1 – List of the proteins

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Replicate Count** | **Total Signal** | **Description** |
| P01275 | 3 | 0.001368761 | Glucagon OS=Homo sapiens OX=9606 GN=GCG PE=1 SV=3 |
| E5RK35 | 2 | 1.33E-04 | Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 PE=1 SV=1 |
| O14828-2 | 2 | 2.79E-05 | Isoform 2 of Secretory carrier-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=SCAMP3 |
| contaminant\_KERATIN10 | 2 | 3.57E-04 |  |
| contaminant\_KERATIN06 | 3 | 5.08E-04 |  |
| K7EPJ9 | 2 | 6.18E-04 | Keratin, type I cytoskeletal 17 (Fragment) OS=Homo sapiens OX=9606 GN=KRT17 PE=1 SV=1 |
| contaminant\_KERATIN12 | 2 | 3.31E-04 |  |
| contaminant\_KERATIN07 | 3 | 4.90E-04 |  |
| P08727 | 2 | 3.57E-04 | Keratin, type I cytoskeletal 19 OS=Homo sapiens OX=9606 GN=KRT19 PE=1 SV=4 |
| C9JM50 | 2 | 7.29E-04 | Keratin, type I cytoskeletal 19 (Fragment) OS=Homo sapiens OX=9606 GN=KRT19 PE=1 SV=1 |
| P19012 | 3 | 5.08E-04 | Keratin, type I cytoskeletal 15 OS=Homo sapiens OX=9606 GN=KRT15 PE=1 SV=3 |
| Q04695 | 2 | 3.31E-04 | Keratin, type I cytoskeletal 17 OS=Homo sapiens OX=9606 GN=KRT17 PE=1 SV=2 |
| F5GWP8 | 2 | 4.09E-04 | Keratin, type I cytoskeletal 17 OS=Homo sapiens OX=9606 GN=KRT17 PE=1 SV=2 |
| Q58FG1 | 3 | 3.94E-04 | Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens OX=9606 GN=HSP90AA4P PE=5 SV=1 |
| Q9NQC3-4 | 2 | 3.31E-05 | Isoform 4 of Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 |
| Q9BV20-2 | 2 | 2.56E-05 | Isoform 2 of Methylthioribose-1-phosphate isomerase OS=Homo sapiens OX=9606 GN=MRI1 |
| Q9BV20 | 2 | 2.23E-05 | Methylthioribose-1-phosphate isomerase OS=Homo sapiens OX=9606 GN=MRI1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9BV20-2 |

2 – List of the proteins

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| --- | --- | --- | --- |
| **Name** | **Replicate Count** | **Total Signal** | **Description** |
| P28289 | 3 | 1.47E-06 | Tropomodulin-1 OS=Homo sapiens OX=9606 GN=TMOD1 PE=1 SV=1 |
| B3KPU0 | 3 | 8.62E-06 | cDNA FLJ32186 fis, clone PLACE6002011, highly similar to PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1 |
| A0A087WVI1 | 3 | 3.87E-06 | PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1 |
| E5RGS7 | 3 | 9.54E-06 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |
| Q96JY6 | 3 | 3.58E-06 | PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1 |
| Q96JY6-3 | 3 | 3.44E-06 | Isoform 3 of PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 |
| Q96JY6-5 | 3 | 2.09E-06 | Isoform 5 of PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2; Additional IDs concatenated into MaxParsimony group: Q96JY6-3, Q96JY6, A0A087WVI1, H7C1D1, Q96JY6-4, C9JS55, B3KPU0, H0YBP7, E5RGS7, A0A087WUQ1 |
| H0YBP7 | 3 | 8.93E-06 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 |
| A0A0D9SFE5 | 3 | 6.81E-05 | Lamin B1, isoform CRA\_a OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=1 |
| A0A0D9SFY5 | 3 | 0.000122198 | Lamin-B1 (Fragment) OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=1 |
| Q9H1E5 | 3 | 2.05E-05 | Thioredoxin-related transmembrane protein 4 OS=Homo sapiens OX=9606 GN=TMX4 PE=1 SV=1 |
| Q8WUZ0 | 3 | 2.37E-05 | B-cell CLL/lymphoma 7 protein family member C OS=Homo sapiens OX=9606 GN=BCL7C PE=1 SV=3 |
| Q8WUZ0-2 | 3 | 2.13E-05 | Isoform 2 of B-cell CLL/lymphoma 7 protein family member C OS=Homo sapiens OX=9606 GN=BCL7C |
| I3L1Q2 | 3 | 1.76E-05 | B-cell CLL/lymphoma 7 protein family member C (Fragment) OS=Homo sapiens OX=9606 GN=BCL7C PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q8WUZ0-2, Q8WUZ0 |
| Q92734-4 | 2 | 3.62E-06 | Isoform 4 of Protein TFG OS=Homo sapiens OX=9606 GN=TFG |
| Q92734-2 | 2 | 2.56E-06 | Isoform 2 of Protein TFG OS=Homo sapiens OX=9606 GN=TFG |
| Q92734-3 | 2 | 3.57E-06 | Isoform 3 of Protein TFG OS=Homo sapiens OX=9606 GN=TFG |
| Q92734 | 2 | 2.54E-06 | Protein TFG OS=Homo sapiens OX=9606 GN=TFG PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q92734-2, Q92734-3, Q92734-4 |
| Q7Z4V5-3 | 3 | 1.14E-05 | Isoform 3 of Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens OX=9606 GN=HDGFL2; Additional IDs concatenated into MaxParsimony group: Q7Z4V5-4, Q7Z4V5, Q7Z4V5-2, A0A087WT54 |
| Q7Z4V5 | 3 | 1.15E-05 | Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens OX=9606 GN=HDGFL2 PE=1 SV=1 |
| Q7Z4V5-4 | 3 | 1.14E-05 | Isoform 4 of Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens OX=9606 GN=HDGFL2 |
| Q7Z4V5-2 | 3 | 1.15E-05 | Isoform 2 of Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens OX=9606 GN=HDGFL2 |
| K7EQH1 | 3 | 5.17E-05 | Uncharacterized protein C18orf25 (Fragment) OS=Homo sapiens OX=9606 GN=C18orf25 PE=1 SV=1 |
| Q96B23-2 | 3 | 2.20E-05 | Isoform 2 of Uncharacterized protein C18orf25 OS=Homo sapiens OX=9606 GN=C18orf25 |
| Q96B23 | 3 | 1.87E-05 | Uncharacterized protein C18orf25 OS=Homo sapiens OX=9606 GN=C18orf25 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q96B23-2, A0A087WVF1, K7EQH1 |
| A0A087WVF1 | 3 | 2.74E-05 | Uncharacterized protein C18orf25 OS=Homo sapiens OX=9606 GN=C18orf25 PE=1 SV=1 |
| A0A1W2PQ55 | 3 | 0.000131446 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| A0A1W2PP40 | 3 | 9.07E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| P0DPI2-2 | 3 | 7.85E-05 | Isoform 2 of Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial OS=Homo sapiens OX=9606 GN=GATD3A |
| A0A096LP12 | 3 | 6.31E-05 | Glutamine amidotransferase-like class 1 domain-containing 3A (Fragment) OS=Homo sapiens OX=9606 GN=GATD3A PE=1 SV=2 |
| A0A096LP73 | 3 | 0.000103246 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 GN=LOC102724023 PE=1 SV=1 |
| A0A0B4J2H4 | 3 | 7.85E-05 | Uncharacterized protein OS=Homo sapiens OX=9606 GN=LOC102724023 PE=1 SV=1 |
| A0A0B4J2D5 | 3 | 6.94E-05 | Glutamine amidotransferase-like class 1 domain-containing protein 3B, mitochondrial OS=Homo sapiens OX=9606 GN=GATD3B PE=1 SV=1 |
| A0A096LPI6 | 3 | 6.66E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=2; Additional IDs concatenated into MaxParsimony group: A0A0B4J2D5, P0DPI2, P0DPI2-2, A0A0B4J2H4, A0A0B4J2D5-2, A0A096LP12, F2Z2Q0, A0A2R8YDR7, A0A2R8Y6K9, A0A096LP73, A0A096LNJ1 |
| A0A0B4J2D5-2 | 3 | 7.85E-05 | Isoform 2 of Glutamine amidotransferase-like class 1 domain-containing protein 3B, mitochondrial OS=Homo sapiens OX=9606 GN=GATD3B |
| F2Z2Q0 | 3 | 6.52E-05 | Glutamine amidotransferase-like class 1 domain-containing 3A OS=Homo sapiens OX=9606 GN=GATD3A PE=1 SV=1 |
| A0A2R8YDR7 | 3 | 7.44E-05 | Glutamine amidotransferase-like class 1 domain-containing 3A (Fragment) OS=Homo sapiens OX=9606 GN=GATD3A PE=1 SV=1 |
| A0A096LNJ1 | 3 | 0.00013344 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 GN=LOC102724023 PE=1 SV=1 |
| P0DPI2 | 3 | 6.94E-05 | Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial OS=Homo sapiens OX=9606 GN=GATD3A PE=1 SV=1 |
| A0A2R8Y6K9 | 3 | 8.68E-05 | Glutamine amidotransferase-like class 1 domain-containing 3A OS=Homo sapiens OX=9606 GN=GATD3A PE=1 SV=1 |
| A0A0D9SEI8 | 3 | 8.52E-05 | Y-box-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=YBX3 PE=1 SV=1 |
| H0Y449 | 2 | 1.26E-05 | Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=YBX1 PE=1 SV=1 |
| Q9Y2T7 | 2 | 6.90E-06 | Y-box-binding protein 2 OS=Homo sapiens OX=9606 GN=YBX2 PE=1 SV=2 |
| P67809 | 2 | 1.45E-05 | Nuclease-sensitive element-binding protein 1 OS=Homo sapiens OX=9606 GN=YBX1 PE=1 SV=3 |
| G3V1A1 | 3 | 1.34E-04 | 60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=1 |
| A0A087WU27 | 3 | 3.70E-05 | Aminopeptidase B (Fragment) OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=1 |
| A0A087WUS4 | 3 | 2.43E-05 | Aminopeptidase B (Fragment) OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=1 |
| Q9H4A4 | 3 | 1.05E-05 | Aminopeptidase B OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A6NKB8, A0A087WU27, A0A087WUS4 |
| A6NKB8 | 3 | 1.12E-05 | Aminopeptidase B OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=1 |
| P26583 | 3 | 2.12E-05 | High mobility group protein B2 OS=Homo sapiens OX=9606 GN=HMGB2 PE=1 SV=2 |
| Q15124 | 3 | 2.70E-06 | Phosphoglucomutase-like protein 5 OS=Homo sapiens OX=9606 GN=PGM5 PE=1 SV=2 |
| Q9UBM7 | 3 | 1.30E-05 | 7-dehydrocholesterol reductase OS=Homo sapiens OX=9606 GN=DHCR7 PE=1 SV=1 |
| P61026 | 2 | 4.20E-05 | Ras-related protein Rab-10 OS=Homo sapiens OX=9606 GN=RAB10 PE=1 SV=1 |
| A0A0U1RRL7 | 2 | 2.93E-05 | Protein MMP24OS OS=Homo sapiens OX=9606 GN=MMP24OS PE=1 SV=1 |
| Q86WC4 | 2 | 1.09E-05 | Osteopetrosis-associated transmembrane protein 1 OS=Homo sapiens OX=9606 GN=OSTM1 PE=1 SV=1 |
| Q96ID5 | 3 | 5.16E-06 | Immunoglobulin superfamily member 21 OS=Homo sapiens OX=9606 GN=IGSF21 PE=2 SV=1 |
| Q02878 | 3 | 3.79E-05 | 60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3 |
| Q96MW5 | 2 | 5.49E-06 | Conserved oligomeric Golgi complex subunit 8 OS=Homo sapiens OX=9606 GN=COG8 PE=1 SV=2 |
| P49257 | 3 | 9.60E-06 | Protein ERGIC-53 OS=Homo sapiens OX=9606 GN=LMAN1 PE=1 SV=2 |
| O15355 | 3 | 3.79E-06 | Protein phosphatase 1G OS=Homo sapiens OX=9606 GN=PPM1G PE=1 SV=1 |
| Q7L311 | 3 | 8.25E-06 | Armadillo repeat-containing X-linked protein 2 OS=Homo sapiens OX=9606 GN=ARMCX2 PE=2 SV=1 |
| Q00577 | 3 | 2.95E-06 | Transcriptional activator protein Pur-alpha OS=Homo sapiens OX=9606 GN=PURA PE=1 SV=2 |
| Q96P70 | 2 | 1.98E-07 | Importin-9 OS=Homo sapiens OX=9606 GN=IPO9 PE=1 SV=3 |
| Q13283 | 3 | 1.53E-05 | Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=1 |
| Q15637-5 | 3 | 4.76E-06 | Isoform 5 of Splicing factor 1 OS=Homo sapiens OX=9606 GN=SF1 |
| P13667 | 3 | 2.10E-05 | Protein disulfide-isomerase A4 OS=Homo sapiens OX=9606 GN=PDIA4 PE=1 SV=2 |
| Q7Z4H8 | 3 | 1.17E-06 | KDEL motif-containing protein 2 OS=Homo sapiens OX=9606 GN=KDELC2 PE=1 SV=2 |
| Q15170-2 | 3 | 6.01E-05 | Isoform 2 of Transcription elongation factor A protein-like 1 OS=Homo sapiens OX=9606 GN=TCEAL1 |
| P49721 | 3 | 2.23E-05 | Proteasome subunit beta type-2 OS=Homo sapiens OX=9606 GN=PSMB2 PE=1 SV=1 |
| P42677 | 3 | 4.18E-05 | 40S ribosomal protein S27 OS=Homo sapiens OX=9606 GN=RPS27 PE=1 SV=3 |
| A0A0X1KG71 | 3 | 7.14E-06 | Negative elongation factor B OS=Homo sapiens OX=9606 GN=NELFB PE=1 SV=1 |
| O43242 | 2 | 7.87E-06 | 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PSMD3 PE=1 SV=2 |
| Q9UPN7 | 2 | 2.19E-06 | Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP6R1 PE=1 SV=5 |
| P11047 | 2 | 2.77E-07 | Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3 |
| P31930 | 3 | 1.80E-05 | Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC1 PE=1 SV=3 |
| P98160 | 3 | 1.77E-06 | Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens OX=9606 GN=HSPG2 PE=1 SV=4 |
| C9J7I0 | 3 | 8.49E-06 | UBAP1-MVB12-associated (UMA)-domain containing protein 1 OS=Homo sapiens OX=9606 GN=UMAD1 PE=2 SV=2 |
| Q9H3N1 | 3 | 2.30E-05 | Thioredoxin-related transmembrane protein 1 OS=Homo sapiens OX=9606 GN=TMX1 PE=1 SV=1 |
| B7ZBB8 | 3 | 6.36E-06 | Protein phosphatase 1 regulatory subunit 3G OS=Homo sapiens OX=9606 GN=PPP1R3G PE=1 SV=1 |
| Q96HY6 | 3 | 7.49E-06 | DDRGK domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DDRGK1 PE=1 SV=2 |
| P35555 | 3 | 3.72E-06 | Fibrillin-1 OS=Homo sapiens OX=9606 GN=FBN1 PE=1 SV=3 |
| P46109 | 3 | 9.96E-06 | Crk-like protein OS=Homo sapiens OX=9606 GN=CRKL PE=1 SV=1 |
| Q6ZMI0 | 3 | 5.84E-07 | Protein phosphatase 1 regulatory subunit 21 OS=Homo sapiens OX=9606 GN=PPP1R21 PE=1 SV=1 |
| O15116 | 3 | 5.90E-06 | U6 snRNA-associated Sm-like protein LSm1 OS=Homo sapiens OX=9606 GN=LSM1 PE=1 SV=1 |
| O00303 | 2 | 2.80E-06 | Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens OX=9606 GN=EIF3F PE=1 SV=1 |
| Q9NX62 | 2 | 3.19E-06 | Inositol monophosphatase 3 OS=Homo sapiens OX=9606 GN=IMPAD1 PE=1 SV=1 |
| Q9NSD9 | 2 | 6.68E-07 | Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens OX=9606 GN=FARSB PE=1 SV=3 |
| P25398 | 2 | 5.42E-05 | 40S ribosomal protein S12 OS=Homo sapiens OX=9606 GN=RPS12 PE=1 SV=3 |
| Q9NSE4 | 2 | 9.91E-07 | Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=IARS2 PE=1 SV=2 |
| Q08211 | 3 | 2.30E-07 | ATP-dependent RNA helicase A OS=Homo sapiens OX=9606 GN=DHX9 PE=1 SV=4 |
| Q9P265 | 3 | 1.18E-06 | Disco-interacting protein 2 homolog B OS=Homo sapiens OX=9606 GN=DIP2B PE=1 SV=3 |
| P47914 | 3 | 5.47E-05 | 60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=1 SV=2 |
| P56181-2 | 2 | 3.90E-06 | Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFV3 |
| Q16658 | 3 | 4.15E-05 | Fascin OS=Homo sapiens OX=9606 GN=FSCN1 PE=1 SV=3 |
| Q99459 | 3 | 9.75E-06 | Cell division cycle 5-like protein OS=Homo sapiens OX=9606 GN=CDC5L PE=1 SV=2 |
| Q02790 | 3 | 3.60E-06 | Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens OX=9606 GN=FKBP4 PE=1 SV=3 |
| Q13151 | 3 | 1.53E-05 | Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens OX=9606 GN=HNRNPA0 PE=1 SV=1 |
| P02750 | 2 | 8.59E-06 | Leucine-rich alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=LRG1 PE=1 SV=2 |
| Q4KMP7 | 3 | 2.45E-06 | TBC1 domain family member 10B OS=Homo sapiens OX=9606 GN=TBC1D10B PE=1 SV=3 |
| P27694 | 3 | 8.93E-07 | Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2 |
| Q9NQS1 | 2 | 7.15E-06 | Cell death regulator Aven OS=Homo sapiens OX=9606 GN=AVEN PE=1 SV=1 |
| P48681 | 3 | 8.93E-06 | Nestin OS=Homo sapiens OX=9606 GN=NES PE=1 SV=2 |
| P48147 | 2 | 9.60E-07 | Prolyl endopeptidase OS=Homo sapiens OX=9606 GN=PREP PE=1 SV=2 |
| Q9BR76 | 3 | 7.70E-05 | Coronin-1B OS=Homo sapiens OX=9606 GN=CORO1B PE=1 SV=1 |
| Q9BX68 | 3 | 1.99E-05 | Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=HINT2 PE=1 SV=1 |
| P20618 | 3 | 6.35E-05 | Proteasome subunit beta type-1 OS=Homo sapiens OX=9606 GN=PSMB1 PE=1 SV=2 |
| P62906 | 3 | 3.03E-05 | 60S ribosomal protein L10a OS=Homo sapiens OX=9606 GN=RPL10A PE=1 SV=2 |
| Q9Y2W2 | 3 | 1.31E-05 | WW domain-binding protein 11 OS=Homo sapiens OX=9606 GN=WBP11 PE=1 SV=1 |
| Q8TBP5 | 3 | 2.25E-05 | Membrane protein FAM174A OS=Homo sapiens OX=9606 GN=FAM174A PE=2 SV=1 |
| P12004 | 2 | 2.10E-06 | Proliferating cell nuclear antigen OS=Homo sapiens OX=9606 GN=PCNA PE=1 SV=1 |
| P46778 | 2 | 1.52E-05 | 60S ribosomal protein L21 OS=Homo sapiens OX=9606 GN=RPL21 PE=1 SV=2 |
| Q9BSH5 | 3 | 1.57E-05 | Haloacid dehalogenase-like hydrolase domain-containing protein 3 OS=Homo sapiens OX=9606 GN=HDHD3 PE=1 SV=1 |
| P07384 | 3 | 5.88E-06 | Calpain-1 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN1 PE=1 SV=1 |
| O75396 | 3 | 2.62E-05 | Vesicle-trafficking protein SEC22b OS=Homo sapiens OX=9606 GN=SEC22B PE=1 SV=4 |
| Q96C86 | 3 | 1.13E-06 | m7GpppX diphosphatase OS=Homo sapiens OX=9606 GN=DCPS PE=1 SV=2 |
| C9JQ00 | 3 | 0.000196239 | Tubulin alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA4A PE=1 SV=1 |
| A0A075B730 | 2 | 9.53E-07 | Epiplakin OS=Homo sapiens OX=9606 GN=EPPK1 PE=1 SV=2 |
| P58107 | 2 | 9.48E-07 | Epiplakin OS=Homo sapiens OX=9606 GN=EPPK1 PE=1 SV=3 |
| V9GYJ7 | 3 | 1.65E-05 | Rab GDP dissociation inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=8 |
| Q5SX90 | 3 | 1.40E-05 | Rab GDP dissociation inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=1 |
| V9GYF8 | 3 | 1.59E-05 | Rab GDP dissociation inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=1 |
| A0A0J9YYI8 | 3 | 0.000169264 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| M0QXZ3 | 3 | 0.000143604 | Complement C3 (Fragment) OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=1 |
| D6RCR6 | 2 | 3.31E-05 | NAD(P) transhydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=1 |
| E9PCX7 | 3 | 1.87E-05 | NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=1 |
| C9K0M0 | 3 | 9.46E-05 | Trifunctional enzyme subunit beta, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=8 |
| C9JE81 | 3 | 7.61E-05 | Trifunctional enzyme subunit beta, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=8 |
| B5MD38 | 3 | 5.14E-05 | Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=1 |
| C9JEY0 | 3 | 8.94E-05 | Trifunctional enzyme subunit beta, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=8 |
| O14979 | 3 | 5.97E-06 | Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens OX=9606 GN=HNRNPDL PE=1 SV=3 |
| D6RBQ9 | 3 | 0.000138236 | Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1 |
| O14979-2 | 3 | 8.34E-06 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens OX=9606 GN=HNRNPDL |
| O14979-3 | 3 | 1.03E-05 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens OX=9606 GN=HNRNPDL |
| A0A087WUK2 | 3 | 6.91E-06 | Heterogeneous nuclear ribonucleoprotein D-like, isoform CRA\_b OS=Homo sapiens OX=9606 GN=HNRNPDL PE=1 SV=1 |
| D6RD83 | 3 | 0.000260337 | Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1 |
| Q68E03 | 3 | 9.93E-05 | Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| B3KM87 | 3 | 3.74E-06 | cDNA FLJ10526 fis, clone NT2RP2000931, highly similar to Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| P43243-2 | 3 | 3.40E-06 | Isoform 2 of Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 |
| B4DT28 | 3 | 3.74E-05 | Heterogeneous nuclear ribonucleoprotein R, isoform CRA\_a OS=Homo sapiens OX=9606 GN=HNRNPR PE=1 SV=1 |
| O60506-5 | 3 | 1.72E-05 | Isoform 5 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP |
| F2Z2I8 | 3 | 0.000413792 | Stomatin-like protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=STOML2 PE=1 SV=1 |
| P16615-4 | 3 | 2.31E-06 | Isoform 4 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2A2 |
| P16615-3 | 3 | 3.48E-06 | Isoform 3 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2A2 |
| P16615-2 | 3 | 3.48E-06 | Isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2A2 |
| H7C5W9 | 3 | 1.83E-06 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment) OS=Homo sapiens OX=9606 GN=ATP2A2 PE=1 SV=1 |
| P16615 | 3 | 3.33E-06 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2A2 PE=1 SV=1 |
| P16615-5 | 3 | 3.48E-06 | Isoform 5 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2A2 |
| X6R2P6 | 3 | 0.000221004 | Programmed cell death protein 5 OS=Homo sapiens OX=9606 GN=PDCD5 PE=1 SV=1 |
| Q3HM38 | 3 | 0.00030388 | Programmed cell death 5 short isoform OS=Homo sapiens OX=9606 GN=PDCD5 PE=1 SV=1 |
| H7C1F6 | 3 | 8.46E-05 | Glutamine amidotransferase-like class 1 domain-containing 3A (Fragment) OS=Homo sapiens OX=9606 GN=GATD3A PE=1 SV=2 |
| A0A096LNH5 | 3 | 9.61E-05 | Uncharacterized protein OS=Homo sapiens OX=9606 GN=LOC102724023 PE=1 SV=1 |
| H7C2G3 | 3 | 8.15E-05 | Glutamine amidotransferase-like class 1 domain-containing 3A (Fragment) OS=Homo sapiens OX=9606 GN=GATD3A PE=1 SV=1 |
| H3BTH3 | 3 | 8.96E-05 | 60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RPL13 PE=1 SV=1 |
| J3QSB4 | 3 | 0.00015839 | 60S ribosomal protein L13 (Fragment) OS=Homo sapiens OX=9606 GN=RPL13 PE=1 SV=1 |
| R4GN83 | 3 | 3.85E-05 | Basigin (Fragment) OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=1 |
| D6RFZ9 | 3 | 4.87E-05 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=8 |
| D6RFX4 | 3 | 4.95E-05 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| D6RAU2 | 3 | 6.53E-05 | Receptor of-activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| E9PD14 | 3 | 6.27E-05 | Receptor of-activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| H0Y8W2 | 3 | 2.14E-05 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| D6R9Z1 | 3 | 4.07E-05 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=8 |
| D6R9L0 | 3 | 3.20E-05 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| H0YAM7 | 2 | 7.48E-06 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| Q9Y4G6 | 3 | 1.27E-06 | Talin-2 OS=Homo sapiens OX=9606 GN=TLN2 PE=1 SV=4 |
| H0YMT1 | 3 | 2.12E-06 | Talin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TLN2 PE=1 SV=1 |
| Q9Y490 | 3 | 3.01E-06 | Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9Y4G6, A0A1B0GVU7, H0YMT1 |
| A0A1B0GVU7 | 3 | 1.99E-06 | Talin-2 OS=Homo sapiens OX=9606 GN=TLN2 PE=1 SV=1 |
| Q5JNZ5 | 3 | 7.09E-05 | Putative 40S ribosomal protein S26-like 1 OS=Homo sapiens OX=9606 GN=RPS26P11 PE=5 SV=1 |
| H0YFY6 | 3 | 5.42E-06 | Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=1 |
| Q14980-5 | 3 | 2.19E-06 | Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 |
| Q14151 | 3 | 1.87E-05 | Scaffold attachment factor B2 OS=Homo sapiens OX=9606 GN=SAFB2 PE=1 SV=1 |
| Q15424 | 3 | 3.18E-05 | Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB PE=1 SV=4 |
| Q15424-3 | 3 | 3.17E-05 | Isoform 3 of Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB; Additional IDs concatenated into MaxParsimony group: Q15424-4, Q15424, Q14151, Q15424-2 |
| Q15424-4 | 3 | 3.17E-05 | Isoform 4 of Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB |
| Q15424-2 | 3 | 2.10E-05 | Isoform 2 of Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB |
| E5RJG6 | 3 | 2.48E-05 | Transforming acidic coiled-coil-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| O75410 | 3 | 8.01E-06 | Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=2 |
| E7EVI4 | 3 | 5.58E-06 | Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| E5RFM9 | 3 | 1.07E-05 | Transforming acidic coiled-coil-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| O75410-3 | 3 | 5.31E-06 | Isoform 3 of Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 |
| R4GMT7 | 3 | 1.03E-05 | Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| O75410-2 | 3 | 7.89E-06 | Isoform 2 of Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1; Additional IDs concatenated into MaxParsimony group: O75410, O75410-7, R4GMT7, E5RFM9, E5RJG6, O75410-3, E7ET87, E7EVI4, H0YAY0 |
| E7ET87 | 3 | 5.32E-06 | Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| H0YAY0 | 3 | 5.77E-06 | Transforming acidic coiled-coil-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| O75410-7 | 3 | 8.17E-06 | Isoform 7 of Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 |
| I3L0K2 | 2 | 2.11E-05 | Thioredoxin domain-containing protein 17 OS=Homo sapiens OX=9606 GN=TXNDC17 PE=1 SV=1 |
| I3L3M7 | 2 | 1.98E-05 | Thioredoxin domain-containing protein 17 OS=Homo sapiens OX=9606 GN=TXNDC17 PE=1 SV=1 |
| Q9BRA2 | 2 | 4.43E-05 | Thioredoxin domain-containing protein 17 OS=Homo sapiens OX=9606 GN=TXNDC17 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: I3L2R6, I3L3M7, I3L0K2 |
| I3L2R6 | 2 | 5.56E-05 | Thioredoxin domain-containing protein 17 OS=Homo sapiens OX=9606 GN=TXNDC17 PE=1 SV=1 |
| P14678-3 | 2 | 2.38E-06 | Isoform SM-B1 of Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens OX=9606 GN=SNRPB; Additional IDs concatenated into MaxParsimony group: P63162-2, P63162, P14678, P14678-2, J3QLE5, Q92611 |
| P63162 | 2 | 2.87E-06 | Small nuclear ribonucleoprotein-associated protein N OS=Homo sapiens OX=9606 GN=SNRPN PE=1 SV=1 |
| J3QLE5 | 2 | 4.07E-06 | Small nuclear ribonucleoprotein-associated protein N (Fragment) OS=Homo sapiens OX=9606 GN=SNRPN PE=1 SV=1 |
| P14678-2 | 2 | 2.98E-06 | Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens OX=9606 GN=SNRPB |
| P63162-2 | 2 | 2.82E-06 | Isoform 2 of Small nuclear ribonucleoprotein-associated protein N OS=Homo sapiens OX=9606 GN=SNRPN |
| Q92611 | 2 | 5.87E-07 | ER degradation-enhancing alpha-mannosidase-like protein 1 OS=Homo sapiens OX=9606 GN=EDEM1 PE=1 SV=1 |
| P14678 | 2 | 2.87E-06 | Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens OX=9606 GN=SNRPB PE=1 SV=2 |
| H0YJC0 | 3 | 5.18E-06 | 26S proteasome regulatory subunit 10B (Fragment) OS=Homo sapiens OX=9606 GN=PSMC6 PE=1 SV=1 |
| H0YJS8 | 3 | 4.50E-06 | 26S proteasome regulatory subunit 10B (Fragment) OS=Homo sapiens OX=9606 GN=PSMC6 PE=1 SV=2 |
| A0A087X2I1 | 3 | 3.36E-06 | 26S proteasome regulatory subunit 10B OS=Homo sapiens OX=9606 GN=PSMC6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P62333, H0YJC0, H0YJS8, H0YJT1, H0YJE9 |
| P62333 | 3 | 3.49E-06 | 26S proteasome regulatory subunit 10B OS=Homo sapiens OX=9606 GN=PSMC6 PE=1 SV=1 |
| H0YJE9 | 2 | 4.44E-06 | 26S proteasome regulatory subunit 10B OS=Homo sapiens OX=9606 GN=PSMC6 PE=1 SV=2 |
| H0YJT1 | 2 | 3.20E-06 | 26S proteasome regulatory subunit 10B OS=Homo sapiens OX=9606 GN=PSMC6 PE=1 SV=2 |
| P09012 | 2 | 3.53E-05 | U1 small nuclear ribonucleoprotein A OS=Homo sapiens OX=9606 GN=SNRPA PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: M0QZG7, M0R2B8, M0R221, M0QXK2, M0R0G9 |
| G3XAN0 | 3 | 7.76E-05 | 40S ribosomal protein S20 OS=Homo sapiens OX=9606 GN=RPS20 PE=1 SV=1 |
| M0R1T5 | 3 | 1.84E-05 | Charged multivesicular body protein 2a (Fragment) OS=Homo sapiens OX=9606 GN=CHMP2A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O43633 |
| O43633 | 3 | 1.88E-05 | Charged multivesicular body protein 2a OS=Homo sapiens OX=9606 GN=CHMP2A PE=1 SV=1 |
| K7ESQ0 | 2 | 3.36E-05 | Ran-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=1 |
| P40429 | 3 | 5.38E-05 | 60S ribosomal protein L13a OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2 |
| Q8J015 | 3 | 6.04E-05 | 60S ribosomal protein L13a OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=1 |
| M0QYS1 | 3 | 5.20E-05 | 60S ribosomal protein L13a (Fragment) OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P40429, Q8J015, Q6NVV1 |
| Q6NVV1 | 3 | 6.52E-05 | Putative 60S ribosomal protein L13a protein RPL13AP3 OS=Homo sapiens OX=9606 GN=RPL13AP3 PE=5 SV=1 |
| S4R398 | 3 | 9.59E-06 | Transportin-1 (Fragment) OS=Homo sapiens OX=9606 GN=TNPO1 PE=1 SV=1 |
| Q92973-3 | 3 | 2.18E-06 | Isoform 3 of Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 |
| Q92973 | 3 | 2.06E-06 | Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q92973-2, Q92973-3, S4R398, O14787-2 |
| O14787-2 | 3 | 1.72E-06 | Isoform 2 of Transportin-2 OS=Homo sapiens OX=9606 GN=TNPO2 |
| Q92973-2 | 3 | 2.08E-06 | Isoform 2 of Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 |
| E9PIR8 | 3 | 1.65E-05 | Pogo transposable element with ZNF domain (Fragment) OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=1 |
| A6PW30 | 3 | 2.97E-05 | Pogo transposable element with ZNF domain (Fragment) OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=1 |
| Q7Z3K3-4 | 3 | 6.88E-06 | Isoform 4 of Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ |
| Q7Z3K3-7 | 3 | 1.85E-06 | Isoform 7 of Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ |
| Q7Z3K3-6 | 3 | 1.78E-06 | Isoform 6 of Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ |
| Q7Z3K3 | 3 | 1.77E-06 | Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q7Z3K3-6, Q7Z3K3-3, Q7Z3K3-2, Q7Z3K3-7, Q7Z3K3-5, Q7Z3K3-4, E9PIR8, E9PJY9, A6PW30 |
| Q7Z3K3-2 | 3 | 1.84E-06 | Isoform 2 of Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ |
| Q7Z3K3-3 | 3 | 1.83E-06 | Isoform 3 of Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ |
| Q7Z3K3-5 | 3 | 1.90E-06 | Isoform 5 of Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ |
| E9PJY9 | 3 | 1.80E-05 | Pogo transposable element with ZNF domain (Fragment) OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=1 |
| E9PKY0 | 2 | 8.86E-06 | Catenin delta-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNND1 PE=1 SV=1 |
| D6R967 | 3 | 1.54E-05 | Inorganic pyrophosphatase 2, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PPA2 PE=1 SV=1 |
| H0Y9D8 | 3 | 1.31E-05 | Inorganic pyrophosphatase 2, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PPA2 PE=1 SV=1 |
| Q5T8Q9 | 3 | 0.000105165 | Glutathione S-transferase OS=Homo sapiens OX=9606 GN=GSTM5 PE=1 SV=1 |
| P46439 | 3 | 9.74E-05 | Glutathione S-transferase Mu 5 OS=Homo sapiens OX=9606 GN=GSTM5 PE=1 SV=3 |
| Q5T8R1 | 3 | 9.74E-05 | Glutathione S-transferase OS=Homo sapiens OX=9606 GN=GSTM5 PE=1 SV=2 |
| D6RI02 | 2 | 2.05E-05 | 40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| D6RAT0 | 2 | 1.93E-06 | 40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| P61247 | 2 | 7.37E-06 | 40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: D6RG13, E9PFI5, H0Y8L7, D6RI02, D6RAT0, D6RB09, D6RAS7, D6RED7, D6RGE0 |
