid regulated kinase 1 | 6 |
| 2 | ENSG00000031698 | seryl-tRNA synthetase 1 | 1 |
| 44 | ENSG00000169247 | SH3 domain and tetratricopeptide repeats 2 | 5 |
| 26 | ENSG00000164054 | shisa family member 5 | 3 |
| 22 | ENSG00000115415 | signal transducer and activator of transcription 1 | 2 |
| 100 | ENSG00000170581 | signal transducer and activator of transcription 2 | 12 |
| 10 | ENSG00000241794 | small proline rich protein 2A | 1 |
| 9 | ENSG00000163216 | small proline rich protein 2D | 1 |
| 61 | ENSG00000102743 | solute carrier family 25 member 15 | 13 |
| 73 | ENSG00000147606 | solute carrier family 26 member 7 | 8 |
| 126 | ENSG00000189120 | Sp6 transcription factor | 17 |
| 67 | ENSG00000161888 | SPC24 component of NDC80 kinetochore complex | 19 |
| 128 | ENSG00000008294 | sperm associated antigen 9 | 17 |
| 152 | ENSG00000130066 | spermidine/spermine N1-acetyltransferase 1 | X |
| 10 | ENSG00000181449 | SRY-box transcription factor 2 | 3 |
| 48 | ENSG00000124766 | SRY-box transcription factor 4 | 6 |
| 67 | ENSG00000205413 | sterile alpha motif domain containing 9 | 7 |
| 68 | ENSG00000177409 | sterile alpha motif domain containing 9 like | 7 |
| 55 | ENSG00000149136 | structure specific recognition protein 1 | 11 |
| 64 | ENSG00000112096 | superoxide dismutase 2 | 6 |
| 8 | ENSG00000173705 | sushi domain containing 5 | 3 |
| 3 | ENSG00000162512 | syndecan 3 | 1 |
| 77 | ENSG00000041982 | tenascin C | 9 |
| 59 | ENSG00000112773 | terminal nucleotidyltransferase 5A | 6 |
| 17 | ENSG00000113407 | threonyl-tRNA synthetase 1 | 5 |
| 14 | ENSG00000071539 | thyroid hormone receptor interactor 13 | 5 |
| 129 | ENSG00000035862 | TIMP metalloproteinase inhibitor 2 | 17 |
| 148 | ENSG00000100234 | TIMP metalloproteinase inhibitor 3 | 22 |
| 63 | ENSG00000118503 | TNF alpha induced protein 3 | 6 |
| 76 | ENSG00000181634 | TNF superfamily member 15 | 9 |
| 70 | ENSG00000105967 | transcription factor EC | 7 |
| 13 | ENSG00000170006 | transmembrane protein 154 | 4 |
| 11 | ENSG00000121895 | transmembrane protein 156 | 4 |
| 153 | ENSG00000147027 | transmembrane protein 47 | X |
| 145 | ENSG00000184012 | transmembrane serine protease 2 | 21 |
| 55 | ENSG00000168394 | transporter 1, ATP binding cassette subfamily B member | 6 |
| 89 | ENSG00000132274 | tripartite motif containing 22 | 11 |
| 99 | ENSG00000167552 | tubulin alpha 1a | 12 |
| 75 | ENSG00000196116 | tudor domain containing 7 | 9 |
| 94 | ENSG00000156587 | ubiquitin conjugating enzyme E2 L6 | 11 |
| 27 | ENSG00000182179 | ubiquitin like modifier activating enzyme 7 | 3 |
| 146 | ENSG00000184979 | ubiquitin specific peptidase 18 | 22 |
| 110 | ENSG00000251002 | uncharacterized LOC105370401 | 14 |
| 20 | ENSG00000286081 | uncharacterized LOC105373682 | 2 |
| 120 | ENSG00000132530 | XIAP associated factor 1 | 17 |
| 142 | ENSG00000124256 | Z-DNA binding protein 1 | 20 |
| 4 | ENSG00000163874 | zinc finger CCCH-type containing 12A | 1 |
| 140 | ENSG00000124201 | zinc finger NFX1-type containing 1 | 20 |
| 116 | ENSG00000162078 | zymogen granule protein 16B | 16 |

Table S6. Deregulated proteins in HTB-43-R cells versus parental cells (HTB-43).

Adjusted *p*-values and *p*-values are indicated. Fold change (FC) values are indicated.

Negative numbers correspond to deregulated proteins and positive numbers to positive proteins.

| Swiss-Prot ID | Protein name | p | p (Corr) | Regulation | FC Resistant vs Parental cells |
|---------------|---|----------|----------|------------|--------------------------------|
| P30041 | Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN] | 6.39E-05 | 1.78E-03 | up | 1.6062549 |
| P23528 | Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN] | 3.79E-03 | 1.48E-02 | down | -1.2341194 |
| P68104 | Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN] | 1.88E-02 | 4.43E-02 | down | -1.2412293 |
| P60174 | Triosephosphate isomerase OS=Homo sapiens GN=TP1 PE=1 SV=3 - [TP1_HUMAN] | 2.00E-02 | 4.65E-02 | up | 1.1414198 |
| Q06830 | Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN] | 2.69E-04 | 3.18E-03 | down | -1.4436241 |
| P62937 | Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN] | 2.92E-03 | 1.27E-02 | down | -1.2447767 |
| P04792 | Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN] | 4.59E-04 | 4.06E-03 | up | 1.5795714 |
| P00558 | Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN] | 1.81E-05 | 1.36E-03 | up | 1.3082011 |
| P35232 | Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1 - [PHB_HUMAN] | 7.32E-03 | 2.27E-02 | up | 1.1551746 |
| P09211 | Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN] | 1.70E-03 | 8.55E-03 | up | 1.276601 |
| P37108 | Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 - [SRP14_HUMAN] | 1.71E-02 | 4.12E-02 | up | 1.1334251 |
| Q99623 | Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN] | 9.38E-04 | 6.11E-03 | up | 1.202131 |
| P07437 | Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TUBB5_HUMAN] | 1.44E-02 | 3.66E-02 | down | -1.3822523 |
| P09382 | Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN] | 5.37E-03 | 1.87E-02 | down | -2.1661763 |
| P15559 | NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN] | 4.90E-04 | 4.30E-03 | up | 1.6138847 |
| P06733 | Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENO1_HUMAN] | 7.00E-03 | 2.22E-02 | down | -1.5024956 |
| P00492 | Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 - [HPRT1_HUMAN] | 6.43E-03 | 2.09E-02 | up | 1.1258961 |
| P60842 | Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [EIF4A1_HUMAN] | 5.87E-05 | 1.78E-03 | down | -1.4718035 |
| P30050 | 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RPL12_HUMAN] | 1.51E-03 | 8.02E-03 | down | -1.1765697 |
| P31946 | 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN] | 1.64E-03 | 8.36E-03 | up | 1.2718947 |
| P18124 | 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RPL7_HUMAN] | 4.76E-03 | 1.70E-02 | down | -1.1101823 |
| P31947 | 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN] | 1.25E-04 | 2.21E-03 | down | -2.0151713 |
| P23284 | Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN] | 3.77E-04 | 3.62E-03 | up | 1.3232296 |
| P00338 | L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN] | 1.39E-03 | 7.57E-03 | down | -1.2208092 |

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| Q14019 | Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3 - [COTL1_HUMAN] | 7.24E-03 | 2.25E-02 | up | 1.5707432 |
| P62258 | 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN] | 1.52E-02 | 3.80E-02 | down | -1.1411275 |
| P23396 | 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN] | 6.81E-03 | 2.18E-02 | down | -1.1796442 |
| P07195 | L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN] | 6.82E-05 | 1.84E-03 | up | 1.232984 |
| Q99714 | 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 - [HCD2_HUMAN] | 4.16E-03 | 1.58E-02 | up | 1.1669333 |
| P07900 | Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN] | 3.92E-03 | 1.51E-02 | up | 1.1636283 |
| P08238 | Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN] | 8.96E-05 | 1.93E-03 | down | -1.5619411 |
| P07737 | Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN] | 7.13E-04 | 5.30E-03 | down | -1.6706427 |
| Q13885 | Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN] | 6.21E-03 | 2.06E-02 | down | -1.7487133 |
| Q9BQE3 | Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN] | 1.30E-02 | 3.41E-02 | down | -1.1826854 |
| P11142 | Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN] | 4.12E-03 | 1.57E-02 | down | -1.1618044 |
| P62701 | 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN] | 3.69E-03 | 1.46E-02 | down | -1.2036382 |
| P07355 | Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN] | 1.65E-02 | 4.03E-02 | down | -1.108626 |
| Q99497 | Protein DJ-1 OS=Homo sapiens GN= PARK7 PE=1 SV=2 - [PARK7_HUMAN] | 1.23E-03 | 7.10E-03 | down | -1.3677577 |
| P00505 | Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN] | 9.53E-05 | 1.99E-03 | up | 1.4605905 |
| P63244 | Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 - [RACK1_HUMAN] | 3.52E-04 | 3.58E-03 | down | -1.1869397 |
| P31949 | Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN] | 1.27E-02 | 3.35E-02 | up | 1.3337348 |
| P30086 | Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN] | 1.65E-04 | 2.44E-03 | up | 1.3983476 |
| P51148 | Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN] | 1.90E-04 | 2.68E-03 | up | 1.3729767 |
| P22392 | Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN] | 8.64E-04 | 5.87E-03 | up | 1.4499636 |
| P0DMV8 | Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1 - [HS71A_HUMAN] | 8.40E-05 | 1.93E-03 | up | 1.3490398 |
| P13639 | Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN] | 3.11E-04 | 3.39E-03 | down | -1.2252377 |
| P50454 | Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN] | 1.10E-04 | 2.10E-03 | down | -1.416099 |
| P24534 | Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN] | 6.69E-03 | 2.15E-02 | down | -1.2675023 |
| Q9HB71 | Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2 - [CYBP_HUMAN] | 1.81E-03 | 8.88E-03 | up | 1.2186345 |
| O43707 | Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN] | 3.61E-03 | 1.44E-02 | up | 1.1556438 |
| P68366 | Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN] | 5.78E-05 | 1.78E-03 | down | -1.2423459 |
| Q9Y277 | Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 - [VDAC3_HUMAN] | 2.92E-04 | 3.28E-03 | down | -1.5041708 |
| O75874 | Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 - [IDHC_HUMAN] | 2.38E-06 | 8.34E-04 | up | 1.7515198 |
| P29692 | Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5 - [EF1D_HUMAN] | 5.81E-03 | 1.98E-02 | down | -1.1551785 |
| Q96KP4 | Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2 - [CNDP2_HUMAN] | 1.35E-04 | 2.34E-03 | up | 1.2593963 |
| P51149 | Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [RAB7A_HUMAN] | 1.59E-03 | 8.29E-03 | up | 1.430655 |
| Q15181 | Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN] | 1.26E-03 | 7.16E-03 | down | -1.2080727 |
| P15880 | 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN] | 1.95E-02 | 4.55E-02 | down | -1.215076 |

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| P46783 | 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN] | 2.39E-03 | 1.10E-02 | down | -1.2302696 |
| P22626 | Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN] | 2.37E-03 | 1.09E-02 | down | -1.1977986 |
| P61106 | Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN] | 2.73E-03 | 1.21E-02 | up | 1.3336896 |
| P15311 | Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN] | 1.62E-04 | 2.44E-03 | up | 1.450627 |
| P11021 | 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN] | 2.86E-04 | 3.27E-03 | up | 1.4802543 |
| P61247 | 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN] | 2.55E-03 | 1.15E-02 | down | -1.1924746 |
| P26641 | Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN] | 1.71E-03 | 8.55E-03 | down | -1.1577983 |
| P30101 | Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN] | 9.50E-04 | 6.11E-03 | up | 1.4193659 |
| Q14247 | Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN] | 1.97E-02 | 4.59E-02 | down | -1.1920252 |
| Q02543 | 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 - [RL18A_HUMAN] | 7.13E-04 | 5.30E-03 | down | -1.1813025 |
| Q02878 | 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN] | 1.49E-02 | 3.75E-02 | down | -1.150198 |
| P16152 | Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN] | 2.03E-02 | 4.68E-02 | up | 1.2413833 |
| P49327 | Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN] | 1.84E-02 | 4.35E-02 | up | 1.1383919 |
| Q01518 | Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 - [CAP1_HUMAN] | 7.91E-04 | 5.60E-03 | down | -1.3925996 |
| P13010 | X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN] | 5.67E-04 | 4.64E-03 | down | -1.3123354 |
| P68036 | Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 - [UB2L3_HUMAN] | 8.69E-03 | 2.58E-02 | up | 1.2318766 |
| P21796 | Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN] | 1.32E-03 | 7.37E-03 | up | 1.236651 |
| P62081 | 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN] | 1.38E-02 | 3.54E-02 | down | -1.2224071 |
| P06576 | ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN] | 3.94E-03 | 1.52E-02 | down | -1.2279522 |
| P62424 | 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN] | 1.67E-04 | 2.44E-03 | down | -1.2012862 |
| P63241 | Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 - [IF5A1_HUMAN] | 2.84E-04 | 3.27E-03 | down | -1.6620091 |
| P17174 | Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3 - [AATC_HUMAN] | 2.10E-02 | 4.81E-02 | down | -1.1220492 |
| P62820 | Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN] | 3.44E-03 | 1.40E-02 | up | 1.2865559 |
| Q05639 | Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 - [EF1A2_HUMAN] | 5.03E-07 | 8.34E-04 | up | 3.5856824 |
| P61019 | Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN] | 3.66E-04 | 3.61E-03 | up | 1.3084416 |
| P12814 | Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN] | 6.70E-03 | 2.15E-02 | up | 1.1193713 |
| P30042 | ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3 - [ES1_HUMAN] | 7.37E-03 | 2.27E-02 | up | 1.1812938 |
| P18669 | Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN] | 5.42E-03 | 1.88E-02 | down | -1.2068174 |
| P48047 | ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN] | 1.35E-02 | 3.49E-02 | down | -1.2747991 |
| Q16881 | Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3 - [TRXR1_HUMAN] | 5.27E-03 | 1.85E-02 | up | 1.1081886 |
| P30085 | UMP-CMP kinase OS=Homo sapiens GN=CMKP1 PE=1 SV=3 - [KCY_HUMAN] | 1.13E-03 | 6.80E-03 | down | -1.6023248 |
| P07237 | Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3 - [PDIA1_HUMAN] | 7.16E-03 | 2.24E-02 | up | 1.2946332 |
| P38646 | Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 - [GRP75_HUMAN] | 5.20E-03 | 1.83E-02 | up | 1.196175 |
| P11413 | Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN] | 2.67E-03 | 1.19E-02 | up | 1.1954743 |

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| P62263 | 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN] | 1.18E-02 | 3.19E-02 | down | -1.3029432 |
| P27348 | 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN] | 9.39E-03 | 2.71E-02 | up | 1.2264786 |
| P08708 | 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 - [RS17_HUMAN] | 1.91E-02 | 4.47E-02 | down | -1.2349489 |
| P25705 | ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN] | 1.17E-03 | 6.90E-03 | down | -1.2573305 |
| Q06323 | Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN] | 1.40E-02 | 3.58E-02 | up | 1.2133229 |
| P55072 | Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN] | 3.22E-03 | 1.34E-02 | down | -1.1345266 |
| Q13509 | Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN] | 2.35E-03 | 1.08E-02 | down | -1.366184 |
| P12235 | ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 - [ADT1_HUMAN] | 2.13E-03 | 1.01E-02 | up | 1.2829441 |
| P83731 | 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24_HUMAN] | 8.73E-04 | 5.88E-03 | down | -1.1736782 |
| P09661 | U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 - [RU2A_HUMAN] | 3.31E-03 | 1.37E-02 | down | -1.1250858 |
| P18621 | 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN] | 5.61E-03 | 1.93E-02 | down | -1.1430866 |
| P22102 | Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 - [PUR2_HUMAN] | 6.71E-05 | 1.84E-03 | down | -1.5227143 |
| P49588 | Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN] | 3.50E-03 | 1.41E-02 | up | 1.4299626 |
| Q08257 | Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 - [QOR_HUMAN] | 1.95E-05 | 1.36E-03 | down | -1.3778034 |
| P02794 | Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2 - [FRIH_HUMAN] | 5.66E-04 | 4.64E-03 | up | 1.9602916 |
| O60506 | Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN] | 1.30E-03 | 7.30E-03 | up | 1.2307497 |
| Q15907 | Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4 - [RB11B_HUMAN] | 3.47E-04 | 3.55E-03 | up | 1.2526463 |
| P11586 | C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN] | 3.78E-04 | 3.62E-03 | down | -1.4721048 |
| P62826 | GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN] | 1.23E-02 | 3.28E-02 | down | -1.3588738 |
| P14625 | Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN] | 2.15E-05 | 1.36E-03 | up | 1.6472217 |
| P27635 | 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10_HUMAN] | 1.58E-02 | 3.89E-02 | down | -1.1761628 |
| P80188 | Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2 - [NGAL_HUMAN] | 2.94E-03 | 1.28E-02 | up | 2.7148077 |
| P68431 | Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN] | 1.11E-02 | 3.04E-02 | down | -1.4482012 |
| P39023 | 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 - [RL3_HUMAN] | 3.22E-03 | 1.34E-02 | down | -1.179685 |
| P62917 | 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN] | 6.32E-03 | 2.08E-02 | down | -1.1288501 |
| P62906 | 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN] | 7.02E-03 | 2.22E-02 | down | -1.1210649 |
| P40925 | Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN] | 4.25E-04 | 3.88E-03 | up | 1.2935199 |
| P46781 | 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN] | 4.72E-03 | 1.69E-02 | down | -1.1730803 |
| Q16658 | Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 - [FSCN1_HUMAN] | 1.81E-03 | 8.88E-03 | down | -1.8247709 |
| P62280 | 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN] | 7.24E-04 | 5.35E-03 | down | -1.2117864 |
| P12956 | X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 - [XRCC6_HUMAN] | 9.95E-05 | 2.01E-03 | down | -1.3034099 |
| P17844 | Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN] | 2.52E-04 | 3.07E-03 | down | -1.3476697 |
| P61353 | 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27_HUMAN] | 6.65E-04 | 5.11E-03 | down | -1.1860358 |
| P62266 | 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN] | 1.35E-02 | 3.49E-02 | down | -1.2439618 |

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| P29401 | Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 - [TKT_HUMAN] | 4.42E-03 | 1.64E-02 | up | 1.203193 |
| P13804 | Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 - [ETFA_HUMAN] | 7.37E-06 | 1.35E-03 | up | 1.5177015 |
| P05161 | Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5 - [ISG15_HUMAN] | 6.08E-05 | 1.78E-03 | down | -2.0635717 |
| Q92841 | Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN] | 3.65E-04 | 3.61E-03 | up | 1.1654038 |
| P00918 | Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN] | 1.44E-02 | 3.66E-02 | up | 1.3509647 |
| Q00610 | Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN] | 9.59E-04 | 6.13E-03 | up | 1.2153449 |
| P62191 | 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN] | 6.86E-03 | 2.19E-02 | down | -1.1891428 |
| Q04760 | Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4 - [LGUL_HUMAN] | 2.11E-02 | 4.82E-02 | up | 1.1353526 |
| P43490 | Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 - [NAMPT_HUMAN] | 1.84E-06 | 8.34E-04 | up | 1.7633975 |
| P26038 | Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN] | 3.04E-03 | 1.29E-02 | down | -1.4272814 |
| O60701 | UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 - [UGDH_HUMAN] | 5.83E-05 | 1.78E-03 | up | 1.2146384 |
| P04843 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 - [RPN1_HUMAN] | 1.66E-02 | 4.04E-02 | up | 1.1063002 |
| P00568 | Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN] | 1.52E-02 | 3.80E-02 | up | 1.2606336 |
| P17980 | 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN] | 4.27E-03 | 1.61E-02 | down | -1.1797079 |
| P46779 | 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN] | 1.52E-02 | 3.80E-02 | down | -1.2236639 |
| P47895 | Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens GN=ALDH1A3 PE=1 SV=2 - [AL1A3_HUMAN] | 2.31E-03 | 1.07E-02 | down | -1.1389194 |
| P13667 | Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN] | 6.37E-05 | 1.78E-03 | up | 1.4710776 |
| Q9NX63 | MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 - [MIC19_HUMAN] | 1.67E-03 | 8.47E-03 | up | 1.286661 |
| P61289 | Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 - [PSME3_HUMAN] | 2.30E-03 | 1.07E-02 | down | -1.100153 |
| P31939 | Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN] | 1.45E-05 | 1.36E-03 | down | -1.2837373 |
| Q96C19 | EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1 - [EFHD2_HUMAN] | 5.46E-05 | 1.78E-03 | down | -2.5403726 |
| P14923 | Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN] | 3.41E-03 | 1.40E-02 | up | 1.227592 |
| Q15084 | Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN] | 4.85E-05 | 1.78E-03 | up | 1.4844995 |
| P36578 | 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN] | 6.73E-03 | 2.16E-02 | down | -1.1735872 |
| P00387 | NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3 - [NB5R3_HUMAN] | 3.01E-03 | 1.28E-02 | up | 1.1891589 |
| O43175 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN] | 1.49E-04 | 2.44E-03 | down | -2.1595984 |
| P51991 | Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_HUMAN] | 1.40E-02 | 3.58E-02 | down | -1.2101227 |
| Q14240 | Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2 - [IF4A2_HUMAN] | 9.63E-03 | 2.75E-02 | up | 1.2813967 |
| Q9UL46 | Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN] | 9.75E-03 | 2.77E-02 | up | 1.209638 |
| P40939 | Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN] | 5.81E-03 | 1.98E-02 | up | 1.198289 |
| P52907 | F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 - [CAZA1_HUMAN] | 9.21E-04 | 6.09E-03 | down | -1.482052 |
| O75347 | Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1 SV=3 - [TBCA_HUMAN] | 6.10E-03 | 2.03E-02 | down | -1.1259292 |
| O00264 | Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN] | 5.31E-03 | 1.86E-02 | up | 1.391766 |
| P35221 | Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN] | 2.30E-03 | 1.07E-02 | up | 1.3006402 |

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| P46777 | 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 - [RL5_HUMAN] | 1.57E-02 | 3.87E-02 | down | -1.133346 |
| P61026 | Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN] | 1.19E-02 | 3.21E-02 | up | 1.2246257 |
| P04080 | Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN] | 1.33E-02 | 3.46E-02 | up | 1.2581038 |
| P61586 | Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN] | 9.88E-03 | 2.79E-02 | up | 1.2297707 |
| P33993 | DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN] | 9.86E-04 | 6.21E-03 | down | -1.3645427 |
| P23526 | Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 - [SAHH_HUMAN] | 1.32E-03 | 7.37E-03 | down | -1.2220912 |
| Q16891 | MICOS complex subunit MIC60 OS=Homo sapiens GN=IMMT PE=1 SV=1 - [MIC60_HUMAN] | 5.65E-03 | 1.94E-02 | up | 1.2135626 |
| P20339 | Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2 - [RAB5A_HUMAN] | 1.16E-02 | 3.15E-02 | up | 1.2418282 |
| P05198 | Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3 - [IF2A_HUMAN] | 4.26E-03 | 1.61E-02 | down | -1.2081513 |
| P62851 | 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN] | 8.74E-03 | 2.58E-02 | down | -1.1635156 |
| Q15149 | Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN] | 4.65E-03 | 1.68E-02 | up | 1.239284 |
| P33316 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=4 - [DUT_HUMAN] | 1.03E-03 | 6.39E-03 | down | -1.6526828 |
| O00303 | Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1 - [EIF3F_HUMAN] | 4.07E-03 | 1.56E-02 | down | -1.1988128 |
| Q92688 | Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 - [AN32B_HUMAN] | 1.34E-03 | 7.38E-03 | up | 1.3922219 |
| P04181 | Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 - [OAT_HUMAN] | 2.08E-02 | 4.78E-02 | up | 1.2362257 |
| P00441 | Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN] | 1.91E-02 | 4.47E-02 | up | 1.169954 |
| P35613 | Basigin OS=Homo sapiens GN=BSG PE=1 SV=2 - [BASI_HUMAN] | 2.83E-03 | 1.24E-02 | down | -1.4603549 |
| P30044 | Peroxisedoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN] | 4.86E-03 | 1.73E-02 | up | 1.3072814 |
| P19338 | Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN] | 6.74E-04 | 5.11E-03 | down | -1.3032299 |
| Q9Y617 | Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN] | 5.72E-04 | 4.65E-03 | up | 1.1873496 |
| Q04828 | Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN] | 1.10E-04 | 2.10E-03 | up | 2.9348218 |
| O43390 | Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN] | 1.15E-04 | 2.14E-03 | down | -1.4232169 |
| Q9NR30 | Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN] | 1.93E-04 | 2.70E-03 | down | -1.6687161 |
| P20700 | Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2 - [LMNB1_HUMAN] | 4.39E-04 | 3.99E-03 | down | -1.4446604 |
| P67809 | Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 - [YBOX1_HUMAN] | 1.67E-02 | 4.04E-02 | down | -1.1535116 |
| P22314 | Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN] | 1.43E-03 | 7.73E-03 | down | -1.1387231 |
| P40429 | 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN] | 7.47E-04 | 5.41E-03 | down | -1.1757252 |
| P11940 | Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 - [PABP1_HUMAN] | 7.66E-04 | 5.50E-03 | down | -1.1792278 |
| P37837 | Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN] | 1.42E-04 | 2.43E-03 | up | 1.5685321 |
| Q9NUQ9 | Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 - [FA49B_HUMAN] | 2.48E-04 | 3.05E-03 | up | 1.3108495 |
| Q99986 | Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 - [VRK1_HUMAN] | 9.19E-04 | 6.09E-03 | down | -1.5845141 |
| Q9BUF5 | Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN] | 4.40E-03 | 1.64E-02 | down | -1.327108 |
| Q13185 | Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 - [CBX3_HUMAN] | 1.03E-02 | 2.88E-02 | down | -1.2591394 |
| Q9Y4L1 | Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN] | 7.35E-04 | 5.38E-03 | up | 1.3731519 |