| D6RG13 | 2 | 8.73E-06 | 40S ribosomal protein S3a (Fragment) OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| H0Y8L7 | 2 | 1.02E-05 | 40S ribosomal protein S3a (Fragment) OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| D6RGE0 | 2 | 6.75E-06 | 40S ribosomal protein S3a (Fragment) OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| D6RED7 | 2 | 4.34E-06 | 40S ribosomal protein S3a (Fragment) OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| D6RAS7 | 2 | 3.51E-06 | 40S ribosomal protein S3a (Fragment) OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| D6RB09 | 2 | 2.27E-06 | 40S ribosomal protein S3a (Fragment) OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=8 |
| E9PFI5 | 2 | 9.49E-06 | 40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1 |
| Q15165-3 | 3 | 9.61E-06 | Isoform 3 of Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 |
| A0A0J9YYF0 | 3 | 3.36E-05 | Serum paraoxonase/arylesterase 2 (Fragment) OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1 |
| A0A0J9YYF3 | 3 | 2.58E-05 | Serum paraoxonase/arylesterase 2 (Fragment) OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1 |
| Q15165-1 | 3 | 9.29E-06 | Isoform 1 of Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 |
| A0A0J9YXU7 | 3 | 1.57E-05 | Serum paraoxonase/arylesterase 2 (Fragment) OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1 |
| J3QT77 | 3 | 9.61E-06 | Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1 |
| Q15165 | 3 | 9.29E-06 | Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=4 |
| G3XAK4 | 3 | 8.12E-06 | Paraoxonase 2, isoform CRA\_c OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1 |
| A0A0J9YYG4 | 3 | 9.29E-06 | Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1 |
| A0A0J9YXF2 | 3 | 8.77E-06 | Paraoxonase 2, isoform CRA\_a OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q15165-1, Q15165, A0A0J9YYG4, Q15165-3, J3QT77, G3XAK4, A0A0J9YXU7, A0A0J9YYF3, A0A0J9YYF0, A0A0J9YVW3 |
| A0A0J9YVW3 | 3 | 5.56E-05 | Serum paraoxonase/arylesterase 2 (Fragment) OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=1 |
| C9JRZ6 | 3 | 4.79E-05 | MICOS complex subunit OS=Homo sapiens OX=9606 GN=CHCHD3 PE=1 SV=2 |
| F8WAR4 | 3 | 4.61E-05 | MICOS complex subunit OS=Homo sapiens OX=9606 GN=CHCHD3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JRZ6, Q9NX63, A0A286YEX5 |
| Q9NX63 | 3 | 4.89E-05 | MICOS complex subunit MIC19 OS=Homo sapiens OX=9606 GN=CHCHD3 PE=1 SV=1 |
| F8WC19 | 3 | 0.000132985 | Splicing factor 3B subunit 1 OS=Homo sapiens OX=9606 GN=SF3B1 PE=1 SV=1 |
| B4DGZ4 | 3 | 3.20E-05 | cDNA FLJ57368, highly similar to Splicing factor 3B subunit 1 OS=Homo sapiens OX=9606 GN=SF3B1 PE=1 SV=1 |
| O75533-2 | 3 | 3.42E-05 | Isoform 2 of Splicing factor 3B subunit 1 OS=Homo sapiens OX=9606 GN=SF3B1 |
| O75533 | 3 | 5.98E-06 | Splicing factor 3B subunit 1 OS=Homo sapiens OX=9606 GN=SF3B1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: B4DGZ4, O75533-2, F8WC19 |
| Q9P2E9-3 | 3 | 4.87E-06 | Isoform 2 of Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 |
| F8W7S5 | 3 | 2.51E-06 | Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=1 |
| A0A087WVV2 | 3 | 2.02E-06 | Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=1 |
| Q9P2E9 | 3 | 3.37E-06 | Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: Q9P2E9-3, A0A087WVV2, F8W7S5 |
| M0QZM9 | 3 | 7.86E-05 | Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=1 |
| M0R0Y2 | 3 | 1.08E-05 | Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=1 |
| P54920 | 3 | 9.33E-06 | Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: M0R2M1, M0R0Y2, M0R031, M0QZN5, M0QZM9 |
| M0QZN5 | 3 | 4.59E-05 | Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=1 |
| M0R2M1 | 3 | 1.03E-05 | Alpha-soluble NSF attachment protein (Fragment) OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=1 |
| M0R031 | 3 | 3.72E-05 | Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=1 |
| O75494-3 | 3 | 1.73E-06 | Isoform 3 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 |
| Q5JRI1 | 3 | 1.84E-06 | Serine/arginine-rich-splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 PE=1 SV=1 |
| O75494 | 3 | 1.21E-06 | Serine/arginine-rich splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O75494-2, O75494-3, O75494-6, O75494-4, Q5JRI1, O75494-5, Q6IQ42 |
| Q6IQ42 | 3 | 4.58E-06 | FUSIP1 protein OS=Homo sapiens OX=9606 GN=SRSF10 PE=1 SV=1 |
| O75494-4 | 3 | 1.83E-06 | Isoform 4 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 |
| O75494-6 | 3 | 1.74E-06 | Isoform 6 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 |
| O75494-2 | 3 | 1.21E-06 | Isoform 2 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 |
| O75494-5 | 3 | 1.91E-06 | Isoform 5 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 |
| E7EX90 | 3 | 7.14E-07 | Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=1 SV=1 |
| Q14203-6 | 3 | 7.06E-07 | Isoform 6 of Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 |
| Q14203 | 3 | 7.02E-07 | Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q14203-6, E7EX90, Q14203-4, Q14203-3, Q14203-2, Q14203-5, Q6AWB1 |
| Q14203-5 | 3 | 7.88E-07 | Isoform 5 of Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 |
| Q6AWB1 | 3 | 1.01E-06 | Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=1 SV=1 |
| Q14203-4 | 3 | 7.16E-07 | Isoform 4 of Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 |
| Q14203-2 | 3 | 7.84E-07 | Isoform p135 of Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 |
| Q14203-3 | 3 | 7.26E-07 | Isoform 3 of Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 |
| P29536-2 | 3 | 3.71E-06 | Isoform 2 of Leiomodin-1 OS=Homo sapiens OX=9606 GN=LMOD1 |
| Q9BV00 | 3 | 7.89E-06 | LMOD1 protein OS=Homo sapiens OX=9606 GN=LMOD1 PE=1 SV=1 |
| P29536 | 3 | 3.54E-06 | Leiomodin-1 OS=Homo sapiens OX=9606 GN=LMOD1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P29536-2, Q9BV00 |
| C9JHW9 | 3 | 1.50E-05 | Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| F8WCF2 | 3 | 4.81E-05 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| A0A087WUM5 | 3 | 0.000195532 | Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens OX=9606 GN=GLIPR2 PE=1 SV=1 |
| Q5SYE7 | 2 | 3.50E-07 | NHS-like protein 1 OS=Homo sapiens OX=9606 GN=NHSL1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5SYE7-2 |
| Q5SYE7-2 | 2 | 3.51E-07 | Isoform 2 of NHS-like protein 1 OS=Homo sapiens OX=9606 GN=NHSL1 |
| Q9UQ80-2 | 3 | 9.05E-06 | Isoform 2 of Proliferation-associated protein 2G4 OS=Homo sapiens OX=9606 GN=PA2G4 |
| Q9UQ80 | 3 | 7.81E-06 | Proliferation-associated protein 2G4 OS=Homo sapiens OX=9606 GN=PA2G4 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9UQ80-2 |
| F5H3K7 | 3 | 7.97E-05 | Ras-related protein Rab-6A (Fragment) OS=Homo sapiens OX=9606 GN=RAB6A PE=1 SV=1 |
| P20340 | 3 | 3.68E-05 | Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P20340-2, P20340-4, P20340-3, F5H3K7 |
| P20340-4 | 3 | 4.37E-05 | Isoform 4 of Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A |
| P20340-3 | 3 | 5.44E-05 | Isoform 3 of Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A |
| P20340-2 | 3 | 3.68E-05 | Isoform 2 of Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A |
| Q9UBV2-2 | 2 | 1.35E-06 | Isoform 2 of Protein sel-1 homolog 1 OS=Homo sapiens OX=9606 GN=SEL1L |
| G3V3B3 | 2 | 2.50E-06 | Protein sel-1 homolog 1 (Fragment) OS=Homo sapiens OX=9606 GN=SEL1L PE=1 SV=1 |
| Q9UBV2 | 2 | 5.13E-07 | Protein sel-1 homolog 1 OS=Homo sapiens OX=9606 GN=SEL1L PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9UBV2-2, G3V3B3 |
| D6R9P3 | 2 | 7.67E-06 | Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=1 |
| D6RD18 | 2 | 7.59E-06 | Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=1 |
| D6RBZ0 | 2 | 6.57E-06 | Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=1 |
| Q99729-2 | 2 | 6.47E-06 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB; Additional IDs concatenated into MaxParsimony group: D6RBZ0, Q99729-3, D6RD18, D6R9P3 |
| Q99729-3 | 2 | 7.54E-06 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB |
| H7C1R1 | 3 | 1.76E-05 | Zinc finger protein 185 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF185 PE=1 SV=2 |
| H7BZT5 | 3 | 5.90E-06 | Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 PE=1 SV=2 |
| O15231-8 | 3 | 4.70E-06 | Isoform 8 of Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 |
| O15231 | 3 | 4.72E-06 | Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 PE=1 SV=3 |
| O15231-6 | 3 | 4.52E-06 | Isoform 6 of Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185; Additional IDs concatenated into MaxParsimony group: O15231-8, O15231-3, O15231, O15231-7, O15231-4, H7BZT5, O15231-5, H0Y704, H7C1R1 |
| O15231-7 | 3 | 4.93E-06 | Isoform 7 of Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 |
| O15231-3 | 3 | 4.72E-06 | Isoform 3 of Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 |
| O15231-4 | 3 | 5.17E-06 | Isoform 4 of Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 |
| H0Y704 | 3 | 7.27E-06 | Zinc finger protein 185 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF185 PE=1 SV=2 |
| O15231-5 | 3 | 6.96E-06 | Isoform 5 of Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 |
| Q99426 | 2 | 1.09E-05 | Tubulin-folding cofactor B OS=Homo sapiens OX=9606 GN=TBCB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q99426-2, K7EK42, K7EP07, K7EL99 |
| K7EK42 | 2 | 1.39E-05 | Tubulin-folding cofactor B OS=Homo sapiens OX=9606 GN=TBCB PE=1 SV=1 |
| Q99426-2 | 2 | 1.37E-05 | Isoform 2 of Tubulin-folding cofactor B OS=Homo sapiens OX=9606 GN=TBCB |
| K7EP07 | 2 | 1.57E-05 | Tubulin-folding cofactor B (Fragment) OS=Homo sapiens OX=9606 GN=TBCB PE=1 SV=8 |
| Q99747 | 3 | 2.61E-06 | Gamma-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPG PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q99747-2 |
| Q99747-2 | 3 | 3.54E-06 | Isoform 2 of Gamma-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPG |
| Q1KMD3 | 3 | 1.30E-05 | Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens OX=9606 GN=HNRNPUL2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H3BQZ7 |
| H3BQZ7 | 3 | 1.30E-05 | HCG2044799 OS=Homo sapiens OX=9606 GN=HNRNPUL2-BSCL2 PE=4 SV=1 |
| P18583-9 | 2 | 2.14E-07 | Isoform I of Protein SON OS=Homo sapiens OX=9606 GN=SON; Additional IDs concatenated into MaxParsimony group: P18583-5, P18583, P18583-7, P18583-4, P18583-3, P18583-10, P18583-2, P18583-6, H7C1M2 |
| P18583-10 | 2 | 2.31E-07 | Isoform J of Protein SON OS=Homo sapiens OX=9606 GN=SON |
| P18583-6 | 2 | 2.50E-07 | Isoform E of Protein SON OS=Homo sapiens OX=9606 GN=SON |
| P18583-5 | 2 | 2.14E-07 | Isoform D of Protein SON OS=Homo sapiens OX=9606 GN=SON |
| P18583 | 2 | 2.17E-07 | Protein SON OS=Homo sapiens OX=9606 GN=SON PE=1 SV=4 |
| P18583-7 | 2 | 2.21E-07 | Isoform G of Protein SON OS=Homo sapiens OX=9606 GN=SON |
| P18583-4 | 2 | 2.27E-07 | Isoform C of Protein SON OS=Homo sapiens OX=9606 GN=SON |
| P18583-3 | 2 | 2.29E-07 | Isoform B of Protein SON OS=Homo sapiens OX=9606 GN=SON |
| P18583-2 | 2 | 2.46E-07 | Isoform A of Protein SON OS=Homo sapiens OX=9606 GN=SON |
| O43681 | 3 | 4.52E-06 | ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A087WXS7, K7ERW9 |
| A0A087WXS7 | 3 | 4.76E-06 | ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=1 |
| K7ERW9 | 3 | 4.50E-06 | Arsenical pump-driving ATPase (Fragment) OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=1 |
| Q9BZF3-2 | 2 | 8.96E-07 | Isoform 2 of Oxysterol-binding protein-related protein 6 OS=Homo sapiens OX=9606 GN=OSBPL6 |
| Q9BZF3 | 2 | 8.62E-07 | Oxysterol-binding protein-related protein 6 OS=Homo sapiens OX=9606 GN=OSBPL6 PE=1 SV=1 |
| Q9BZF3-4 | 2 | 8.91E-07 | Isoform 4 of Oxysterol-binding protein-related protein 6 OS=Homo sapiens OX=9606 GN=OSBPL6 |
| Q9BZF3-6 | 2 | 1.58E-06 | Isoform 6 of Oxysterol-binding protein-related protein 6 OS=Homo sapiens OX=9606 GN=OSBPL6 |
| Q9BZF3-3 | 2 | 8.58E-07 | Isoform 3 of Oxysterol-binding protein-related protein 6 OS=Homo sapiens OX=9606 GN=OSBPL6 |
| Q9BZF3-5 | 2 | 8.39E-07 | Isoform 5 of Oxysterol-binding protein-related protein 6 OS=Homo sapiens OX=9606 GN=OSBPL6; Additional IDs concatenated into MaxParsimony group: Q9BZF3-3, Q9BZF3, Q9BZF3-4, Q9BZF3-2, Q9BZF3-6 |
| A0A0A0MSS4 | 3 | 4.14E-05 | Nuclear migration protein nudC (Fragment) OS=Homo sapiens OX=9606 GN=NUDC PE=1 SV=1 |
| A0A0A0MSU9 | 3 | 2.96E-05 | Nuclear migration protein nudC (Fragment) OS=Homo sapiens OX=9606 GN=NUDC PE=1 SV=1 |
| Q9Y266 | 3 | 1.66E-05 | Nuclear migration protein nudC OS=Homo sapiens OX=9606 GN=NUDC PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0A0MSU9, A0A0A0MSS4 |
| H0YJ21 | 3 | 1.34E-05 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=2 |
| A0A2R8YGC7 | 3 | 1.77E-05 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1 |
| A0A2R8Y6I5 | 3 | 1.04E-05 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1 |
| A0A2R8Y542 | 3 | 1.25E-05 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1 |
| H0YKU2 | 3 | 0.00018605 | Proteasome activator complex subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=1 |
| A0A2R8Y619 | 2 | 0.00084211 | Histone H2B OS=Homo sapiens OX=9606 PE=1 SV=1 |
| F5H3X6 | 3 | 0.000105424 | Prohibitin-2 (Fragment) OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=2 |
| F5H2D2 | 3 | 7.09E-05 | Prohibitin-2 OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=1 |
| I3L0S0 | 2 | 6.36E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=1 |
| H7BYR4 | 3 | 1.42E-06 | Calcium-dependent secretion activator 2 (Fragment) OS=Homo sapiens OX=9606 GN=CADPS2 PE=1 SV=1 |
| F8W8P5 | 3 | 1.07E-06 | Calcium-dependent secretion activator 2 OS=Homo sapiens OX=9606 GN=CADPS2 PE=1 SV=2 |
| Q86UW7-3 | 3 | 1.02E-06 | Isoform 3 of Calcium-dependent secretion activator 2 OS=Homo sapiens OX=9606 GN=CADPS2 |
| C9IYE1 | 3 | 9.84E-07 | Calcium-dependent secretion activator 2 OS=Homo sapiens OX=9606 GN=CADPS2 PE=1 SV=1 |
| Q86UW7 | 3 | 9.82E-07 | Calcium-dependent secretion activator 2 OS=Homo sapiens OX=9606 GN=CADPS2 PE=1 SV=2 |
| H7C538 | 3 | 2.09E-05 | Calcium-dependent secretion activator 1 (Fragment) OS=Homo sapiens OX=9606 GN=CADPS PE=1 SV=1 |
| Q86UW7-2 | 3 | 1.01E-06 | Isoform 2 of Calcium-dependent secretion activator 2 OS=Homo sapiens OX=9606 GN=CADPS2 |
| A0A0C4DGY2 | 3 | 2.60E-05 | Calcium-dependent secretion activator 1 OS=Homo sapiens OX=9606 GN=CADPS PE=1 SV=1 |
| A0A087X1P3 | 3 | 9.79E-07 | Calcium-dependent secretion activator 2 OS=Homo sapiens OX=9606 GN=CADPS2 PE=1 SV=1 |
| C9JSZ1 | 3 | 0.00016104 | Far upstream element-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=1 |
| Q9NYU2 | 3 | 5.94E-06 | UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens OX=9606 GN=UGGT1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9NYU2-2, H7BZG0 |
| Q9NYU2-2 | 3 | 6.04E-06 | Isoform 2 of UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens OX=9606 GN=UGGT1 |
| P49368-2 | 3 | 1.92E-05 | Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606 GN=CCT3 |
| B4DUR8 | 3 | 1.94E-05 | T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606 GN=CCT3 PE=1 SV=1 |
| P49368 | 3 | 1.78E-05 | T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606 GN=CCT3 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P49368-2, B4DUR8, Q5SZX6 |
| Q5SZX6 | 2 | 3.42E-06 | T-complex protein 1 subunit gamma (Fragment) OS=Homo sapiens OX=9606 GN=CCT3 PE=1 SV=1 |
| K7EKQ2 | 3 | 1.21E-05 | Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1 |
| K7EQA9 | 3 | 3.49E-05 | Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1 |
| K7EIU0 | 2 | 3.45E-05 | Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1 |
| Q13428-8 | 3 | 1.54E-05 | Isoform 8 of Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 |
| H0Y8Y7 | 3 | 2.08E-05 | Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 PE=1 SV=2 |
| E7ETY2 | 3 | 1.46E-05 | Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 PE=1 SV=1 |
| Q13428-7 | 3 | 1.50E-05 | Isoform 7 of Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 |
| Q13428-2 | 3 | 1.54E-05 | Isoform 2 of Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 |
| Q13428-5 | 3 | 2.16E-05 | Isoform 5 of Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 |
| Q13428-6 | 3 | 1.50E-05 | Isoform 6 of Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 |
| Q13428-4 | 3 | 1.43E-05 | Isoform 4 of Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1; Additional IDs concatenated into MaxParsimony group: Q13428-3, E7ETY2, Q13428, Q13428-7, Q13428-6, J3KQ96, Q13428-8, Q13428-2, H0Y8Y7, Q13428-5 |
| J3KQ96 | 3 | 1.54E-05 | Treacle protein (Fragment) OS=Homo sapiens OX=9606 GN=TCOF1 PE=1 SV=1 |
| Q13428-3 | 3 | 1.46E-05 | Isoform 3 of Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 |
| Q13428 | 3 | 1.46E-05 | Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 PE=1 SV=3 |
| O00154-4 | 3 | 2.25E-05 | Isoform 4 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 |
| O00154 | 3 | 2.00E-05 | Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O00154-7, O00154-5, O00154-4, O00154-6, O00154-3, K7EKP8, O00154-2 |
| O00154-5 | 3 | 2.17E-05 | Isoform 5 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 |
| O00154-2 | 3 | 2.20E-05 | Isoform 2 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 |
| O00154-7 | 3 | 2.05E-05 | Isoform 7 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 |
| O00154-6 | 3 | 2.31E-05 | Isoform 6 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 |
| O00154-3 | 3 | 1.91E-05 | Isoform 3 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 |
| K7EKP8 | 3 | 1.94E-05 | Cytosolic acyl coenzyme A thioester hydrolase (Fragment) OS=Homo sapiens OX=9606 GN=ACOT7 PE=1 SV=8 |
| C9JRC4 | 3 | 4.52E-05 | Protein phosphatase 1 regulatory subunit 7 (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1 |
| Q8NHP1 | 3 | 1.12E-06 | Aflatoxin B1 aldehyde reductase member 4 OS=Homo sapiens OX=9606 GN=AKR7L PE=2 SV=6 |
| C9J1E1 | 3 | 1.68E-05 | Biliverdin reductase A (Fragment) OS=Homo sapiens OX=9606 GN=BLVRA PE=1 SV=1 |
| Q5T5P2-8 | 3 | 2.59E-05 | Isoform 7 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P2-10 | 3 | 1.64E-05 | Isoform 10 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P2 | 3 | 1.21E-05 | Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5T5P2-3, Q5T5P2-10, Q5T5P2-7, Q5T5P2-2, Q5T5P2-9, Q5T5P2-6, Q5T5P2-8, Q5T5P2-4, Q5T5P1, Q5T5P0 |
| Q5T5P2-9 | 3 | 1.86E-05 | Isoform 9 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P2-6 | 3 | 2.52E-05 | Isoform 6 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P2-4 | 3 | 2.71E-05 | Isoform 4 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P2-2 | 3 | 1.75E-05 | Isoform 2 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P0 | 3 | 1.14E-05 | Sickle tail protein homolog (Fragment) OS=Homo sapiens OX=9606 GN=KIAA1217 PE=1 SV=1 |
| Q5T5P2-7 | 3 | 1.74E-05 | Isoform 5 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P2-3 | 3 | 1.60E-05 | Isoform 3 of Sickle tail protein homolog OS=Homo sapiens OX=9606 GN=KIAA1217 |
| Q5T5P1 | 3 | 9.60E-06 | Sickle tail protein homolog (Fragment) OS=Homo sapiens OX=9606 GN=KIAA1217 PE=1 SV=2 |
| E5RIT6 | 2 | 1.28E-05 | 60S ribosomal protein L26-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=RPL26L1 PE=1 SV=1 |
| P61254 | 2 | 1.88E-05 | 60S ribosomal protein L26 OS=Homo sapiens OX=9606 GN=RPL26 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UNX3, J3QRC4, E5RIT6, J3QQV1, J3QQQ9, J3QRI7 |
| J3QQQ9 | 2 | 1.53E-05 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |
| J3QRC4 | 2 | 1.21E-05 | 60S ribosomal protein L26 (Fragment) OS=Homo sapiens OX=9606 GN=RPL26 PE=4 SV=1 |
| J3QQV1 | 2 | 1.49E-05 | 60S ribosomal protein L26 OS=Homo sapiens OX=9606 GN=RPL26 PE=4 SV=1 |
| J3QRI7 | 2 | 1.53E-05 | 60S ribosomal protein L26 (Fragment) OS=Homo sapiens OX=9606 GN=RPL26 PE=4 SV=1 |
| Q9UNX3 | 2 | 1.13E-05 | 60S ribosomal protein L26-like 1 OS=Homo sapiens OX=9606 GN=RPL26L1 PE=1 SV=1 |
| Q9ULV4 | 2 | 6.45E-06 | Coronin-1C OS=Homo sapiens OX=9606 GN=CORO1C PE=1 SV=1 |
| Q9ULV4-2 | 2 | 6.37E-06 | Isoform 2 of Coronin-1C OS=Homo sapiens OX=9606 GN=CORO1C |
| B4E3S0 | 2 | 8.28E-06 | Coronin OS=Homo sapiens OX=9606 GN=CORO1C PE=1 SV=1 |
| Q9ULV4-3 | 2 | 5.80E-06 | Isoform 3 of Coronin-1C OS=Homo sapiens OX=9606 GN=CORO1C; Additional IDs concatenated into MaxParsimony group: Q9ULV4-2, Q9ULV4, B4E3S0, H0YHL7 |
| Q12906-5 | 3 | 1.78E-05 | Isoform 5 of Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 |
| Q12906-6 | 3 | 1.74E-05 | Isoform 6 of Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 |
| Q12906-4 | 3 | 1.76E-05 | Isoform 4 of Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 |
| K7EKJ9 | 3 | 3.54E-05 | Interleukin enhancer-binding factor 3 (Fragment) OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=1 |
| Q12906-3 | 3 | 1.61E-05 | Isoform 3 of Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 |
| K7EQR9 | 3 | 8.43E-06 | Interleukin enhancer-binding factor 3 (Fragment) OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=1 |
| Q12906 | 3 | 1.37E-05 | Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3 |
| Q12906-7 | 3 | 1.37E-05 | Isoform 7 of Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3; Additional IDs concatenated into MaxParsimony group: Q12906, Q12906-3, Q12906-6, Q12906-2, Q12906-4, Q12906-5, K7EKJ9, K7EQR9 |
| Q12906-2 | 3 | 1.75E-05 | Isoform 2 of Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 |
| P23229 | 3 | 3.43E-06 | Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: P23229-6, P23229-9, P23229-3, P23229-5, P23229-2, P23229-4, P23229-7, H7BZ97 |
| P23229-6 | 3 | 3.48E-06 | Isoform Alpha-6X1X2A of Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 |
| H7BZ97 | 3 | 3.43E-06 | Integrin alpha-6 (Fragment) OS=Homo sapiens OX=9606 GN=ITGA6 PE=1 SV=1 |
| P23229-7 | 3 | 1.22E-06 | Isoform 7 of Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 |
| P23229-3 | 3 | 3.55E-06 | Isoform Alpha-6X1B of Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 |
| P23229-2 | 3 | 3.61E-06 | Isoform Alpha-6X1A of Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 |
| P23229-4 | 3 | 3.63E-06 | Isoform Alpha-6X2A of Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 |
| P23229-9 | 3 | 3.53E-06 | Isoform 9 of Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 |
| P23229-5 | 3 | 3.57E-06 | Isoform Alpha-6X2B of Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 |
| Q5H9R7 | 3 | 1.31E-05 | Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=2 |
| H7BXH2 | 3 | 1.39E-05 | Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=1 |
| E9PQP7 | 3 | 1.79E-05 | Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=1 |
| Q5H9R7-6 | 3 | 1.36E-05 | Isoform 6 of Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 |
| Q5H9R7-4 | 3 | 1.45E-05 | Isoform 4 of Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 |
| E9PKF6 | 3 | 1.37E-05 | Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=1 |
| Q5H9R7-5 | 3 | 1.30E-05 | Isoform 5 of Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3; Additional IDs concatenated into MaxParsimony group: Q5H9R7, Q5H9R7-2, Q5H9R7-6, E9PKF6, H7BXH2, Q5H9R7-4, Q5H9R7-3, E9PQP7, H0YEN2, H0YEV0 |
| Q5H9R7-2 | 3 | 1.32E-05 | Isoform 2 of Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 |
| Q5H9R7-3 | 3 | 1.45E-05 | Isoform 3 of Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 |
| H0YEV0 | 3 | 0.000105168 | Serine/threonine-protein phosphatase 6 regulatory subunit 3 (Fragment) OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=1 |
| H0YEN2 | 3 | 1.98E-05 | Serine/threonine-protein phosphatase 6 regulatory subunit 3 (Fragment) OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=1 |
| Q13907 | 2 | 1.27E-06 | Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens OX=9606 GN=IDI1 PE=1 SV=2 |
| Q13907-2 | 2 | 1.01E-06 | Isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens OX=9606 GN=IDI1; Additional IDs concatenated into MaxParsimony group: Q13907 |
| H3BQW8 | 3 | 2.94E-05 | Hydroxyacylglutathione hydrolase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HAGH PE=1 SV=1 |
| Q16775-3 | 3 | 1.99E-05 | Isoform 3 of Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=HAGH |
| Q13200 | 3 | 3.84E-06 | 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PSMD2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q13200-3, Q13200-2 |
| Q13200-3 | 3 | 4.48E-06 | Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PSMD2 |
| Q13200-2 | 3 | 4.65E-06 | Isoform 2 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PSMD2 |
| P14868 | 3 | 3.36E-05 | Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=DARS PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P14868-2, H7BZ35 |
| H7BZ35 | 2 | 5.18E-05 | Aspartate--tRNA ligase, cytoplasmic (Fragment) OS=Homo sapiens OX=9606 GN=DARS PE=1 SV=1 |
| P14868-2 | 3 | 4.20E-05 | Isoform 2 of Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=DARS |
| P07954-2 | 3 | 1.21E-05 | Isoform Cytoplasmic of Fumarate hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=FH |
| P07954 | 3 | 1.10E-05 | Fumarate hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=FH PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P07954-2 |
| H3BNP9 | 3 | 2.02E-05 | Sulfide:quinone oxidoreductase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SQOR PE=1 SV=1 |
| Q9Y6N5 | 3 | 5.75E-06 | Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens OX=9606 GN=SQOR PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H3BNP9 |
| A0A1B0GVU0 | 2 | 3.11E-05 | Alpha-aminoadipic semialdehyde dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| F8VVF2 | 2 | 2.64E-05 | Alpha-aminoadipic semialdehyde dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=2 |
| H0YHM6 | 2 | 2.13E-05 | Alpha-aminoadipic semialdehyde dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=8 |
| Q9UJU6-2 | 3 | 1.54E-05 | Isoform 2 of Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL |
| F8WC20 | 2 | 4.43E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| F8WFE1 | 2 | 2.55E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| F8WBG8 | 2 | 1.73E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| Q9UJU6-5 | 3 | 1.35E-05 | Isoform 5 of Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL |
| F8WBB2 | 2 | 3.58E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| F8WCK3 | 2 | 5.29E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| Q9UJU6-6 | 3 | 1.74E-05 | Isoform 6 of Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL |
| Q9UJU6-4 | 3 | 1.31E-05 | Isoform 4 of Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL |
| Q9UJU6-3 | 3 | 1.51E-05 | Isoform 3 of Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL; Additional IDs concatenated into MaxParsimony group: Q9UJU6-2, Q9UJU6, B4DDD6, Q9UJU6-6, H0Y5J4, Q9UJU6-4, Q9UJU6-5, F8WBG8, F8WFE1, F8WBB2, F8WC20, F2Z3E3, F8WCK3, F8WB73, F2Z2V3 |
| F8WB73 | 2 | 6.82E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| Q9UJU6 | 3 | 1.54E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| F2Z2V3 | 2 | 7.83E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| F2Z3E3 | 2 | 4.41E-05 | Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| B4DDD6 | 3 | 1.63E-05 | cDNA FLJ59450, highly similar to Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| H0Y5J4 | 3 | 1.23E-05 | Drebrin-like protein (Fragment) OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1 |
| P36776-3 | 3 | 2.19E-06 | Isoform 3 of Lon protease homolog, mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 |
| P36776 | 3 | 1.74E-06 | Lon protease homolog, mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P36776-2, K7EKE6, K7EJE8, P36776-3 |
| K7EJE8 | 3 | 2.02E-06 | Lon protease homolog, mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 PE=1 SV=1 |
| P36776-2 | 3 | 1.87E-06 | Isoform 2 of Lon protease homolog, mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 |
| K7EKE6 | 3 | 1.98E-06 | Lon protease homolog, mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 PE=1 SV=1 |
| Q9Y2Q3-4 | 3 | 1.46E-05 | Isoform 4 of Glutathione S-transferase kappa 1 OS=Homo sapiens OX=9606 GN=GSTK1 |
| Q9Y2Q3 | 3 | 1.19E-05 | Glutathione S-transferase kappa 1 OS=Homo sapiens OX=9606 GN=GSTK1 PE=1 SV=3 |