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| Q13242 | Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 - [SRSF9_HUMAN] | 9.52E-04 | 6.11E-03 | down | -1.2412403 |
| P42330 | Aldo-keto reductase family 1 member C3 OS=Homo sapiens GN=AKR1C3 PE=1 SV=4 - [AK1C3_HUMAN] | 1.41E-03 | 7.65E-03 | up | 2.4039125 |
| P12268 | Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 - [IMDH2_HUMAN] | 4.93E-04 | 4.30E-03 | down | -1.2885474 |
| Q99798 | Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 - [ACON_HUMAN] | 7.45E-04 | 5.41E-03 | up | 1.3294115 |
| Q03135 | Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4 - [CAV1_HUMAN] | 1.70E-02 | 4.10E-02 | down | -1.1861877 |
| Q13310 | Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1 - [PABP4_HUMAN] | 8.23E-05 | 1.93E-03 | down | -1.4894267 |
| O76003 | Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 - [GLRX3_HUMAN] | 8.96E-04 | 5.99E-03 | down | -1.3019738 |
| Q01081 | Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3 - [U2AF1_HUMAN] | 1.28E-02 | 3.36E-02 | down | -1.1551194 |
| P27824 | Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN] | 8.45E-03 | 2.51E-02 | up | 1.2374053 |
| O95433 | Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1 - [AHSA1_HUMAN] | 1.64E-05 | 1.36E-03 | down | -1.598835 |
| P62333 | 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN] | 4.87E-03 | 1.73E-02 | down | -1.24646 |
| P30740 | Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1 - [ILEU_HUMAN] | 1.15E-02 | 3.13E-02 | up | 1.199689 |
| P62913 | 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN] | 3.52E-03 | 1.41E-02 | down | -1.2254583 |
| P47756 | F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 - [CAPZB_HUMAN] | 8.98E-05 | 1.93E-03 | down | -1.361371 |
| Q9P258 | Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN] | 1.63E-04 | 2.44E-03 | down | -1.5995828 |
| Q92598 | Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN] | 8.57E-04 | 5.84E-03 | down | -1.1677066 |
| P38117 | Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 - [ETFB_HUMAN] | 6.18E-05 | 1.78E-03 | up | 1.4257207 |
| P50914 | 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14_HUMAN] | 3.58E-03 | 1.43E-02 | down | -1.2302359 |
| P09972 | Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN] | 9.05E-03 | 2.65E-02 | up | 1.2637615 |
| P35579 | Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN] | 7.89E-05 | 1.93E-03 | down | -1.3237699 |
| P31153 | S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 - [METK2_HUMAN] | 1.72E-02 | 4.13E-02 | down | -1.2178786 |
| P49915 | GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 - [GUAA_HUMAN] | 7.50E-04 | 5.41E-03 | down | -1.1682175 |
| Q9UKM9 | RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN] | 5.28E-04 | 4.49E-03 | down | -1.1826164 |
| P15924 | Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN] | 2.90E-04 | 3.28E-03 | down | -1.4416785 |
| Q9Y265 | RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN] | 1.68E-02 | 4.07E-02 | up | 1.109814 |
| P98179 | RNA-binding protein 3 OS=Homo sapiens GN=RBM3 PE=1 SV=1 - [RBM3_HUMAN] | 8.32E-04 | 5.74E-03 | down | -2.3412771 |
| P62879 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN] | 3.31E-03 | 1.37E-02 | down | -1.1979517 |
| Q53GQ0 | Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 - [DHB12_HUMAN] | 4.31E-03 | 1.62E-02 | up | 1.3972734 |
| P09110 | 3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 - [THIK_HUMAN] | 2.72E-04 | 3.20E-03 | up | 1.2407163 |
| Q9NTK5 | Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN] | 6.14E-04 | 4.89E-03 | down | -1.3208947 |
| O00571 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN] | 1.66E-02 | 4.03E-02 | down | -1.2072935 |
| Q9NX40 | OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 - [OCAD1_HUMAN] | 1.49E-03 | 7.96E-03 | up | 1.1379675 |
| P30048 | Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN] | 3.05E-03 | 1.29E-02 | down | -1.1892427 |
| P14868 | Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN] | 6.66E-03 | 2.15E-02 | down | -1.161467 |

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| P53396 | ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN] | 1.69E-04 | 2.44E-03 | up | 1.3355421 |
| Q9HAV7 | GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2 - [GRPE1_HUMAN] | 1.45E-02 | 3.68E-02 | up | 1.3305161 |
| P13693 | Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 - [TCTP_HUMAN] | 2.90E-04 | 3.28E-03 | down | -1.2956079 |
| P06748 | Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN] | 1.44E-03 | 7.75E-03 | down | -1.2478081 |
| Q86VP6 | Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN] | 1.54E-03 | 8.10E-03 | up | 1.1377778 |
| P55084 | Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN] | 3.42E-04 | 3.55E-03 | up | 1.2763329 |
| P07339 | Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN] | 6.07E-03 | 2.03E-02 | up | 1.1749836 |
| P16615 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN] | 2.10E-03 | 9.98E-03 | up | 1.4429438 |
| P07384 | Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN] | 7.07E-05 | 1.86E-03 | up | 1.4105902 |
| Q12931 | Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN] | 7.43E-03 | 2.27E-02 | up | 1.1836349 |
| O15372 | Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1 - [EIF3H_HUMAN] | 1.59E-03 | 8.28E-03 | down | -1.2745551 |
| Q9Y547 | Intraflagellar transport protein 25 homolog OS=Homo sapiens GN=HSPB11 PE=1 SV=1 - [IFT25_HUMAN] | 5.95E-05 | 1.78E-03 | down | -1.5542209 |
| P48163 | NADP-dependent malic enzyme OS=Homo sapiens GN=ME1 PE=1 SV=1 - [MAOX_HUMAN] | 3.25E-04 | 3.46E-03 | up | 1.3942713 |
| P46926 | Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1 - [GNPI1_HUMAN] | 2.08E-05 | 1.36E-03 | up | 1.8899547 |
| O76021 | Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3 - [RL1D1_HUMAN] | 7.43E-03 | 2.27E-02 | down | -1.1990682 |
| P54577 | Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN] | 6.78E-03 | 2.17E-02 | up | 1.2195108 |
| P06493 | Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3 - [CDK1_HUMAN] | 3.08E-04 | 3.39E-03 | down | -1.476753 |
| P49591 | Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN] | 1.01E-04 | 2.01E-03 | down | -1.4985554 |
| O75608 | Acyl-protein thioesterase 1 OS=Homo sapiens GN=LYPLA1 PE=1 SV=1 - [LYPA1_HUMAN] | 6.94E-04 | 5.21E-03 | up | 1.6011112 |
| Q9Y696 | Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 - [CLIC4_HUMAN] | 1.52E-04 | 2.44E-03 | down | -1.4006624 |
| O75083 | WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN] | 2.81E-03 | 1.24E-02 | up | 1.1481489 |
| Q13151 | Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROAO_HUMAN] | 9.43E-04 | 6.11E-03 | down | -1.2118063 |
| P27144 | Adenylate kinase 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 - [KAD4_HUMAN] | 3.46E-03 | 1.41E-02 | down | -1.3533028 |
| P23381 | Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN] | 4.46E-03 | 1.65E-02 | up | 1.2812287 |
| Q96K17 | Transcription factor BTF3 homolog 4 OS=Homo sapiens GN=BTF3L4 PE=1 SV=1 - [BT3L4_HUMAN] | 5.85E-03 | 1.98E-02 | down | -1.4531513 |
| P32119 | Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN] | 9.14E-03 | 2.65E-02 | up | 1.1597544 |
| P52565 | Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=3 - [GDIR1_HUMAN] | 4.39E-03 | 1.64E-02 | up | 1.1318933 |
| Q15233 | Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 - [NONO_HUMAN] | 4.47E-04 | 4.02E-03 | down | -1.1952565 |
| Q96AG4 | Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 - [LRC59_HUMAN] | 8.19E-03 | 2.46E-02 | up | 1.1533757 |
| Q9UBX3 | Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2 - [DIC_HUMAN] | 1.11E-03 | 6.70E-03 | up | 1.5409805 |
| P13796 | Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN] | 1.93E-05 | 1.36E-03 | up | 4.9645185 |
| O15511 | Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3 - [ARPC5_HUMAN] | 2.00E-02 | 4.64E-02 | up | 1.2004961 |
| O75431 | Metaxin-2 OS=Homo sapiens GN=MTX2 PE=1 SV=1 - [MTX2_HUMAN] | 4.09E-03 | 1.56E-02 | up | 1.2855476 |
| Q01813 | ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 - [PFKAP_HUMAN] | 8.80E-03 | 2.59E-02 | up | 1.1276958 |

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| Q9Y2X3 | Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 - [NOP58_HUMAN] | 8.53E-04 | 5.84E-03 | down | -1.2856553 |
| P54886 | Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN] | 3.96E-04 | 3.73E-03 | down | -1.4123482 |
| P51665 | 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2 - [PSMD7_HUMAN] | 1.72E-02 | 4.13E-02 | down | -1.1022326 |
| P55060 | Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN] | 1.90E-03 | 9.15E-03 | down | -1.1749027 |
| O75396 | Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN] | 3.44E-05 | 1.72E-03 | down | -2.1398134 |
| P16402 | Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2 - [H13_HUMAN] | 4.48E-03 | 1.65E-02 | down | -1.5689797 |
| Q14566 | DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN] | 3.42E-04 | 3.55E-03 | down | -1.5707914 |
| Q14103 | Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 - [HNRPD_HUMAN] | 1.41E-02 | 3.60E-02 | up | 1.1316749 |
| P46940 | Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN] | 7.40E-03 | 2.27E-02 | down | -1.1817677 |
| P21333 | Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN] | 3.00E-03 | 1.28E-02 | down | -1.3866814 |
| P62829 | 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN] | 9.45E-03 | 2.71E-02 | down | -1.1723456 |
| O00151 | PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4 - [PDLI1_HUMAN] | 2.28E-05 | 1.38E-03 | down | -1.7290163 |
| P36957 | Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4 - [ODO2_HUMAN] | 1.10E-02 | 3.03E-02 | down | -1.1369902 |
| P48506 | Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 - [GSH1_HUMAN] | 3.72E-05 | 1.78E-03 | up | 1.7526379 |
| O00429 | Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 - [DNM1L_HUMAN] | 1.58E-02 | 3.89E-02 | up | 1.1522093 |
| P06737 | Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN] | 4.23E-05 | 1.78E-03 | down | -1.8788105 |
| Q9Y3A5 | Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=1 SV=4 - [SBDS_HUMAN] | 6.68E-04 | 5.11E-03 | down | -1.3808237 |
| P04179 | Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2 - [SODM_HUMAN] | 2.47E-03 | 1.13E-02 | up | 1.3963857 |
| Q9BVK6 | Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2 - [TMED9_HUMAN] | 3.03E-03 | 1.29E-02 | up | 1.3050512 |
| O00233 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 - [PSMD9_HUMAN] | 5.17E-04 | 4.41E-03 | down | -1.390694 |
| Q08J23 | tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 - [NSUN2_HUMAN] | 1.19E-02 | 3.22E-02 | down | -1.2152523 |
| P35998 | 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN] | 1.35E-03 | 7.38E-03 | down | -1.1426486 |
| P27797 | Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN] | 4.06E-04 | 3.77E-03 | up | 1.5843748 |
| O43795 | Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3 - [MYO1B_HUMAN] | 1.52E-04 | 2.44E-03 | down | -1.2396137 |
| P24539 | ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [AT5F1_HUMAN] | 3.09E-04 | 3.39E-03 | down | -1.2738857 |
| Q14204 | Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN] | 6.09E-05 | 1.78E-03 | up | 1.6032346 |
| Q13162 | Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN] | 4.84E-05 | 1.78E-03 | up | 1.8027271 |
| Q13200 | 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 - [PSMD2_HUMAN] | 1.34E-02 | 3.47E-02 | down | -1.2142394 |
| Q13057 | Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4 - [COASY_HUMAN] | 2.49E-03 | 1.13E-02 | up | 1.1592919 |
| P09758 | Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3 - [TACD2_HUMAN] | 9.11E-03 | 2.65E-02 | down | -1.2121285 |
| Q14152 | Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1 - [EIF3A_HUMAN] | 3.84E-03 | 1.49E-02 | down | -1.1910186 |
| P41091 | Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 - [IF2G_HUMAN] | 2.29E-04 | 2.87E-03 | down | -1.2338092 |
| P16949 | Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 - [STMN1_HUMAN] | 5.90E-03 | 1.98E-02 | down | -1.3613175 |
| P22676 | Calretinin OS=Homo sapiens GN=CALB2 PE=2 SV=2 - [CALB2_HUMAN] | 3.13E-06 | 8.76E-04 | up | 3.1833932 |

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| Q9BY44 | Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=1 SV=3 - [EIF2A_HUMAN] | 1.25E-02 | 3.30E-02 | down | -1.2347101 |
| P30838 | Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 - [AL3A1_HUMAN] | 9.71E-06 | 1.36E-03 | up | 1.8669542 |
| Q15785 | Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2 - [TOM34_HUMAN] | 1.63E-03 | 8.34E-03 | down | -1.2463759 |
| Q06210 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN] | 1.21E-03 | 7.05E-03 | up | 1.3379711 |
| Q13136 | Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1 PE=1 SV=1 - [LIPA1_HUMAN] | 5.42E-04 | 4.57E-03 | down | -1.3497835 |
| P21964 | Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 - [COMT_HUMAN] | 1.37E-02 | 3.52E-02 | up | 1.3126211 |
| P31689 | DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 - [DNJA1_HUMAN] | 1.18E-02 | 3.19E-02 | down | -1.3605753 |
| Q9UHX1 | Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1 - [PUF60_HUMAN] | 8.15E-03 | 2.45E-02 | down | -1.1477194 |
| Q9BT78 | COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1 - [CSN4_HUMAN] | 3.47E-03 | 1.41E-02 | up | 1.1351424 |
| Q9Y310 | tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1 - [RTCB_HUMAN] | 2.17E-02 | 4.93E-02 | up | 1.1991403 |
| P27105 | Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3 - [STOM_HUMAN] | 1.55E-03 | 8.14E-03 | down | -1.3997545 |
| P51572 | B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3 - [BAP31_HUMAN] | 1.83E-02 | 4.34E-02 | up | 1.2099215 |
| P61221 | ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 - [ABCE1_HUMAN] | 2.61E-03 | 1.17E-02 | down | -1.1531037 |
| P63172 | Dynein light chain Tctex-type 1 OS=Homo sapiens GN=DYNLT1 PE=1 SV=1 - [DYLT1_HUMAN] | 1.58E-02 | 3.88E-02 | up | 1.6481178 |
| P55786 | Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN] | 5.44E-03 | 1.88E-02 | up | 1.1913173 |
| Q16851 | UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - [UGPA_HUMAN] | 4.64E-05 | 1.78E-03 | up | 1.4884177 |
| O95336 | 6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2 - [6PGL_HUMAN] | 1.04E-03 | 6.43E-03 | up | 1.148455 |
| Q15005 | Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3 - [SPCS2_HUMAN] | 4.79E-03 | 1.70E-02 | up | 1.3009044 |
| Q9Y624 | Junctional adhesion molecule A OS=Homo sapiens GN=F11R PE=1 SV=1 - [JAM1_HUMAN] | 3.31E-04 | 3.50E-03 | up | 1.5451335 |
| Q96AE4 | Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN] | 3.97E-03 | 1.53E-02 | down | -1.3270313 |
| P56192 | Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 - [SYMC_HUMAN] | 3.71E-03 | 1.46E-02 | down | -1.137392 |
| P32969 | 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [RL9_HUMAN] | 5.86E-03 | 1.98E-02 | down | -1.1909722 |
| Q9HA64 | Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 - [KT3K_HUMAN] | 7.98E-03 | 2.41E-02 | up | 1.3307159 |
| P49736 | DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4 - [MCM2_HUMAN] | 4.51E-04 | 4.03E-03 | down | -1.5317193 |
| Q9NV17 | ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2 - [ATD3A_HUMAN] | 2.23E-03 | 1.05E-02 | down | -1.5860535 |
| P28074 | Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN] | 9.95E-04 | 6.23E-03 | down | -1.5448285 |
| P21281 | V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 - [VATB2_HUMAN] | 7.79E-04 | 5.55E-03 | up | 1.5195359 |
| O60547 | GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS PE=1 SV=1 - [GMDS_HUMAN] | 1.20E-03 | 7.02E-03 | up | 1.40803 |
| P60228 | Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 - [EIF3E_HUMAN] | 7.08E-03 | 2.22E-02 | down | -1.2316507 |
| Q02218 | 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3 - [ODO1_HUMAN] | 3.68E-03 | 1.46E-02 | down | -1.2107928 |
| P38606 | V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 - [VATA_HUMAN] | 7.61E-03 | 2.32E-02 | up | 1.2802314 |
| O95881 | Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1 - [TXD12_HUMAN] | 3.54E-04 | 3.58E-03 | down | -1.6267446 |
| Q5VWZ2 | Lysophospholipase-like protein 1 OS=Homo sapiens GN=LYPLAL1 PE=1 SV=3 - [LYPL1_HUMAN] | 9.66E-04 | 6.16E-03 | up | 1.2498306 |
| P14324 | Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4 - [FPSP_HUMAN] | 1.09E-02 | 3.02E-02 | up | 1.227648 |

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| P18206 | Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 - [VINC_HUMAN] | 1.35E-02 | 3.49E-02 | down | -1.2371044 |
| P15374 | Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN] | 2.02E-02 | 4.67E-02 | up | 1.2342337 |
| Q15382 | GTP-binding protein Rheb OS=Homo sapiens GN=RHEB PE=1 SV=1 - [RHEB_HUMAN] | 4.97E-03 | 1.76E-02 | up | 1.4957985 |
| P15153 | Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 - [RAC2_HUMAN] | 3.71E-04 | 3.61E-03 | up | 2.020465 |
| Q9BR76 | Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 - [COR1B_HUMAN] | 5.38E-03 | 1.88E-02 | up | 1.1234653 |
| P55263 | Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 - [ADK_HUMAN] | 6.36E-03 | 2.08E-02 | down | -1.3790295 |
| P12081 | Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2 - [SYHC_HUMAN] | 8.68E-04 | 5.87E-03 | down | -1.2718859 |
| P39748 | Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1 - [FEN1_HUMAN] | 3.01E-04 | 3.36E-03 | up | 1.3293201 |
| Q12907 | Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1 - [LMAN2_HUMAN] | 3.07E-05 | 1.63E-03 | up | 1.4461673 |
| Q722W4 | Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 - [ZCCHV_HUMAN] | 1.50E-04 | 2.44E-03 | down | -1.8808278 |
| Q9Y3F4 | Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 - [STRAP_HUMAN] | 3.73E-04 | 3.61E-03 | down | -1.5498998 |
| Q8TC12 | Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2 - [RDH11_HUMAN] | 3.19E-03 | 1.34E-02 | down | -1.3041362 |
| P30043 | Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN] | 6.34E-04 | 4.98E-03 | up | 1.7419794 |
| Q03169 | Tumor necrosis factor alpha-induced protein 2 OS=Homo sapiens GN=TNFAIP2 PE=2 SV=2 - [TNAP2_HUMAN] | 4.31E-05 | 1.78E-03 | up | 2.116569 |
| P30405 | Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Homo sapiens GN=PPIF PE=1 SV=1 - [PPIF_HUMAN] | 4.55E-03 | 1.66E-02 | down | -1.2422752 |
| O95831 | Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN] | 5.82E-03 | 1.98E-02 | up | 1.2126722 |
| P62942 | Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2 - [FKB1A_HUMAN] | 1.28E-02 | 3.36E-02 | up | 1.3899764 |
| Q9Y376 | Calcium-binding protein 39 OS=Homo sapiens GN=CAB39 PE=1 SV=1 - [CAB39_HUMAN] | 1.19E-03 | 6.95E-03 | down | -1.4694296 |
| P13995 | Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 PE=1 SV=2 - [MTDC_HUMAN] | 7.02E-03 | 2.22E-02 | down | -1.2777969 |
| P36871 | Phosphoglucosmutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 - [PGM1_HUMAN] | 1.53E-04 | 2.44E-03 | down | -1.757677 |
| Q14258 | E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 - [TRI25_HUMAN] | 1.43E-04 | 2.43E-03 | up | 1.6760329 |
| Q724W1 | L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN] | 2.76E-04 | 3.20E-03 | up | 1.5713593 |
| Q9Y262 | Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 - [EIF3L_HUMAN] | 8.17E-03 | 2.45E-02 | down | -1.1597643 |
| Q96RS6 | NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 - [NUDC1_HUMAN] | 1.85E-03 | 9.01E-03 | up | 1.1416517 |
| P48637 | Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1 - [GSHB_HUMAN] | 1.20E-02 | 3.23E-02 | down | -1.2317704 |
| Q00059 | Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1 - [TFAM_HUMAN] | 1.86E-02 | 4.38E-02 | down | -1.1820513 |
| Q03252 | Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=4 - [LMNB2_HUMAN] | 6.05E-03 | 2.03E-02 | down | -1.1603619 |
| O14933 | Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens GN=UBE2L6 PE=1 SV=4 - [UB2L6_HUMAN] | 3.24E-03 | 1.34E-02 | up | 1.6019629 |
| P30519 | Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2 - [HMOX2_HUMAN] | 2.17E-02 | 4.93E-02 | up | 1.1141288 |
| O95373 | Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN] | 1.02E-02 | 2.87E-02 | down | -1.1922915 |
| Q96DI7 | U5 small nuclear ribonucleoprotein 40 kDa protein OS=Homo sapiens GN=SNRNP40 PE=1 SV=1 - [SNR40_HUMAN] | 1.81E-03 | 8.88E-03 | down | -1.3128988 |
| P26583 | High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN] | 1.26E-02 | 3.34E-02 | up | 1.3599427 |
| Q9Y5M8 | Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 - [SRPRB_HUMAN] | 3.88E-04 | 3.69E-03 | up | 1.4659659 |
| Q96HS1 | Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2 - [PGAM5_HUMAN] | 3.57E-04 | 3.59E-03 | down | -1.2412837 |

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|--------|---|----------|----------|------|------------|
| Q5JTV8 | Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2 - [TOIP1_HUMAN] | 1.16E-02 | 3.15E-02 | up | 1.2489173 |
| Q92820 | Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN] | 7.11E-05 | 1.86E-03 | up | 3.1326673 |
| P11172 | Uridine 5'-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1 - [UMPS_HUMAN] | 8.03E-04 | 5.65E-03 | up | 1.3767604 |
| Q9NQR4 | Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN] | 1.78E-03 | 8.86E-03 | up | 1.1305518 |
| Q9UL25 | Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3 - [RAB21_HUMAN] | 8.73E-03 | 2.58E-02 | up | 1.1660937 |
| P35270 | Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1 - [SPRE_HUMAN] | 9.94E-03 | 2.80E-02 | up | 1.4115462 |
| P15121 | Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 - [ALDR_HUMAN] | 1.68E-03 | 8.49E-03 | up | 1.3091357 |
| Q13247 | Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2 - [SRSF6_HUMAN] | 1.72E-02 | 4.13E-02 | down | -1.1612135 |
| O75533 | Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN] | 1.06E-04 | 2.07E-03 | down | -1.3605387 |
| Q9NSD9 | Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN] | 1.01E-05 | 1.36E-03 | down | -1.247156 |
| Q727H5 | Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens GN=TMED4 PE=1 SV=1 - [TMED4_HUMAN] | 3.20E-03 | 1.34E-02 | down | -1.314663 |
| O95299 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1 - [NDUAA_HUMAN] | 1.04E-02 | 2.90E-02 | up | 1.2588991 |
| Q92599 | Septin-8 OS=Homo sapiens GN=SEPT8 PE=1 SV=4 - [SEPT8_HUMAN] | 2.20E-02 | 4.97E-02 | up | 1.1200876 |
| Q96IU4 | Protein ABHD14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1 - [ABHEB_HUMAN] | 2.18E-05 | 1.36E-03 | up | 1.8066789 |
| Q13148 | TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 - [TADBP_HUMAN] | 1.82E-02 | 4.32E-02 | down | -1.3657229 |
| P26440 | Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN] | 1.61E-04 | 2.44E-03 | up | 1.5149204 |
| P20073 | Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 - [ANXA7_HUMAN] | 7.69E-03 | 2.34E-02 | down | -1.1948313 |
| Q99436 | Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1 - [PSB7_HUMAN] | 1.65E-02 | 4.03E-02 | down | -1.14481 |
| Q99447 | Ethanolamine-phosphate cytidyltransferase OS=Homo sapiens GN=PCYT2 PE=1 SV=1 - [PCY2_HUMAN] | 3.90E-04 | 3.69E-03 | up | 1.9419681 |
| P24752 | Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN] | 2.01E-04 | 2.73E-03 | up | 1.4854594 |
| P36542 | ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HUMAN] | 7.54E-05 | 1.91E-03 | down | -1.4592322 |
| P62714 | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 - [PP2AB_HUMAN] | 1.15E-03 | 6.83E-03 | up | 1.2826419 |
| P33992 | DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5_HUMAN] | 1.66E-04 | 2.44E-03 | down | -1.2432284 |
| Q16531 | DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN] | 1.82E-04 | 2.60E-03 | up | 1.2106942 |
| P19367 | Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HXK1_HUMAN] | 5.34E-03 | 1.87E-02 | down | -1.2471868 |
| P12429 | Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN] | 9.44E-03 | 2.71E-02 | up | 1.108245 |
| Q96P70 | Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3 - [IPO9_HUMAN] | 1.68E-02 | 4.06E-02 | up | 1.1196529 |
| P45954 | Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN] | 3.90E-05 | 1.78E-03 | up | 1.1744773 |
| Q9Y5B9 | FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 - [SP16H_HUMAN] | 1.46E-02 | 3.68E-02 | down | -1.176356 |
| Q86W42 | THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1 - [THOC6_HUMAN] | 1.74E-02 | 4.15E-02 | up | 1.2216566 |
| P35222 | Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN] | 2.00E-04 | 2.73E-03 | down | -1.1231141 |
| P52292 | Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 - [IMA1_HUMAN] | 5.66E-04 | 4.64E-03 | down | -1.3627762 |
| Q9H2U2 | Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2 - [IPYR2_HUMAN] | 3.58E-03 | 1.43E-02 | up | 1.383827 |
| P08754 | Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 - [GNAI3_HUMAN] | 5.07E-04 | 4.38E-03 | down | -1.5921568 |

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| P13861 | cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2 - [KAP2_HUMAN] | 2.99E-03 | 1.28E-02 | down | -1.5732346 |
| P13928 | Annexin A8 OS=Homo sapiens GN=ANXA8 PE=1 SV=3 - [ANXA8_HUMAN] | 6.20E-04 | 4.92E-03 | down | -1.3408294 |
| Q8TEX9 | Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2 - [IPO4_HUMAN] | 2.20E-02 | 4.97E-02 | down | -1.1967877 |
| P07205 | Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN] | 1.29E-02 | 3.38E-02 | up | 1.2785542 |
| P01116 | GTPase KRas OS=Homo sapiens GN=KRAS PE=1 SV=1 - [RASK_HUMAN] | 1.09E-02 | 3.02E-02 | down | -1.2984385 |
| Q16563 | Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=1 SV=1 - [SYPL1_HUMAN] | 2.06E-03 | 9.82E-03 | up | 1.2860348 |
| Q9NWW4 | UPF0587 protein C1orf123 OS=Homo sapiens GN=C1orf123 PE=1 SV=1 - [CA123_HUMAN] | 1.29E-03 | 7.28E-03 | down | -1.3113347 |
| O75340 | Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1 - [PDCD6_HUMAN] | 4.91E-04 | 4.30E-03 | down | -2.1625555 |
| P34896 | Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN] | 1.24E-03 | 7.10E-03 | down | -1.3914781 |
| O75947 | ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN] | 7.32E-04 | 5.38E-03 | down | -1.2155179 |
| Q7L2H7 | Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 - [EIF3M_HUMAN] | 8.78E-04 | 5.89E-03 | down | -1.139839 |
| Q14512 | Fibroblast growth factor-binding protein 1 OS=Homo sapiens GN=FGFBP1 PE=1 SV=1 - [FGFP1_HUMAN] | 2.12E-02 | 4.84E-02 | up | 1.4420913 |
| Q86UP2 | Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1 - [KTN1_HUMAN] | 1.60E-04 | 2.44E-03 | down | -1.4343544 |
| O96019 | Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1 - [ACL6A_HUMAN] | 9.03E-04 | 6.01E-03 | down | -1.2459966 |
| O95861 | 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1 - [BPNT1_HUMAN] | 3.25E-04 | 3.46E-03 | up | 1.7618325 |
| Q92616 | eIF-2-alpha kinase activator GCN1 OS=Homo sapiens GN=GCN1 PE=1 SV=6 - [GCN1_HUMAN] | 4.19E-04 | 3.84E-03 | down | -1.2707899 |
| Q9Y678 | Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 - [COPG1_HUMAN] | 9.68E-02 | 2.76E-02 | up | 1.1939502 |
| Q08380 | Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN] | 2.14E-04 | 2.81E-03 | up | 1.935903 |
| Q14558 | Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=2 - [KPRA_HUMAN] | 3.39E-04 | 3.55E-03 | up | 1.3550591 |
| Q13126 | S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP PE=1 SV=2 - [MTAP_HUMAN] | 5.82E-05 | 1.78E-03 | up | 1.3452346 |
| P22059 | Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1 - [OSBP1_HUMAN] | 1.81E-02 | 4.31E-02 | up | 1.2997214 |
| P30566 | Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN] | 6.61E-03 | 2.14E-02 | down | -1.1616874 |
| Q15029 | 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - [U5S1_HUMAN] | 1.52E-02 | 3.80E-02 | down | -1.109069 |
| Q9Y446 | Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1 - [PKP3_HUMAN] | 2.60E-04 | 3.11E-03 | down | -1.6296604 |
| P33991 | DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5 - [MCM4_HUMAN] | 1.58E-04 | 2.44E-03 | down | -1.4498371 |
| Q12797 | Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3 - [ASPH_HUMAN] | 5.06E-05 | 1.78E-03 | up | 1.4420688 |
| P12532 | Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN] | 1.91E-06 | 8.34E-04 | up | 3.3859243 |
| Q9H307 | Pinin OS=Homo sapiens GN=PNN PE=1 SV=4 - [PININ_HUMAN] | 8.10E-03 | 2.44E-02 | down | -1.192626 |
| P53007 | Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN] | 4.00E-04 | 3.74E-03 | up | 1.2346582 |
| Q9Y490 | Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN] | 3.53E-03 | 1.42E-02 | down | -1.1710095 |
| Q9Y295 | Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1 - [DRG1_HUMAN] | 1.05E-03 | 6.45E-03 | down | -1.2131886 |
| Q13283 | Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 - [G3BP1_HUMAN] | 1.06E-02 | 2.93E-02 | down | -1.1862748 |
| Q6P2Q9 | Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN] | 1.13E-03 | 6.82E-03 | down | -1.2123522 |
| Q00325 | Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN] | 1.14E-02 | 3.12E-02 | up | 1.1472305 |