| Q9Y2Q3-2 | 3 | 9.50E-06 | Isoform 2 of Glutathione S-transferase kappa 1 OS=Homo sapiens OX=9606 GN=GSTK1; Additional IDs concatenated into MaxParsimony group: Q9Y2Q3, E9PFN5, Q9Y2Q3-4, Q9Y2Q3-3 |
| E9PFN5 | 3 | 1.41E-05 | Glutathione S-transferase kappa OS=Homo sapiens OX=9606 GN=GSTK1 PE=1 SV=1 |
| P43304-2 | 3 | 4.69E-06 | Isoform 2 of Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=GPD2 |
| P43304 | 3 | 3.88E-06 | Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=GPD2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P43304-2 |
| A0MZ66-7 | 3 | 6.14E-05 | Isoform 7 of Shootin-1 OS=Homo sapiens OX=9606 GN=SHTN1 |
| A0MZ66-6 | 3 | 2.24E-05 | Isoform 6 of Shootin-1 OS=Homo sapiens OX=9606 GN=SHTN1 |
| A0MZ66-3 | 3 | 2.07E-05 | Isoform 3 of Shootin-1 OS=Homo sapiens OX=9606 GN=SHTN1; Additional IDs concatenated into MaxParsimony group: A0MZ66, A0MZ66-6, A0MZ66-5, A0MZ66-7 |
| A0MZ66 | 3 | 2.13E-05 | Shootin-1 OS=Homo sapiens OX=9606 GN=SHTN1 PE=1 SV=4 |
| A0MZ66-5 | 3 | 2.36E-05 | Isoform 5 of Shootin-1 OS=Homo sapiens OX=9606 GN=SHTN1 |
| F5H5P8 | 3 | 2.08E-06 | cGMP-dependent 3',5'-cyclic phosphodiesterase (Fragment) OS=Homo sapiens OX=9606 GN=PDE2A PE=1 SV=8 |
| O00408-6 | 3 | 2.28E-07 | Isoform 6 of cGMP-dependent 3',5'-cyclic phosphodiesterase OS=Homo sapiens OX=9606 GN=PDE2A |
| F5H130 | 3 | 1.24E-06 | cGMP-dependent 3',5'-cyclic phosphodiesterase (Fragment) OS=Homo sapiens OX=9606 GN=PDE2A PE=1 SV=1 |
| O00408-2 | 3 | 1.94E-07 | Isoform PDE2A1 of cGMP-dependent 3',5'-cyclic phosphodiesterase OS=Homo sapiens OX=9606 GN=PDE2A; Additional IDs concatenated into MaxParsimony group: O00408-6, F5H130, F5H5P8 |
| H0YE28 | 3 | 5.14E-05 | Selenoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=SELENOH PE=1 SV=1 |
| A0A087WYP2 | 3 | 3.99E-05 | Selenoprotein H OS=Homo sapiens OX=9606 GN=SELENOH PE=1 SV=1 |
| Q8IZQ5 | 3 | 3.96E-05 | Selenoprotein H OS=Homo sapiens OX=9606 GN=SELENOH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A087WYP2, H0YE28 |
| G5E9J0 | 3 | 7.13E-05 | Arp2/3 complex 34 kDa subunit OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1 |
| G5E9S7 | 3 | 0.000170703 | Actin related protein 2/3 complex, subunit 2, 34kDa, isoform CRA\_e OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1 |
| C9JTV5 | 3 | 7.29E-05 | Arp2/3 complex 34 kDa subunit (Fragment) OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=8 |
| O15144 | 3 | 2.16E-05 | Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: G5E9J0, C9JTV5, G5E9S7 |
| F5H1N7 | 2 | 7.83E-07 | Uncharacterized protein KIAA1211 OS=Homo sapiens OX=9606 GN=KIAA1211 PE=1 SV=1 |
| A0A1B0GWF1 | 2 | 2.48E-06 | Uncharacterized protein KIAA1211 (Fragment) OS=Homo sapiens OX=9606 GN=KIAA1211 PE=1 SV=1 |
| Q6ZU35 | 2 | 7.79E-07 | Uncharacterized protein KIAA1211 OS=Homo sapiens OX=9606 GN=KIAA1211 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: F5H1N7, A0A2R8Y6P1, A0A1B0GWF1 |
| A0A2R8Y6P1 | 2 | 2.03E-06 | Uncharacterized protein KIAA1211 (Fragment) OS=Homo sapiens OX=9606 GN=KIAA1211 PE=1 SV=1 |
| I3L1U7 | 2 | 3.71E-06 | Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens OX=9606 GN=PAM16 PE=4 SV=1 |
| P57737-3 | 3 | 6.00E-07 | Isoform 3 of Coronin-7 OS=Homo sapiens OX=9606 GN=CORO7; Additional IDs concatenated into MaxParsimony group: A0A0A6YYL4, I3L3T0, I3L0X9, I3L1U7, Q9Y3D7 |
| I3L3T0 | 2 | 3.30E-06 | HCG15164, isoform CRA\_b OS=Homo sapiens OX=9606 GN=PAM16 PE=4 SV=1 |
| A0A0A6YYL4 | 3 | 6.00E-07 | Coronin OS=Homo sapiens OX=9606 GN=CORO7-PAM16 PE=3 SV=1 |
| Q9Y3D7 | 2 | 3.83E-06 | Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens OX=9606 GN=PAM16 PE=1 SV=2 |
| I3L0X9 | 2 | 3.49E-06 | Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens OX=9606 GN=PAM16 PE=4 SV=1 |
| Q06124-3 | 3 | 3.24E-06 | Isoform 3 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 |
| Q06124 | 3 | 2.50E-06 | Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q06124-2, Q06124-3, A0A1W2PPU4 |
| Q06124-2 | 3 | 2.52E-06 | Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 |
| A0A1W2PPU4 | 3 | 6.91E-06 | Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 PE=1 SV=1 |
| O60885 | 3 | 2.82E-06 | Bromodomain-containing protein 4 OS=Homo sapiens OX=9606 GN=BRD4 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: O60885-3, Q15059, O60885-2, M0QZD9, Q15059-2 |
| M0QZD9 | 3 | 6.71E-06 | Bromodomain-containing protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=BRD4 PE=1 SV=1 |
| O60885-3 | 3 | 4.83E-06 | Isoform B of Bromodomain-containing protein 4 OS=Homo sapiens OX=9606 GN=BRD4 |
| Q15059 | 3 | 5.28E-06 | Bromodomain-containing protein 3 OS=Homo sapiens OX=9606 GN=BRD3 PE=1 SV=1 |
| O60885-2 | 3 | 5.31E-06 | Isoform C of Bromodomain-containing protein 4 OS=Homo sapiens OX=9606 GN=BRD4 |
| Q15059-2 | 3 | 6.90E-06 | Isoform 2 of Bromodomain-containing protein 3 OS=Homo sapiens OX=9606 GN=BRD3 |
| A0A1W2PRH9 | 3 | 0.000313399 | Mitochondrial import inner membrane translocase subunit Tim9 OS=Homo sapiens OX=9606 GN=TIMM9 PE=1 SV=1 |
| G3V502 | 3 | 0.000284908 | Mitochondrial import inner membrane translocase subunit Tim9 OS=Homo sapiens OX=9606 GN=TIMM9 PE=1 SV=1 |
| A0A1W2PQS5 | 3 | 0.000308261 | Mitochondrial import inner membrane translocase subunit Tim9 OS=Homo sapiens OX=9606 GN=TIMM9 PE=1 SV=1 |
| A0A087WYS1 | 2 | 1.27E-06 | UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens OX=9606 GN=UGP2 PE=1 SV=1 |
| Q16851-2 | 2 | 1.30E-06 | Isoform 2 of UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens OX=9606 GN=UGP2 |
| Q16851 | 2 | 1.27E-06 | UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens OX=9606 GN=UGP2 PE=1 SV=5 |
| E7EUC7 | 2 | 1.25E-06 | UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens OX=9606 GN=UGP2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087WYS1, Q16851, Q16851-2 |
| Q99439-2 | 2 | 1.45E-06 | Isoform 2 of Calponin-2 OS=Homo sapiens OX=9606 GN=CNN2 |
| Q99439 | 2 | 1.27E-06 | Calponin-2 OS=Homo sapiens OX=9606 GN=CNN2 PE=1 SV=4 |
| B4DUT8 | 2 | 1.19E-06 | Calponin OS=Homo sapiens OX=9606 GN=CNN2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q99439, B4DDF4, Q99439-2, A0A087X271, K7ES69 |
| A0A087X271 | 2 | 2.19E-06 | Calponin (Fragment) OS=Homo sapiens OX=9606 GN=CNN2 PE=1 SV=1 |
| K7ES69 | 2 | 2.65E-06 | Calponin-2 OS=Homo sapiens OX=9606 GN=CNN2 PE=1 SV=1 |
| B4DDF4 | 2 | 1.32E-06 | Calponin OS=Homo sapiens OX=9606 GN=CNN2 PE=1 SV=1 |
| Q9NQW7-2 | 3 | 1.11E-06 | Isoform 2 of Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1 |
| Q9NQW7-3 | 3 | 1.20E-06 | Isoform 3 of Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1; Additional IDs concatenated into MaxParsimony group: Q9NQW7-4, Q9NQW7, Q9NQW7-2, Q5T6H7 |
| Q5T6H7 | 3 | 1.45E-06 | Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1 PE=1 SV=1 |
| Q9NQW7 | 3 | 1.29E-06 | Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1 PE=1 SV=3 |
| Q9NQW7-4 | 3 | 1.04E-06 | Isoform 4 of Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1 |
| A0A087WWY5 | 2 | 0.000140556 | Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 |
| A0A0G2JQT1 | 2 | 1.26E-05 | Cytoplasmic FMR1-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=4 |
| A0A0G2JRV9 | 2 | 6.72E-05 | Cytoplasmic FMR1-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 |
| Q7L576 | 2 | 8.64E-06 | Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 |
| E7EW33 | 2 | 1.02E-05 | Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens OX=9606 GN=CYFIP2 PE=1 SV=1 |
| A0A087WVE1 | 2 | 5.76E-05 | Cytoplasmic FMR1-interacting protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP2 PE=1 SV=1 |
| A0A087WU52 | 2 | 7.17E-05 | Cytoplasmic FMR1-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 |
| E7EVJ5 | 2 | 8.82E-06 | Cytoplasmic FMR1-interacting protein OS=Homo sapiens OX=9606 GN=CYFIP2 PE=1 SV=1 |
| H7C229 | 2 | 9.69E-06 | Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens OX=9606 GN=CYFIP2 PE=1 SV=2 |
| A0A087WWL1 | 2 | 6.72E-05 | Cytoplasmic FMR1-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 |
| Q96F07-2 | 2 | 8.64E-06 | Isoform 2 of Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens OX=9606 GN=CYFIP2 |
| A0A0G2JRF5 | 2 | 0.000140556 | Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 |
| A0A087WWZ1 | 2 | 3.67E-05 | Cytoplasmic FMR1-interacting protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP2 PE=1 SV=1 |
| A0A0G2JRX2 | 2 | 7.17E-05 | Cytoplasmic FMR1-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 |
| A0A0G2JR96 | 2 | 1.26E-05 | Cytoplasmic FMR1-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=4 |
| A0A087WTQ3 | 2 | 4.88E-05 | Cytoplasmic FMR1-interacting protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CYFIP2 PE=1 SV=1 |
| A0A087WV63 | 2 | 0.000152433 | Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens OX=9606 GN=CYFIP2 PE=4 SV=1 |
| Q96F07 | 2 | 8.47E-06 | Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens OX=9606 GN=CYFIP2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q96F07-2, Q7L576, E7EVJ5, H7C229, E7EW33, A0A0G2JQT1, A0A0G2JR96, A0A087WWZ1, A0A087WTQ3, A0A087WVE1, A0A0G2JRV9, A0A087WWL1, A0A087WU52, A0A0G2JRX2, A0A0G2JRF5, A0A087WWY5, A0A087WV63 |
| A0A2U3TZL5 | 3 | 0.000112958 | CD59 glycoprotein (Fragment) OS=Homo sapiens OX=9606 GN=CD59 PE=4 SV=1 |
| E9PNW4 | 3 | 0.000125509 | CD59 glycoprotein OS=Homo sapiens OX=9606 PE=1 SV=1 |
| E9PR17 | 3 | 0.000104269 | CD59 glycoprotein OS=Homo sapiens OX=9606 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P13987, A0A2U3TZL5, E9PNW4 |
| P13987 | 3 | 0.000105898 | CD59 glycoprotein OS=Homo sapiens OX=9606 GN=CD59 PE=1 SV=1 |
| P49720 | 2 | 1.86E-06 | Proteasome subunit beta type-3 OS=Homo sapiens OX=9606 GN=PSMB3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A087WUL2 |
| A0A087WUL2 | 2 | 2.64E-06 | Proteasome subunit beta type-3 (Fragment) OS=Homo sapiens OX=9606 GN=PSMB3 PE=1 SV=1 |
| P35658 | 3 | 3.96E-07 | Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=2 |
| B7ZAV2 | 3 | 9.04E-07 | cDNA, FLJ79316, highly similar to Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=1 |
| E9PKD2 | 3 | 1.67E-06 | Nuclear pore complex protein Nup214 (Fragment) OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=1 |
| H0Y837 | 3 | 8.56E-07 | Nuclear pore complex protein Nup214 (Fragment) OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=1 |
| P35658-3 | 3 | 3.96E-07 | Isoform 3 of Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 |
| A0A0A0MSW3 | 3 | 5.45E-07 | Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=1 |
| P35658-2 | 3 | 3.98E-07 | Isoform 2 of Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 |
| P35658-5 | 3 | 3.95E-07 | Isoform 5 of Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214; Additional IDs concatenated into MaxParsimony group: P35658-3, P35658, P35658-4, P35658-2, A0A0A0MSW3, H0Y837, B7ZAV2, E9PKD2 |
| P35658-4 | 3 | 3.98E-07 | Isoform 4 of Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 |
| Q9H019 | 2 | 4.72E-07 | Mitochondrial fission regulator 1-like OS=Homo sapiens OX=9606 GN=MTFR1L PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9H019-3, E9PLD2 |
| E9PLD2 | 2 | 7.07E-07 | Mitochondrial fission regulator 1-like OS=Homo sapiens OX=9606 GN=MTFR1L PE=1 SV=1 |
| Q9H019-3 | 2 | 4.93E-07 | Isoform 3 of Mitochondrial fission regulator 1-like OS=Homo sapiens OX=9606 GN=MTFR1L |
| Q16822-3 | 2 | 6.69E-06 | Isoform 3 of Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 |
| H0YMU6 | 2 | 3.16E-05 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=1 |
| H0YML5 | 2 | 7.14E-06 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=1 |
| H0YM31 | 3 | 9.48E-06 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=2 |
| H0YNG4 | 2 | 3.00E-05 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=1 |
| Q16822-2 | 3 | 1.09E-05 | Isoform 2 of Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 |
| H0YMA5 | 2 | 2.77E-05 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=1 |
| A0A0A0MS74 | 3 | 1.09E-05 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=1 |
| Q16822 | 3 | 7.54E-06 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: H0YM31, Q16822-3, H0YML5, Q16822-2, A0A0A0MS74, H0YMA5, H0YNG4, H0YMU6 |
| M0QYH3 | 3 | 4.80E-05 | Far upstream element-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=1 |
| M0QXW7 | 3 | 6.99E-05 | Far upstream element-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=1 |
| Q5SSJ5-3 | 3 | 6.19E-05 | Isoform 3 of Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 |
| H0YE58 | 3 | 1.99E-05 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| H0YEL7 | 3 | 3.45E-05 | Acetyl-CoA acetyltransferase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ACAT1 PE=1 SV=1 |
| H0YJH7 | 3 | 1.77E-05 | Lamina-associated polypeptide 2, isoforms beta/gamma (Fragment) OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=1 |
| D6RIT9 | 3 | 7.99E-05 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| D6RF07 | 3 | 0.000298917 | OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| D6RA54 | 3 | 0.000125002 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| Q9NX40-3 | 3 | 7.35E-05 | Isoform 3 of OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 |
| D6RG39 | 3 | 8.04E-05 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| D6RC55 | 3 | 0.00012277 | OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| Q9NX40-4 | 3 | 7.09E-05 | Isoform 4 of OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 |
| D6RDI5 | 3 | 0.000141755 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| D6R918 | 3 | 0.000188359 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| Q9NX40-2 | 3 | 7.35E-05 | Isoform 2 of OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 |
| D6RBC5 | 3 | 0.000171877 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| A0A0A0MRL0 | 3 | 1.61E-05 | Interleukin enhancer-binding factor 2 OS=Homo sapiens OX=9606 GN=ILF2 PE=1 SV=1 |
| A0A2R8Y783 | 3 | 1.81E-05 | Protein 4.1 (Fragment) OS=Homo sapiens OX=9606 GN=EPB41 PE=1 SV=1 |
| H3BTK3 | 2 | 6.63E-05 | Calcium-regulated heat-stable protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=1 |
| I3L3X8 | 2 | 5.01E-05 | Calcium-regulated heat-stable protein 1 OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=1 |
| H3BSW7 | 2 | 4.21E-05 | Calcium-regulated heat-stable protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=1 |
| H3BUY4 | 2 | 3.80E-05 | Calcium-regulated heat-stable protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=1 |
| Q9Y2V2 | 3 | 5.55E-05 | Calcium-regulated heat-stable protein 1 OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H3BNU9, H3BPY5, H3BUY4, H3BSW7, I3L3X8, H3BTK3 |
| H3BNU9 | 2 | 3.60E-05 | Calcium-regulated heat-stable protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=1 |
| H3BPY5 | 2 | 3.77E-05 | Calcium-regulated heat-stable protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=8 |
| H0YF29 | 3 | 7.96E-06 | UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens OX=9606 GN=C8orf82 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q6P1X6, Q6P1X6-2 |
| Q6P1X6 | 3 | 9.62E-06 | UPF0598 protein C8orf82 OS=Homo sapiens OX=9606 GN=C8orf82 PE=1 SV=2 |
| Q6P1X6-2 | 3 | 9.99E-06 | Isoform 2 of UPF0598 protein C8orf82 OS=Homo sapiens OX=9606 GN=C8orf82 |
| P51003 | 2 | 2.39E-06 | Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOLA PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: G3XAH6 |
| G3XAH6 | 2 | 2.46E-06 | Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOLA PE=1 SV=1 |
| H0YJ66 | 3 | 0.000126747 | Dehydrogenase/reductase SDR family member 7 (Fragment) OS=Homo sapiens OX=9606 GN=DHRS7 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087X0Z7, Q9Y394, Q9Y394-2 |
| Q9Y394 | 3 | 0.000149181 | Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 PE=1 SV=1 |
| Q9Y394-2 | 3 | 0.00017499 | Isoform 2 of Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 |
| A0A087X0Z7 | 3 | 0.000134501 | Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 PE=1 SV=1 |
| Q96AQ6-3 | 3 | 4.76E-06 | Isoform 3 of Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens OX=9606 GN=PBXIP1 |
| Q96AQ6-2 | 3 | 4.66E-06 | Isoform 2 of Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens OX=9606 GN=PBXIP1 |
| Q5T173 | 3 | 1.00E-05 | Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens OX=9606 GN=PBXIP1 PE=1 SV=1 |
| Q96AQ6 | 3 | 4.47E-06 | Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens OX=9606 GN=PBXIP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q96AQ6-2, Q96AQ6-3, Q5T173 |
| Q9Y285 | 3 | 2.78E-06 | Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=3 |
| K7EK06 | 3 | 8.40E-06 | Phenylalanine--tRNA ligase alpha subunit (Fragment) OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=8 |
| K7ER16 | 3 | 6.00E-06 | Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=1 |
| K7EPH2 | 3 | 2.81E-06 | Phenylalanine--tRNA ligase alpha subunit (Fragment) OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=8 |
| K7ER00 | 3 | 2.57E-06 | Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9Y285, Q9Y285-2, K7ER16, K7EK06, K7EPH2 |
| Q9Y285-2 | 3 | 2.96E-06 | Isoform 2 of Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FARSA |
| O15027-2 | 3 | 3.05E-06 | Isoform 2 of Protein transport protein Sec16A OS=Homo sapiens OX=9606 GN=SEC16A |
| O15027-3 | 3 | 3.02E-06 | Isoform 3 of Protein transport protein Sec16A OS=Homo sapiens OX=9606 GN=SEC16A |
| O15027 | 3 | 2.99E-06 | Protein transport protein Sec16A OS=Homo sapiens OX=9606 GN=SEC16A PE=1 SV=3 |
| F1T0I1 | 3 | 2.79E-06 | Protein transport protein sec16 OS=Homo sapiens OX=9606 GN=SEC16A PE=1 SV=1 |
| J3KNL6 | 3 | 2.76E-06 | Protein transport protein sec16 OS=Homo sapiens OX=9606 GN=SEC16A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F1T0I1, O15027-5, O15027, O15027-3, O15027-4, O15027-2 |
| O15027-4 | 3 | 3.02E-06 | Isoform 4 of Protein transport protein Sec16A OS=Homo sapiens OX=9606 GN=SEC16A |
| O15027-5 | 3 | 2.96E-06 | Isoform 5 of Protein transport protein Sec16A OS=Homo sapiens OX=9606 GN=SEC16A |
| F8VYK5 | 3 | 1.46E-05 | Coatomer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1 |
| F8W651 | 3 | 1.09E-05 | Coatomer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1 |
| P61923-2 | 3 | 1.03E-05 | Isoform 2 of Coatomer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 |
| P61923-4 | 3 | 7.01E-06 | Isoform 4 of Coatomer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 |
| F8VVA7 | 3 | 6.55E-06 | Coatomer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P61923-4, P61923, P61923-3, P61923-2, F8W651, F8VYK5 |
| P61923-3 | 3 | 8.42E-06 | Isoform 3 of Coatomer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 |
| P61923 | 3 | 7.32E-06 | Coatomer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1 |
| Q15459 | 3 | 1.68E-06 | Splicing factor 3A subunit 1 OS=Homo sapiens OX=9606 GN=SF3A1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q15459-2 |
| Q15459-2 | 3 | 1.83E-06 | Isoform 2 of Splicing factor 3A subunit 1 OS=Homo sapiens OX=9606 GN=SF3A1 |
| A2A274 | 3 | 2.66E-06 | Aconitate hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q99798 |
| Q99798 | 3 | 2.75E-06 | Aconitate hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=2 |
| H3BVG0 | 2 | 2.41E-06 | Nuclear pore complex protein Nup93 OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q8N1F7, H3BM93, H3BRI8, H3BV11 |
| H3BM93 | 2 | 1.19E-05 | Nuclear pore complex protein Nup93 (Fragment) OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=1 |
| H3BRI8 | 2 | 1.41E-05 | Nuclear pore complex protein Nup93 (Fragment) OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=1 |
| Q8N1F7 | 2 | 2.59E-06 | Nuclear pore complex protein Nup93 OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=2 |
| H3BV11 | 2 | 1.56E-05 | Nuclear pore complex protein Nup93 (Fragment) OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=1 |
| E9PQM0 | 2 | 4.40E-07 | Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens OX=9606 GN=PTPMT1 PE=1 SV=1 |
| Q8WUK0 | 2 | 3.68E-07 | Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens OX=9606 GN=PTPMT1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PQM0, Q8WUK0-3, Q8WUK0-2 |
| Q8WUK0-2 | 2 | 5.39E-07 | Isoform 2 of Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens OX=9606 GN=PTPMT1 |
| Q8WUK0-3 | 2 | 4.89E-07 | Isoform 3 of Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens OX=9606 GN=PTPMT1 |
| O94925 | 3 | 7.89E-06 | Glutaminase kidney isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O94925-3, O94925-2 |
| O94925-2 | 3 | 3.12E-05 | Isoform 2 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS |
| O94925-3 | 3 | 8.83E-06 | Isoform 3 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS |
| U3KQF1 | 3 | 0.00010725 | Lysosomal protective protein OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=1 |
| X6R8A1 | 3 | 1.77E-05 | Carboxypeptidase OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: X6R5C5, P10619, P10619-2, U3KQU6, U3KQ41, U3KQF1 |
| X6R5C5 | 3 | 1.83E-05 | Carboxypeptidase OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=1 |
| P10619-2 | 3 | 1.90E-05 | Isoform 2 of Lysosomal protective protein OS=Homo sapiens OX=9606 GN=CTSA |
| P10619 | 3 | 1.83E-05 | Lysosomal protective protein OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=2 |
| U3KQU6 | 3 | 3.81E-05 | Carboxypeptidase OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=1 |
| U3KQ41 | 3 | 8.07E-05 | Lysosomal protective protein (Fragment) OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=8 |
| P00367 | 2 | 2.54E-06 | Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens OX=9606 GN=GLUD1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P00367-3, P00367-2 |
| Q8IY67 | 3 | 2.27E-06 | Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1 |
| Q8IY67-2 | 3 | 1.86E-06 | Isoform 2 of Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 |
| A0A087WZ13 | 3 | 1.86E-06 | Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1 |
| E9PAU2 | 3 | 1.82E-06 | Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q8IY67-2, A0A087WZ13, Q8IY67 |
| Q15631 | 2 | 3.90E-06 | Translin OS=Homo sapiens OX=9606 GN=TSN PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PGT1, H7C1D4 |
| H7C1D4 | 2 | 4.81E-06 | Translin (Fragment) OS=Homo sapiens OX=9606 GN=TSN PE=1 SV=1 |
| E9PGT1 | 2 | 3.99E-06 | Translin OS=Homo sapiens OX=9606 GN=TSN PE=1 SV=1 |
| Q5VW32 | 3 | 3.19E-06 | BRO1 domain-containing protein BROX OS=Homo sapiens OX=9606 GN=BROX PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5VW32-2 |
| Q5VW32-2 | 3 | 3.46E-06 | Isoform 2 of BRO1 domain-containing protein BROX OS=Homo sapiens OX=9606 GN=BROX |
| A0A0U1RQH7 | 3 | 8.85E-06 | RNA-binding protein 39 (Fragment) OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=1 |
| Q5QP23 | 2 | 1.78E-06 | RNA-binding protein 39 (Fragment) OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=1 |
| Q14498 | 3 | 4.09E-06 | RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q14498-2, Q14498-3, G3XAC6, H0Y4X3, A0A0U1RQH7, Q5QP23 |
| Q14498-3 | 3 | 4.27E-06 | Isoform 3 of RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 |
| G3XAC6 | 3 | 5.13E-06 | RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=1 |
| H0Y4X3 | 2 | 1.61E-06 | RNA-binding protein 39 (Fragment) OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=8 |
| Q14498-2 | 3 | 4.14E-06 | Isoform 2 of RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 |
| Reverse\_Q9UBF2-2 | 3 | 3.07E-06 |  |
| Reverse\_Q9UBF2 | 3 | 2.56E-06 | ; Additional IDs concatenated into MaxParsimony group: Reverse\_Q9UBF2-2 |
| Reverse\_Q16270 | 3 | 9.05E-06 | ; Additional IDs concatenated into MaxParsimony group: Reverse\_Q16270-2 |
| Reverse\_Q16270-2 | 3 | 9.15E-06 |  |
| A1L2Z2 | 3 | 6.42E-06 | MYH14 protein OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=1 |
| E5RHJ1 | 2 | 2.48E-05 | Iduronate 2-sulfatase (Fragment) OS=Homo sapiens OX=9606 GN=IDS PE=4 SV=1 |
| H3BTP7 | 2 | 4.01E-05 | 60S ribosomal protein L4 (Fragment) OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=1 |
| H3BU31 | 3 | 0.000104709 | 60S ribosomal protein L4 (Fragment) OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=1 |
| P01011-3 | 3 | 3.78E-05 | Isoform 3 of Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 |
| Q5RI18 | 3 | 2.34E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=9 |
| A0A1W2PPH7 | 3 | 2.57E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PQ74 | 3 | 3.79E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PRZ7 | 3 | 4.67E-05 | Heterogeneous nuclear ribonucleoprotein U (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PQL0 | 3 | 2.68E-05 | Heterogeneous nuclear ribonucleoprotein U (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PP34 | 3 | 2.58E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PPL4 | 3 | 2.58E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| H0YHL1 | 3 | 5.98E-06 | Dynactin subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=1 |
| H0YI98 | 3 | 1.94E-05 | Dynactin subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=1 |
| H0YA91 | 3 | 1.04E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| R4GN64 | 3 | 2.38E-05 | Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens OX=9606 GN=SLC25A13 PE=1 SV=1 |
| Q9UJS0-2 | 3 | 5.41E-06 | Isoform 2 of Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens OX=9606 GN=SLC25A13; Additional IDs concatenated into MaxParsimony group: Q9UJS0, R4GN64 |
| Q9UJS0 | 3 | 5.42E-06 | Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens OX=9606 GN=SLC25A13 PE=1 SV=2 |
| Q5VVC8 | 3 | 4.98E-05 | 60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 PE=1 SV=2 |
| P62913 | 3 | 4.67E-05 | 60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P62913-2, Q5VVC8 |
| P62913-2 | 3 | 4.70E-05 | Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 |
| O00429 | 3 | 4.22E-06 | Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=2 |
| O00429-2 | 3 | 4.29E-06 | Isoform 4 of Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L |
| O00429-5 | 3 | 4.38E-06 | Isoform 5 of Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L |
| O00429-7 | 3 | 4.62E-06 | Isoform 7 of Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L |
| G8JLD5 | 3 | 4.37E-06 | Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=1 |
| O00429-8 | 3 | 4.21E-06 | Isoform 8 of Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L |
| O00429-6 | 3 | 4.15E-06 | Isoform 6 of Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L; Additional IDs concatenated into MaxParsimony group: O00429-8, O00429, O00429-2, G8JLD5, O00429-5, O00429-3, O00429-4, O00429-7 |
| O00429-3 | 3 | 4.38E-06 | Isoform 2 of Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L |
| O00429-4 | 3 | 4.45E-06 | Isoform 3 of Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L |
| O75477 | 3 | 4.93E-06 | Erlin-1 OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=1 |
| B0QZ43 | 3 | 6.20E-06 | Erlin-1 (Fragment) OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=1 |
| Q8WWM7-8 | 3 | 5.49E-06 | Isoform 8 of Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L |
| Q8WWM7-4 | 3 | 5.49E-06 | Isoform 4 of Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L |
| Q8WWM7-5 | 3 | 5.49E-06 | Isoform 5 of Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L |
| Q8WWM7-6 | 3 | 5.92E-06 | Isoform 6 of Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L |
| E9PKF8 | 3 | 7.85E-06 | Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=8 |
| D3DQV9 | 3 | 1.60E-06 | Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P78344, P78344-2, H0Y3P2, E9PKF8, H0YE22 |
| P78344-2 | 3 | 1.67E-06 | Isoform 2 of Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 |
| H0Y3P2 | 3 | 1.67E-06 | Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1 |
| P78344 | 3 | 1.60E-06 | Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1 |
| H0YE22 | 3 | 3.97E-06 | Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1 |
| A6NEM2 | 3 | 3.34E-06 | Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCFC1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P51610-4, P51610-2, H7C1C4 |
| P51610-2 | 3 | 4.11E-06 | Isoform 2 of Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCFC1 |