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| Q15393 | Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN] | 1.72E-02 | 4.13E-02 | down | -1.1477252 |
| Q9Y320 | Thioredoxin-related transmembrane protein 2 OS=Homo sapiens GN=TMX2 PE=1 SV=1 - [TMX2_HUMAN] | 6.58E-04 | 5.10E-03 | up | 1.483777 |
| P28062 | Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 - [PSB8_HUMAN] | 1.18E-04 | 2.15E-03 | up | 1.6555768 |
| P09622 | Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 - [DLDH_HUMAN] | 1.64E-05 | 1.36E-03 | up | 1.3070242 |
| Q9NZM1 | Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 - [MYOF_HUMAN] | 6.07E-05 | 1.78E-03 | down | -1.2412878 |
| P49321 | Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 - [NASP_HUMAN] | 3.48E-03 | 1.41E-02 | down | -1.6916473 |
| P48147 | Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 - [PPCE_HUMAN] | 6.69E-03 | 2.15E-02 | up | 1.1596283 |
| P00966 | Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN] | 4.41E-05 | 1.78E-03 | up | 2.498901 |
| O15067 | Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 - [PUR4_HUMAN] | 3.37E-03 | 1.39E-02 | down | -1.4083506 |
| Q15257 | Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PTPA PE=1 SV=3 - [PTPA_HUMAN] | 1.51E-02 | 3.78E-02 | up | 1.2398322 |
| P42224 | Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 - [STAT1_HUMAN] | 1.33E-02 | 3.46E-02 | down | -1.1049707 |
| P50416 | Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 - [CPT1A_HUMAN] | 4.26E-03 | 1.61E-02 | up | 1.353562 |
| P41252 | Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 - [SYIC_HUMAN] | 2.52E-03 | 1.14E-02 | up | 1.4402844 |
| Q9P035 | Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=HACD3 PE=1 SV=2 - [HACD3_HUMAN] | 3.75E-03 | 1.47E-02 | up | 1.4539803 |
| Q9BX40 | Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B PE=1 SV=1 - [LS14B_HUMAN] | 1.30E-02 | 3.41E-02 | up | 1.4748756 |
| P50897 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1 - [PPT1_HUMAN] | 1.35E-02 | 3.49E-02 | down | -1.321179 |
| Q722K6 | Endoplasmic reticulum metalloproteinase 1 OS=Homo sapiens GN=ERMP1 PE=1 SV=2 - [ERMP1_HUMAN] | 8.34E-03 | 2.50E-02 | up | 1.1831948 |
| P18031 | Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 - [PTN1_HUMAN] | 5.80E-03 | 1.98E-02 | up | 1.2737365 |
| P47755 | F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 - [CAZA2_HUMAN] | 1.50E-04 | 2.44E-03 | up | 1.701005 |
| Q99439 | Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 - [CNN2_HUMAN] | 1.62E-04 | 2.44E-03 | down | -2.8696566 |
| O75964 | ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3 - [ATP5L_HUMAN] | 1.22E-02 | 3.26E-02 | down | -1.3232837 |
| O43291 | Kunitz-type protease inhibitor 2 OS=Homo sapiens GN=SPINT2 PE=1 SV=2 - [SPIT2_HUMAN] | 4.22E-03 | 1.60E-02 | up | 1.1236874 |
| O75475 | PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1_HUMAN] | 7.64E-05 | 1.91E-03 | down | -2.1883593 |
| P30443 | HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 - [1A01_HUMAN] | 3.73E-04 | 3.61E-03 | up | 1.4614594 |
| Q9BUL8 | Programmed cell death protein 10 OS=Homo sapiens GN=PDCD10 PE=1 SV=1 - [PDC10_HUMAN] | 8.06E-03 | 2.44E-02 | up | 1.1784003 |
| P09525 | Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 - [ANXA4_HUMAN] | 2.15E-04 | 2.81E-03 | up | 1.8130257 |
| Q56VL3 | OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 - [OCAD2_HUMAN] | 1.53E-02 | 3.81E-02 | up | 1.549294 |
| Q8N884 | Cyclic GMP-AMP synthase OS=Homo sapiens GN=MB21D1 PE=1 SV=2 - [CGAS_HUMAN] | 5.43E-04 | 4.57E-03 | down | -1.2495068 |
| P48507 | Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1 - [GSH0_HUMAN] | 1.37E-02 | 3.53E-02 | down | -1.1450833 |
| O94826 | Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70 PE=1 SV=1 - [TOM70_HUMAN] | 7.40E-03 | 2.27E-02 | up | 1.1188831 |
| Q8WWM7 | Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2 - [ATX2L_HUMAN] | 1.19E-02 | 3.21E-02 | down | -1.1336836 |
| Q96TA1 | Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN] | 2.18E-04 | 2.81E-03 | up | 2.2896135 |
| Q9Y394 | Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7 PE=1 SV=1 - [DHRS7_HUMAN] | 9.43E-04 | 6.11E-03 | up | 1.1681348 |
| P53621 | Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 - [COPA_HUMAN] | 1.29E-02 | 3.39E-02 | up | 1.1597196 |

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| Q9UKZ1 | CCR4-NOT transcription complex subunit 11 OS=Homo sapiens GN=CNOT11 PE=1 SV=1 - [CNO11_HUMAN] | 2.13E-02 | 4.85E-02 | up | 1.2121085 |
| Q15050 | Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 - [RRS1_HUMAN] | 4.57E-03 | 1.66E-02 | up | 1.3037481 |
| P21283 | V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4 - [VATC1_HUMAN] | 1.71E-03 | 8.55E-03 | up | 1.450572 |
| Q14498 | RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39_HUMAN] | 8.25E-04 | 5.71E-03 | down | -1.2205482 |
| P23921 | Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 - [RIR1_HUMAN] | 1.53E-02 | 3.81E-02 | down | -1.4626693 |
| Q16222 | UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3 - [UAP1_HUMAN] | 2.91E-03 | 1.27E-02 | down | -1.4034836 |
| Q9BV19 | Uncharacterized protein C1orf50 OS=Homo sapiens GN=C1orf50 PE=1 SV=2 - [CA050_HUMAN] | 1.30E-03 | 7.31E-03 | down | -1.3427149 |
| Q13724 | Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS PE=1 SV=5 - [MOGS_HUMAN] | 9.50E-04 | 6.11E-03 | up | 1.4345765 |
| P14550 | Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3 - [AK1A1_HUMAN] | 2.21E-03 | 1.04E-02 | down | -1.3957207 |
| Q13547 | Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1 - [HDAC1_HUMAN] | 1.43E-03 | 7.73E-03 | down | -1.342396 |
| Q15645 | Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2 - [PCH2_HUMAN] | 1.56E-04 | 2.44E-03 | down | -1.3168436 |
| O60716 | Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN] | 1.10E-02 | 3.03E-02 | up | 1.1260769 |
| Q86TX2 | Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 - [ACOT1_HUMAN] | 7.14E-03 | 2.23E-02 | up | 1.2569525 |
| Q3LXA3 | Triokinase/FMN cyclase OS=Homo sapiens GN=TKFC PE=1 SV=2 - [TKFC_HUMAN] | 8.49E-05 | 1.93E-03 | up | 1.2506938 |
| P21291 | Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3 - [CSRP1_HUMAN] | 6.90E-04 | 5.21E-03 | up | 1.6530378 |
| P51809 | Vesicle-associated membrane protein 7 OS=Homo sapiens GN=VAMP7 PE=1 SV=3 - [VAMP7_HUMAN] | 4.54E-03 | 1.66E-02 | down | -1.2780358 |
| P18463 | HLA class I histocompatibility antigen, B-37 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 - [1B37_HUMAN] | 5.91E-05 | 1.78E-03 | up | 2.1537585 |
| O00159 | Unconventional myosin-1c OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN] | 5.05E-03 | 1.78E-02 | down | -1.3109862 |
| P46108 | Adapter molecule crk OS=Homo sapiens GN=CRK PE=1 SV=2 - [CRK_HUMAN] | 1.25E-02 | 3.32E-02 | down | -1.2291358 |
| P23919 | Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN] | 4.63E-05 | 1.78E-03 | down | -1.6315895 |
| Q93009 | Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2 - [UBP7_HUMAN] | 2.47E-03 | 1.13E-02 | up | 1.3057977 |
| P50995 | Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN] | 1.10E-03 | 6.70E-03 | up | 1.2172781 |
| Q96A33 | Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1 - [CCD47_HUMAN] | 1.17E-04 | 2.15E-03 | up | 1.4912884 |
| Q9BS26 | Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 - [ERP44_HUMAN] | 2.65E-03 | 1.19E-02 | up | 1.3178169 |
| O00203 | AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3 - [AP3B1_HUMAN] | 6.88E-03 | 2.19E-02 | up | 1.2140434 |
| Q14914 | Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN] | 9.36E-06 | 1.36E-03 | down | -1.5355291 |
| Q9BQ52 | Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=ELAC2 PE=1 SV=2 - [RNZ2_HUMAN] | 5.20E-03 | 1.83E-02 | down | -1.6913863 |
| O75494 | Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10 PE=1 SV=1 - [SRS10_HUMAN] | 5.83E-03 | 1.98E-02 | down | -1.3410664 |
| Q9UHB6 | LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1 - [LIMA1_HUMAN] | 1.44E-02 | 3.66E-02 | down | -1.5125822 |
| P09874 | Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN] | 1.04E-02 | 2.90E-02 | up | 1.3567923 |
| P06746 | DNA polymerase beta OS=Homo sapiens GN=POLB PE=1 SV=3 - [DPOLB_HUMAN] | 1.53E-03 | 8.06E-03 | down | -1.1838535 |
| P00533 | Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 - [EGFR_HUMAN] | 1.64E-04 | 2.44E-03 | down | -2.0065012 |
| P58107 | Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN] | 8.65E-05 | 1.93E-03 | down | -1.2566304 |
| P55884 | Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 - [EIF3B_HUMAN] | 5.64E-04 | 4.64E-03 | down | -1.3158051 |