| P51610-4 | 3 | 3.34E-06 | Isoform 4 of Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCFC1 |
| P51610 | 3 | 3.97E-06 | Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCFC1 PE=1 SV=2 |
| H7C1C4 | 2 | 4.47E-06 | Host cell factor 1 (Fragment) OS=Homo sapiens OX=9606 GN=HCFC1 PE=1 SV=1 |
| Q12802-4 | 3 | 4.80E-06 | Isoform 3 of A-kinase anchor protein 13 OS=Homo sapiens OX=9606 GN=AKAP13 |
| H0YMW2 | 3 | 2.57E-06 | A-kinase anchor protein 13 (Fragment) OS=Homo sapiens OX=9606 GN=AKAP13 PE=1 SV=1 |
| Q12802 | 3 | 4.76E-06 | A-kinase anchor protein 13 OS=Homo sapiens OX=9606 GN=AKAP13 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q12802-2, Q12802-4, H0YMW2 |
| Q12802-2 | 3 | 4.75E-06 | Isoform 2 of A-kinase anchor protein 13 OS=Homo sapiens OX=9606 GN=AKAP13 |
| E5RJD2 | 3 | 2.09E-05 | 2,4-dienoyl-CoA reductase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=DECR1 PE=1 SV=1 |
| E5RID6 | 3 | 4.51E-05 | 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens OX=9606 GN=DECR1 PE=1 SV=1 |
| Q16698 | 3 | 1.37E-05 | 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens OX=9606 GN=DECR1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q16698-2, E5RFV2, E5RJG7, E5RID6, E5RJD2 |
| E5RFV2 | 3 | 2.24E-05 | 2,4-dienoyl-CoA reductase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=DECR1 PE=1 SV=1 |
| E5RJG7 | 3 | 2.54E-05 | 2,4-dienoyl-CoA reductase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=DECR1 PE=1 SV=1 |
| Q16698-2 | 3 | 1.41E-05 | Isoform 2 of 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens OX=9606 GN=DECR1 |
| P50213-2 | 2 | 4.92E-06 | Isoform 2 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=IDH3A |
| H7C3D5 | 3 | 2.74E-05 | Reticulophagy regulator 2 (Fragment) OS=Homo sapiens OX=9606 GN=RETREG2 PE=1 SV=1 |
| Q8NC44 | 3 | 1.02E-05 | Reticulophagy regulator 2 OS=Homo sapiens OX=9606 GN=RETREG2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H7C3D5 |
| P18206-2 | 3 | 2.07E-06 | Isoform 1 of Vinculin OS=Homo sapiens OX=9606 GN=VCL |
| P18206 | 3 | 1.94E-06 | Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P18206-2 |
| P62753 | 3 | 3.17E-05 | 40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A2A3R5, A2A3R7 |
| A2A3R5 | 3 | 3.62E-05 | 40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1 |
| A2A3R7 | 3 | 2.57E-05 | 40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1 |
| F8WF02 | 3 | 1.75E-05 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=PDHB PE=1 SV=1 |
| C9J634 | 3 | 1.26E-05 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=PDHB PE=1 SV=1 |
| Q5JSH3 | 3 | 3.12E-06 | WD repeat-containing protein 44 OS=Homo sapiens OX=9606 GN=WDR44 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5JSH3-2, Q5JSH3-4, H7BY83 |
| Q5JSH3-4 | 3 | 3.46E-06 | Isoform 4 of WD repeat-containing protein 44 OS=Homo sapiens OX=9606 GN=WDR44 |
| H7BY83 | 3 | 1.39E-06 | WD repeat-containing protein 44 (Fragment) OS=Homo sapiens OX=9606 GN=WDR44 PE=1 SV=1 |
| Q5JSH3-2 | 3 | 3.15E-06 | Isoform 2 of WD repeat-containing protein 44 OS=Homo sapiens OX=9606 GN=WDR44 |
| Q13148 | 2 | 2.59E-06 | TAR DNA-binding protein 43 OS=Homo sapiens OX=9606 GN=TARDBP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q13148-4, A0A087WX29 |
| A0A087WX29 | 2 | 4.41E-06 | TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens OX=9606 GN=TARDBP PE=1 SV=1 |
| Q9H2G2-2 | 3 | 2.33E-06 | Isoform 2 of STE20-like serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=SLK |
| Q9H2G2 | 3 | 2.27E-06 | STE20-like serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=SLK PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9H2G2-2 |
| P53367-2 | 3 | 3.38E-06 | Isoform A of Arfaptin-1 OS=Homo sapiens OX=9606 GN=ARFIP1 |
| P53367-3 | 3 | 5.96E-06 | Isoform 3 of Arfaptin-1 OS=Homo sapiens OX=9606 GN=ARFIP1 |
| P53367 | 3 | 3.09E-06 | Arfaptin-1 OS=Homo sapiens OX=9606 GN=ARFIP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P53367-2, P53367-3 |
| Q6NVY1 | 3 | 1.26E-05 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=HIBCH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: B9A058, H7C126 |
| B9A058 | 3 | 2.56E-05 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=HIBCH PE=1 SV=1 |
| H7C126 | 3 | 0.000109961 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HIBCH PE=1 SV=1 |
| D6RCD0 | 2 | 8.22E-07 | Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens OX=9606 GN=HSD17B11 PE=1 SV=2 |
| Q8NBQ5 | 2 | 7.02E-07 | Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens OX=9606 GN=HSD17B11 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: D6RCD0 |
| E9PBS1 | 3 | 6.44E-06 | Multifunctional protein ADE2 (Fragment) OS=Homo sapiens OX=9606 GN=PAICS PE=1 SV=1 |
| P22234-2 | 3 | 6.16E-06 | Isoform 2 of Multifunctional protein ADE2 OS=Homo sapiens OX=9606 GN=PAICS; Additional IDs concatenated into MaxParsimony group: P22234, E9PBS1 |
| P22234 | 3 | 6.26E-06 | Multifunctional protein ADE2 OS=Homo sapiens OX=9606 GN=PAICS PE=1 SV=3 |
| K7ELC7 | 3 | 3.38E-05 | 60S ribosomal protein L27 (Fragment) OS=Homo sapiens OX=9606 GN=RPL27 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P61353 |
| P61353 | 3 | 4.76E-05 | 60S ribosomal protein L27 OS=Homo sapiens OX=9606 GN=RPL27 PE=1 SV=2 |
| A0A2R8Y891 | 3 | 1.72E-06 | ATP-dependent 6-phosphofructokinase OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P08237-3, P08237, P08237-2, F8VZI0 |
| P08237 | 3 | 1.95E-06 | ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=2 |
| P08237-2 | 3 | 2.03E-06 | Isoform 2 of ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens OX=9606 GN=PFKM |
| F8VZI0 | 3 | 2.09E-06 | ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=9 |
| P08237-3 | 3 | 1.79E-06 | Isoform 3 of ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens OX=9606 GN=PFKM |
| Q9Y2I8-2 | 2 | 2.59E-07 | Isoform 2 of WD repeat-containing protein 37 OS=Homo sapiens OX=9606 GN=WDR37; Additional IDs concatenated into MaxParsimony group: Q9Y2I8, Q9Y2I8-3, A0A087WTQ2, E7EQ49, C9JGR9 |
| Q9Y2I8-3 | 2 | 4.85E-07 | Isoform 3 of WD repeat-containing protein 37 OS=Homo sapiens OX=9606 GN=WDR37 |
| A0A087WTQ2 | 2 | 4.87E-07 | WD repeat-containing protein 37 OS=Homo sapiens OX=9606 GN=WDR37 PE=1 SV=1 |
| E7EQ49 | 2 | 5.14E-07 | WD repeat-containing protein 37 OS=Homo sapiens OX=9606 GN=WDR37 PE=1 SV=1 |
| C9JGR9 | 2 | 6.13E-07 | WD repeat-containing protein 37 (Fragment) OS=Homo sapiens OX=9606 GN=WDR37 PE=1 SV=1 |
| Q9Y2I8 | 2 | 2.59E-07 | WD repeat-containing protein 37 OS=Homo sapiens OX=9606 GN=WDR37 PE=1 SV=2 |
| P31948-3 | 2 | 2.09E-06 | Isoform 3 of Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 |
| P31948-2 | 2 | 1.84E-06 | Isoform 2 of Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1; Additional IDs concatenated into MaxParsimony group: P31948, P31948-3 |
| P31948 | 2 | 1.99E-06 | Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1 |
| M0QXU7 | 2 | 5.14E-07 | Mitochondrial import inner membrane translocase subunit TIM44 (Fragment) OS=Homo sapiens OX=9606 GN=TIMM44 PE=1 SV=1 |
| O43615 | 2 | 3.10E-07 | Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens OX=9606 GN=TIMM44 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0QXU7 |
| Q9H8S9 | 3 | 4.29E-06 | MOB kinase activator 1A OS=Homo sapiens OX=9606 GN=MOB1A PE=1 SV=4 |
| Q7L9L4 | 3 | 4.29E-06 | MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B PE=1 SV=3 |
| Q7L9L4-2 | 3 | 4.19E-06 | Isoform 2 of MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B; Additional IDs concatenated into MaxParsimony group: Q7L9L4, Q9H8S9 |
| I3L4P8 | 3 | 9.19E-06 | Heme oxygenase 2 (Fragment) OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=8 |
| A0A1B0GXH0 | 3 | 9.12E-06 | Heme oxygenase 2 (Fragment) OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=1 |
| P30519-2 | 3 | 4.16E-06 | Isoform 2 of Heme oxygenase 2 OS=Homo sapiens OX=9606 GN=HMOX2 |
| I3L1F5 | 3 | 5.02E-06 | Heme oxygenase 2 (Fragment) OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=1 |
| I3L463 | 3 | 9.05E-06 | Heme oxygenase 2 (Fragment) OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=1 |
| P30519 | 3 | 3.78E-06 | Heme oxygenase 2 OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=2 |
| I3L159 | 3 | 5.21E-06 | Heme oxygenase 2 (Fragment) OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=1 |
| A0A087WT44 | 3 | 3.23E-06 | Heme oxygenase 2 OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P30519, P30519-2, I3L1F5, I3L159, I3L463, A0A1B0GXH0, I3L4P8, I3L276 |
| I3L276 | 3 | 1.09E-05 | Heme oxygenase 2 (Fragment) OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=1 |
| Q96S66-3 | 3 | 1.12E-05 | Isoform 3 of Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 |
| Q96S66 | 3 | 8.77E-06 | Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q96S66-2, Q96S66-3, Q96S66-4 |
| Q96S66-4 | 3 | 1.32E-05 | Isoform 4 of Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 |
| Q96S66-2 | 3 | 9.65E-06 | Isoform 2 of Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 |
| P26368-2 | 2 | 1.12E-06 | Isoform 2 of Splicing factor U2AF 65 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF2 |
| P26368 | 2 | 1.11E-06 | Splicing factor U2AF 65 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P26368-2, K7ENG2 |
| K7ENG2 | 2 | 1.71E-06 | U2 snRNP auxiliary factor large subunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=1 SV=1 |
| Q5UCC4 | 2 | 2.60E-06 | ER membrane protein complex subunit 10 OS=Homo sapiens OX=9606 GN=EMC10 PE=1 SV=1 |
| M0R2A0 | 2 | 1.83E-06 | ER membrane protein complex subunit 10 OS=Homo sapiens OX=9606 GN=EMC10 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5UCC4, Q5UCC4-2 |
| Q5UCC4-2 | 2 | 2.68E-06 | Isoform 2 of ER membrane protein complex subunit 10 OS=Homo sapiens OX=9606 GN=EMC10 |
| K7EQT9 | 3 | 0.001784994 | Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| M0R2T0 | 3 | 6.97E-05 | Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1 |
| M0R019 | 3 | 5.47E-05 | Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=8 |
| M0R0N3 | 2 | 3.56E-05 | Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=8 |
| M0QYQ7 | 2 | 4.47E-05 | Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1 |
| M0R0Y6 | 2 | 9.89E-05 | Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1 |
| A0A2R8Y815 | 2 | 1.54E-05 | Catenin beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| P14923 | 2 | 1.33E-06 | Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3 |
| P53675-2 | 3 | 3.23E-06 | Isoform 2 of Clathrin heavy chain 2 OS=Homo sapiens OX=9606 GN=CLTCL1 |
| P53675 | 3 | 3.12E-06 | Clathrin heavy chain 2 OS=Homo sapiens OX=9606 GN=CLTCL1 PE=1 SV=2 |
| J3KS13 | 3 | 7.52E-06 | Clathrin heavy chain 1 OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=1 |
| A0A087WX41 | 3 | 4.06E-06 | Clathrin heavy chain 2 OS=Homo sapiens OX=9606 GN=CLTCL1 PE=1 SV=1 |
| K7EJJ5 | 3 | 1.24E-05 | Clathrin heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=1 |
| B7Z2U2 | 2 | 1.81E-05 | TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 PE=1 SV=1 |
| B0QY01 | 3 | 2.17E-05 | Target of Myb protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TOM1 PE=1 SV=8 |
| Q6ZVM7-5 | 2 | 1.46E-05 | Isoform 5 of TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 |
| Q6ZVM7-3 | 2 | 1.52E-05 | Isoform 3 of TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 |
| Q6ZVM7 | 2 | 1.39E-05 | TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 PE=1 SV=1 |
| Q6ZVM7-4 | 2 | 2.93E-05 | Isoform 4 of TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 |
| F5H3S6 | 2 | 1.81E-05 | TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 PE=1 SV=1 |
| Q6ZVM7-2 | 2 | 1.54E-05 | Isoform 2 of TOM1-like protein 2 OS=Homo sapiens OX=9606 GN=TOM1L2 |
| F8WBC0 | 2 | 0.000125519 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=4 SV=1 |
| E5RGV0 | 3 | 2.29E-05 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| E5RGH4 | 3 | 2.09E-05 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| D6RBM0 | 3 | 1.68E-05 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| D6RIU0 | 3 | 1.24E-05 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| E7EN40 | 3 | 2.14E-05 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| P29803 | 3 | 3.05E-05 | Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial OS=Homo sapiens OX=9606 GN=PDHA2 PE=1 SV=1 |
| Q5JPU3 | 2 | 7.17E-05 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens OX=9606 GN=PDHA1 PE=1 SV=1 |
| Q5JPU0 | 3 | 7.29E-05 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens OX=9606 GN=PDHA1 PE=1 SV=1 |
| Q5JPU1 | 3 | 6.40E-05 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PDHA1 PE=1 SV=1 |
| Q5JPT9 | 3 | 6.47E-05 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PDHA1 PE=1 SV=8 |
| P08559-2 | 3 | 7.04E-05 | Isoform 2 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens OX=9606 GN=PDHA1 |
| P08559-4 | 3 | 6.53E-05 | Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens OX=9606 GN=PDHA1; Additional IDs concatenated into MaxParsimony group: P08559-2, P08559, P08559-3, Q5JPU1, Q5JPT9, Q5JPU0, P29803, Q5JPU2, Q5JPU3 |
| Q5JPU2 | 3 | 8.69E-05 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PDHA1 PE=1 SV=1 |
| P08559 | 3 | 7.17E-05 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens OX=9606 GN=PDHA1 PE=1 SV=3 |
| P08559-3 | 3 | 7.79E-05 | Isoform 3 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens OX=9606 GN=PDHA1 |
| Q08257-2 | 2 | 1.33E-05 | Isoform 2 of Quinone oxidoreductase OS=Homo sapiens OX=9606 GN=CRYZ |
| B1AH78 | 3 | 6.11E-06 | Ras-related C3 botulinum toxin substrate 2 (Fragment) OS=Homo sapiens OX=9606 GN=RAC2 PE=1 SV=1 |
| B1AH77 | 3 | 2.86E-05 | Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens OX=9606 GN=RAC2 PE=1 SV=1 |
| J3KSC4 | 3 | 3.25E-05 | Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens OX=9606 GN=RAC3 PE=1 SV=1 |
| P60763 | 3 | 2.20E-05 | Ras-related C3 botulinum toxin substrate 3 OS=Homo sapiens OX=9606 GN=RAC3 PE=1 SV=1 |
| P15153 | 3 | 2.20E-05 | Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens OX=9606 GN=RAC2 PE=1 SV=1 |
| P63000 | 3 | 2.47E-05 | Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens OX=9606 GN=RAC1 PE=1 SV=1 |
| J3QLK0 | 3 | 3.11E-05 | Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens OX=9606 GN=RAC3 PE=1 SV=1 |
| B1AH80 | 3 | 2.29E-05 | Ras-related C3 botulinum toxin substrate 2 (Rho family, small GTP binding protein Rac2), isoform CRA\_c OS=Homo sapiens OX=9606 GN=RAC2 PE=1 SV=1 |
| P49748 | 3 | 9.40E-06 | Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ACADVL PE=1 SV=1 |
| P49748-2 | 3 | 9.73E-06 | Isoform 2 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ACADVL |
| G3V1M7 | 3 | 5.31E-06 | Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ACADVL PE=1 SV=2 |
| P49748-3 | 3 | 9.08E-06 | Isoform 3 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ACADVL; Additional IDs concatenated into MaxParsimony group: P49748, P49748-2, G3V1M7 |
| E5RHI8 | 2 | 3.04E-05 | Protein FAM114A2 (Fragment) OS=Homo sapiens OX=9606 GN=FAM114A2 PE=1 SV=1 |
| E5RGF9 | 2 | 1.81E-05 | Protein FAM114A2 (Fragment) OS=Homo sapiens OX=9606 GN=FAM114A2 PE=1 SV=1 |
| Q9NRY5 | 2 | 7.82E-06 | Protein FAM114A2 OS=Homo sapiens OX=9606 GN=FAM114A2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: E5RGF9, E5RFK2, E5RHI8, E7ESJ7 |
| E5RFK2 | 2 | 2.29E-05 | Protein FAM114A2 (Fragment) OS=Homo sapiens OX=9606 GN=FAM114A2 PE=1 SV=1 |
| M0QYL7 | 3 | 2.56E-05 | Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=1 |
| M0R1W6 | 3 | 2.31E-05 | Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=1 |
| H0YJ40 | 3 | 3.24E-05 | SRA stem-loop-interacting RNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SLIRP PE=1 SV=1 |
| Q9GZT3 | 3 | 2.85E-05 | SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLIRP PE=1 SV=1 |
| A0A087WUN7 | 3 | 3.38E-05 | SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLIRP PE=1 SV=1 |
| H0YJI1 | 3 | 6.47E-05 | SRA stem-loop-interacting RNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SLIRP PE=1 SV=1 |
| H0YJW7 | 3 | 6.88E-06 | SRA stem-loop-interacting RNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SLIRP PE=1 SV=1 |
| Q9GZT3-2 | 3 | 2.91E-05 | Isoform 2 of SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLIRP |
| G3V2S9 | 3 | 2.51E-05 | SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLIRP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9GZT3, Q9GZT3-2, G3V4X6, H0YJ40, A0A087WUN7, H0YJW7, H0YJI1 |
| G3V4X6 | 3 | 3.17E-05 | SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLIRP PE=1 SV=1 |
| K7EPS6 | 3 | 3.03E-05 | Hepatoma-derived growth factor-related protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=HDGFL2 PE=1 SV=2 |
| A0A087WX58 | 3 | 6.81E-05 | Hepatoma-derived growth factor-related protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=HDGFL2 PE=1 SV=1 |
| A0A087WUQ6 | 3 | 1.34E-05 | Glutathione peroxidase OS=Homo sapiens OX=9606 GN=GPX1 PE=1 SV=1 |
| P07203-2 | 2 | 9.96E-06 | Isoform 2 of Glutathione peroxidase 1 OS=Homo sapiens OX=9606 GN=GPX1 |
| P07203 | 3 | 1.33E-05 | Glutathione peroxidase 1 OS=Homo sapiens OX=9606 GN=GPX1 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A087WUQ6, A0A2R8Y6B6, P07203-2 |
| A0A2R8Y6B6 | 3 | 1.72E-05 | Glutathione peroxidase 1 OS=Homo sapiens OX=9606 GN=GPX1 PE=1 SV=1 |
| O60749 | 3 | 7.98E-06 | Sorting nexin-2 OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: D6RC15 |
| D6RC15 | 2 | 1.10E-05 | Sorting nexin-2 (Fragment) OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=8 |
| U3KQ56 | 3 | 1.96E-05 | Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens OX=9606 GN=GRHPR PE=1 SV=1 |
| H0YH82 | 3 | 1.85E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8W642 | 3 | 2.44E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8VX68 | 3 | 1.34E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8VPF9 | 3 | 2.51E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=8 |
| F8VRP1 | 3 | 1.38E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=8 |
| F8VX07 | 3 | 1.41E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8VZK9 | 3 | 2.01E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=8 |
| F8VPA1 | 3 | 2.45E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8W1S4 | 3 | 2.24E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| A0A0C4DGI3 | 3 | 1.35E-05 | Citrate synthase OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| A0A0D9SFL3 | 2 | 2.36E-06 | RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1 |
| H7BY36 | 2 | 4.48E-06 | RNA-binding protein EWS (Fragment) OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1 |
| C9JGE3 | 2 | 2.23E-06 | EWS RNA-binding protein variant 6 OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=2 |
| Q01844-2 | 2 | 2.37E-06 | Isoform EWS-B of RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 |
| Q9UKV3 | 3 | 4.15E-06 | Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UKV3-5, E7EQT4, S4R3H4, Q9UKV3-2, Q9UKV3-3, G3V3B0, G3V3T3 |
| Q9UKV3-2 | 2 | 1.39E-06 | Isoform 2 of Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 |
| S4R3H4 | 3 | 4.34E-06 | Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=1 |
| G3V3B0 | 2 | 1.47E-06 | Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=1 |
| Q9UKV3-3 | 2 | 1.47E-06 | Isoform 3 of Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 |
| E7EQT4 | 3 | 4.28E-06 | Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=2 |
| Q9UKV3-5 | 2 | 4.14E-06 | Isoform 4 of Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 |
| P24821-5 | 3 | 4.19E-07 | Isoform 5 of Tenascin OS=Homo sapiens OX=9606 GN=TNC |
| P24821-6 | 3 | 4.43E-07 | Isoform 6 of Tenascin OS=Homo sapiens OX=9606 GN=TNC |
| P24821-2 | 3 | 3.97E-07 | Isoform 2 of Tenascin OS=Homo sapiens OX=9606 GN=TNC |
| P24821-3 | 3 | 3.77E-07 | Isoform 3 of Tenascin OS=Homo sapiens OX=9606 GN=TNC |
| E9PC84 | 3 | 3.59E-07 | Tenascin OS=Homo sapiens OX=9606 GN=TNC PE=1 SV=1 |
| P24821 | 3 | 3.15E-07 | Tenascin OS=Homo sapiens OX=9606 GN=TNC PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P24821-4, J3QSU6, E9PC84, F5H7V9, P24821-3, P24821-2, P24821-5, P24821-6 |
| F5H7V9 | 3 | 3.77E-07 | Tenascin OS=Homo sapiens OX=9606 GN=TNC PE=1 SV=1 |
| J3QSU6 | 3 | 3.43E-07 | Tenascin OS=Homo sapiens OX=9606 GN=TNC PE=1 SV=1 |
| P24821-4 | 3 | 3.28E-07 | Isoform 4 of Tenascin OS=Homo sapiens OX=9606 GN=TNC |
| Q9BZZ5-2 | 3 | 4.60E-06 | Isoform 2 of Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 |
| Q9BZZ5-1 | 3 | 4.61E-06 | Isoform 1 of Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 |
| Q9BZZ5 | 3 | 4.42E-06 | Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9BZZ5-6, G3V1C3, Q9BZZ5-2, Q9BZZ5-5, Q9BZZ5-3, Q9BZZ5-1 |
| Q9BZZ5-5 | 3 | 4.48E-06 | Isoform 5 of Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 |
| Q9BZZ5-6 | 3 | 3.93E-06 | Isoform 6 of Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 |
| Q9BZZ5-3 | 3 | 5.21E-06 | Isoform 3 of Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 |
| G3V1C3 | 3 | 4.54E-06 | Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 PE=1 SV=1 |
| H7C5S0 | 2 | 5.93E-06 | Actin-like protein 6A (Fragment) OS=Homo sapiens OX=9606 GN=ACTL6A PE=1 SV=1 |
| O96019 | 2 | 2.22E-06 | Actin-like protein 6A OS=Homo sapiens OX=9606 GN=ACTL6A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H7C5S0 |
| F8W727 | 3 | 7.76E-05 | 60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P62910, D3YTB1 |
| P62910 | 3 | 8.80E-05 | 60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=2 |
| D3YTB1 | 3 | 8.93E-05 | 60S ribosomal protein L32 (Fragment) OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=1 |
| A0A2R8YG21 | 3 | 7.71E-06 | Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=1 |
| A0A2R8Y688 | 3 | 5.10E-06 | Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=1 |
| Q7Z6Z7 | 3 | 4.26E-06 | E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens OX=9606 GN=HUWE1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q7Z6Z7-3, Q7Z6Z7-2 |
| Q7Z6Z7-2 | 3 | 4.27E-06 | Isoform 2 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens OX=9606 GN=HUWE1 |
| Q7Z6Z7-3 | 3 | 4.27E-06 | Isoform 3 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens OX=9606 GN=HUWE1 |
| C9JNW5 | 3 | 6.34E-05 | 60S ribosomal protein L24 OS=Homo sapiens OX=9606 GN=RPL24 PE=1 SV=1 |
| C9JXB8 | 3 | 7.86E-05 | 60S ribosomal protein L24 OS=Homo sapiens OX=9606 GN=RPL24 PE=1 SV=1 |
| P83731 | 3 | 6.06E-05 | 60S ribosomal protein L24 OS=Homo sapiens OX=9606 GN=RPL24 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JNW5, C9JXB8 |
| Q14894 | 2 | 8.88E-06 | Ketimine reductase mu-crystallin OS=Homo sapiens OX=9606 GN=CRYM PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: I3L2W5, I3NI53, I3L325, I3L3Y1, I3L3J9 |
| I3NI53 | 2 | 7.08E-06 | Ketimine reductase mu-crystallin (Fragment) OS=Homo sapiens OX=9606 GN=CRYM PE=1 SV=1 |
| I3L3J9 | 2 | 3.20E-05 | Ketimine reductase mu-crystallin (Fragment) OS=Homo sapiens OX=9606 GN=CRYM PE=1 SV=8 |
| I3L325 | 2 | 7.45E-06 | Ketimine reductase mu-crystallin (Fragment) OS=Homo sapiens OX=9606 GN=CRYM PE=1 SV=1 |
| I3L2W5 | 2 | 6.01E-06 | Ketimine reductase mu-crystallin OS=Homo sapiens OX=9606 GN=CRYM PE=1 SV=1 |
| P28074-3 | 3 | 8.86E-05 | Isoform 3 of Proteasome subunit beta type-5 OS=Homo sapiens OX=9606 GN=PSMB5 |
| P28074 | 3 | 5.39E-05 | Proteasome subunit beta type-5 OS=Homo sapiens OX=9606 GN=PSMB5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P28074-3 |
| A0A0C4DFS6 | 3 | 3.25E-05 | Protein sprouty homolog 4 OS=Homo sapiens OX=9606 GN=SPRY4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9C004, Q9C004-2, D6RB56 |
| Q9C004 | 3 | 3.51E-05 | Protein sprouty homolog 4 OS=Homo sapiens OX=9606 GN=SPRY4 PE=1 SV=2 |
| Q9C004-2 | 3 | 9.89E-05 | Isoform C of Protein sprouty homolog 4 OS=Homo sapiens OX=9606 GN=SPRY4 |
| D6RB56 | 3 | 6.48E-05 | Protein sprouty homolog 4 (Fragment) OS=Homo sapiens OX=9606 GN=SPRY4 PE=1 SV=1 |
| Q5T624 | 3 | 2.30E-05 | Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=1 |
| P49321-2 | 3 | 2.16E-05 | Isoform 2 of Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP |
| P49321 | 3 | 1.31E-05 | Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P49321-2, Q5T624, E9PI86 |
| E9PI86 | 3 | 3.80E-05 | Nuclear autoantigenic sperm protein (Fragment) OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=1 |
| Q9NP79-2 | 2 | 3.36E-06 | Isoform 2 of Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens OX=9606 GN=VTA1 |
| A0A087WY55 | 2 | 2.67E-06 | Chromosome 6 open reading frame 55, isoform CRA\_b OS=Homo sapiens OX=9606 GN=VTA1 PE=1 SV=1 |
| J3QR09 | 3 | 7.23E-05 | Ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1 |
| P84098 | 3 | 7.12E-05 | 60S ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: J3KTE4, J3QR09 |
| J3KTE4 | 3 | 7.20E-05 | Ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1 |
| A0FGR8-2 | 3 | 5.47E-06 | Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 |
| A0FGR8-5 | 3 | 1.41E-05 | Isoform 5 of Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 |
| A0FGR8-6 | 3 | 5.18E-06 | Isoform 6 of Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2; Additional IDs concatenated into MaxParsimony group: A0FGR8, A0A087WXU3, A0FGR8-2, H7BXI1, A0FGR8-5 |
| H7BXI1 | 3 | 5.52E-06 | Extended synaptotagmin-2 (Fragment) OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1 |
| A0FGR8 | 3 | 5.30E-06 | Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1 |
| A0A087WXU3 | 3 | 5.30E-06 | Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1 |
| Q99627 | 2 | 1.13E-05 | COP9 signalosome complex subunit 8 OS=Homo sapiens OX=9606 GN=COPS8 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PGT6, Q99627-2, H7C3S9 |
| H7C3S9 | 2 | 2.84E-05 | COP9 signalosome complex subunit 8 (Fragment) OS=Homo sapiens OX=9606 GN=COPS8 PE=1 SV=1 |
| Q99627-2 | 2 | 1.47E-05 | Isoform 2 of COP9 signalosome complex subunit 8 OS=Homo sapiens OX=9606 GN=COPS8 |
| E9PGT6 | 2 | 1.36E-05 | COP9 signalosome complex subunit 8 OS=Homo sapiens OX=9606 GN=COPS8 PE=1 SV=1 |
| Q8IYB3 | 3 | 3.73E-06 | Serine/arginine repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1 PE=1 SV=2 |
| A9Z1X7 | 3 | 3.70E-06 | Serine/arginine repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q8IYB3, Q8IYB3-2 |
| Q8IYB3-2 | 3 | 3.74E-06 | Isoform 2 of Serine/arginine repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1 |
| Q66K74-2 | 3 | 1.25E-06 | Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens OX=9606 GN=MAP1S |
| Q66K74 | 3 | 1.22E-06 | Microtubule-associated protein 1S OS=Homo sapiens OX=9606 GN=MAP1S PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q66K74-2 |
| A0A087WTA8 | 3 | 3.44E-06 | Collagen alpha-2(I) chain OS=Homo sapiens OX=9606 GN=COL1A2 PE=1 SV=1 |
| P08123 | 3 | 3.44E-06 | Collagen alpha-2(I) chain OS=Homo sapiens OX=9606 GN=COL1A2 PE=1 SV=7; Additional IDs concatenated into MaxParsimony group: A0A087WTA8 |
| C9J459 | 3 | 5.57E-05 | Anion exchange protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=1 |
| P04920-3 | 3 | 3.16E-06 | Isoform 3 of Anion exchange protein 2 OS=Homo sapiens OX=9606 GN=SLC4A2 |
| C9J722 | 3 | 2.69E-05 | Anion exchange protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=1 |
| P04920 | 3 | 3.14E-06 | Anion exchange protein 2 OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P04920-3, P04920-2, C9J9M9, C9J035, C9J722, C9JVC2, C9J459 |
| C9J035 | 3 | 2.60E-05 | Anion exchange protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=8 |
| P04920-2 | 3 | 3.18E-06 | Isoform B1 of Anion exchange protein 2 OS=Homo sapiens OX=9606 GN=SLC4A2 |
| C9J9M9 | 3 | 2.31E-05 | Anion exchange protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=1 |
| C9JVC2 | 3 | 3.07E-05 | Anion exchange protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=1 |
| H0YIV9 | 3 | 1.05E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=3 SV=1; Additional IDs concatenated into MaxParsimony group: O43716, F8VRU3 |
| F8VRU3 | 3 | 1.45E-05 | Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial OS=Homo sapiens OX=9606 GN=GATC PE=4 SV=1 |
| O43716 | 3 | 1.29E-05 | Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial OS=Homo sapiens OX=9606 GN=GATC PE=1 SV=1 |
| E9PB61 | 3 | 4.14E-05 | THO complex subunit 4 OS=Homo sapiens OX=9606 GN=ALYREF PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q86V81 |
| Q86V81 | 3 | 4.25E-05 | THO complex subunit 4 OS=Homo sapiens OX=9606 GN=ALYREF PE=1 SV=3 |
| P59998-4 | 2 | 4.41E-05 | Isoform 4 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens OX=9606 GN=ARPC4 |
| R4GN08 | 2 | 4.47E-05 | Actin-related protein 2/3 complex subunit 4 (Fragment) OS=Homo sapiens OX=9606 GN=ARPC4 PE=1 SV=1 |
| H7C0A3 | 3 | 3.62E-05 | ARPC4-TTLL3 readthrough (Fragment) OS=Homo sapiens OX=9606 GN=ARPC4-TTLL3 PE=4 SV=1 |
| P59998-3 | 3 | 3.23E-05 | Isoform 3 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens OX=9606 GN=ARPC4; Additional IDs concatenated into MaxParsimony group: F8WCF6, P59998, H7C0A3, P59998-4, R4GN08 |
| P59998 | 3 | 3.60E-05 | Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens OX=9606 GN=ARPC4 PE=1 SV=3 |
| F8WCF6 | 3 | 3.34E-05 | Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens OX=9606 GN=ARPC4-TTLL3 PE=3 SV=1 |
| Q9Y6C9 | 3 | 8.65E-06 | Mitochondrial carrier homolog 2 OS=Homo sapiens OX=9606 GN=MTCH2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PIE4 |
| E9PIE4 | 3 | 1.00E-05 | Mitochondrial carrier homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=MTCH2 PE=1 SV=8 |
| E7EX53 | 3 | 5.58E-05 | Ribosomal protein L15 (Fragment) OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=1 |
| A0A2R8Y738 | 3 | 5.38E-05 | Ribosomal protein L15 (Fragment) OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=1 |
| P61313 | 3 | 4.77E-05 | 60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E7EQV9, A0A2R8YEM3, P61313-2, A0A2R8Y738, E7EX53 |
| E7EQV9 | 3 | 4.27E-05 | Ribosomal protein L15 (Fragment) OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=1 |
| P61313-2 | 3 | 5.12E-05 | Isoform 2 of 60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 |
| A0A2R8YEM3 | 3 | 4.39E-05 | Ribosomal protein L15 (Fragment) OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=1 |
| J3QKT2 | 3 | 1.06E-05 | Cytosolic non-specific dipeptidase (Fragment) OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=1 |
| J3QRH4 | 3 | 1.30E-05 | Cytosolic non-specific dipeptidase (Fragment) OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=1 |
| A0A2R8Y623 | 3 | 2.36E-05 | 40S ribosomal protein S7 (Fragment) OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1 |
| A0A2R8YF49 | 3 | 4.42E-06 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1; Additional IDs concatenated into MaxParsimony group: Q12774, A0A2R8YFR7, A5YM69, C9J591 |
| A0A2R8YFR7 | 3 | 4.75E-06 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |
| Q12774 | 3 | 4.42E-06 | Rho guanine nucleotide exchange factor 5 OS=Homo sapiens OX=9606 GN=ARHGEF5 PE=1 SV=3 |
| M0QZP8 | 3 | 8.07E-06 | Immunity-related GTPase family Q protein (Fragment) OS=Homo sapiens OX=9606 GN=IRGQ PE=1 SV=1 |
| P61769 | 3 | 3.75E-05 | Beta-2-microglobulin OS=Homo sapiens OX=9606 GN=B2M PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F5H6I0, H0YLF3 |
| F5H6I0 | 3 | 4.41E-05 | Beta-2-microglobulin OS=Homo sapiens OX=9606 GN=B2M PE=1 SV=2 |
| H0YLF3 | 3 | 6.28E-05 | Beta-2-microglobulin (Fragment) OS=Homo sapiens OX=9606 GN=B2M PE=1 SV=1 |
| F5H324 | 2 | 3.02E-06 | Arylsulfatase E OS=Homo sapiens OX=9606 GN=ARSE PE=1 SV=1 |
| F5GYY5 | 2 | 2.68E-06 | Arylsulfatase E OS=Homo sapiens OX=9606 GN=ARSE PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P51690, F5H324 |
| P51690 | 2 | 2.79E-06 | Arylsulfatase E OS=Homo sapiens OX=9606 GN=ARSE PE=1 SV=2 |
| Q6P2E9-2 | 3 | 1.64E-06 | Isoform 2 of Enhancer of mRNA-decapping protein 4 OS=Homo sapiens OX=9606 GN=EDC4 |
| Q6P2E9 | 3 | 1.19E-06 | Enhancer of mRNA-decapping protein 4 OS=Homo sapiens OX=9606 GN=EDC4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q6P2E9-2 |
| P53621 | 2 | 1.85E-07 | Coatomer subunit alpha OS=Homo sapiens OX=9606 GN=COPA PE=1 SV=2 |
| P53621-2 | 2 | 1.83E-07 | Isoform 2 of Coatomer subunit alpha OS=Homo sapiens OX=9606 GN=COPA; Additional IDs concatenated into MaxParsimony group: P53621 |
| E5RIE0 | 3 | 4.27E-06 | Catenin alpha-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=8 |
| G3XAM7 | 3 | 1.61E-06 | Catenin (Cadherin-associated protein), alpha 1, 102kDa, isoform CRA\_a OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| E5RGY6 | 3 | 3.59E-06 | Catenin alpha-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| E5RIB1 | 3 | 2.32E-06 | Catenin alpha-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| E5RFM3 | 3 | 5.31E-06 | Catenin alpha-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| E5RJL0 | 3 | 4.95E-06 | Catenin alpha-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| E5RG03 | 3 | 3.20E-06 | Catenin alpha-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| P35221 | 3 | 1.50E-06 | Catenin alpha-1 OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| P35221-2 | 3 | 1.46E-06 | Isoform 2 of Catenin alpha-1 OS=Homo sapiens OX=9606 GN=CTNNA1; Additional IDs concatenated into MaxParsimony group: P35221, G3XAM7, P26232-5, P26232-2, P26232-3, P26232-6, A0A0A0MRI5, P26232-4, P35221-3, A0A0A0MTJ6, E5RIB1, E5RG03, E5RGY6, H0YBB8, E5RHV7, C9IZ88, E5RIE0, E5RJL0, E5RFM3, C9J144 |
| E5RHV7 | 3 | 4.06E-06 | Catenin alpha-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1 |
| H3BS70 | 3 | 9.96E-06 | Enoyl-CoA delta isomerase 1, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ECI1 PE=1 SV=1 |
| P42126-2 | 3 | 7.83E-06 | Isoform 2 of Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens OX=9606 GN=ECI1 |
| P42126 | 3 | 7.39E-06 | Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens OX=9606 GN=ECI1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P42126-2, Q96DC0, H3BS70 |
| Q96DC0 | 3 | 9.18E-06 | DCI protein OS=Homo sapiens OX=9606 GN=ECI1 PE=1 SV=1 |
| Q6YN16 | 2 | 6.98E-06 | Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens OX=9606 GN=HSDL2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q6YN16-2 |
| Q6YN16-2 | 2 | 8.46E-06 | Isoform 2 of Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens OX=9606 GN=HSDL2 |
| P35659 | 2 | 9.75E-06 | Protein DEK OS=Homo sapiens OX=9606 GN=DEK PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B4DFG0, D6R9L5 |
| B4DFG0 | 2 | 1.05E-05 | cDNA FLJ53031, highly similar to Protein DEK OS=Homo sapiens OX=9606 GN=DEK PE=1 SV=1 |
| D6R9L5 | 2 | 2.42E-05 | Protein DEK (Fragment) OS=Homo sapiens OX=9606 GN=DEK PE=1 SV=1 |
| B4DQI4 | 2 | 3.08E-06 | Protein ABHD14B OS=Homo sapiens OX=9606 GN=ABHD14B PE=1 SV=1 |
| Q96IU4 | 2 | 2.76E-06 | Protein ABHD14B OS=Homo sapiens OX=9606 GN=ABHD14B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B4DQI4 |
| Q9HDC9-2 | 3 | 1.68E-06 | Isoform 2 of Adipocyte plasma membrane-associated protein OS=Homo sapiens OX=9606 GN=APMAP |
| Q9HDC9 | 3 | 1.17E-06 | Adipocyte plasma membrane-associated protein OS=Homo sapiens OX=9606 GN=APMAP PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H0Y512, Q9HDC9-2 |
| H0Y512 | 3 | 1.19E-06 | Adipocyte plasma membrane-associated protein (Fragment) OS=Homo sapiens OX=9606 GN=APMAP PE=1 SV=1 |
| F8VR84 | 2 | 4.76E-06 | UPF0160 protein MYG1, mitochondrial OS=Homo sapiens OX=9606 GN=C12orf10 PE=1 SV=1 |
| Q9HB07 | 2 | 2.70E-06 | UPF0160 protein MYG1, mitochondrial OS=Homo sapiens OX=9606 GN=C12orf10 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F8VQQ3, F8VR84 |
| F8VQQ3 | 2 | 3.37E-06 | UPF0160 protein MYG1, mitochondrial OS=Homo sapiens OX=9606 GN=C12orf10 PE=1 SV=1 |
| D6RA32 | 2 | 2.60E-06 | Microtubule-associated protein 1B (Fragment) OS=Homo sapiens OX=9606 GN=MAP1B PE=1 SV=2 |
| D6RCL2 | 2 | 1.56E-05 | Microtubule-associated protein 1B OS=Homo sapiens OX=9606 GN=MAP1B PE=1 SV=2 |
| D6RGJ3 | 2 | 1.31E-05 | Microtubule-associated protein 1B (Fragment) OS=Homo sapiens OX=9606 GN=MAP1B PE=1 SV=1 |
| H3BRI0 | 2 | 0.000127826 | Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens OX=9606 GN=COX5A PE=1 SV=1 |
| Q12888-2 | 3 | 1.06E-05 | Isoform 2 of TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1; Additional IDs concatenated into MaxParsimony group: Q12888-3, Q12888, A6NNK5, C9JXV0 |
| A6NNK5 | 3 | 1.08E-05 | TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2 |
| Q12888-3 | 3 | 1.06E-05 | Isoform 3 of TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 |
| C9JXV0 | 3 | 2.02E-05 | TP53-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=1 |
| Q12888 | 3 | 1.06E-05 | TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2 |
| A0A087X2I4 | 3 | 7.20E-05 | Proteasome subunit beta type OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=1 |
| I3L3X7 | 3 | 0.000150314 | Proteasome subunit beta type-6 (Fragment) OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=1 |
| M0R055 | 3 | 1.55E-05 | ELAV-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=1 |
| H0Y561 | 3 | 0.000109335 | 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens OX=9606 GN=PSMD4 PE=1 SV=1 |
| A0A0G2JMB2 | 3 | 1.15E-05 | Immunoglobulin heavy constant alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA2 PE=1 SV=1 |
| Q6PIK3 | 3 | 1.03E-05 | HCG1995540, isoform CRA\_b OS=Homo sapiens OX=9606 GN=RAB4B PE=1 SV=1 |
| Q8WUD1-2 | 3 | 8.26E-06 | Isoform 2 of Ras-related protein Rab-2B OS=Homo sapiens OX=9606 GN=RAB2B |
| Q8WUD1 | 3 | 5.78E-06 | Ras-related protein Rab-2B OS=Homo sapiens OX=9606 GN=RAB2B PE=1 SV=1 |
| E9PKL7 | 3 | 6.89E-06 | Ras-related protein Rab-2A OS=Homo sapiens OX=9606 GN=RAB2A PE=1 SV=1 |
| P49773 | 3 | 0.000170808 | Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: D6RD60, D6RE99, D6REP8, D6RC06 |
| D6RE99 | 3 | 0.000275921 | Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=1 |
| D6RC06 | 3 | 0.000331105 | Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=1 |
| D6RD60 | 3 | 0.00020895 | Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=1 |
| D6REP8 | 3 | 0.000275921 | Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=1 |
| H0YCY6 | 3 | 2.03E-06 | Triokinase/FMN cyclase (Fragment) OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=1 |
| Q3LXA3-2 | 3 | 2.03E-06 | Isoform 2 of Triokinase/FMN cyclase OS=Homo sapiens OX=9606 GN=TKFC |
| I3L252 | 3 | 4.95E-06 | Triokinase/FMN cyclase (Fragment) OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=1 |
| O95831 | 3 | 2.78E-06 | Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O95831-3, O95831-2, E9PMA0, O95831-5 |
| O95831-2 | 3 | 4.96E-06 | Isoform 2 of Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 |
| O95831-3 | 3 | 2.80E-06 | Isoform 3 of Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 |
| E9PMA0 | 3 | 4.85E-06 | Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 PE=1 SV=1 |
| O95831-5 | 3 | 5.09E-06 | Isoform 5 of Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 |
| Q9UJU2-5 | 3 | 3.41E-05 | Isoform 5 of Lymphoid enhancer-binding factor 1 OS=Homo sapiens OX=9606 GN=LEF1 |
| Q9UJU2-6 | 3 | 3.28E-05 | Isoform 6 of Lymphoid enhancer-binding factor 1 OS=Homo sapiens OX=9606 GN=LEF1 |
| Q9UJU2 | 3 | 3.17E-05 | Lymphoid enhancer-binding factor 1 OS=Homo sapiens OX=9606 GN=LEF1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UJU2-6, Q9UJU2-5, Q9UJU2-2 |
| Q9UJU2-2 | 3 | 3.85E-05 | Isoform 2 of Lymphoid enhancer-binding factor 1 OS=Homo sapiens OX=9606 GN=LEF1 |
| H7C2F7 | 3 | 2.79E-05 | Trafficking protein particle complex subunit 12 (Fragment) OS=Homo sapiens OX=9606 GN=TRAPPC12 PE=1 SV=1 |
| Q8WVT3 | 3 | 8.42E-06 | Trafficking protein particle complex subunit 12 OS=Homo sapiens OX=9606 GN=TRAPPC12 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H7C2F7 |
| Q5UIP0-2 | 2 | 2.37E-08 | Isoform 2 of Telomere-associated protein RIF1 OS=Homo sapiens OX=9606 GN=RIF1 |
| Q5UIP0 | 2 | 2.35E-08 | Telomere-associated protein RIF1 OS=Homo sapiens OX=9606 GN=RIF1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5UIP0-2, H7C2B5 |
| H7C2B5 | 2 | 7.78E-08 | Telomere-associated protein RIF1 (Fragment) OS=Homo sapiens OX=9606 GN=RIF1 PE=1 SV=1 |
| F8WDF3 | 2 | 4.07E-05 | Programmed cell death protein 10 OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1 |
| C9JND6 | 2 | 1.64E-05 | Programmed cell death protein 10 (Fragment) OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1 |
| C9J932 | 2 | 3.04E-05 | Programmed cell death protein 10 (Fragment) OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1 |
| Q9BUL8 | 2 | 1.13E-05 | Programmed cell death protein 10 OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9J5C3, C9J6F3, C9JND6, C9JSA3, H7C5M9, C9J932, F8WDF3 |
| C9JSA3 | 2 | 1.79E-05 | Programmed cell death protein 10 (Fragment) OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1 |
| C9J5C3 | 2 | 1.19E-05 | Programmed cell death protein 10 (Fragment) OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1 |
| C9J6F3 | 2 | 1.29E-05 | Programmed cell death protein 10 OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1 |
| H7C5M9 | 2 | 1.97E-05 | Programmed cell death protein 10 (Fragment) OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1 |
| Q16555 | 2 | 3.26E-06 | Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 PE=1 SV=1 |
| Q16555-2 | 2 | 3.48E-06 | Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 |
| A0A1C7CYX9 | 2 | 2.76E-06 | Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q16555, Q16555-2 |
| E9PC15 | 2 | 6.71E-07 | Acylglycerol kinase, mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=1 |
| Q53H12 | 2 | 6.26E-07 | Acylglycerol kinase, mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PC15, E9PG39 |
| E9PG39 | 2 | 1.08E-06 | Acylglycerol kinase, mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=1 |
| I3L246 | 3 | 3.02E-05 | 40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 SV=1 |
| H3BN98 | 3 | 1.41E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=2; Additional IDs concatenated into MaxParsimony group: P62244, I3L246, I3L3P7 |
| P62244 | 3 | 2.58E-05 | 40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 SV=2 |
| I3L3P7 | 3 | 3.35E-05 | 40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 SV=1 |
| A0A2R8Y7T2 | 3 | 1.41E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A2R8YCW1 | 3 | 1.08E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A2R8YFR4 | 3 | 1.06E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| O15523 | 3 | 9.44E-06 | ATP-dependent RNA helicase DDX3Y OS=Homo sapiens OX=9606 GN=DDX3Y PE=1 SV=2 |
| A0A2R8Y5G6 | 3 | 1.12E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A0D9SF53 | 3 | 9.51E-06 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A2R8Y645 | 3 | 9.74E-06 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A0D9SG12 | 3 | 1.08E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| J3KRZ1 | 3 | 5.89E-05 | Probable ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1 |
| A0A2R8YDT5 | 3 | 1.42E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| F6S8Q4 | 3 | 1.11E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A2R8YFS5 | 3 | 1.05E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| O15523-2 | 3 | 9.48E-06 | Isoform 2 of ATP-dependent RNA helicase DDX3Y OS=Homo sapiens OX=9606 GN=DDX3Y |
| O00571-2 | 3 | 1.08E-05 | Isoform 2 of ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X |
| A0A2R8YF78 | 3 | 1.09E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A0J9YVQ7 | 3 | 4.64E-06 | ATP-dependent RNA helicase DDX3X (Fragment) OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=2 |
| A0A2R8YDH3 | 3 | 1.18E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A2U3TZJ9 | 3 | 1.05E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=4 SV=1 |
| A0A2R8Y4A4 | 3 | 1.05E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A0D9SFB3 | 3 | 1.09E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |
| A0A087WVZ1 | 3 | 5.45E-06 | ATP-dependent RNA helicase DDX3X (Fragment) OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=2 |
| J3QSF1 | 3 | 6.39E-05 | Probable ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1 |
| O00571 | 3 | 1.05E-05 | ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=3 |
| P40227 | 3 | 2.13E-05 | T-complex protein 1 subunit zeta OS=Homo sapiens OX=9606 GN=CCT6A PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P40227-2 |
| P40227-2 | 3 | 2.20E-05 | Isoform 2 of T-complex protein 1 subunit zeta OS=Homo sapiens OX=9606 GN=CCT6A |
| F8WCY6 | 2 | 1.57E-05 | Ras-related protein Rab-5A OS=Homo sapiens OX=9606 GN=RAB5A PE=1 SV=1 |
| F8VSF8 | 2 | 1.32E-05 | Ras-related protein Rab-5C (Fragment) OS=Homo sapiens OX=9606 GN=RAB5C PE=4 SV=1 |
| F8WD79 | 2 | 1.50E-05 | Ras-related protein Rab-5A OS=Homo sapiens OX=9606 GN=RAB5A PE=1 SV=1 |
| F8VPW9 | 2 | 1.33E-05 | Ras-related protein Rab-5B OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1 |
| F8VWZ7 | 2 | 1.23E-05 | Ras-related protein Rab-5B (Fragment) OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1 |
| P05091-2 | 3 | 1.65E-05 | Isoform 2 of Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 |
| P05091 | 3 | 1.50E-05 | Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P05091-2, F8VP50 |
| F8VP50 | 3 | 1.27E-06 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=3 |
| F8VXH9 | 3 | 2.44E-05 | Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1 |
| P57721-5 | 3 | 9.46E-06 | Isoform 5 of Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 |
| F8W0G4 | 3 | 2.47E-05 | Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1 |
| P57721-3 | 3 | 9.60E-06 | Isoform 3 of Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 |
| P57721 | 3 | 8.95E-06 | Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 PE=2 SV=2 |
| P57721-4 | 3 | 8.98E-06 | Isoform 4 of Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 |
| E9PFP8 | 3 | 9.20E-06 | Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 PE=1 SV=1 |
| P57721-2 | 3 | 9.63E-06 | Isoform 2 of Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 |
| J3QT27 | 3 | 1.03E-05 | Poly(rC)-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=PCBP3 PE=1 SV=1 |
| Q5T8U3 | 3 | 0.000161739 | 60S ribosomal protein L7a (Fragment) OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=1 |
| P62424 | 3 | 0.000116136 | 60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5T8U3, Q5T8U2 |
| Q5T8U2 | 3 | 0.000130338 | 60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=1 |
| F8WB72 | 2 | 2.90E-05 | 60S ribosomal protein L35a OS=Homo sapiens OX=9606 GN=RPL35A PE=1 SV=1 |
| F8WBS5 | 2 | 3.00E-05 | 60S ribosomal protein L35a OS=Homo sapiens OX=9606 GN=RPL35A PE=1 SV=1 |
| C9K025 | 2 | 1.76E-05 | 60S ribosomal protein L35a (Fragment) OS=Homo sapiens OX=9606 GN=RPL35A PE=1 SV=1 |
| P18077 | 2 | 6.14E-05 | 60S ribosomal protein L35a OS=Homo sapiens OX=9606 GN=RPL35A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9K025, F8WB72, F8WBS5 |
| P05090 | 3 | 6.42E-05 | Apolipoprotein D OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1 |
| C9JF17 | 3 | 5.65E-05 | Apolipoprotein D (Fragment) OS=Homo sapiens OX=9606 GN=APOD PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P05090 |
| Q9UBF2 | 3 | 1.30E-06 | Coatomer subunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 PE=1 SV=1 |
| Q9Y678 | 3 | 1.30E-06 | Coatomer subunit gamma-1 OS=Homo sapiens OX=9606 GN=COPG1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UBF2, Q9UBF2-2 |
| Q9UBF2-2 | 3 | 1.56E-06 | Isoform 2 of Coatomer subunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 |
| P36551 | 3 | 8.28E-06 | Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens OX=9606 GN=CPOX PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H0YA22 |
| H0YA22 | 3 | 2.08E-05 | Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CPOX PE=1 SV=1 |
| H3BP04 | 2 | 1.18E-06 | Cytochrome b-c1 complex subunit 2, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=1 |
| H3BUI9 | 2 | 1.58E-06 | Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=1 |
| H3BUE4 | 2 | 1.80E-06 | Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=1 |
| H3BRG4 | 2 | 5.06E-07 | Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=1 |
| H3BSJ9 | 2 | 6.21E-07 | Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=1 |
| P50851 | 2 | 3.60E-07 | Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens OX=9606 GN=LRBA PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P50851-2, E9PEM5 |
| P50851-2 | 2 | 3.62E-07 | Isoform 2 of Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens OX=9606 GN=LRBA |
| E9PEM5 | 2 | 4.00E-07 | Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens OX=9606 GN=LRBA PE=1 SV=1 |
| P30038-2 | 3 | 5.11E-06 | Isoform 2 of Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH4A1 |
| Q9UFG5-2 | 3 | 3.66E-06 | Isoform 2 of UPF0449 protein C19orf25 OS=Homo sapiens OX=9606 GN=C19orf25; Additional IDs concatenated into MaxParsimony group: K7EK56, Q9UFG5 |
| K7EK56 | 3 | 3.68E-06 | UPF0449 protein C19orf25 OS=Homo sapiens OX=9606 GN=C19orf25 PE=1 SV=1 |
| Q9UFG5 | 3 | 4.99E-06 | UPF0449 protein C19orf25 OS=Homo sapiens OX=9606 GN=C19orf25 PE=1 SV=2 |
| Q8WUM4-2 | 3 | 1.62E-06 | Isoform 2 of Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 GN=PDCD6IP; Additional IDs concatenated into MaxParsimony group: Q8WUM4 |
| Q8WUM4 | 3 | 1.63E-06 | Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 GN=PDCD6IP PE=1 SV=1 |
| Q5JVP2 | 3 | 1.87E-05 | Prostaglandin reductase 1 (Fragment) OS=Homo sapiens OX=9606 GN=PTGR1 PE=1 SV=1 |
| Q14914 | 3 | 6.77E-06 | Prostaglandin reductase 1 OS=Homo sapiens OX=9606 GN=PTGR1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q14914-2, Q5JVP2 |
| Q14914-2 | 3 | 7.40E-06 | Isoform 2 of Prostaglandin reductase 1 OS=Homo sapiens OX=9606 GN=PTGR1 |
| J3QLP3 | 3 | 2.28E-06 | von Willebrand factor A domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=VWA1 PE=1 SV=1 |
| Q6PCB0 | 3 | 1.60E-06 | von Willebrand factor A domain-containing protein 1 OS=Homo sapiens OX=9606 GN=VWA1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: J3QLP3, J3QRR0 |
| J3QRR0 | 3 | 2.58E-06 | von Willebrand factor A domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=VWA1 PE=1 SV=1 |
| O43402 | 2 | 1.35E-05 | ER membrane protein complex subunit 8 OS=Homo sapiens OX=9606 GN=EMC8 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: M0R1B0 |
| M0R1B0 | 2 | 2.84E-05 | ER membrane protein complex subunit 8 (Fragment) OS=Homo sapiens OX=9606 GN=EMC8 PE=1 SV=1 |
| K7EIS0 | 2 | 4.84E-06 | Tubulin gamma chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBG1 PE=1 SV=1 |
| P23258 | 2 | 2.84E-06 | Tubulin gamma-1 chain OS=Homo sapiens OX=9606 GN=TUBG1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9NRH3, K7EIS0, K7EKE5 |
| Q9NRH3 | 2 | 2.84E-06 | Tubulin gamma-2 chain OS=Homo sapiens OX=9606 GN=TUBG2 PE=2 SV=1 |
| K7EKE5 | 2 | 9.49E-06 | Tubulin gamma-1 chain OS=Homo sapiens OX=9606 GN=TUBG1 PE=4 SV=1 |
| Reverse\_Q7Z6I6 | 3 | 7.17E-05 | ; Additional IDs concatenated into MaxParsimony group: Reverse\_Q7Z6I6-3, Reverse\_A0A0A0MRJ8 |
| Reverse\_Q7Z6I6-3 | 3 | 8.28E-05 |  |
| Reverse\_A0A0A0MRJ8 | 3 | 8.54E-05 |  |
| A0A1X7SCE1 | 2 | 0.000126296 | Glial fibrillary acidic protein (Fragment) OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 |
| K7EJU1 | 2 | 0.000170093 | Glial fibrillary acidic protein (Fragment) OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 |
| P12036-2 | 2 | 4.38E-05 | Isoform 2 of Neurofilament heavy polypeptide OS=Homo sapiens OX=9606 GN=NEFH |
| E7ESP9 | 2 | 4.81E-05 | Neurofilament medium polypeptide OS=Homo sapiens OX=9606 GN=NEFM PE=1 SV=1 |
| E7EMV2 | 2 | 6.04E-05 | Neurofilament medium polypeptide OS=Homo sapiens OX=9606 GN=NEFM PE=1 SV=1 |
| P12036 | 2 | 4.11E-05 | Neurofilament heavy polypeptide OS=Homo sapiens OX=9606 GN=NEFH PE=1 SV=4 |
| P07197-2 | 2 | 7.81E-05 | Isoform 2 of Neurofilament medium polypeptide OS=Homo sapiens OX=9606 GN=NEFM |
| P07196 | 2 | 7.77E-05 | Neurofilament light polypeptide OS=Homo sapiens OX=9606 GN=NEFL PE=1 SV=3 |
| P07197 | 2 | 4.61E-05 | Neurofilament medium polypeptide OS=Homo sapiens OX=9606 GN=NEFM PE=1 SV=3 |
| Q16352 | 2 | 8.45E-05 | Alpha-internexin OS=Homo sapiens OX=9606 GN=INA PE=1 SV=2 |
| Q8WW12-3 | 3 | 0.000142319 | Isoform 3 of PEST proteolytic signal-containing nuclear protein OS=Homo sapiens OX=9606 GN=PCNP |
| E7ETT4 | 2 | 3.75E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1 |
| C9JQS9 | 2 | 3.38E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1 |
| E7EX59 | 2 | 3.32E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JQS9, P05166-2, E9PDR0, P05166, E7ETT1, E7EUY3, F8WBI9, E7ETT4, E9PEC3 |
| E9PDR0 | 2 | 3.44E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1 |
| E9PEC3 | 2 | 2.59E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1 |
| P05166 | 2 | 3.51E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=3 |
| E7ETT1 | 2 | 3.64E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1 |
| P05166-2 | 2 | 3.38E-06 | Isoform 2 of Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB |
| E7EUY3 | 2 | 3.66E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1 |
| F8WBI9 | 2 | 4.67E-06 | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE=1 SV=1 |
| G3V4X5 | 3 | 4.11E-05 | Proteasome endopeptidase complex OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=1 |
| H0YJ03 | 3 | 5.79E-05 | Proteasome subunit alpha type-3 (Fragment) OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=1 |
| C9JLK2 | 2 | 6.00E-06 | Acylamino-acid-releasing enzyme (Fragment) OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=1 |
| H7C1U0 | 2 | 7.92E-06 | Acylamino-acid-releasing enzyme (Fragment) OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=1 |
| P62277 | 3 | 5.13E-05 | 40S ribosomal protein S13 OS=Homo sapiens OX=9606 GN=RPS13 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: J3KMX5 |
| J3KMX5 | 3 | 5.24E-05 | 40S ribosomal protein S13 OS=Homo sapiens OX=9606 GN=RPS13 PE=1 SV=1 |
| H3BQI7 | 3 | 9.50E-06 | Inactive hydroxysteroid dehydrogenase-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=HSDL1 PE=1 SV=1 |
| H3BT52 | 3 | 9.24E-06 | Inactive hydroxysteroid dehydrogenase-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=HSDL1 PE=1 SV=1 |
| Q3SXM5-2 | 3 | 3.73E-06 | Isoform 2 of Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens OX=9606 GN=HSDL1 |
| Q9NY27 | 3 | 1.51E-05 | Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PPP4R2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9NY27-3, Q9NY27-2 |
| Q9NY27-2 | 3 | 1.75E-05 | Isoform 2 of Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PPP4R2 |
| Q9NY27-3 | 3 | 1.74E-05 | Isoform 3 of Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PPP4R2 |
| P10155 | 3 | 2.24E-06 | 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=TROVE2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P10155-4, P10155-5, P10155-3, P10155-2 |
| P10155-3 | 3 | 2.32E-06 | Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=TROVE2 |
| P10155-4 | 3 | 2.25E-06 | Isoform 4 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=TROVE2 |
| P10155-2 | 3 | 5.87E-06 | Isoform Short of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=TROVE2 |
| P10155-5 | 3 | 2.29E-06 | Isoform 5 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=TROVE2 |
| P10644 | 3 | 4.23E-06 | cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR1A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P10644-2, K7EM13 |
| K7EM13 | 3 | 1.05E-05 | cAMP-dependent protein kinase type I-alpha regulatory subunit (Fragment) OS=Homo sapiens OX=9606 GN=PRKAR1A PE=1 SV=1 |
| P10644-2 | 3 | 4.78E-06 | Isoform 2 of cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR1A |
| Q5QNZ2 | 2 | 2.27E-05 | ATP synthase peripheral stalk-membrane subunit b OS=Homo sapiens OX=9606 GN=ATP5PB PE=1 SV=1 |
| P24539 | 2 | 1.73E-05 | ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5QNZ2 |
| F8W6C1 | 3 | 1.29E-05 | Spectrin beta chain, non-erythrocytic 1 (Fragment) OS=Homo sapiens OX=9606 GN=SPTBN1 PE=1 SV=1 |
| A0A087WYC1 | 3 | 6.18E-06 | Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=1 |
| A0A087WTS8 | 3 | 9.09E-06 | Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=1 |