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| P09417 | Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN] | 1.74E-04 | 2.50E-03 | up | 1.6191547 |
| Q8WUA7 | TBC1 domain family member 22A OS=Homo sapiens GN=TBC1D22A PE=1 SV=2 - [TB22A_HUMAN] | 1.53E-02 | 3.81E-02 | up | 1.2787445 |
| P17812 | CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2 - [PYRG1_HUMAN] | 6.05E-04 | 4.84E-03 | down | -1.5289824 |
| Q8TBX8 | Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens GN=PIP4K2C PE=1 SV=3 - [PI42C_HUMAN] | 1.13E-02 | 3.09E-02 | up | 1.1981641 |
| P07954 | Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN] | 2.61E-03 | 1.17E-02 | up | 1.586866 |
| Q9H788 | SH2 domain-containing protein 4A OS=Homo sapiens GN=SH2D4A PE=1 SV=1 - [SH24A_HUMAN] | 2.03E-02 | 4.67E-02 | up | 1.3383296 |
| Q9P2E9 | Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN] | 9.20E-03 | 2.66E-02 | up | 1.3453128 |
| Q9NPH2 | Inositol-3-phosphate synthase 1 OS=Homo sapiens GN=ISYNA1 PE=1 SV=1 - [INO1_HUMAN] | 3.67E-03 | 1.45E-02 | down | -1.439747 |
| Q00341 | Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2 - [VIGLN_HUMAN] | 8.02E-05 | 1.93E-03 | down | -1.256816 |
| Q9NR45 | Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN] | 1.60E-03 | 8.30E-03 | up | 2.017355 |
| P51116 | Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 - [FXR2_HUMAN] | 9.66E-03 | 2.76E-02 | down | -1.4320009 |
| P07686 | Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN] | 5.18E-06 | 1.13E-03 | up | 2.9749308 |
| P61163 | Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 - [ACTZ_HUMAN] | 7.69E-03 | 2.34E-02 | down | -1.3391565 |
| Q00403 | Transcription initiation factor IIB OS=Homo sapiens GN=GTF2B PE=1 SV=1 - [TF2B_HUMAN] | 9.04E-05 | 1.93E-03 | down | -1.6268498 |
| Q6IBS0 | Twintilin-2 OS=Homo sapiens GN=TW2F2 PE=1 SV=2 - [TW2F2_HUMAN] | 1.29E-03 | 7.28E-03 | down | -1.3557509 |
| O60437 | Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4 - [PEPL_HUMAN] | 1.86E-03 | 9.03E-03 | up | 1.3550858 |
| P45974 | Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN] | 6.92E-03 | 2.20E-02 | up | 1.3926362 |
| O75746 | Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2 - [CMC1_HUMAN] | 5.58E-03 | 1.93E-02 | up | 1.1514953 |
| Q9H488 | GDP-fucose protein O-fucosyltransferase 1 OS=Homo sapiens GN=POFUT1 PE=1 SV=1 - [OFUT1_HUMAN] | 9.77E-04 | 6.18E-03 | down | -1.2536441 |
| Q9GZL7 | Ribosome biogenesis protein WDR12 OS=Homo sapiens GN=WDR12 PE=1 SV=2 - [WDR12_HUMAN] | 8.79E-03 | 2.59E-02 | down | -1.407055 |
| Q96GA7 | Serine dehydratase-like OS=Homo sapiens GN=SDSL PE=1 SV=1 - [SDSL_HUMAN] | 2.61E-04 | 3.11E-03 | up | 1.6641517 |
| Q8N1G4 | Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1 - [LRC47_HUMAN] | 5.98E-03 | 2.01E-02 | down | -1.2038138 |
| Q9UBU8 | Mortality factor 4-like protein 1 OS=Homo sapiens GN=MORF4L1 PE=1 SV=2 - [MO4L1_HUMAN] | 1.44E-02 | 3.66E-02 | down | -1.2230835 |
| Q9Y5Z4 | Heme-binding protein 2 OS=Homo sapiens GN=HEBP2 PE=1 SV=1 - [HEBP2_HUMAN] | 3.13E-04 | 3.39E-03 | up | 1.6592985 |
| Q9BQG0 | Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN] | 1.48E-03 | 7.93E-03 | down | -1.2400677 |
| P63279 | SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1 - [UBC9_HUMAN] | 3.04E-04 | 3.37E-03 | up | 1.4283125 |
| O00154 | Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3 - [BACH_HUMAN] | 3.49E-03 | 1.41E-02 | down | -1.4204521 |
| Q9Y2Z0 | Protein SGT1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3 - [SGT1_HUMAN] | 4.44E-03 | 1.65E-02 | down | -1.4518747 |
| Q969L2 | Protein MAL2 OS=Homo sapiens GN=MAL2 PE=1 SV=1 - [MAL2_HUMAN] | 3.08E-03 | 1.30E-02 | up | 1.3011281 |
| Q14232 | Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=1 SV=1 - [EI2BA_HUMAN] | 4.68E-03 | 1.68E-02 | down | -1.2916558 |
| Q9Y6N5 | Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [SQRD_HUMAN] | 3.78E-03 | 1.48E-02 | up | 1.2973895 |
| Q96T76 | MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 - [MMS19_HUMAN] | 5.72E-03 | 1.96E-02 | down | -1.409594 |
| P25205 | DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN] | 2.47E-03 | 1.13E-02 | down | -1.3640145 |
| P36543 | V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1 - [VATE1_HUMAN] | 1.72E-03 | 8.57E-03 | up | 1.5892648 |

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| Q9P0V9 | Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2 - [SEP10_HUMAN] | 2.29E-04 | 2.87E-03 | down | -3.1691968 |
| P36776 | Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN] | 3.47E-04 | 3.55E-03 | up | 1.681468 |
| Q9H6F5 | Coiled-coil domain-containing protein 86 OS=Homo sapiens GN=CCDC86 PE=1 SV=1 - [CCD86_HUMAN] | 1.12E-04 | 2.11E-03 | down | -1.461012 |
| P52815 | 39S ribosomal protein L12, mitochondrial OS=Homo sapiens GN=MRPL12 PE=1 SV=2 - [RM12_HUMAN] | 2.06E-02 | 4.73E-02 | up | 1.1835872 |
| Q9BSH4 | Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1 - [TACO1_HUMAN] | 4.45E-04 | 4.02E-03 | up | 1.3613174 |
| Q9Y266 | Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 - [NUDC_HUMAN] | 3.32E-05 | 1.71E-03 | down | -1.9088488 |
| P10114 | Ras-related protein Rap-2a OS=Homo sapiens GN=RAP2A PE=1 SV=1 - [RAP2A_HUMAN] | 6.37E-04 | 4.98E-03 | up | 1.537162 |
| Q9BZE4 | Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1_HUMAN] | 1.66E-03 | 8.45E-03 | down | -1.2020156 |
| P19623 | Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 - [SPEE_HUMAN] | 3.50E-06 | 8.76E-04 | down | -2.0793793 |
| Q9Y478 | 5'-AMP-activated protein kinase subunit beta-1 OS=Homo sapiens GN=PRKAB1 PE=1 SV=4 - [AAKB1_HUMAN] | 4.13E-03 | 1.57E-02 | up | 1.2668242 |
| Q53H12 | Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=1 SV=2 - [AGK_HUMAN] | 8.42E-04 | 5.78E-03 | up | 1.1963671 |
| O94979 | Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=3 - [SC31A_HUMAN] | 1.90E-02 | 4.45E-02 | up | 1.2902408 |
| Q8NF37 | Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 - [PCAT1_HUMAN] | 4.63E-03 | 1.68E-02 | down | -1.2672658 |
| P00749 | Urokinase-type plasminogen activator OS=Homo sapiens GN=PLAU PE=1 SV=2 - [UROK_HUMAN] | 7.36E-03 | 2.27E-02 | up | 1.5188869 |
| Q9BSD7 | Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 - [NTPCR_HUMAN] | 2.74E-04 | 3.20E-03 | up | 2.0379148 |
| Q96GX9 | Methylthioribulose-1-phosphate dehydratase OS=Homo sapiens GN=APIP PE=1 SV=1 - [MTNB_HUMAN] | 1.61E-03 | 8.31E-03 | up | 1.1866856 |
| Q9NZ08 | Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3 - [ERAP1_HUMAN] | 1.10E-03 | 6.69E-03 | up | 1.6819026 |
| O60841 | Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN] | 1.50E-02 | 3.77E-02 | down | -1.174676 |
| P50895 | Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN] | 1.95E-03 | 9.38E-03 | down | -1.5468674 |
| Q96RP9 | Elongation factor G, mitochondrial OS=Homo sapiens GN=GFM1 PE=1 SV=2 - [EFGM_HUMAN] | 6.30E-03 | 2.08E-02 | up | 1.2896384 |
| P56537 | Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 - [IF6_HUMAN] | 1.31E-04 | 2.30E-03 | down | -1.5281272 |
| Q9Y570 | Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 - [PPME1_HUMAN] | 6.32E-03 | 2.08E-02 | up | 1.1573726 |
| Q9Y5X3 | Sorting nexin-5 OS=Homo sapiens GN=SNX5 PE=1 SV=1 - [SNX5_HUMAN] | 4.21E-03 | 1.60E-02 | up | 1.2299447 |
| P51812 | Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 - [KS6A3_HUMAN] | 1.07E-02 | 2.96E-02 | up | 1.1284436 |
| Q8NFJ5 | Retinoic acid-induced protein 3 OS=Homo sapiens GN=GPRC5A PE=1 SV=2 - [RAI3_HUMAN] | 6.05E-05 | 1.78E-03 | up | 2.446458 |
| Q12788 | Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2 - [TBL3_HUMAN] | 8.94E-03 | 2.62E-02 | down | -1.3035139 |
| Q14344 | Guanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2 - [GNA13_HUMAN] | 1.24E-04 | 2.21E-03 | up | 1.4162366 |
| Q92530 | Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 - [PSMF1_HUMAN] | 2.28E-03 | 1.07E-02 | down | -1.3225527 |
| O43813 | LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1 - [LANC1_HUMAN] | 2.18E-04 | 2.81E-03 | up | 2.9125082 |
| P04040 | Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN] | 2.54E-05 | 1.44E-03 | up | 2.2587867 |
| Q99541 | Perilipin-2 OS=Homo sapiens GN=PLIN2 PE=1 SV=2 - [PLIN2_HUMAN] | 2.80E-03 | 1.24E-02 | up | 1.4395255 |
| Q16666 | Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16 PE=1 SV=3 - [IF16_HUMAN] | 1.26E-05 | 1.36E-03 | up | 1.8990318 |
| P55265 | Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] | 1.00E-04 | 2.01E-03 | up | 1.4333954 |
| P61421 | V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1 - [VAOD1_HUMAN] | 4.58E-04 | 4.06E-03 | up | 1.5366842 |

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| Q6UXH1 | Cysteine-rich with EGF-like domain protein 2 OS=Homo sapiens GN=CRELD2 PE=1 SV=1 - [CRELD2_HUMAN] | 6.74E-04 | 5.11E-03 | up | 2.1996548 |
| Q15021 | Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 - [CND1_HUMAN] | 7.50E-04 | 5.41E-03 | down | -1.3730582 |
| Q9BWS9 | Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1 - [CHID1_HUMAN] | 5.47E-04 | 4.58E-03 | up | 1.3908793 |
| Q9NZT2 | Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3 - [OGFR_HUMAN] | 9.10E-03 | 2.65E-02 | up | 1.1740304 |
| O60610 | Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 - [DIAP1_HUMAN] | 1.96E-02 | 4.56E-02 | down | -1.1406935 |
| O14684 | Prostaglandin E synthase OS=Homo sapiens GN=PTGES PE=1 SV=2 - [PTGES_HUMAN] | 3.80E-03 | 1.48E-02 | up | 3.5154588 |
| P27701 | CD82 antigen OS=Homo sapiens GN=CD82 PE=1 SV=1 - [CD82_HUMAN] | 1.61E-03 | 8.31E-03 | up | 1.598229 |
| O76027 | Annexin A9 OS=Homo sapiens GN=ANXA9 PE=1 SV=3 - [ANXA9_HUMAN] | 7.57E-05 | 1.91E-03 | up | 2.784713 |
| Q92879 | CUGBP Elav-like family member 1 OS=Homo sapiens GN=CELF1 PE=1 SV=2 - [CELF1_HUMAN] | 9.71E-04 | 6.16E-03 | down | -1.2149919 |
| P06865 | Beta-hexosaminidase subunit alpha OS=Homo sapiens GN=HEXA PE=1 SV=2 - [HEXA_HUMAN] | 1.99E-05 | 1.36E-03 | up | 2.9524713 |
| Q14134 | Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2 - [TRI29_HUMAN] | 1.13E-02 | 3.10E-02 | down | -1.1202435 |
| Q9UBB4 | Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1 - [ATX10_HUMAN] | 1.86E-03 | 9.03E-03 | up | 1.5241088 |
| Q9BQ39 | ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1 - [DDX50_HUMAN] | 6.10E-03 | 2.03E-02 | down | -1.8190496 |
| O60749 | Sorting nexin-2 OS=Homo sapiens GN=SNX2 PE=1 SV=2 - [SNX2_HUMAN] | 3.62E-04 | 3.61E-03 | up | 1.3565215 |
| Q9BW04 | Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2 - [SARG_HUMAN] | 2.92E-03 | 1.27E-02 | down | -1.5747366 |
| P00390 | Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 - [GSHR_HUMAN] | 6.31E-05 | 1.78E-03 | up | 2.4924774 |
| P45983 | Mitogen-activated protein kinase 8 OS=Homo sapiens GN=MAPK8 PE=1 SV=2 - [MK08_HUMAN] | 2.55E-04 | 3.08E-03 | down | -2.2800934 |
| Q99848 | Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2 - [EBP2_HUMAN] | 7.70E-04 | 5.51E-03 | down | -1.6622479 |
| P51659 | Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3 - [DHB4_HUMAN] | 5.55E-05 | 1.78E-03 | up | 1.5258179 |
| Q14978 | Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2 - [NOLC1_HUMAN] | 8.47E-05 | 1.93E-03 | down | -1.6888846 |
| Q9UHY1 | Nuclear receptor-binding protein OS=Homo sapiens GN=NRBP1 PE=1 SV=1 - [NRBP_HUMAN] | 9.43E-03 | 2.71E-02 | up | 1.3206558 |
| P15104 | Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 - [GLNA_HUMAN] | 4.48E-03 | 1.65E-02 | up | 1.3073772 |
| Q8IU00 | Trafficking protein particle complex subunit 5 OS=Homo sapiens GN=TRAPPC5 PE=1 SV=1 - [TPPCS_HUMAN] | 6.42E-03 | 2.09E-02 | up | 1.3734064 |
| P13798 | Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN] | 1.64E-02 | 4.02E-02 | down | -1.1407412 |
| Q9UI12 | V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1 - [VATH_HUMAN] | 1.57E-03 | 8.21E-03 | up | 1.4507337 |
| P51648 | Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN] | 1.94E-04 | 2.70E-03 | down | -1.3439752 |
| P50402 | Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 - [EMD_HUMAN] | 7.09E-03 | 2.22E-02 | down | -1.5698254 |
| P49189 | 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN] | 1.59E-05 | 1.36E-03 | up | 1.4587952 |
| Q9Y3A4 | Ribosomal RNA-processing protein 7 homolog A OS=Homo sapiens GN=RRP7A PE=1 SV=2 - [RRP7A_HUMAN] | 9.10E-03 | 2.65E-02 | down | -1.2266407 |
| P52306 | Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3 - [GDS1_HUMAN] | 1.56E-02 | 3.85E-02 | down | -1.121545 |
| Q08AF3 | Schlafen family member 5 OS=Homo sapiens GN=SLFN5 PE=1 SV=1 - [SLFN5_HUMAN] | 7.92E-04 | 5.60E-03 | up | 1.9826893 |
| O75643 | U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 - [U520_HUMAN] | 9.52E-03 | 2.73E-02 | down | -1.1944007 |
| Q9H4A5 | Golgi phosphoprotein 3-like OS=Homo sapiens GN=GOLPH3L PE=1 SV=1 - [GLP3L_HUMAN] | 7.45E-03 | 2.27E-02 | up | 1.9586179 |
| Q9BPX3 | Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1 - [CND3_HUMAN] | 9.49E-04 | 6.11E-03 | down | -1.3318311 |