| Q8WXC6-1 | 3 | 2.70E-06 | Isoform 2 of COP9 signalosome complex subunit 9 OS=Homo sapiens OX=9606 GN=COPS9 |
| J3KRI4 | 2 | 2.68E-05 | Cytoplasmic dynein 1 light intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1LI2 PE=1 SV=1 |
| J3KRZ2 | 2 | 1.90E-05 | Cytoplasmic dynein 1 light intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1LI2 PE=1 SV=1 |
| O43237 | 2 | 1.01E-05 | Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1LI2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O43237-2, J3KRI4, J3KRZ2 |
| O43237-2 | 2 | 1.19E-05 | Isoform 2 of Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1LI2 |
| Q9Y426-3 | 3 | 3.84E-07 | Isoform 3 of C2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=C2CD2 |
| Q9Y426 | 3 | 3.81E-07 | C2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=C2CD2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9Y426-3, Q9Y426-2 |
| Q9Y426-2 | 3 | 4.90E-07 | Isoform 2 of C2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=C2CD2 |
| J3QRD1 | 3 | 6.57E-07 | Fatty aldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH3A2 PE=1 SV=1 |
| P51648 | 3 | 5.32E-07 | Fatty aldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH3A2 PE=1 SV=1 |
| P51648-2 | 3 | 5.08E-07 | Isoform 2 of Fatty aldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH3A2; Additional IDs concatenated into MaxParsimony group: P51648, J3QRD1 |
| O43432 | 3 | 4.52E-06 | Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens OX=9606 GN=EIF4G3 PE=1 SV=2 |
| A0A0U1RQK7 | 3 | 4.04E-06 | Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens OX=9606 GN=EIF4G3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0A0MSA7, O43432-3, O43432, O43432-2 |
| O43432-2 | 3 | 9.25E-06 | Isoform 2 of Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens OX=9606 GN=EIF4G3 |
| A0A0A0MSA7 | 3 | 4.42E-06 | Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens OX=9606 GN=EIF4G3 PE=1 SV=1 |
| O43432-3 | 3 | 4.51E-06 | Isoform 3 of Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens OX=9606 GN=EIF4G3 |
| P02751-2 | 2 | 1.49E-05 | Isoform 2 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-16 | 2 | 1.46E-05 | Isoform 16 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| Q9H254-2 | 2 | 4.90E-07 | Isoform 2 of Spectrin beta chain, non-erythrocytic 4 OS=Homo sapiens OX=9606 GN=SPTBN4 |
| Q9H254 | 2 | 2.50E-07 | Spectrin beta chain, non-erythrocytic 4 OS=Homo sapiens OX=9606 GN=SPTBN4 PE=1 SV=2 |
| Q9H254-4 | 2 | 2.98E-07 | Isoform 4 of Spectrin beta chain, non-erythrocytic 4 OS=Homo sapiens OX=9606 GN=SPTBN4 |
| C9JY79 | 2 | 2.50E-07 | Spectrin beta chain OS=Homo sapiens OX=9606 GN=SPTBN4 PE=1 SV=2 |
| M0QZQ3 | 2 | 3.21E-07 | Spectrin beta chain OS=Homo sapiens OX=9606 GN=SPTBN4 PE=1 SV=1 |
| P38159 | 3 | 0.000149147 | RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P38159-2, H3BT71, H0Y6E7, Q96E39, H3BUY5, P38159-3, H3BR27, A0A1B0GUK8, H3BNC1, Q8N7X1, O75526 |
| P38159-3 | 3 | 6.62E-05 | Isoform 3 of RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX |
| Q96E39 | 3 | 7.60E-05 | RNA binding motif protein, X-linked-like-1 OS=Homo sapiens OX=9606 GN=RBMXL1 PE=1 SV=1 |
| O75526 | 3 | 6.61E-06 | RNA-binding motif protein, X-linked-like-2 OS=Homo sapiens OX=9606 GN=RBMXL2 PE=1 SV=3 |
| H3BUY5 | 3 | 0.000116887 | RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=1 |
| H3BR27 | 3 | 0.00016633 | RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=1 |
| H3BNC1 | 3 | 0.00028056 | RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=1 |
| A0A1B0GUK8 | 3 | 5.08E-05 | RNA-binding motif protein, X-linked-like-1 (Fragment) OS=Homo sapiens OX=9606 GN=RBMXL1 PE=1 SV=1 |
| Q8N7X1 | 3 | 2.43E-06 | RNA-binding motif protein, X-linked-like-3 OS=Homo sapiens OX=9606 GN=RBMXL3 PE=2 SV=2 |
| H3BT71 | 3 | 0.000129131 | RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=1 |
| P38159-2 | 3 | 0.000147416 | Isoform 2 of RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX |
| H0Y6E7 | 3 | 0.0001309 | RNA-binding motif protein, X chromosome (Fragment) OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=2 |
| D6R9C9 | 3 | 1.99E-05 | Protein NOXP20 (Fragment) OS=Homo sapiens OX=9606 GN=FAM114A1 PE=1 SV=8 |
| E9PFL9 | 3 | 5.65E-06 | Lupus La protein OS=Homo sapiens OX=9606 GN=SSB PE=1 SV=1 |
| E9PGX9 | 3 | 5.77E-06 | Lupus La protein (Fragment) OS=Homo sapiens OX=9606 GN=SSB PE=1 SV=1 |
| E7ERC4 | 3 | 4.11E-06 | Lupus La protein (Fragment) OS=Homo sapiens OX=9606 GN=SSB PE=1 SV=1 |
| P26641-2 | 3 | 1.38E-05 | Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EEF1G; Additional IDs concatenated into MaxParsimony group: P26641 |
| P26641 | 3 | 1.54E-05 | Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EEF1G PE=1 SV=3 |
| P21333-2 | 3 | 4.28E-06 | Isoform 2 of Filamin-A OS=Homo sapiens OX=9606 GN=FLNA |
| F8WE98 | 3 | 7.11E-06 | Filamin-A (Fragment) OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=2 |
| P21333 | 3 | 4.27E-06 | Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P21333-2, Q60FE5, A0A087WWY3, F8WE98 |
| A0A087WWY3 | 3 | 3.52E-06 | Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1 |
| Q60FE5 | 3 | 4.31E-06 | Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1 |
| O00231-2 | 2 | 2.16E-06 | Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens OX=9606 GN=PSMD11; Additional IDs concatenated into MaxParsimony group: O00231, J3QRY4 |
| J3QRY4 | 2 | 4.89E-06 | 26S proteasome non-ATPase regulatory subunit 11 (Fragment) OS=Homo sapiens OX=9606 GN=PSMD11 PE=1 SV=8 |
| O00231 | 2 | 2.17E-06 | 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens OX=9606 GN=PSMD11 PE=1 SV=3 |
| B4DUA4 | 3 | 6.16E-05 | Serine/arginine-rich-splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 PE=1 SV=1 |
| Q13243 | 3 | 3.13E-05 | Serine/arginine-rich splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 PE=1 SV=1 |
| Q13243-3 | 3 | 3.16E-05 | Isoform SRP40-4 of Serine/arginine-rich splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 |
| Q13247 | 3 | 2.53E-05 | Serine/arginine-rich splicing factor 6 OS=Homo sapiens OX=9606 GN=SRSF6 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q13247-3, Q08170, A0A0D9SEM4, Q13243, Q13243-3, B4DUA4, B4DJK0 |
| Q08170 | 3 | 1.66E-05 | Serine/arginine-rich splicing factor 4 OS=Homo sapiens OX=9606 GN=SRSF4 PE=1 SV=2 |
| Q13247-3 | 3 | 2.60E-05 | Isoform SRP55-3 of Serine/arginine-rich splicing factor 6 OS=Homo sapiens OX=9606 GN=SRSF6 |
| A0A0D9SEM4 | 3 | 2.17E-05 | Serine/arginine-rich-splicing factor 4 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF4 PE=1 SV=1 |
| B4DJK0 | 3 | 6.86E-05 | Serine/arginine-rich-splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 PE=1 SV=1 |
| Q99832 | 2 | 4.56E-07 | T-complex protein 1 subunit eta OS=Homo sapiens OX=9606 GN=CCT7 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q99832-3, F8WAM2 |
| F8WAM2 | 2 | 2.53E-06 | T-complex protein 1 subunit eta (Fragment) OS=Homo sapiens OX=9606 GN=CCT7 PE=1 SV=1 |
| Q99832-3 | 2 | 4.96E-07 | Isoform 3 of T-complex protein 1 subunit eta OS=Homo sapiens OX=9606 GN=CCT7 |
| E9PFE3 | 2 | 1.85E-06 | Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1 |
| Q9Y6E2 | 3 | 9.24E-07 | Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E7ETZ4, Q75MG1, E7EMS9, Q9Y6E2-2, F8WDX8, C9JF98, E9PFE3 |
| E7EMS9 | 2 | 1.43E-06 | Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1 |
| Q9Y6E2-2 | 2 | 1.48E-06 | Isoform 2 of Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=BZW2 |
| F8WDX8 | 2 | 1.75E-06 | Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1 |
| Q75MG1 | 3 | 1.41E-06 | Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1 |
| E7ETZ4 | 3 | 9.49E-07 | Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1 |
| C9JF98 | 2 | 1.84E-06 | Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=8 |
| P56134-3 | 3 | 1.61E-05 | Isoform 3 of ATP synthase subunit f, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5J2 |
| C9JJT5 | 3 | 1.64E-05 | ATP5MF-PTCD1 readthrough OS=Homo sapiens OX=9606 GN=ATP5MF-PTCD1 PE=4 SV=2 |
| C9JU26 | 3 | 9.03E-06 | ATP synthase membrane subunit f OS=Homo sapiens OX=9606 GN=ATP5MF PE=1 SV=1 |
| P56134-4 | 3 | 1.81E-05 | Isoform 4 of ATP synthase subunit f, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5J2 |
| G3V325 | 3 | 1.18E-06 | ATP5MF-PTCD1 readthrough OS=Homo sapiens OX=9606 GN=ATP5MF-PTCD1 PE=4 SV=1; Additional IDs concatenated into MaxParsimony group: C9JU26, P56134, P56134-2, P56134-3, C9JJT5, P56134-4 |
| P56134-2 | 3 | 1.01E-05 | Isoform 2 of ATP synthase subunit f, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5J2 |
| P56134 | 3 | 9.42E-06 | ATP synthase subunit f, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5J2 PE=1 SV=3 |
| P52209-2 | 3 | 1.11E-05 | Isoform 2 of 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens OX=9606 GN=PGD |
| K7EMN2 | 3 | 3.25E-05 | 6-phosphogluconate dehydrogenase, decarboxylating (Fragment) OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=1 |
| P52209 | 3 | 1.08E-05 | 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P52209-2, K7EPF6, K7EM49, K7EMN2 |
| K7EPF6 | 3 | 2.01E-05 | 6-phosphogluconate dehydrogenase, decarboxylating (Fragment) OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=1 |
| K7EM49 | 3 | 2.54E-05 | 6-phosphogluconate dehydrogenase, decarboxylating (Fragment) OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=1 |
| Q12904 | 2 | 3.07E-06 | Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens OX=9606 GN=AIMP1 PE=1 SV=2 |
| Q12904-2 | 2 | 2.85E-06 | Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens OX=9606 GN=AIMP1; Additional IDs concatenated into MaxParsimony group: Q12904 |
| P14209-3 | 3 | 8.84E-05 | Isoform 3 of CD99 antigen OS=Homo sapiens OX=9606 GN=CD99 |
| A0A096LP69 | 3 | 8.12E-05 | CD99 antigen OS=Homo sapiens OX=9606 GN=CD99 PE=1 SV=1 |
| P14209 | 3 | 8.08E-05 | CD99 antigen OS=Homo sapiens OX=9606 GN=CD99 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A096LP69, P14209-3 |
| A0A087X225 | 3 | 0.000358563 | Ras GTPase-activating-like protein IQGAP1 (Fragment) OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1 |
| A0A087WWP1 | 3 | 1.68E-05 | Ras GTPase-activating-like protein IQGAP1 (Fragment) OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1 |
| H0YLE8 | 3 | 2.49E-05 | Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1 |
| Q6NUK1-2 | 2 | 1.04E-05 | Isoform 2 of Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens OX=9606 GN=SLC25A24 |
| O75083 | 3 | 2.31E-05 | WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: O75083-3 |
| O75083-3 | 3 | 5.74E-06 | Isoform 2 of WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=WDR1 |
| H0YDD4 | 3 | 5.59E-06 | Acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Homo sapiens OX=9606 GN=DLAT PE=1 SV=1 |
| E9PEJ4 | 3 | 5.65E-06 | Acetyltransferase component of pyruvate dehydrogenase complex OS=Homo sapiens OX=9606 GN=DLAT PE=1 SV=1 |
| P10515 | 3 | 5.11E-06 | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens OX=9606 GN=DLAT PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: E9PEJ4, H0YDD4 |
| Q14974-2 | 3 | 9.54E-07 | Isoform 2 of Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 |
| J3KTM9 | 3 | 1.01E-06 | Importin subunit beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=1 |
| P62195-2 | 2 | 3.29E-06 | Isoform 2 of 26S proteasome regulatory subunit 8 OS=Homo sapiens OX=9606 GN=PSMC5 |
| P62195 | 2 | 3.22E-06 | 26S proteasome regulatory subunit 8 OS=Homo sapiens OX=9606 GN=PSMC5 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P62195-2, J3QQM1 |
| J3QQM1 | 2 | 4.97E-06 | 26S proteasome regulatory subunit 8 (Fragment) OS=Homo sapiens OX=9606 GN=PSMC5 PE=1 SV=1 |
| P52434-4 | 2 | 5.48E-05 | Isoform 4 of DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H; Additional IDs concatenated into MaxParsimony group: P52434, C9JLU1, P52434-3 |
| P52434 | 2 | 6.39E-05 | DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H PE=1 SV=4 |
| C9JLU1 | 2 | 6.48E-05 | DNA-directed RNA polymerases I, II, and III subunit RPABC3 (Fragment) OS=Homo sapiens OX=9606 GN=POLR2H PE=1 SV=8 |
| P52434-3 | 2 | 8.41E-05 | Isoform 3 of DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H |
| P51571 | 3 | 3.43E-06 | Translocon-associated protein subunit delta OS=Homo sapiens OX=9606 GN=SSR4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A6NLM8 |
| A6NLM8 | 3 | 4.01E-06 | Translocon-associated protein subunit delta OS=Homo sapiens OX=9606 GN=SSR4 PE=1 SV=1 |
| E9PNX1 | 2 | 1.03E-05 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PLA6 | 2 | 2.46E-05 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=8 |
| E9PR70 | 2 | 7.10E-06 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| H0YEP8 | 3 | 1.54E-05 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PJH8 | 2 | 1.40E-05 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PMI5 | 2 | 8.41E-06 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PK86 | 2 | 8.48E-06 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PKH2 | 3 | 4.28E-06 | Serpin H1 OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PQ34 | 2 | 1.47E-05 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PPV6 | 2 | 6.46E-06 | Serpin H1 OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=1 |
| E9PIG2 | 2 | 1.27E-05 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=2 |
| P50454 | 3 | 9.46E-06 | Serpin H1 OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PPV6, E9PR70, E9PMI5, E9PK86, E9PNX1, E9PKH2, E9PRS3, E9PIG2, E9PJH8, E9PQ34, E9PLA6, H0YEP8 |
| E9PRS3 | 2 | 1.26E-05 | Serpin H1 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=8 |
| E9PK03 | 3 | 2.50E-06 | Copper chaperone for superoxide dismutase OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1 |
| P23526-2 | 3 | 6.35E-06 | Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=AHCY |
| K7EN98 | 3 | 6.31E-06 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| G3V3J6 | 3 | 1.56E-05 | HCG1983504, isoform CRA\_b OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=1 |
| G3V3W7 | 3 | 9.86E-06 | Tubulin beta-3 chain OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=1 |
| K7ES63 | 3 | 6.98E-05 | Tubulin beta chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| K7EPE5 | 3 | 6.08E-06 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| K7ERA8 | 3 | 7.80E-06 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| K7ESQ3 | 3 | 8.93E-06 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| K7EQT3 | 3 | 8.25E-06 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| K7EJZ4 | 3 | 7.46E-06 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| K7EJ64 | 3 | 8.25E-06 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| K7EL29 | 3 | 6.60E-06 | Tubulin beta-6 chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| A0A2R8Y6I8 | 3 | 0.00079697 | Alpha-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1 |
| E9PDD6 | 2 | 9.54E-06 | Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1 |
| Q9BXK5-2 | 2 | 8.35E-06 | Isoform 1 of Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 |
| D6RA73 | 3 | 0.000337202 | Stress-70 protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=1 |
| D6RJI2 | 3 | 0.000220069 | Stress-70 protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=1 |
| H0YBG6 | 2 | 1.40E-05 | Stress-70 protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=1 |
| B5MCT8 | 3 | 8.84E-05 | 40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=1 |
| P46781 | 3 | 6.93E-05 | 40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A0A024R4M0, C9JM19, B5MCT8, A8MXK4, F2Z3C0 |
| A0A024R4M0 | 3 | 6.93E-05 | 40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=1 |
| F2Z3C0 | 2 | 3.69E-05 | 40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=1 |
| A8MXK4 | 2 | 3.60E-05 | 40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=1 |
| C9JM19 | 3 | 7.88E-05 | 40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=1 |
| C9JLS9 | 3 | 1.13E-05 | 26S proteasome regulatory subunit 7 (Fragment) OS=Homo sapiens OX=9606 GN=PSMC2 PE=1 SV=1 |
| P35998 | 3 | 5.92E-06 | 26S proteasome regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSMC2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: C9JLS9 |
| Q2TB90 | 3 | 4.34E-06 | Putative hexokinase HKDC1 OS=Homo sapiens OX=9606 GN=HKDC1 PE=1 SV=3 |
| Q92538 | 3 | 2.08E-06 | Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=GBF1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q92538-2, Q92538-3 |
| Q92538-2 | 3 | 2.08E-06 | Isoform 2 of Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=GBF1 |
| Q92538-3 | 3 | 2.08E-06 | Isoform 3 of Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=GBF1 |
| E9PK47 | 3 | 2.79E-06 | Alpha-1,4 glucan phosphorylase OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=1 |
| P06737 | 3 | 5.30E-06 | Glycogen phosphorylase, liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: E9PK47, P06737-2 |
| P06737-2 | 3 | 5.52E-06 | Isoform 2 of Glycogen phosphorylase, liver form OS=Homo sapiens OX=9606 GN=PYGL |
| M0QZS6 | 3 | 1.53E-06 | SUMO-activating enzyme subunit 1 OS=Homo sapiens OX=9606 GN=SAE1 PE=1 SV=1 |
| Q9UBE0 | 3 | 1.17E-06 | SUMO-activating enzyme subunit 1 OS=Homo sapiens OX=9606 GN=SAE1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: M0QZS6 |
| H0YFX4 | 3 | 1.99E-05 | 4F2 cell-surface antigen heavy chain (Fragment) OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| Q5W0S5 | 2 | 5.94E-05 | UV excision repair protein RAD23 homolog B (Fragment) OS=Homo sapiens OX=9606 GN=RAD23B PE=1 SV=1 |
| P54725-3 | 2 | 1.10E-05 | Isoform 3 of UV excision repair protein RAD23 homolog A OS=Homo sapiens OX=9606 GN=RAD23A |
| P07305 | 3 | 0.000196036 | Histone H1.0 OS=Homo sapiens OX=9606 GN=H1F0 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P07305-2 |
| P07305-2 | 3 | 0.000214864 | Isoform 2 of Histone H1.0 OS=Homo sapiens OX=9606 GN=H1F0 |
| Q02252-2 | 3 | 6.03E-06 | Isoform 2 of Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 |
| Q02252 | 3 | 5.88E-06 | Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q02252-2, G3V4Z4 |
| G3V4Z4 | 3 | 7.51E-06 | Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 PE=1 SV=1 |
| D6RFN0 | 3 | 6.33E-06 | COP9 signalosome complex subunit 4 OS=Homo sapiens OX=9606 GN=COPS4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: D6RAX7, Q9BT78, Q9BT78-2 |
| D6RAX7 | 3 | 6.61E-06 | COP9 constitutive photomorphogenic-like protein subunit 4 isoform 2 OS=Homo sapiens OX=9606 GN=COPS4 PE=1 SV=1 |
| Q9BT78 | 3 | 6.83E-06 | COP9 signalosome complex subunit 4 OS=Homo sapiens OX=9606 GN=COPS4 PE=1 SV=1 |
| Q9BT78-2 | 3 | 7.88E-06 | Isoform 2 of COP9 signalosome complex subunit 4 OS=Homo sapiens OX=9606 GN=COPS4 |
| Q9NQ48 | 3 | 4.82E-06 | Leucine zipper transcription factor-like protein 1 OS=Homo sapiens OX=9606 GN=LZTFL1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NQ48-2, Q9NQ48-3, H7C488 |
| Q9NQ48-2 | 3 | 5.11E-06 | Isoform 2 of Leucine zipper transcription factor-like protein 1 OS=Homo sapiens OX=9606 GN=LZTFL1 |
| H7C488 | 3 | 6.13E-06 | Leucine zipper transcription factor-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=LZTFL1 PE=1 SV=1 |
| Q9NQ48-3 | 3 | 5.62E-06 | Isoform 3 of Leucine zipper transcription factor-like protein 1 OS=Homo sapiens OX=9606 GN=LZTFL1 |
| Q9UHK6-5 | 3 | 9.65E-07 | Isoform 4 of Alpha-methylacyl-CoA racemase OS=Homo sapiens OX=9606 GN=AMACR; Additional IDs concatenated into MaxParsimony group: Q9UHK6, D6RB81 |
| D6RB81 | 3 | 1.04E-06 | Alpha-methylacyl-CoA racemase OS=Homo sapiens OX=9606 GN=AMACR PE=1 SV=1 |
| Q9UHK6 | 3 | 9.95E-07 | Alpha-methylacyl-CoA racemase OS=Homo sapiens OX=9606 GN=AMACR PE=1 SV=2 |
| Q07666-2 | 3 | 5.85E-05 | Isoform 2 of KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRBS1 |
| Q07666 | 3 | 5.52E-05 | KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRBS1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q07666-2, Q07666-3 |
| Q07666-3 | 3 | 6.06E-05 | Isoform 3 of KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRBS1 |
| F8VPC7 | 3 | 0.000517647 | Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1 |
| P17174-2 | 2 | 3.78E-06 | Isoform 2 of Aspartate aminotransferase, cytoplasmic OS=Homo sapiens OX=9606 GN=GOT1 |
| Q9H0L4 | 3 | 7.02E-06 | Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens OX=9606 GN=CSTF2T PE=1 SV=1 |
| P15924-3 | 3 | 1.41E-06 | Isoform DSPIa of Desmoplakin OS=Homo sapiens OX=9606 GN=DSP |
| P15924 | 3 | 1.36E-06 | Desmoplakin OS=Homo sapiens OX=9606 GN=DSP PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P15924-3, P15924-2 |
| P15924-2 | 3 | 1.51E-06 | Isoform DPII of Desmoplakin OS=Homo sapiens OX=9606 GN=DSP |
| Q96I99 | 3 | 1.70E-06 | Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=SUCLG2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H0Y852 |
| H0Y852 | 2 | 2.54E-06 | Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SUCLG2 PE=1 SV=1 |
| P12110 | 2 | 8.71E-07 | Collagen alpha-2(VI) chain OS=Homo sapiens OX=9606 GN=COL6A2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P12110-2, P12110-3 |
| P12110-2 | 2 | 9.67E-07 | Isoform 2C2A of Collagen alpha-2(VI) chain OS=Homo sapiens OX=9606 GN=COL6A2 |
| P12110-3 | 2 | 1.07E-06 | Isoform 2C2A' of Collagen alpha-2(VI) chain OS=Homo sapiens OX=9606 GN=COL6A2 |
| K7EJM4 | 3 | 0.000623922 | Synaptic vesicle membrane protein VAT-1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=1 |
| K7ENI6 | 3 | 2.82E-05 | TMEM256-PLSCR3 readthrough (NMD candidate) OS=Homo sapiens OX=9606 GN=TMEM256-PLSCR3 PE=4 SV=1 |
| K7ERE1 | 3 | 1.70E-05 | TMEM256-PLSCR3 readthrough (NMD candidate) OS=Homo sapiens OX=9606 GN=TMEM256-PLSCR3 PE=4 SV=1 |
| Q8N2U0 | 3 | 1.02E-05 | Transmembrane protein 256 OS=Homo sapiens OX=9606 GN=TMEM256 PE=3 SV=1; Additional IDs concatenated into MaxParsimony group: K7ERE1, K7ENI6 |
| Q9H0E2-2 | 3 | 0.000188555 | Isoform 2 of Toll-interacting protein OS=Homo sapiens OX=9606 GN=TOLLIP |
| E7EN89 | 3 | 0.000157129 | Toll interacting protein, isoform CRA\_b OS=Homo sapiens OX=9606 GN=TOLLIP PE=1 SV=2 |
| A2IDB2 | 3 | 5.06E-05 | 14-3-3 protein eta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAH PE=1 SV=1 |
| F8WDN2 | 3 | 1.21E-05 | Thioredoxin, mitochondrial OS=Homo sapiens OX=9606 GN=TXN2 PE=1 SV=1 |
| contaminant\_GR78\_SCHPO | 3 | 1.55E-05 | 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN... |
| G3V0E5 | 3 | 5.31E-06 | Transferrin receptor (P90, CD71), isoform CRA\_c OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=1 |
| Q9HAV7 | 2 | 1.02E-06 | GrpE protein homolog 1, mitochondrial OS=Homo sapiens OX=9606 GN=GRPEL1 PE=1 SV=2 |
| Q9NXV6 | 2 | 3.12E-06 | CDKN2A-interacting protein OS=Homo sapiens OX=9606 GN=CDKN2AIP PE=1 SV=3 |
| P53618 | 2 | 6.12E-07 | Coatomer subunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3 |
| Q6PL24 | 2 | 6.35E-06 | Protein TMED8 OS=Homo sapiens OX=9606 GN=TMED8 PE=1 SV=1 |
| P63172 | 2 | 8.42E-07 | Dynein light chain Tctex-type 1 OS=Homo sapiens OX=9606 GN=DYNLT1 PE=1 SV=1 |
| P0CG12 | 2 | 6.28E-06 | Chromosome transmission fidelity protein 8 homolog isoform 2 OS=Homo sapiens OX=9606 GN=CHTF8 PE=1 SV=1 |
| Q9NPF4 | 2 | 4.16E-06 | Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens OX=9606 GN=OSGEP PE=1 SV=1 |
| Q9BTY2 | 2 | 2.27E-06 | Plasma alpha-L-fucosidase OS=Homo sapiens OX=9606 GN=FUCA2 PE=1 SV=2 |
| Q16762 | 2 | 1.13E-05 | Thiosulfate sulfurtransferase OS=Homo sapiens OX=9606 GN=TST PE=1 SV=4 |
| E5RJU4 | 2 | 1.26E-05 | Transforming acidic coiled-coil-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| O60313-11 | 2 | 2.15E-07 | Isoform 5 of Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 |
| A0A2R8Y3X5 | 2 | 2.46E-07 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| O60313-13 | 2 | 2.28E-07 | Isoform 7 of Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 |
| A0A2R8YFD1 | 2 | 3.38E-07 | Dynamin-like 120 kDa protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| O60313-9 | 2 | 2.19E-07 | Isoform 3 of Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 |
| E5KLJ9 | 2 | 2.15E-07 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| O60313-10 | 2 | 2.07E-07 | Isoform 4 of Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 |
| C9J5V9 | 2 | 1.01E-05 | Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=YBX1 PE=1 SV=1 |
| O95834-2 | 2 | 1.93E-06 | Isoform 2 of Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 |
| A0A0C4DGQ7 | 2 | 2.46E-06 | Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1 |
| K7EKG3 | 2 | 3.27E-06 | Echinoderm microtubule-associated protein-like 2 (Fragment) OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1 |
| C9JRL6 | 2 | 1.74E-06 | Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=2 |
| K7EII6 | 2 | 6.71E-06 | Echinoderm microtubule-associated protein-like 2 (Fragment) OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1 |
| O95834 | 2 | 2.36E-06 | Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1 |
| O95834-3 | 2 | 1.80E-06 | Isoform 3 of Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2; Additional IDs concatenated into MaxParsimony group: O95834-2, K7EIK7, O95834, K7EII6, C9JRL6, A0A0C4DGQ7, K7EKG3, K7ELB2 |
| K7EIK7 | 2 | 1.98E-06 | Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1 |
| A2A2S5 | 2 | 6.14E-06 | Ribosome-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=1 |
| Q9NQR4 | 2 | 2.91E-06 | Omega-amidase NIT2 OS=Homo sapiens OX=9606 GN=NIT2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H7C579 |
| H7C579 | 2 | 3.03E-06 | Omega-amidase NIT2 (Fragment) OS=Homo sapiens OX=9606 GN=NIT2 PE=1 SV=8 |
| A0A0A0MSK5 | 2 | 1.13E-06 | Torsin-1A-interacting protein 1 OS=Homo sapiens OX=9606 GN=TOR1AIP1 PE=1 SV=1 |
| H0YD16 | 2 | 2.63E-06 | Torsin-1A-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TOR1AIP1 PE=1 SV=1 |
| Q5JTV8 | 2 | 8.94E-07 | Torsin-1A-interacting protein 1 OS=Homo sapiens OX=9606 GN=TOR1AIP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A0A0MSK5, H0YD16, H0YDU3 |
| H0YDU3 | 2 | 2.70E-06 | Torsin-1A-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TOR1AIP1 PE=1 SV=2 |
| P52815 | 2 | 5.67E-06 | 39S ribosomal protein L12, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL12 PE=1 SV=2 |
| B4DLN1 | 2 | 2.54E-06 | cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier OS=Homo sapiens OX=9606 PE=2 SV=1; Additional IDs concatenated into MaxParsimony group: P52815 |
| A0A1B0GU38 | 2 | 1.94E-06 | Serpin B8 OS=Homo sapiens OX=9606 GN=SERPINB8 PE=1 SV=1 |
| C9JVA8 | 2 | 3.06E-06 | Serpin B8 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINB8 PE=1 SV=1 |
| P50452 | 2 | 1.34E-06 | Serpin B8 OS=Homo sapiens OX=9606 GN=SERPINB8 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A1B0GU38, P50452-2, H7BXK7, C9JVA8, C9JTJ8 |
| P50452-2 | 2 | 2.07E-06 | Isoform 2 of Serpin B8 OS=Homo sapiens OX=9606 GN=SERPINB8 |
| H7BXK7 | 2 | 2.65E-06 | Serpin B8 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINB8 PE=1 SV=1 |
| C9JTJ8 | 2 | 4.04E-06 | Serpin B8 (Fragment) OS=Homo sapiens OX=9606 GN=SERPINB8 PE=1 SV=1 |
| A0A140T9W2 | 2 | 1.70E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| P30484 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-46 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P13746-2 | 2 | 4.99E-06 | Isoform 2 of HLA class I histocompatibility antigen, A-11 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A |
| P30504 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, Cw-4 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A1W2PSE7 | 2 | 1.64E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A1W2PQS8 | 2 | 5.69E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P04222 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, Cw-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=2 |