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| Q7L1Q6 | Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 - [BZW1_HUMAN] | 1.14E-03 | 6.82E-03 | down | -1.6815206 |
| Q9Y276 | Mitochondrial chaperone BCS1 OS=Homo sapiens GN=BCS1L PE=1 SV=1 - [BCS1_HUMAN] | 1.65E-03 | 8.39E-03 | down | -1.7372831 |
| P51159 | Ras-related protein Rab-27A OS=Homo sapiens GN=RAB27A PE=1 SV=3 - [RB27A_HUMAN] | 5.87E-03 | 1.98E-02 | up | 1.4642688 |
| P49642 | DNA primase small subunit OS=Homo sapiens GN=PRIM1 PE=1 SV=1 - [PRI1_HUMAN] | 8.14E-04 | 5.71E-03 | down | -1.7366599 |
| P48449 | Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1 - [ERG7_HUMAN] | 1.62E-03 | 8.34E-03 | up | 1.4240606 |
| Q8NFH3 | Nucleoporin Nup43 OS=Homo sapiens GN=NUP43 PE=1 SV=1 - [NUP43_HUMAN] | 8.42E-03 | 2.51E-02 | down | -1.2197393 |
| Q15533 | Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 - [TPSN_HUMAN] | 8.24E-04 | 5.71E-03 | up | 2.064553 |
| Q6NUK1 | Calcium-binding mitochondrial carrier protein ScaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2 - [SCMC1_HUMAN] | 9.74E-05 | 2.01E-03 | down | -1.4782157 |
| Q86U38 | Nucleolar protein 9 OS=Homo sapiens GN=NOP9 PE=1 SV=1 - [NOP9_HUMAN] | 4.46E-03 | 1.65E-02 | up | 1.517769 |
| P49959 | Double-strand break repair protein MRE11 OS=Homo sapiens GN=MRE11 PE=1 SV=3 - [MRE11_HUMAN] | 5.43E-03 | 1.88E-02 | up | 1.2570578 |
| Q9UDY2 | Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2 - [ZO2_HUMAN] | 2.01E-04 | 2.73E-03 | up | 1.7104182 |
| P11182 | Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3 - [ODB2_HUMAN] | 1.92E-02 | 4.50E-02 | down | -1.4291689 |
| O95747 | Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 - [OXSR1_HUMAN] | 1.02E-03 | 6.38E-03 | up | 1.2839477 |
| P57768 | Sorting nexin-16 OS=Homo sapiens GN=SNX16 PE=1 SV=2 - [SNX16_HUMAN] | 1.95E-02 | 4.56E-02 | up | 1.4950898 |
| P46459 | Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3 - [NSF_HUMAN] | 7.70E-06 | 1.35E-03 | up | 1.8119555 |
| Q14744 | Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 - [ANM5_HUMAN] | 1.65E-02 | 4.03E-02 | down | -1.2156925 |
| O60762 | Dolichol-phosphate mannosyltransferase subunit 1 OS=Homo sapiens GN=DPM1 PE=1 SV=1 - [DPM1_HUMAN] | 7.37E-03 | 2.27E-02 | up | 1.2151911 |
| O95478 | Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens GN=NSA2 PE=1 SV=1 - [NSA2_HUMAN] | 8.41E-03 | 2.51E-02 | down | -1.2447759 |
| Q13308 | Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2 - [PTK7_HUMAN] | 1.23E-03 | 7.10E-03 | down | -1.2785714 |
| P35580 | Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN] | 2.49E-04 | 3.05E-03 | down | -1.4624026 |
| Q99747 | Gamma-soluble NSF attachment protein OS=Homo sapiens GN=NAPG PE=1 SV=1 - [SNAG_HUMAN] | 1.99E-06 | 8.34E-04 | up | 1.301351 |
| P31937 | 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN] | 1.25E-03 | 7.12E-03 | up | 1.3404347 |
| Q9Y285 | Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN] | 2.13E-02 | 4.85E-02 | down | -1.2721947 |
| P25685 | DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 - [DNJB1_HUMAN] | 2.55E-05 | 1.44E-03 | up | 1.2354383 |
| Q9NRJ5 | Poly(A) polymerase beta OS=Homo sapiens GN=PAPOLB PE=2 SV=1 - [PAPOB_HUMAN] | 4.30E-05 | 1.78E-03 | down | -1.7611123 |
| Q9HCC0 | Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN] | 1.55E-02 | 3.84E-02 | up | 1.4034 |
| O60906 | Sphingomyelin phosphodiesterase 2 OS=Homo sapiens GN=SMPD2 PE=1 SV=2 - [NSMA_HUMAN] | 2.00E-03 | 9.60E-03 | up | 1.2967778 |
| O95834 | Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2 PE=1 SV=1 - [EMAL2_HUMAN] | 1.24E-03 | 7.10E-03 | up | 1.4021201 |
| Q14787 | Transportin-2 OS=Homo sapiens GN=TNPO2 PE=1 SV=3 - [TNPO2_HUMAN] | 1.04E-03 | 6.44E-03 | up | 1.4744554 |
| P48735 | Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 - [IDHP_HUMAN] | 2.26E-04 | 2.86E-03 | up | 1.4327364 |
| Q9UIA9 | Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3 - [XPO7_HUMAN] | 1.15E-03 | 6.83E-03 | up | 1.2675384 |
| Q9NSE4 | Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2 - [SYIM_HUMAN] | 4.46E-03 | 1.65E-02 | up | 1.7426889 |
| Q16186 | Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 - [ADRM1_HUMAN] | 2.97E-03 | 1.28E-02 | down | -1.2287655 |
| Q2TAY7 | WD40 repeat-containing protein SMU1 OS=Homo sapiens GN=SMU1 PE=1 SV=2 - [SMU1_HUMAN] | 1.40E-02 | 3.58E-02 | down | -1.2146875 |

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| Q16831 | Uridine phosphorylase 1 OS=Homo sapiens GN=UPP1 PE=1 SV=1 - [UPP1_HUMAN] | 1.17E-03 | 6.92E-03 | up | 1.583172 |
| Q9Y6K5 | 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3 - [OAS3_HUMAN] | 9.42E-05 | 1.99E-03 | up | 1.3342782 |
| Q9Y6M1 | Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2 - [IF2B2_HUMAN] | 9.42E-03 | 2.71E-02 | down | -3.6895058 |
| Q5C9Z4 | Nucleolar MIF4G domain-containing protein 1 OS=Homo sapiens GN=NOM1 PE=1 SV=1 - [NOM1_HUMAN] | 1.08E-03 | 6.59E-03 | up | 1.6000432 |
| Q9H9A6 | Leucine-rich repeat-containing protein 40 OS=Homo sapiens GN=LRRC40 PE=1 SV=1 - [LRC40_HUMAN] | 0.00E+00 | 0.00E+00 | down | -16 |
| Q9UJ70 | N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4 - [NAGK_HUMAN] | 3.27E-03 | 1.36E-02 | up | 1.7269212 |
| Q9H6W3 | Ribosomal oxygenase 1 OS=Homo sapiens GN=RIOX1 PE=1 SV=2 - [RIOX1_HUMAN] | 6.41E-03 | 2.09E-02 | down | -1.1208888 |
| Q86V21 | Acetoacetyl-CoA synthetase OS=Homo sapiens GN=AACS PE=1 SV=1 - [AACS_HUMAN] | 1.64E-05 | 1.36E-03 | down | -2.0512118 |
| Q6PI48 | Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1 - [SYDM_HUMAN] | 9.37E-04 | 6.11E-03 | up | 1.5726361 |
| Q9Y3Z3 | Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2 - [SAMH1_HUMAN] | 3.71E-04 | 3.61E-03 | up | 1.4277416 |
| O75400 | Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 - [PR40A_HUMAN] | 2.01E-02 | 4.65E-02 | down | -1.1814973 |
| O15127 | Secretory carrier-associated membrane protein 2 OS=Homo sapiens GN=SCAMP2 PE=1 SV=2 - [SCAM2_HUMAN] | 3.00E-03 | 1.28E-02 | up | 1.3049076 |
| Q9ULX3 | RNA-binding protein NOB1 OS=Homo sapiens GN=NOB1 PE=1 SV=1 - [NOB1_HUMAN] | 2.22E-04 | 2.84E-03 | down | -1.5035427 |
| O14896 | Interferon regulatory factor 6 OS=Homo sapiens GN=IRF6 PE=1 SV=1 - [IRF6_HUMAN] | 2.95E-03 | 1.28E-02 | up | 1.4686584 |
| O60264 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 - [SMCA5_HUMAN] | 1.43E-02 | 3.65E-02 | down | -1.2105724 |
| O94925 | Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1 - [GLSK_HUMAN] | 4.17E-04 | 3.84E-03 | down | -1.2727522 |
| Q96S44 | TP53-regulating kinase OS=Homo sapiens GN=TP53RK PE=1 SV=2 - [PRPK_HUMAN] | 3.50E-03 | 1.41E-02 | up | 1.2900254 |
| P52566 | Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDI2 PE=1 SV=3 - [GDIR2_HUMAN] | 1.86E-05 | 1.36E-03 | up | 2.3920696 |
| P22307 | Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN] | 9.14E-03 | 2.65E-02 | down | -1.2692349 |
| Q9P2R7 | Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=1 SV=3 - [SUCB1_HUMAN] | 9.00E-05 | 1.93E-03 | up | 1.4459355 |
| Q93050 | V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3 - [VPP1_HUMAN] | 1.23E-04 | 2.21E-03 | up | 1.9227544 |
| Q08722 | Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1 - [CD47_HUMAN] | 2.18E-04 | 2.81E-03 | up | 1.6584599 |
| Q9Y5A7 | NEDD8 ultimate buster 1 OS=Homo sapiens GN=NUB1 PE=1 SV=2 - [NUB1_HUMAN] | 1.24E-02 | 3.29E-02 | up | 1.7533697 |
| O43663 | Protein regulator of cytokinesis 1 OS=Homo sapiens GN=PRC1 PE=1 SV=2 - [PRC1_HUMAN] | 6.62E-04 | 5.11E-03 | down | -1.7139791 |
| Q13045 | Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2 - [FLII_HUMAN] | 4.69E-03 | 1.68E-02 | down | -1.2113197 |
| Q9N666 | Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2 - [MBOA7_HUMAN] | 1.21E-02 | 3.25E-02 | down | -1.274538 |
| Q15003 | Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=1 SV=3 - [CND2_HUMAN] | 1.01E-02 | 2.85E-02 | down | -1.472106 |
| P46087 | Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN] | 8.93E-03 | 2.62E-02 | down | -1.1640453 |
| Q9Y6M7 | Sodium bicarbonate cotransporter 3 OS=Homo sapiens GN=SLC4A7 PE=1 SV=2 - [S4A7_HUMAN] | 2.01E-02 | 4.65E-02 | down | -1.1880937 |
| Q9GZR7 | ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=1 SV=1 - [DDX24_HUMAN] | 2.95E-03 | 1.28E-02 | down | -1.3916662 |
| Q16775 | Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN] | 1.33E-03 | 7.37E-03 | up | 1.845707 |
| P27694 | Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2 - [RFA1_HUMAN] | 3.38E-03 | 1.39E-02 | down | -1.3268305 |
| Q15020 | Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 - [SART3_HUMAN] | 1.51E-03 | 8.02E-03 | up | 1.1961639 |
| Q9UNQ2 | Probable dimethyladenosine transferase OS=Homo sapiens GN=DIMT1 PE=1 SV=1 - [DIM1_HUMAN] | 1.78E-02 | 4.25E-02 | down | -1.1958653 |