| P30456 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-43 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30450 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-26 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| P10319 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-58 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P13746 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-11 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P04439 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| Q5SRN5 | 2 | 4.99E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| P01891 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-68 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=4 |
| A0A1W2PPF8 | 2 | 5.46E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30443 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30490 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-52 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P30501 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, Cw-2 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| Q29960-2 | 2 | 1.85E-06 | Isoform 2 of HLA class I histocompatibility antigen, Cw-16 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C |
| P16188 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-30 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| A0A1W2PS24 | 2 | 5.69E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30447 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-23 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A1W2PRT9 | 2 | 5.11E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T9X5 | 2 | 4.99E-06 | HLA class I histocompatibility antigen, A-3 alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T937 | 2 | 1.78E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A140T9U0 | 2 | 1.64E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| P30685 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-35 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| A0A1W2PPQ2 | 2 | 5.46E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30455 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, A-36 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30510 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, Cw-14 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=2 |
| Q95604 | 2 | 1.62E-06 | HLA class I histocompatibility antigen, Cw-17 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| P01892 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30498 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-78 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| A0A140TA03 | 2 | 4.60E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| P18465 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-57 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P30491 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-53 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P30459 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-74 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A1W2PR61 | 2 | 5.69E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T955 | 2 | 6.19E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T930 | 2 | 1.52E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0G2JPD3, A0A0G2JL56, A0A140T9M0, Q95604, A0A140T912, A0A140T913, A0A140T9X5, A0A0G2JIF2, Q5SRN5, A0A140T8Y4, P13746-2, A0A140T9U0, A0A1W2PSE7, Q29960, P30508, P04222, P30504, P30510, Q07000, P30501, P30453, A0A140T9I0, P30459, B0UXQ0, P30457, P16189, P05534, P01892, P10314, P30455, P18462, P16190, P30512, P30456, P30447, P30450, P16188, P10316, P30443, P01891, P13746, P04439, P30492, P30464, P30495, Q29940, P30484, P10319, P30493, P30490, A0A1W2PRT9, P30685, P30498, P18464, P18465, P30491, A0A140T9W2, A0A140T9Z6, A0A1W2PS39, A0A1W2PQD0, A0A1W2PPF8, A0A1W2PPQ2, A0A140T937, Q9GJ45, Q29960-2, A0A1W2PRZ0, A0A1W2PQS8, A0A1W2PR61, A0A1W2PS24, Q5SRN7, A0A140T955, A0A0G2JI36, A0A140T933, A0A140T8W8, A0A140T941, A0A140T975, A0A140T9M5, A0A140T9T1, A0A140T953, A0A140TA13, A0A140T9Z4, A0A140TA03 |
| P30453 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-34 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T8Y4 | 2 | 4.99E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30493 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-55 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P05534 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-24 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| P18464 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-51 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| A0A0G2JPD3 | 2 | 4.70E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T912 | 2 | 1.62E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A140T9Z6 | 2 | 5.41E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T9Z4 | 2 | 4.60E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A140T933 | 2 | 6.19E-06 | HLA class I histocompatibility antigen, A-3 alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T913 | 2 | 4.99E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T9M0 | 2 | 1.62E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A140T975 | 2 | 6.19E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| Q5SRN7 | 2 | 6.19E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| A0A140T9M5 | 2 | 2.31E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A0G2JI36 | 2 | 2.02E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T8W8 | 2 | 6.19E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P10314 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-32 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| B0UXQ0 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A1W2PRZ0 | 2 | 1.86E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| Q9GJ45 | 2 | 5.68E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A1W2PS39 | 2 | 5.46E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140TA13 | 2 | 2.69E-06 | HLA class I histocompatibility antigen, B-46 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P30457 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-66 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30508 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, Cw-12 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=2 |
| P30492 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-54 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| A0A0G2JL56 | 2 | 1.53E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P16190 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-33 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=3 |
| P30512 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-29 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| Q29960 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, Cw-16 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A0G2JIF2 | 2 | 1.63E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P30464 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-15 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=2 |
| P10316 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-69 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| Q07000 | 2 | 1.65E-06 | HLA class I histocompatibility antigen, Cw-15 alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| P30495 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-56 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| P18462 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-25 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T953 | 2 | 2.45E-06 | HLA class I histocompatibility antigen, B-46 alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| A0A140T941 | 2 | 6.19E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| P16189 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-31 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2 |
| A0A1W2PQD0 | 2 | 1.78E-06 | HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| A0A140T9T1 | 2 | 2.31E-06 | HLA class I histocompatibility antigen, Cw-6 alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=1 |
| A0A140T9I0 | 2 | 5.07E-06 | HLA class I histocompatibility antigen, A-3 alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=1 |
| Q29940 | 2 | 1.67E-06 | HLA class I histocompatibility antigen, B-59 alpha chain OS=Homo sapiens OX=9606 GN=HLA-B PE=1 SV=1 |
| F8VRY7 | 2 | 1.85E-06 | 3'(2'),5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1 |
| O95861-3 | 2 | 2.08E-06 | Isoform 3 of 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 |
| D6R9A6 | 2 | 1.86E-05 | High mobility group protein B2 (Fragment) OS=Homo sapiens OX=9606 GN=HMGB2 PE=1 SV=1 |
| Q13733 | 2 | 2.52E-06 | Sodium/potassium-transporting ATPase subunit alpha-4 OS=Homo sapiens OX=9606 GN=ATP1A4 PE=1 SV=3 |
| H3BQH2 | 2 | 1.58E-06 | Cadherin-11 (Fragment) OS=Homo sapiens OX=9606 GN=CDH11 PE=1 SV=1 |
| A0A087WYS0 | 2 | 1.64E-05 | MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=1 |
| Q68CR8 | 2 | 2.63E-05 | Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| B7ZBQ0 | 2 | 3.58E-05 | Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| B4DDC6 | 2 | 1.93E-05 | cDNA FLJ59832, moderately similar to Prostaglandin E synthase 3 (EC 5.3.99.3) OS=Homo sapiens OX=9606 GN=PTGES3 PE=1 SV=1 |
| A0A087WYT3 | 2 | 1.46E-05 | Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q15185, Q15185-4, Q15185-2, B4DDC6 |
| Q15185 | 2 | 1.50E-05 | Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 PE=1 SV=1 |
| Q15185-4 | 2 | 1.72E-05 | Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 |
| Q15185-2 | 2 | 1.89E-05 | Isoform 2 of Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 |
| E5RHG9 | 2 | 3.38E-05 | Cytochrome b-c1 complex subunit 7 OS=Homo sapiens OX=9606 GN=UQCRB PE=1 SV=1 |
| P14927 | 2 | 2.31E-05 | Cytochrome b-c1 complex subunit 7 OS=Homo sapiens OX=9606 GN=UQCRB PE=1 SV=2 |
| B7Z2R2 | 2 | 1.60E-05 | Cytochrome b-c1 complex subunit 7 OS=Homo sapiens OX=9606 GN=UQCRB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P14927-2, P14927, E5RHG9 |
| P14927-2 | 2 | 1.84E-05 | Isoform 2 of Cytochrome b-c1 complex subunit 7 OS=Homo sapiens OX=9606 GN=UQCRB |
| Q9C0E8-2 | 2 | 7.19E-06 | Isoform 2 of Endoplasmic reticulum junction formation protein lunapark OS=Homo sapiens OX=9606 GN=LNPK |
| Q9C0E8-4 | 2 | 6.62E-06 | Isoform 4 of Endoplasmic reticulum junction formation protein lunapark OS=Homo sapiens OX=9606 GN=LNPK; Additional IDs concatenated into MaxParsimony group: Q9C0E8, Q9C0E8-2, Q9C0E8-3 |
| Q9C0E8 | 2 | 7.10E-06 | Endoplasmic reticulum junction formation protein lunapark OS=Homo sapiens OX=9606 GN=LNPK PE=1 SV=2 |
| Q9C0E8-3 | 2 | 9.97E-06 | Isoform 3 of Endoplasmic reticulum junction formation protein lunapark OS=Homo sapiens OX=9606 GN=LNPK |
| H7C1H2 | 2 | 2.99E-06 | 26S proteasome non-ATPase regulatory subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=PSMD2 PE=1 SV=1 |
| H0YCF6 | 2 | 8.86E-07 | Cytoskeleton-associated protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CKAP5 PE=1 SV=8 |
| Q14008 | 2 | 1.69E-07 | Cytoskeleton-associated protein 5 OS=Homo sapiens OX=9606 GN=CKAP5 PE=1 SV=3 |
| Q14008-3 | 2 | 1.69E-07 | Isoform 3 of Cytoskeleton-associated protein 5 OS=Homo sapiens OX=9606 GN=CKAP5; Additional IDs concatenated into MaxParsimony group: Q14008, Q14008-2, H0YEK7, H0YCF6 |
| H0YEK7 | 2 | 7.74E-07 | Cytoskeleton-associated protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CKAP5 PE=1 SV=2 |
| Q14008-2 | 2 | 1.74E-07 | Isoform 2 of Cytoskeleton-associated protein 5 OS=Homo sapiens OX=9606 GN=CKAP5 |
| Q8N3V7-2 | 2 | 2.95E-07 | Isoform 2 of Synaptopodin OS=Homo sapiens OX=9606 GN=SYNPO |
| Q8N3V7 | 2 | 2.87E-07 | Synaptopodin OS=Homo sapiens OX=9606 GN=SYNPO PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8N3V7-2, Q8N3V7-3 |
| Q8N3V7-3 | 2 | 3.89E-07 | Isoform 3 of Synaptopodin OS=Homo sapiens OX=9606 GN=SYNPO |
| A0A1B0GTI0 | 2 | 4.52E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| A0A1B0GTR6 | 2 | 4.27E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| A0A1B0GV94 | 2 | 3.33E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| A0A087WZY0 | 2 | 4.50E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=2 |
| A0A1B0GU14 | 2 | 2.56E-05 | Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| A0A1B0GWJ7 | 2 | 4.43E-06 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1 |
| A0A1B0GTV7 | 2 | 3.70E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| A0A1B0GUE8 | 2 | 3.40E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| A0A1C7CYZ2 | 2 | 4.39E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| A0A1B0GVL0 | 2 | 7.38E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=4 SV=1 |
| C9J931 | 2 | 2.23E-05 | GTP-binding protein Rheb OS=Homo sapiens OX=9606 GN=RHEB PE=1 SV=1 |
| Q15382 | 2 | 9.56E-06 | GTP-binding protein Rheb OS=Homo sapiens OX=9606 GN=RHEB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9J931 |
| H0YN18 | 2 | 2.72E-05 | Proteasome endopeptidase complex OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1 |
| P25789 | 2 | 3.16E-05 | Proteasome subunit alpha type-4 OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0YL69, H0YN18, H0YMZ1, P25789-2 |
| H0YMZ1 | 2 | 3.75E-05 | Proteasome subunit alpha type (Fragment) OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=8 |
| H0YL69 | 2 | 3.49E-05 | Proteasome subunit alpha type (Fragment) OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1 |
| P25789-2 | 2 | 3.29E-05 | Isoform 2 of Proteasome subunit alpha type-4 OS=Homo sapiens OX=9606 GN=PSMA4 |
| Q04900-2 | 2 | 3.20E-05 | Isoform 2 of Sialomucin core protein 24 OS=Homo sapiens OX=9606 GN=CD164 |
| Q04900 | 2 | 3.07E-05 | Sialomucin core protein 24 OS=Homo sapiens OX=9606 GN=CD164 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q04900-2, Q04900-3, Q04900-4, Q04900-5 |
| Q04900-5 | 2 | 3.86E-05 | Isoform 5 of Sialomucin core protein 24 OS=Homo sapiens OX=9606 GN=CD164 |
| Q04900-4 | 2 | 3.40E-05 | Isoform 4 of Sialomucin core protein 24 OS=Homo sapiens OX=9606 GN=CD164 |
| Q04900-3 | 2 | 3.29E-05 | Isoform 3 of Sialomucin core protein 24 OS=Homo sapiens OX=9606 GN=CD164 |
| O14497 | 2 | 5.33E-06 | AT-rich interactive domain-containing protein 1A OS=Homo sapiens OX=9606 GN=ARID1A PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O14497-2 |
| O14497-2 | 2 | 5.89E-06 | Isoform 2 of AT-rich interactive domain-containing protein 1A OS=Homo sapiens OX=9606 GN=ARID1A |
| O94985-2 | 2 | 2.48E-07 | Isoform 2 of Calsyntenin-1 OS=Homo sapiens OX=9606 GN=CLSTN1 |
| Q5SR54 | 2 | 3.08E-07 | Calsyntenin-1 (Fragment) OS=Homo sapiens OX=9606 GN=CLSTN1 PE=1 SV=1 |
| O94985 | 2 | 2.45E-07 | Calsyntenin-1 OS=Homo sapiens OX=9606 GN=CLSTN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O94985-2, Q5SR54 |
| A6NC58 | 2 | 1.54E-06 | Zinc finger MYM-type protein 3 OS=Homo sapiens OX=9606 GN=ZMYM3 PE=1 SV=1 |
| A6NL54 | 2 | 1.08E-06 | Zinc finger MYM-type protein 3 OS=Homo sapiens OX=9606 GN=ZMYM3 PE=1 SV=1 |
| Q14202-2 | 2 | 3.97E-07 | Isoform 2 of Zinc finger MYM-type protein 3 OS=Homo sapiens OX=9606 GN=ZMYM3 |
| A6NHB5 | 2 | 3.93E-07 | Zinc finger MYM-type protein 3 OS=Homo sapiens OX=9606 GN=ZMYM3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q14202, Q14202-2, A6NHN7, A6NL54, Q14202-3, A6NC58 |
| Q14202 | 2 | 3.93E-07 | Zinc finger MYM-type protein 3 OS=Homo sapiens OX=9606 GN=ZMYM3 PE=1 SV=2 |
| A6NHN7 | 2 | 4.21E-07 | Zinc finger MYM-type protein 3 OS=Homo sapiens OX=9606 GN=ZMYM3 PE=1 SV=1 |
| Q14202-3 | 2 | 1.09E-06 | Isoform 3 of Zinc finger MYM-type protein 3 OS=Homo sapiens OX=9606 GN=ZMYM3 |
| E9PM36 | 2 | 2.02E-05 | 40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=1 |
| H0YEN5 | 2 | 2.20E-05 | 40S ribosomal protein S2 (Fragment) OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=1 |
| P15880 | 2 | 1.46E-05 | 40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PQD7, E9PMM9, H0YEN5, E9PM36, E9PPT0, I3L404, H0YE27, H3BNG3 |
| I3L404 | 2 | 2.72E-05 | 40S ribosomal protein S2 (Fragment) OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=1 |
| E9PMM9 | 2 | 1.97E-05 | 40S ribosomal protein S2 (Fragment) OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=1 |
| E9PQD7 | 2 | 1.82E-05 | 40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=1 |
| H0YJB9 | 2 | 3.30E-06 | RNA transcription, translation and transport factor protein (Fragment) OS=Homo sapiens OX=9606 GN=RTRAF PE=1 SV=1 |
| Q9Y224 | 2 | 1.75E-06 | RNA transcription, translation and transport factor protein OS=Homo sapiens OX=9606 GN=RTRAF PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: G3V4C6, H0YJB9 |
| G3V4C6 | 2 | 2.21E-06 | RNA transcription, translation and transport factor protein OS=Homo sapiens OX=9606 GN=RTRAF PE=1 SV=1 |
| E7EPB3 | 2 | 7.24E-06 | 60S ribosomal protein L14 OS=Homo sapiens OX=9606 GN=RPL14 PE=1 SV=1 |
| P50914 | 2 | 4.17E-06 | 60S ribosomal protein L14 OS=Homo sapiens OX=9606 GN=RPL14 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: E7EPB3 |
| F2Z2Z8 | 2 | 1.72E-05 | Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens OX=9606 GN=PBXIP1 PE=1 SV=1 |
| A0A1W2PQD4 | 2 | 6.11E-06 | Heterogeneous nuclear ribonucleoprotein U (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PPE9 | 2 | 4.16E-05 | Heterogeneous nuclear ribonucleoprotein U (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| Q5SQT3 | 2 | 4.43E-05 | Histone H2A (Fragment) OS=Homo sapiens OX=9606 GN=H2AFY2 PE=1 SV=8 |
| Q9P0M6 | 2 | 2.88E-05 | Core histone macro-H2A.2 OS=Homo sapiens OX=9606 GN=H2AFY2 PE=1 SV=3 |
| E7EQR6 | 2 | 2.98E-06 | T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 |
| F5H282 | 2 | 3.60E-06 | T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 |
| I3L4P4 | 2 | 7.42E-05 | Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV=1 |
| Q96QK1 | 2 | 6.90E-06 | Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: I3L4P4, A0A1W2PP10, I3L4S0 |
| I3L4S0 | 2 | 8.51E-05 | Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV=1 |
| A0A1W2PP10 | 2 | 7.59E-05 | Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV=1 |
| Q9UMR2-3 | 2 | 2.90E-06 | Isoform 3 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens OX=9606 GN=DDX19B |
| H3BQK0 | 2 | 3.61E-06 | ATP-dependent RNA helicase DDX19B OS=Homo sapiens OX=9606 GN=DDX19B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F6QDS0, Q9UMR2, Q9NUU7, Q9UMR2-4, Q9UMR2-2, I3L0H8, I3L352, Q9NUU7-2, Q9UMR2-3, H3BN59, H3BMQ5, H3BTB3 |
| Q9UMR2-4 | 2 | 3.86E-06 | Isoform 4 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens OX=9606 GN=DDX19B |
| Q9NUU7-2 | 2 | 2.76E-06 | Isoform 2 of ATP-dependent RNA helicase DDX19A OS=Homo sapiens OX=9606 GN=DDX19A |
| F6QDS0 | 2 | 3.65E-06 | HCG2043426, isoform CRA\_b OS=Homo sapiens OX=9606 GN=hCG\_2043426 PE=1 SV=1 |
| Q9NUU7 | 2 | 3.66E-06 | ATP-dependent RNA helicase DDX19A OS=Homo sapiens OX=9606 GN=DDX19A PE=1 SV=1 |
| I3L0H8 | 2 | 3.91E-06 | ATP-dependent RNA helicase DDX19A OS=Homo sapiens OX=9606 GN=DDX19A PE=1 SV=1 |
| Q9UMR2 | 2 | 3.65E-06 | ATP-dependent RNA helicase DDX19B OS=Homo sapiens OX=9606 GN=DDX19B PE=1 SV=1 |
| Q9UMR2-2 | 2 | 3.90E-06 | Isoform 2 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens OX=9606 GN=DDX19B |
| I3L352 | 2 | 2.71E-06 | ATP-dependent RNA helicase DDX19A (Fragment) OS=Homo sapiens OX=9606 GN=DDX19A PE=1 SV=1 |
| O75746-2 | 2 | 2.86E-06 | Isoform 2 of Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens OX=9606 GN=SLC25A12 |
| O75746 | 2 | 2.41E-06 | Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens OX=9606 GN=SLC25A12 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: O75746-2 |
| Q9C0C2 | 2 | 6.40E-07 | 182 kDa tankyrase-1-binding protein OS=Homo sapiens OX=9606 GN=TNKS1BP1 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: Q9C0C2-2 |
| Q9C0C2-2 | 2 | 1.37E-06 | Isoform 2 of 182 kDa tankyrase-1-binding protein OS=Homo sapiens OX=9606 GN=TNKS1BP1 |
| P35611-6 | 2 | 2.71E-06 | Isoform 6 of Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 |
| P35611 | 2 | 2.43E-06 | Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=2 |
| E7ENY0 | 2 | 2.70E-06 | Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=1 |
| D6RJE2 | 2 | 2.60E-05 | Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=1 |
| P35611-5 | 2 | 3.51E-06 | Isoform 5 of Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 |
| P35611-3 | 2 | 2.33E-06 | Isoform 3 of Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1; Additional IDs concatenated into MaxParsimony group: P35611, E7ENY0, P35611-6, P35611-4, E7EV99, P35611-2, P35611-5, A0A0A0MSR2, D6RF25, D6RAH3, D6RJE2 |
| E7EV99 | 2 | 2.83E-06 | Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=1 |
| D6RF25 | 2 | 1.26E-05 | Alpha-adducin (Fragment) OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=8 |
| D6RAH3 | 2 | 1.31E-05 | Alpha-adducin (Fragment) OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=1 |
| P35611-2 | 2 | 2.84E-06 | Isoform 2 of Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 |
| P35611-4 | 2 | 2.71E-06 | Isoform 4 of Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 |
| A0A0A0MSR2 | 2 | 4.48E-06 | Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=1 |
| A0A2R8Y765 | 2 | 3.70E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| A0A2R8Y855 | 2 | 2.79E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| Q969G3-2 | 2 | 2.82E-06 | Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 |
| Q969G3-6 | 2 | 3.50E-06 | Isoform 6 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 |
| A0A2R8Y7I9 | 2 | 3.08E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| A0A2R8YES3 | 2 | 2.95E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| Q969G3-3 | 2 | 3.00E-06 | Isoform 3 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 |
| B4DGM3 | 2 | 2.61E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| J3QKS7 | 2 | 3.57E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment) OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=2 |
| Q969G3-4 | 2 | 2.72E-06 | Isoform 4 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 |
| A0A2R8Y7U4 | 2 | 3.45E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| Q969G3 | 2 | 2.49E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: B4DGM3, Q969G3-4, A0A2R8Y855, Q969G3-2, A0A2R8YES3, Q969G3-3, A0A2R8Y4T4, A0A2R8Y7I9, Q969G3-5, A0A2U3TZQ7, A0A2R8Y7U4, Q969G3-6, J3QKS7, A0A2R8Y765, K7EMQ8, H7C048 |
| H7C048 | 2 | 6.52E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment) OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| Q969G3-5 | 2 | 3.12E-06 | Isoform 5 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 |
| A0A2U3TZQ7 | 2 | 3.29E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=4 SV=1 |
| K7EMQ8 | 2 | 5.79E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment) OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| A0A2R8Y4T4 | 2 | 3.06E-06 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=1 |
| Q5TEJ7 | 2 | 1.28E-05 | Replication protein A 32 kDa subunit (Fragment) OS=Homo sapiens OX=9606 GN=RPA2 PE=1 SV=1 |
| P15927-3 | 2 | 6.39E-06 | Isoform 3 of Replication protein A 32 kDa subunit OS=Homo sapiens OX=9606 GN=RPA2; Additional IDs concatenated into MaxParsimony group: P15927-2, P15927, Q5TEJ7 |
| P15927 | 2 | 8.48E-06 | Replication protein A 32 kDa subunit OS=Homo sapiens OX=9606 GN=RPA2 PE=1 SV=1 |
| P15927-2 | 2 | 8.23E-06 | Isoform 2 of Replication protein A 32 kDa subunit OS=Homo sapiens OX=9606 GN=RPA2 |
| H0YLX1 | 2 | 3.95E-05 | Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=1 |
| Q9P035 | 2 | 2.70E-06 | Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=2 |
| H3BPZ1 | 2 | 2.90E-06 | Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=1 |
| H3BS72 | 2 | 2.44E-06 | Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9P035, H3BPZ1, Q9P035-2, H3BRL8, H3BMZ1 |
| A0A0U1RQF0 | 2 | 2.76E-07 | Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=1 |
| P49327 | 2 | 2.75E-07 | Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A0A0U1RQF0 |
| A0A0A0MRX2 | 2 | 4.39E-06 | DDRGK domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DDRGK1 PE=1 SV=1 |
| Q96HY6-2 | 2 | 4.18E-06 | Isoform 2 of DDRGK domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DDRGK1 |
| H0YAG8 | 2 | 9.09E-06 | Alcohol dehydrogenase class-3 (Fragment) OS=Homo sapiens OX=9606 GN=ADH5 PE=1 SV=1 |
| P62820-3 | 2 | 3.73E-05 | Isoform 3 of Ras-related protein Rab-1A OS=Homo sapiens OX=9606 GN=RAB1A |
| P62820-2 | 2 | 3.41E-05 | Isoform 2 of Ras-related protein Rab-1A OS=Homo sapiens OX=9606 GN=RAB1A |
| E9PLD0 | 2 | 2.39E-05 | Ras-related protein Rab-1B OS=Homo sapiens OX=9606 GN=RAB1B PE=1 SV=1 |
| Q92928 | 2 | 2.01E-05 | Putative Ras-related protein Rab-1C OS=Homo sapiens OX=9606 GN=RAB1C PE=5 SV=2; Additional IDs concatenated into MaxParsimony group: Q9H0U4, E9PLD0, P62820, E7END7, P62820-2, P62820-3 |
| P62820 | 2 | 2.35E-05 | Ras-related protein Rab-1A OS=Homo sapiens OX=9606 GN=RAB1A PE=1 SV=3 |
| Q9H0U4 | 2 | 2.01E-05 | Ras-related protein Rab-1B OS=Homo sapiens OX=9606 GN=RAB1B PE=1 SV=1 |
| E7END7 | 2 | 2.78E-05 | Ras-related protein Rab-1A OS=Homo sapiens OX=9606 GN=RAB1A PE=1 SV=1 |
| Q8NBM8 | 2 | 3.43E-07 | Prenylcysteine oxidase-like OS=Homo sapiens OX=9606 GN=PCYOX1L PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E7EVZ5 |
| E7EVZ5 | 2 | 4.19E-07 | Prenylcysteine oxidase-like OS=Homo sapiens OX=9606 GN=PCYOX1L PE=1 SV=1 |
| Q9NZT2-2 | 2 | 2.03E-06 | Isoform 2 of Opioid growth factor receptor OS=Homo sapiens OX=9606 GN=OGFR |
| A0A0A0MRN5 | 2 | 2.13E-06 | Opioid growth factor receptor, isoform CRA\_d OS=Homo sapiens OX=9606 GN=OGFR PE=1 SV=1 |
| Q9NZT2 | 2 | 1.97E-06 | Opioid growth factor receptor OS=Homo sapiens OX=9606 GN=OGFR PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9NZT2-2, A0A0A0MRN5 |
| A6NJU6 | 2 | 1.31E-05 | ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=2 |
| C9IZL7 | 2 | 8.04E-05 | Non-POU domain-containing octamer-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=NONO PE=1 SV=1 |
| P49321-3 | 2 | 5.69E-06 | Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP |
| P49321-4 | 2 | 8.54E-07 | Isoform 4 of Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP |
| E9PPR5 | 2 | 7.73E-07 | Nuclear autoantigenic sperm protein (Fragment) OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=8 |
| H0YEX5 | 2 | 2.59E-06 | Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=1 |
| Q5VU79 | 2 | 4.93E-06 | Ubiquitin-associated protein 2-like (Fragment) OS=Homo sapiens OX=9606 GN=UBAP2L PE=1 SV=1 |
| Q5VU78 | 2 | 4.67E-06 | Ubiquitin-associated protein 2-like (Fragment) OS=Homo sapiens OX=9606 GN=UBAP2L PE=1 SV=1 |
| Q96JB5 | 2 | 2.22E-06 | CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3 PE=1 SV=2 |
| Q96JB5-3 | 2 | 3.99E-06 | Isoform 3 of CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3 |
| J3QRM1 | 2 | 4.13E-06 | CDK5 regulatory subunit-associated protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=CDK5RAP3 PE=1 SV=1 |
| Q96JB5-2 | 2 | 2.68E-06 | Isoform 2 of CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3 |
| Q96JB5-4 | 2 | 2.11E-06 | Isoform 4 of CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3; Additional IDs concatenated into MaxParsimony group: Q96JB5, Q96JB5-2, Q96JB5-3, J3QRM1 |
| P52594-4 | 2 | 5.28E-06 | Isoform 4 of Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=AGFG1; Additional IDs concatenated into MaxParsimony group: P52594, P52594-3, P52594-2 |
| P52594-2 | 2 | 5.91E-06 | Isoform 2 of Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=AGFG1 |
| P52594 | 2 | 5.49E-06 | Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=AGFG1 PE=1 SV=2 |
| P52594-3 | 2 | 5.51E-06 | Isoform 3 of Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=AGFG1 |
| Q9NTJ5 | 2 | 7.47E-07 | Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens OX=9606 GN=SACM1L PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9NTJ5-2, E9PGZ4, C9JV50 |
| Q9NTJ5-2 | 2 | 8.33E-07 | Isoform 2 of Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens OX=9606 GN=SACM1L |
| C9JV50 | 2 | 2.34E-06 | Phosphatidylinositide phosphatase SAC1 (Fragment) OS=Homo sapiens OX=9606 GN=SACM1L PE=1 SV=1 |
| E9PGZ4 | 2 | 9.06E-07 | Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens OX=9606 GN=SACM1L PE=1 SV=1 |
| C9JHN8 | 2 | 1.94E-06 | Golgi to ER traffic protein 4 homolog (Fragment) OS=Homo sapiens OX=9606 GN=GET4 PE=1 SV=1 |