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| Q9BSJ8 | Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN] | 9.08E-03 | 2.65E-02 | down | -1.1641192 |
| Q96SQ9 | Cytochrome P450 2S1 OS=Homo sapiens GN=CYP2S1 PE=1 SV=2 - [CP2S1_HUMAN] | 4.65E-03 | 1.68E-02 | down | -1.2561288 |
| Q14956 | Transmembrane glycoprotein NMB OS=Homo sapiens GN=GPNMB PE=1 SV=2 - [GPNMB_HUMAN] | 3.20E-03 | 1.34E-02 | up | 3.8122861 |
| Q13416 | Origin recognition complex subunit 2 OS=Homo sapiens GN=ORC2 PE=1 SV=2 - [ORC2_HUMAN] | 1.15E-02 | 3.14E-02 | down | -1.5569828 |
| O95347 | Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2 - [SMC2_HUMAN] | 9.79E-03 | 2.77E-02 | down | -1.2051346 |
| Q9BRR6 | ADP-dependent glucokinase OS=Homo sapiens GN=ADPGK PE=1 SV=1 - [ADPGK_HUMAN] | 7.05E-03 | 2.22E-02 | up | 1.2796909 |
| P16070 | CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3 - [CD44_HUMAN] | 7.18E-03 | 2.24E-02 | down | -1.4455993 |
| P54687 | Branched-chain-amino-acid aminotransferase, cytosolic OS=Homo sapiens GN=BCAT1 PE=1 SV=3 - [BCAT1_HUMAN] | 1.80E-03 | 8.88E-03 | up | 1.7024701 |
| P16278 | Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2 - [BGAL_HUMAN] | 1.68E-05 | 1.36E-03 | up | 2.674876 |
| Q9UJU6 | Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN] | 6.18E-03 | 2.05E-02 | down | -1.4999853 |
| P27708 | CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN] | 5.77E-03 | 1.97E-02 | down | -1.4113257 |
| Q9H4I3 | TraB domain-containing protein OS=Homo sapiens GN=TRABD PE=1 SV=1 - [TRABD_HUMAN] | 1.04E-02 | 2.90E-02 | up | 1.2781523 |
| O43865 | S-adenosylhomocysteine hydrolase-like protein 1 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2 - [SAHH2_HUMAN] | 6.29E-04 | 4.96E-03 | down | -1.2098899 |
| Q02880 | DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3 - [TOP2B_HUMAN] | 1.22E-02 | 3.26E-02 | up | 1.2403648 |
| Q13033 | Striatin-3 OS=Homo sapiens GN=STRN3 PE=1 SV=3 - [STRN3_HUMAN] | 9.75E-03 | 2.77E-02 | down | -1.2795827 |
| Q8NBM4 | Ubiquitin-associated domain-containing protein 2 OS=Homo sapiens GN=UBAC2 PE=1 SV=1 - [UBAC2_HUMAN] | 1.22E-02 | 3.26E-02 | up | 1.1888158 |
| P0DMP2 | SLIT-ROBO Rho GTPase-activating protein 2B OS=Homo sapiens GN=SRGAP2B PE=3 SV=1 - [SRG2B_HUMAN] | 9.83E-03 | 2.78E-02 | up | 1.8545426 |
| Q14534 | Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=1 SV=3 - [ERG1_HUMAN] | 5.62E-04 | 4.64E-03 | up | 1.6891527 |
| Q5H9R7 | Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=1 SV=2 - [PP6R3_HUMAN] | 3.03E-05 | 1.63E-03 | down | -1.119556 |
| Q8NI36 | WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1 - [WDR36_HUMAN] | 8.51E-03 | 2.53E-02 | down | -1.5635501 |
| Q5K651 | Sterile alpha motif domain-containing protein 9 OS=Homo sapiens GN=SAMD9 PE=1 SV=1 - [SAMD9_HUMAN] | 1.84E-02 | 4.35E-02 | down | -1.5779779 |
| P78347 | General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 - [GTF2I_HUMAN] | 1.34E-03 | 7.37E-03 | down | -1.1755334 |
| Q13823 | Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 - [NOG2_HUMAN] | 6.56E-04 | 5.10E-03 | down | -1.3253435 |
| Q9UHL4 | Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3 - [DPP2_HUMAN] | 5.16E-04 | 4.41E-03 | up | 1.5832589 |
| Q13188 | Serine/threonine-protein kinase 3 OS=Homo sapiens GN=STK3 PE=1 SV=2 - [STK3_HUMAN] | 4.66E-03 | 1.68E-02 | up | 1.9148835 |
| Q9Y2T3 | Guanine deaminase OS=Homo sapiens GN=GDA PE=1 SV=1 - [GUAD_HUMAN] | 2.31E-03 | 1.07E-02 | up | 2.248735 |
| P53985 | Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 - [MOT1_HUMAN] | 1.49E-02 | 3.76E-02 | down | -1.4588302 |
| O95400 | CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens GN=CD2BP2 PE=1 SV=1 - [CD2B2_HUMAN] | 4.61E-03 | 1.67E-02 | down | -1.4955467 |
| Q02040 | A-kinase anchor protein 17A OS=Homo sapiens GN=AKAP17A PE=1 SV=2 - [AK17A_HUMAN] | 5.98E-04 | 4.82E-03 | up | 1.7645462 |
| Q96JB2 | Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3 - [COG3_HUMAN] | 1.46E-03 | 7.84E-03 | up | 1.3927218 |
| O94832 | Unconventional myosin-IId OS=Homo sapiens GN=MYO1D PE=1 SV=2 - [MYO1D_HUMAN] | 8.98E-03 | 2.63E-02 | up | 1.6863748 |
| Q15643 | Thyroid receptor-interacting protein 11 OS=Homo sapiens GN=TRIP11 PE=1 SV=3 - [TRIPB_HUMAN] | 6.09E-03 | 2.03E-02 | down | -1.2959384 |
| Q92609 | TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5 PE=1 SV=1 - [TBCD5_HUMAN] | 1.02E-04 | 2.02E-03 | up | 1.5077848 |
| Q8N442 | Translation factor GUF1, mitochondrial OS=Homo sapiens GN=GUF1 PE=1 SV=1 - [GUF1_HUMAN] | 1.34E-03 | 7.37E-03 | up | 1.5227385 |

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| P12955 | Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 - [PEPD_HUMAN] | 1.19E-02 | 3.21E-02 | up | 1.461973 |
| P80303 | Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2 - [NUCB2_HUMAN] | 1.87E-03 | 9.03E-03 | up | 1.867417 |
| Q9NTJ3 | Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2 - [SMC4_HUMAN] | 9.91E-04 | 6.22E-03 | down | -1.351252 |
| Q92538 | Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2 - [GBF1_HUMAN] | 1.72E-03 | 8.57E-03 | down | -1.4695753 |
| Q5T160 | Probable arginine--tRNA ligase, mitochondrial OS=Homo sapiens GN=RARS2 PE=1 SV=1 - [SYRM_HUMAN] | 6.44E-03 | 2.09E-02 | up | 1.3845218 |
| O75815 | Breast cancer anti-estrogen resistance protein 3 OS=Homo sapiens GN=BCAR3 PE=1 SV=1 - [BCAR3_HUMAN] | 2.90E-03 | 1.27E-02 | down | -1.8781439 |
| Q96AY3 | Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1 - [FKB10_HUMAN] | 4.07E-04 | 3.77E-03 | down | -1.9798253 |
| O15131 | Importin subunit alpha-6 OS=Homo sapiens GN=KPNA5 PE=1 SV=2 - [IMA6_HUMAN] | 1.24E-03 | 7.10E-03 | down | -1.4166344 |
| Q7Z406 | Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN] | 8.23E-04 | 5.71E-03 | up | 1.4848014 |
| Q01650 | Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2 - [LAT1_HUMAN] | 2.12E-02 | 4.84E-02 | down | -1.2028178 |
| P11388 | DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN] | 3.62E-03 | 1.44E-02 | down | -1.4372797 |
| P18583 | Protein SON OS=Homo sapiens GN=SON PE=1 SV=4 - [SON_HUMAN] | 3.83E-03 | 1.49E-02 | down | -1.358802 |
| Q02241 | Kinesin-like protein KIF23 OS=Homo sapiens GN=KIF23 PE=1 SV=3 - [KIF23_HUMAN] | 1.83E-02 | 4.34E-02 | down | -1.435417 |
| P51649 | Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN] | 6.95E-04 | 5.21E-03 | up | 2.3108363 |
| O75153 | Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2 - [CLU_HUMAN] | 2.65E-03 | 1.19E-02 | down | -1.6971428 |
| Q63HN8 | E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3 - [RN213_HUMAN] | 3.18E-04 | 3.42E-03 | up | 2.2583714 |
| Q12768 | WASH complex subunit 5 OS=Homo sapiens GN=WASHC5 PE=1 SV=1 - [WASC5_HUMAN] | 4.64E-03 | 1.68E-02 | up | 1.2072117 |
| Q9H6T3 | RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 PE=1 SV=2 - [RPAP3_HUMAN] | 1.73E-02 | 4.14E-02 | down | -1.3079689 |
| Q9H9E3 | Conserved oligomeric Golgi complex subunit 4 OS=Homo sapiens GN=COG4 PE=1 SV=3 - [COG4_HUMAN] | 2.23E-03 | 1.05E-02 | up | 1.1368095 |
| O60341 | Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=2 - [KDM1A_HUMAN] | 5.99E-04 | 4.82E-03 | up | 1.5121465 |
| A0MZ66 | Shootin-1 OS=Homo sapiens GN=SHTN1 PE=1 SV=4 - [SHOT1_HUMAN] | 2.05E-03 | 9.81E-03 | down | -1.4179077 |
| O14617 | AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=1 SV=1 - [AP3D1_HUMAN] | 1.82E-02 | 4.32E-02 | up | 1.3282548 |
| Q6IA69 | Glutamine-dependent NAD(+) synthetase OS=Homo sapiens GN=NADSYN1 PE=1 SV=3 - [NADE_HUMAN] | 8.40E-03 | 2.51E-02 | up | 1.7894685 |
| Q15436 | Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 - [SC23A_HUMAN] | 3.21E-03 | 1.34E-02 | down | -1.1793545 |
| O14964 | Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1 - [HGS_HUMAN] | 2.16E-02 | 4.92E-02 | up | 1.2667841 |
| P26006 | Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5 - [ITA3_HUMAN] | 7.39E-03 | 2.27E-02 | down | -1.2150097 |
| Q8IZL8 | Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens GN=PELP1 PE=1 SV=2 - [PELP1_HUMAN] | 2.70E-03 | 1.20E-02 | up | 1.2021981 |
| Q13409 | Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN] | 2.48E-03 | 1.13E-02 | up | 1.6033486 |
| Q9Y5K6 | CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN] | 1.33E-03 | 7.37E-03 | up | 1.1512592 |
| Q92922 | SWI/SNF complex subunit SMARCC1 OS=Homo sapiens GN=SMARCC1 PE=1 SV=3 - [SMRC1_HUMAN] | 4.36E-03 | 1.63E-02 | down | -1.512285 |
| P26358 | DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2 - [DNMT1_HUMAN] | 2.08E-04 | 2.79E-03 | down | -1.7789246 |
| P06396 | Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1 - [GELS_HUMAN] | 1.79E-02 | 4.27E-02 | up | 1.2887648 |
| Q32P28 | Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=P3H1 PE=1 SV=2 - [P3H1_HUMAN] | 2.98E-03 | 1.28E-02 | down | -2.4484682 |
| Q5UIP0 | Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN] | 8.06E-05 | 1.93E-03 | down | -2.498625 |

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|--------|---|----------|----------|------|------------|
| Q9NW13 | RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3 - [RBM28_HUMAN] | 2.03E-04 | 2.73E-03 | down | -1.2218133 |
| Q03519 | Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 - [TAP2_HUMAN] | 5.73E-04 | 4.65E-03 | up | 2.892575 |
| Q93034 | Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4 - [CUL5_HUMAN] | 1.02E-02 | 2.87E-02 | up | 1.3159928 |
| Q5T0N5 | Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L PE=1 SV=3 - [FBP1L_HUMAN] | 2.36E-04 | 2.93E-03 | down | -1.4343518 |
| Q9NV11 | Fanconi anemia group I protein OS=Homo sapiens GN=FANCI PE=1 SV=4 - [FANCI_HUMAN] | 1.67E-02 | 4.04E-02 | down | -1.2644907 |
| Q8IYB3 | Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2 - [SRRM1_HUMAN] | 3.91E-03 | 1.51E-02 | down | -1.440327 |
| O95202 | LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1 - [LETM1_HUMAN] | 1.46E-02 | 3.68E-02 | up | 1.1514128 |
| O95104 | Splicing factor, arginine/serine-rich 15 OS=Homo sapiens GN=SCAF4 PE=1 SV=3 - [SFR15_HUMAN] | 1.23E-02 | 3.27E-02 | up | 1.2844826 |
| Q9Y4W6 | AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 - [AFG32_HUMAN] | 6.36E-03 | 2.08E-02 | up | 1.4096694 |
| P78344 | Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1 - [IF4G2_HUMAN] | 1.41E-03 | 7.65E-03 | down | -1.3584572 |
| Q14690 | Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 - [RRP5_HUMAN] | 1.16E-03 | 6.86E-03 | down | -1.2546092 |
| Q08378 | Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2 - [GOGA3_HUMAN] | 1.18E-03 | 6.92E-03 | down | -1.2846271 |
| Q9Y6D6 | Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2 - [BIG1_HUMAN] | 1.22E-02 | 3.26E-02 | up | 1.5689297 |
| Q9Y3R5 | Protein dopey-2 OS=Homo sapiens GN=DOPEY2 PE=1 SV=5 - [DOP2_HUMAN] | 7.37E-03 | 2.27E-02 | up | 1.7305596 |
| Q9UDT6 | CAP-Gly domain-containing linker protein 2 OS=Homo sapiens GN=CLIP2 PE=1 SV=1 - [CLIP2_HUMAN] | 1.03E-02 | 2.88E-02 | down | -1.2741673 |
| P09884 | DNA polymerase alpha catalytic subunit OS=Homo sapiens GN=POLA1 PE=1 SV=2 - [DPOLA_HUMAN] | 7.88E-03 | 2.39E-02 | down | -2.207869 |
| Q9Y4B6 | DDB1- and CUL4-associated factor 1 OS=Homo sapiens GN=DCAF1 PE=1 SV=3 - [DCAF1_HUMAN] | 6.24E-03 | 2.06E-02 | up | 1.6140684 |
| Q14689 | Disco-interacting protein 2 homolog A OS=Homo sapiens GN=DIP2A PE=1 SV=2 - [DIP2A_HUMAN] | 1.79E-03 | 8.88E-03 | down | -1.2471621 |
| Q9Y5S2 | Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2 - [MRCKB_HUMAN] | 3.70E-03 | 1.46E-02 | up | 1.5261877 |
| Q9ULL4 | Plexin-B3 OS=Homo sapiens GN=PLXNB3 PE=1 SV=2 - [PLXB3_HUMAN] | 1.60E-02 | 3.92E-02 | up | 1.1816063 |