| C9JPA8 | 2 | 2.19E-06 | Golgi to ER traffic protein 4 homolog (Fragment) OS=Homo sapiens OX=9606 GN=GET4 PE=1 SV=2 |
| Q7L5D6 | 2 | 9.93E-07 | Golgi to ER traffic protein 4 homolog OS=Homo sapiens OX=9606 GN=GET4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q7L5D6-2, C9JHN8, C9JPA8 |
| Q7L5D6-2 | 2 | 1.19E-06 | Isoform 2 of Golgi to ER traffic protein 4 homolog OS=Homo sapiens OX=9606 GN=GET4 |
| B5MBZ0 | 2 | 1.04E-06 | Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens OX=9606 GN=EML4 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9HC35, Q9HC35-2 |
| Q9HC35 | 2 | 1.05E-06 | Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens OX=9606 GN=EML4 PE=1 SV=3 |
| Q9HC35-2 | 2 | 1.12E-06 | Isoform 2 of Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens OX=9606 GN=EML4 |
| S4R3S4 | 2 | 1.48E-05 | Aldehyde dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ALDH2 PE=1 SV=1 |
| F8W1W3 | 2 | 3.84E-06 | Dynamin-1-like protein (Fragment) OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=8 |
| F8VUJ9 | 2 | 3.75E-06 | Dynamin-1-like protein (Fragment) OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=1 |
| B4DPZ9 | 2 | 4.14E-06 | cDNA FLJ59948, highly similar to Dynamin-1-like protein (EC 3.6.5.5) OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=1 |
| H0YNU8 | 2 | 1.19E-05 | Tropomodulin-3 (Fragment) OS=Homo sapiens OX=9606 GN=TMOD3 PE=1 SV=1 |
| Q9NYL9 | 2 | 1.12E-06 | Tropomodulin-3 OS=Homo sapiens OX=9606 GN=TMOD3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0YNU8 |
| Q96TA1 | 2 | 8.21E-06 | Niban-like protein 1 OS=Homo sapiens OX=9606 GN=FAM129B PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q96TA1-2 |
| Q96TA1-2 | 2 | 8.35E-06 | Isoform 2 of Niban-like protein 1 OS=Homo sapiens OX=9606 GN=FAM129B |
| P28838 | 2 | 2.30E-06 | Cytosol aminopeptidase OS=Homo sapiens OX=9606 GN=LAP3 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P28838-2 |
| P28838-2 | 2 | 2.45E-06 | Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens OX=9606 GN=LAP3 |
| P30419 | 2 | 7.09E-06 | Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens OX=9606 GN=NMT1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P30419-2, B7Z8J4, K7EN82 |
| P30419-2 | 2 | 1.32E-06 | Isoform Short of Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens OX=9606 GN=NMT1 |
| B7Z8J4 | 2 | 2.57E-05 | cDNA FLJ54222, highly similar to Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) OS=Homo sapiens OX=9606 GN=NMT1 PE=1 SV=1 |
| K7EN82 | 2 | 7.63E-06 | Glycylpeptide N-tetradecanoyltransferase 1 (Fragment) OS=Homo sapiens OX=9606 GN=NMT1 PE=1 SV=1 |
| P09543 | 2 | 1.40E-06 | 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens OX=9606 GN=CNP PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P09543-2 |
| P09543-2 | 2 | 1.47E-06 | Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens OX=9606 GN=CNP |
| C9JJE5 | 2 | 3.90E-05 | Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment) OS=Homo sapiens OX=9606 GN=IDH1 PE=1 SV=1 |
| C9JLU6 | 2 | 3.31E-05 | Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment) OS=Homo sapiens OX=9606 GN=IDH1 PE=1 SV=8 |
| H7C0J0 | 2 | 9.26E-06 | Neural cell adhesion molecule L1-like protein (Fragment) OS=Homo sapiens OX=9606 GN=CHL1 PE=1 SV=2 |
| Q14152 | 2 | 5.03E-07 | Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens OX=9606 GN=EIF3A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q14152-2 |
| Q14152-2 | 2 | 5.16E-07 | Isoform 2 of Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens OX=9606 GN=EIF3A |
| C9J8Q5 | 2 | 2.17E-06 | Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH5A1 PE=1 SV=1 |
| P51649-2 | 2 | 2.01E-06 | Isoform 2 of Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH5A1; Additional IDs concatenated into MaxParsimony group: P51649, C9J8Q5 |
| P51649 | 2 | 2.06E-06 | Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH5A1 PE=1 SV=2 |
| C9J5W6 | 2 | 2.05E-05 | Transgelin OS=Homo sapiens OX=9606 GN=TAGLN3 PE=1 SV=1 |
| Q9UI15 | 2 | 1.18E-05 | Transgelin-3 OS=Homo sapiens OX=9606 GN=TAGLN3 PE=1 SV=2 |
| A0A087X1A9 | 2 | 1.44E-05 | Vesicle-trafficking protein SEC22b (Fragment) OS=Homo sapiens OX=9606 GN=SEC22B PE=1 SV=1 |
| H0Y5C6 | 2 | 1.12E-05 | Filamin-A (Fragment) OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=1 |
| Q3KQU3 | 2 | 2.71E-06 | MAP7 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MAP7D1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q3KQU3-4, Q3KQU3-2 |
| Q3KQU3-4 | 2 | 2.83E-06 | Isoform 4 of MAP7 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MAP7D1 |
| Q3KQU3-2 | 2 | 2.84E-06 | Isoform 2 of MAP7 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MAP7D1 |

3 – List of the proteins

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Replicate Count** | **Total Signal** | **Description** |
| F5H479 | 2 | 3.33E-05 | Ragulator complex protein LAMTOR1 OS=Homo sapiens OX=9606 GN=LAMTOR1 PE=1 SV=1 |
| F5GX19 | 2 | 2.32E-05 | Ragulator complex protein LAMTOR1 OS=Homo sapiens OX=9606 GN=LAMTOR1 PE=1 SV=1 |
| F5H3Y3 | 2 | 2.06E-05 | Ragulator complex protein LAMTOR1 OS=Homo sapiens OX=9606 GN=LAMTOR1 PE=1 SV=1 |
| H0YFI1 | 2 | 4.17E-05 | Ragulator complex protein LAMTOR1 (Fragment) OS=Homo sapiens OX=9606 GN=LAMTOR1 PE=1 SV=1 |
| F8VP67 | 3 | 3.31E-05 | Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=1 |
| contaminant\_KERATIN20 | 3 | 3.89E-05 |  |
| F8VUG2 | 3 | 1.37E-05 | Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=1 |
| P05787 | 3 | 3.89E-05 | Keratin, type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7 |
| F8W1U3 | 3 | 1.30E-05 | Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=1 |
| P05787-2 | 3 | 3.68E-05 | Isoform 2 of Keratin, type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 |
| Q6UXI9-3 | 3 | 3.58E-06 | Isoform 3 of Nephronectin OS=Homo sapiens OX=9606 GN=NPNT |
| Q6UXI9-6 | 3 | 3.66E-06 | Isoform 6 of Nephronectin OS=Homo sapiens OX=9606 GN=NPNT |
| D6RH31 | 3 | 3.50E-06 | Nephronectin (Fragment) OS=Homo sapiens OX=9606 GN=NPNT PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q6UXI9-3, Q6UXI9-6, Q6UXI9, H0YAK9 |
| H0YAK9 | 3 | 3.74E-06 | Nephronectin (Fragment) OS=Homo sapiens OX=9606 GN=NPNT PE=1 SV=1 |
| Q6UXI9 | 3 | 3.77E-06 | Nephronectin OS=Homo sapiens OX=9606 GN=NPNT PE=2 SV=3 |
| P61970 | 3 | 2.29E-04 | Nuclear transport factor 2 OS=Homo sapiens OX=9606 GN=NUTF2 PE=1 SV=1 |
| Q9NX46 | 2 | 3.24E-06 | Poly(ADP-ribose) glycohydrolase ARH3 OS=Homo sapiens OX=9606 GN=ADPRHL2 PE=1 SV=1 |
| E5RG43 | 3 | 1.07E-03 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| E5RIF9 | 3 | 1.08E-03 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| P05155 | 3 | 1.20E-05 | Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 PE=1 SV=2 |
| P05155-2 | 3 | 1.34E-05 | Isoform 2 of Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 |
| P05155-3 | 3 | 1.19E-05 | Isoform 3 of Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 |
| H9KV48 | 3 | 1.19E-05 | Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 PE=1 SV=1 |
| E9PGN7 | 3 | 1.10E-05 | Plasma protease C1 inhibitor OS=Homo sapiens OX=9606 GN=SERPING1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P05155-3, P05155, H9KV48, P05155-2 |
| E9PKC6 | 2 | 4.25E-05 | CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=1 |
| F8VWU0 | 2 | 6.71E-06 | Decorin (Fragment) OS=Homo sapiens OX=9606 GN=DCN PE=1 SV=1 |
| P07585-4 | 2 | 6.98E-06 | Isoform D of Decorin OS=Homo sapiens OX=9606 GN=DCN |
| F8VUF6 | 2 | 6.75E-06 | Decorin (Fragment) OS=Homo sapiens OX=9606 GN=DCN PE=1 SV=1 |
| P07585 | 2 | 3.35E-06 | Decorin OS=Homo sapiens OX=9606 GN=DCN PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P07585-2, P07585-3, F8VWU0, F8VUF6, F8VNV6, F8VXZ8, P07585-4, F8VX58, F8VSI3, F8VU58, F8VNW0, P07585-5 |
| F8VXZ8 | 2 | 6.90E-06 | Decorin (Fragment) OS=Homo sapiens OX=9606 GN=DCN PE=1 SV=1 |
| F8VX58 | 2 | 1.01E-05 | Decorin (Fragment) OS=Homo sapiens OX=9606 GN=DCN PE=1 SV=1 |
| Q5VY30 | 2 | 1.67E-05 | Retinol-binding protein OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=2 |
| P02753 | 2 | 1.66E-05 | Retinol-binding protein 4 OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q5VY30 |
| C9J177 | 2 | 1.90E-06 | Protein phosphatase 1 regulatory subunit 7 (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1 |
| Q15435-2 | 2 | 1.73E-06 | Isoform 2 of Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 |
| Q15435-5 | 2 | 2.49E-06 | Isoform 5 of Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 |
| Q15435-4 | 2 | 2.32E-06 | Isoform 4 of Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 |
| P13688-5 | 2 | 4.01E-06 | Isoform 5 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| P31997 | 2 | 5.30E-06 | Carcinoembryonic antigen-related cell adhesion molecule 8 OS=Homo sapiens OX=9606 GN=CEACAM8 PE=1 SV=2 |
| P13688-11 | 2 | 5.02E-06 | Isoform 11 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| P13688-8 | 2 | 3.98E-06 | Isoform 8 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| P06731 | 2 | 2.63E-06 | Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens OX=9606 GN=CEACAM5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A0A024R0K5, P06731-2, P13688, A0A087WYX0, P13688-10, P13688-8, P13688-5, P13688-6, P13688-2, P13688-9, P13688-11, P13688-4, P31997, P13688-3 |
| P13688-4 | 2 | 5.27E-06 | Isoform 4 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| A0A024R0K5 | 2 | 2.63E-06 | Carcinoembryonic antigen-related cell adhesion molecule 5, isoform CRA\_a OS=Homo sapiens OX=9606 GN=CEACAM5 PE=1 SV=1 |
| P13688-2 | 2 | 4.43E-06 | Isoform 2 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| P13688 | 2 | 3.51E-06 | Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 PE=1 SV=2 |
| P06731-2 | 2 | 2.64E-06 | Isoform 2 of Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens OX=9606 GN=CEACAM5 |
| P13688-9 | 2 | 4.63E-06 | Isoform 9 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| P13688-3 | 2 | 5.76E-06 | Isoform 3 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| A0A087WYX0 | 2 | 3.53E-06 | Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens OX=9606 GN=CEACAM5 PE=1 SV=1 |
| P13688-6 | 2 | 4.30E-06 | Isoform 6 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| P13688-10 | 2 | 3.95E-06 | Isoform 10 of Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CEACAM1 |
| P50895 | 2 | 2.83E-06 | Basal cell adhesion molecule OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A087WXM8 |
| A0A087WXM8 | 2 | 3.03E-06 | Basal cell adhesion molecule OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=1 |
| Reverse\_C9J931 | 3 | 2.27E-05 |  |
| Reverse\_Q15382 | 2 | 7.06E-06 | ; Additional IDs concatenated into MaxParsimony group: Reverse\_C9J931 |
| P24666-4 | 2 | 2.50E-05 | Isoform 4 of Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 |
| P24666 | 2 | 1.77E-05 | Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P24666-2, P24666-3, P24666-4, G5E9R5, F2Z2Q9 |
| P24666-3 | 2 | 2.26E-05 | Isoform 3 of Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 |
| G5E9R5 | 2 | 3.50E-05 | Acid phosphatase 1, soluble, isoform CRA\_d OS=Homo sapiens OX=9606 GN=ACP1 PE=1 SV=1 |
| F2Z2Q9 | 2 | 4.00E-05 | Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 PE=1 SV=1 |
| P24666-2 | 2 | 1.77E-05 | Isoform 2 of Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 |
| A0A0C4DGD1 | 3 | 8.17E-06 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| H7C5T9 | 2 | 2.20E-06 | Neuroserpin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINI1 PE=1 SV=1 |
| Q9HB40 | 2 | 1.05E-05 | Retinoid-inducible serine carboxypeptidase OS=Homo sapiens OX=9606 GN=SCPEP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9HB40-2 |
| Q9HB40-2 | 2 | 1.61E-05 | Isoform 2 of Retinoid-inducible serine carboxypeptidase OS=Homo sapiens OX=9606 GN=SCPEP1 |
| O60493-3 | 3 | 1.91E-05 | Isoform 3 of Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 |
| E9PPZ2 | 2 | 2.61E-05 | Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1 |
| E9PJF9 | 2 | 3.47E-05 | Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1 |
| B8ZZU8 | 3 | 6.49E-05 | Elongin-B OS=Homo sapiens OX=9606 GN=ELOB PE=1 SV=1 |
| Q15370 | 3 | 6.22E-05 | Elongin-B OS=Homo sapiens OX=9606 GN=ELOB PE=1 SV=1 |
| Q15370-2 | 3 | 4.56E-05 | Isoform 2 of Elongin-B OS=Homo sapiens OX=9606 GN=ELOB; Additional IDs concatenated into MaxParsimony group: I3L0M9, Q15370, B8ZZU8, A0A0B4J296 |
| I3L0M9 | 3 | 5.24E-05 | Elongin-B (Fragment) OS=Homo sapiens OX=9606 GN=ELOB PE=1 SV=1 |
| H0YGT2 | 2 | 1.55E-05 | Cation-dependent mannose-6-phosphate receptor (Fragment) OS=Homo sapiens OX=9606 GN=M6PR PE=1 SV=1 |
| P25774 | 3 | 2.50E-05 | Cathepsin S OS=Homo sapiens OX=9606 GN=CTSS PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P25774-2, U3KQE7, U3KPS4 |
| P25774-2 | 3 | 2.34E-05 | Isoform 2 of Cathepsin S OS=Homo sapiens OX=9606 GN=CTSS |
| U3KPS4 | 3 | 6.51E-05 | Cathepsin S (Fragment) OS=Homo sapiens OX=9606 GN=CTSS PE=1 SV=1 |
| U3KQE7 | 3 | 5.61E-05 | Cathepsin S (Fragment) OS=Homo sapiens OX=9606 GN=CTSS PE=1 SV=1 |
| G3XAN8 | 2 | 1.12E-05 | Mitochondrial import inner membrane translocase subunit Tim8 B OS=Homo sapiens OX=9606 GN=TIMM8B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9Y5J9 |
| Q9Y5J9 | 2 | 1.32E-05 | Mitochondrial import inner membrane translocase subunit Tim8 B OS=Homo sapiens OX=9606 GN=TIMM8B PE=1 SV=1 |
| O15511 | 3 | 8.95E-05 | Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens OX=9606 GN=ARPC5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: B1ALC0 |
| Q14444-2 | 2 | 2.28E-06 | Isoform 2 of Caprin-1 OS=Homo sapiens OX=9606 GN=CAPRIN1 |
| Q14444 | 2 | 2.23E-06 | Caprin-1 OS=Homo sapiens OX=9606 GN=CAPRIN1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q14444-2, G3V153 |
| G3V153 | 2 | 2.52E-06 | Caprin-1 OS=Homo sapiens OX=9606 GN=CAPRIN1 PE=1 SV=1 |
| Q9Y2Y0-2 | 2 | 6.04E-06 | Isoform 2 of ADP-ribosylation factor-like protein 2-binding protein OS=Homo sapiens OX=9606 GN=ARL2BP |
| H3BU49 | 2 | 7.46E-06 | ADP-ribosylation factor-like protein 2-binding protein OS=Homo sapiens OX=9606 GN=ARL2BP PE=1 SV=1 |
| Q9Y2Y0 | 2 | 5.63E-06 | ADP-ribosylation factor-like protein 2-binding protein OS=Homo sapiens OX=9606 GN=ARL2BP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9Y2Y0-2, H3BU49 |
| Q9Y2Q5 | 2 | 6.30E-06 | Ragulator complex protein LAMTOR2 OS=Homo sapiens OX=9606 GN=LAMTOR2 PE=1 SV=1 |
| Q9Y2Q5-3 | 2 | 8.29E-06 | Isoform 3 of Ragulator complex protein LAMTOR2 OS=Homo sapiens OX=9606 GN=LAMTOR2 |
| Q9Y2Q5-2 | 2 | 5.25E-06 | Isoform 2 of Ragulator complex protein LAMTOR2 OS=Homo sapiens OX=9606 GN=LAMTOR2; Additional IDs concatenated into MaxParsimony group: Q9Y2Q5, Q9Y2Q5-3 |
| Q5R3I4 | 2 | 3.54E-07 | Tetratricopeptide repeat protein 38 OS=Homo sapiens OX=9606 GN=TTC38 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H7C089 |
| H7C089 | 2 | 1.39E-06 | Tetratricopeptide repeat protein 38 (Fragment) OS=Homo sapiens OX=9606 GN=TTC38 PE=1 SV=1 |
| Q8TBX8-2 | 2 | 1.69E-07 | Isoform 2 of Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens OX=9606 GN=PIP4K2C |
| P02462 | 2 | 8.15E-07 | Collagen alpha-1(IV) chain OS=Homo sapiens OX=9606 GN=COL4A1 PE=1 SV=4 |
| O43924 | 2 | 3.09E-06 | Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta OS=Homo sapiens OX=9606 GN=PDE6D PE=1 SV=1 |
| K7EN31 | 2 | 2.48E-06 | Ran-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=8 |
| Q14746-2 | 2 | 9.54E-08 | Isoform 2 of Conserved oligomeric Golgi complex subunit 2 OS=Homo sapiens OX=9606 GN=COG2 |
| B7Z2Y2 | 2 | 1.04E-07 | Conserved oligomeric Golgi complex subunit 2 OS=Homo sapiens OX=9606 GN=COG2 PE=1 SV=1 |
| Q14746 | 2 | 9.53E-08 | Conserved oligomeric Golgi complex subunit 2 OS=Homo sapiens OX=9606 GN=COG2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q14746-2, B7Z2Y2 |
| C9JUK7 | 3 | 8.34E-05 | Leukosialin (Fragment) OS=Homo sapiens OX=9606 GN=SPN PE=1 SV=1 |
| Q9H169-3 | 2 | 1.14E-04 | Isoform 3 of Stathmin-4 OS=Homo sapiens OX=9606 GN=STMN4 |
| Q9H169-2 | 2 | 8.84E-05 | Isoform 2 of Stathmin-4 OS=Homo sapiens OX=9606 GN=STMN4 |
| Q9H169 | 2 | 1.01E-04 | Stathmin-4 OS=Homo sapiens OX=9606 GN=STMN4 PE=2 SV=1 |
| E7EVN3 | 2 | 7.40E-05 | Stathmin-4 OS=Homo sapiens OX=9606 GN=STMN4 PE=1 SV=1 |
| E5RIR6 | 2 | 8.27E-05 | Stathmin-4 OS=Homo sapiens OX=9606 GN=STMN4 PE=1 SV=1 |
| Q9H169-4 | 2 | 9.41E-05 | Isoform 4 of Stathmin-4 OS=Homo sapiens OX=9606 GN=STMN4 |
| H3BNK3 | 2 | 1.22E-04 | Acyl carrier protein (Fragment) OS=Homo sapiens OX=9606 GN=NDUFAB1 PE=1 SV=1 |
| Q5JS37-2 | 2 | 7.42E-06 | Isoform 2 of NHL repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=NHLRC3 |
| C9J973 | 2 | 1.34E-05 | NHL repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=NHLRC3 PE=1 SV=1 |
| Q9Y3P9-3 | 2 | 8.57E-07 | Isoform 3 of Rab GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RABGAP1 |
| B5MCD9 | 2 | 3.67E-06 | Rab GTPase-activating protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=RABGAP1 PE=1 SV=1 |
| Q9Y3P9 | 2 | 3.84E-07 | Rab GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RABGAP1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9Y3P9-3, Q9Y3P9-4, B5MCD9, C9JGR5 |
| C9JGR5 | 2 | 6.22E-06 | Rab GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RABGAP1 PE=1 SV=2 |
| Q9Y3P9-4 | 2 | 1.55E-06 | Isoform 4 of Rab GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RABGAP1 |
| B4DWR3 | 2 | 1.72E-06 | Prefoldin subunit 3 OS=Homo sapiens OX=9606 GN=VBP1 PE=1 SV=1 |
| P61758 | 3 | 2.36E-06 | Prefoldin subunit 3 OS=Homo sapiens OX=9606 GN=VBP1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: B4DWR3 |
| G3V5T7 | 3 | 1.89E-05 | GTPase KRas OS=Homo sapiens OX=9606 GN=KRAS PE=4 SV=1 |
| G3V4K2 | 3 | 3.30E-05 | GTPase KRas OS=Homo sapiens OX=9606 GN=KRAS PE=4 SV=1 |
| Q9Y2R0 | 3 | 3.85E-05 | Cytochrome c oxidase assembly factor 3 homolog, mitochondrial OS=Homo sapiens OX=9606 GN=COA3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: K7EPV0 |
| P55957 | 3 | 1.68E-05 | BH3-interacting domain death agonist OS=Homo sapiens OX=9606 GN=BID PE=1 SV=1 |
| P55957-2 | 3 | 1.36E-05 | Isoform 2 of BH3-interacting domain death agonist OS=Homo sapiens OX=9606 GN=BID; Additional IDs concatenated into MaxParsimony group: P55957 |
| H0YN06 | 3 | 8.00E-05 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| Q8N357 | 3 | 5.22E-06 | Solute carrier family 35 member F6 OS=Homo sapiens OX=9606 GN=SLC35F6 PE=1 SV=1 |
| Q9H7N4 | 2 | 3.00E-07 | Splicing factor, arginine/serine-rich 19 OS=Homo sapiens OX=9606 GN=SCAF1 PE=1 SV=3 |
| P56277 | 2 | 3.07E-05 | Cx9C motif-containing protein 4 OS=Homo sapiens OX=9606 GN=CMC4 PE=1 SV=1 |
| Q3C1V8 | 2 | 9.05E-06 | Brain-specific homeobox protein homolog OS=Homo sapiens OX=9606 GN=BSX PE=2 SV=2 |
| O15173-2 | 3 | 2.44E-04 | Isoform 2 of Membrane-associated progesterone receptor component 2 OS=Homo sapiens OX=9606 GN=PGRMC2 |
| U3KQM0 | 3 | 2.11E-05 | Membrane-associated progesterone receptor component 2 OS=Homo sapiens OX=9606 GN=PGRMC2 PE=1 SV=1 |
| O15173 | 3 | 2.70E-04 | Membrane-associated progesterone receptor component 2 OS=Homo sapiens OX=9606 GN=PGRMC2 PE=1 SV=1 |
| F8W1J0 | 3 | 1.65E-05 | 3'(2'),5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1 |
| F8VZG4 | 3 | 2.06E-05 | 3'(2'),5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1 |
| O95861-4 | 3 | 1.03E-05 | Isoform 4 of 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 |
| Q04637-7 | 3 | 7.41E-07 | Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 |
| Q04637-6 | 3 | 7.41E-07 | Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 |
| E9PJF7 | 2 | 1.98E-05 | Translationally-controlled tumor protein (Fragment) OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1 |
| J3KPG2 | 2 | 2.01E-05 | Translationally-controlled tumor protein OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1 |
| A0A1B0GUS4 | 2 | 1.50E-06 | Ubiquitin-conjugating enzyme E2 L5 OS=Homo sapiens OX=9606 GN=UBE2L5 PE=2 SV=1 |
| P68036-2 | 2 | 1.89E-06 | Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens OX=9606 GN=UBE2L3 |
| P68036 | 2 | 1.50E-06 | Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens OX=9606 GN=UBE2L3 PE=1 SV=1 |
| P68036-3 | 2 | 1.09E-06 | Isoform 3 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens OX=9606 GN=UBE2L3; Additional IDs concatenated into MaxParsimony group: P68036, P68036-2, A0A1B0GUS4 |
| J3KQJ1 | 3 | 5.89E-06 | Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A8MXB9, Q8NBJ7, J3QT17, E9PBT8, Q8NBJ7-5, Q8NBJ7-2 |
| Q8NBJ7-2 | 3 | 8.84E-06 | Isoform 2 of Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 |
| Q8NBJ7 | 3 | 6.26E-06 | Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=2 |
| A8MXB9 | 3 | 6.17E-06 | Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=2 |
| Q9P206-3 | 2 | 5.75E-07 | Isoform 3 of Uncharacterized protein KIAA1522 OS=Homo sapiens OX=9606 GN=KIAA1522 |
| Q9P206 | 2 | 5.81E-07 | Uncharacterized protein KIAA1522 OS=Homo sapiens OX=9606 GN=KIAA1522 PE=1 SV=2 |
| Q9P206-2 | 2 | 5.50E-07 | Isoform 2 of Uncharacterized protein KIAA1522 OS=Homo sapiens OX=9606 GN=KIAA1522; Additional IDs concatenated into MaxParsimony group: Q9P206-3, Q9P206 |
| P02730-2 | 3 | 7.41E-07 | Isoform 2 of Band 3 anion transport protein OS=Homo sapiens OX=9606 GN=SLC4A1 |
| P02730 | 3 | 6.88E-07 | Band 3 anion transport protein OS=Homo sapiens OX=9606 GN=SLC4A1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P02730-2, A0A0A0MS98 |
| A0A0A0MS98 | 3 | 1.15E-06 | Band 3 anion transport protein OS=Homo sapiens OX=9606 GN=SLC4A1 PE=1 SV=1 |
| P07108-6 | 2 | 1.92E-05 | Isoform 6 of Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI |
| Q96HQ2-2 | 3 | 4.01E-05 | Isoform 2 of CDKN2AIP N-terminal-like protein OS=Homo sapiens OX=9606 GN=CDKN2AIPNL |
| Reverse\_A0A1B0GTQ4 | 2 | 1.15E-04 |  |
| Q7Z406-4 | 2 | 6.46E-07 | Isoform 4 of Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 |
| Q7Z406-5 | 2 | 7.78E-07 | Isoform 5 of Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 |
| C9IZN5 | 2 | 5.67E-06 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (Fragment) OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=1 |
| A0A087X1G1 | 2 | 5.22E-06 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=1 |
| H7BYD0 | 2 | 4.71E-06 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (Fragment) OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=1 |
| Q16718 | 2 | 4.55E-06 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q16718-2, H7BYD0, A0A087X1G1, C9IZN5, F8WAS3 |
| Q16718-2 | 2 | 4.55E-06 | Isoform 2 of NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens OX=9606 GN=NDUFA5 |
| F8WAS3 | 2 | 7.53E-06 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=1 |
| Q9UKY7 | 2 | 2.01E-05 | Protein CDV3 homolog OS=Homo sapiens OX=9606 GN=CDV3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UKY7-2, H0Y8K3 |
| Q9UKY7-2 | 2 | 2.44E-05 | Isoform 2 of Protein CDV3 homolog OS=Homo sapiens OX=9606 GN=CDV3 |
| E9PNP3 | 2 | 2.06E-05 | Mth938 domain-containing protein OS=Homo sapiens OX=9606 GN=AAMDC PE=1 SV=1 |
| E9PR47 | 2 | 1.73E-05 | Mth938 domain-containing protein OS=Homo sapiens OX=9606 GN=AAMDC PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PNP3, Q9H7C9, E9PIQ4 |
| Q9H7C9 | 2 | 2.38E-05 | Mth938 domain-containing protein OS=Homo sapiens OX=9606 GN=AAMDC PE=1 SV=1 |
| E9PIQ4 | 2 | 3.23E-05 | Mth938 domain-containing protein OS=Homo sapiens OX=9606 GN=AAMDC PE=1 SV=1 |
| P25787 | 2 | 6.87E-07 | Proteasome subunit alpha type-2 OS=Homo sapiens OX=9606 GN=PSMA2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A024RA52, H3BT36 |
| A0A024RA52 | 2 | 6.87E-07 | Proteasome subunit alpha type OS=Homo sapiens OX=9606 GN=PSMA2 PE=1 SV=1 |
| D6RFM2 | 3 | 3.59E-05 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=1 |
| Q6UWV6 | 2 | 4.47E-07 | Ectonucleotide pyrophosphatase/phosphodiesterase family member 7 OS=Homo sapiens OX=9606 GN=ENPP7 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9Y6X5 |
| Q9Y6X5 | 2 | 4.52E-07 | Bis(5'-adenosyl)-triphosphatase ENPP4 OS=Homo sapiens OX=9606 GN=ENPP4 PE=1 SV=3 |
| H3BPG0 | 2 | 1.42E-05 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=COX4I1 PE=1 SV=1 |
| O75381-2 | 2 | 4.22E-06 | Isoform 2 of Peroxisomal membrane protein PEX14 OS=Homo sapiens OX=9606 GN=PEX14 |
| O75381 | 2 | 3.73E-06 | Peroxisomal membrane protein PEX14 OS=Homo sapiens OX=9606 GN=PEX14 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O75381-2 |
| F8VR34 | 2 | 3.22E-06 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8VVB5 | 2 | 4.97E-06 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| P12724 | 3 | 2.88E-06 | Eosinophil cationic protein OS=Homo sapiens OX=9606 GN=RNASE3 PE=1 SV=2 |
| Q96FQ6 | 3 | 9.51E-06 | Protein S100-A16 OS=Homo sapiens OX=9606 GN=S100A16 PE=1 SV=1 |
| P04040 | 3 | 1.97E-05 | Catalase OS=Homo sapiens OX=9606 GN=CAT PE=1 SV=3 |
| P04003 | 2 | 6.30E-06 | C4b-binding protein alpha chain OS=Homo sapiens OX=9606 GN=C4BPA PE=1 SV=2 |
| Reverse\_Q5M9N0 | 2 | 8.54E-07 |  |
| P60880-2 | 2 | 6.84E-06 | Isoform 2 of Synaptosomal-associated protein 25 OS=Homo sapiens OX=9606 GN=SNAP25 |
| P11166 | 2 | 2.43E-06 | Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens OX=9606 GN=SLC2A1 PE=1 SV=2 |
| Q7Z7N9 | 2 | 3.30E-06 | Transmembrane protein 179B OS=Homo sapiens OX=9606 GN=TMEM179B PE=1 SV=1 |
| P08185 | 3 | 3.77E-06 | Corticosteroid-binding globulin OS=Homo sapiens OX=9606 GN=SERPINA6 PE=1 SV=1 |
| P06702 | 3 | 2.64E-05 | Protein S100-A9 OS=Homo sapiens OX=9606 GN=S100A9 PE=1 SV=1 |
| A0A0J9YXE1 | 3 | 1.91E-05 | Protein canopy homolog 4 (Fragment) OS=Homo sapiens OX=9606 GN=CNPY4 PE=1 SV=1 |
| P40855-5 | 2 | 6.94E-07 | Isoform 5 of Peroxisomal biogenesis factor 19 OS=Homo sapiens OX=9606 GN=PEX19 |
| Q5QNY5 | 2 | 7.71E-07 | Peroxisomal biogenesis factor 19 (Fragment) OS=Homo sapiens OX=9606 GN=PEX19 PE=1 SV=1 |
| E9PS71 | 2 | 1.09E-06 | Peroxisomal biogenesis factor 19 OS=Homo sapiens OX=9606 GN=PEX19 PE=1 SV=1 |
| Q96M27-3 | 2 | 4.40E-06 | Isoform 3 of Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 |
| Q96M27-4 | 2 | 6.54E-06 | Isoform 4 of Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 |
| Q96M27-5 | 2 | 4.86E-06 | Isoform 5 of Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 |
| Q96M27-2 | 2 | 4.38E-06 | Isoform 2 of Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1; Additional IDs concatenated into MaxParsimony group: Q96M27-3, Q96M27, Q96M27-5, Q96M27-4 |
| Q96M27 | 2 | 4.57E-06 | Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 PE=1 SV=1 |
| Q92747 | 3 | 1.78E-05 | Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens OX=9606 GN=ARPC1A PE=2 SV=2 |
| O14556 | 2 | 6.19E-05 | Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens OX=9606 GN=GAPDHS PE=1 SV=2 |
| E5RID5 | 2 | 2.18E-05 | Carbonic anhydrase 2 OS=Homo sapiens OX=9606 GN=CA2 PE=1 SV=1 |
| E5RK37 | 2 | 2.09E-05 | Carbonic anhydrase 2 OS=Homo sapiens OX=9606 GN=CA2 PE=1 SV=1 |
| K7EKX1 | 3 | 2.09E-05 | Glucosidase 2 subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=1 |
| K7EJ70 | 3 | 2.03E-05 | Glucosidase 2 subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=1 |
| D3YTI2 | 2 | 3.30E-05 | Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 PE=1 SV=1 |
| E5RGU8 | 3 | 1.20E-03 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| E5RFL2 | 3 | 1.00E-03 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| E5RII2 | 3 | 9.73E-04 | Carbonic anhydrase 1 OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| K7EJH8 | 3 | 5.91E-06 | Alpha-actinin-4 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=1 |
| G3V2W4 | 3 | 4.52E-06 | Alpha-actinin-1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1 |
| D6RC54 | 3 | 5.05E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| D6RAA8 | 2 | 3.35E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| H0Y7L5 | 3 | 1.24E-05 | Apolipoprotein E (Fragment) OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=2 |
| E9PEV4 | 3 | 1.55E-05 | Apolipoprotein E (Fragment) OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1 |
| E7ERP7 | 3 | 1.52E-05 | Apolipoprotein E (Fragment) OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1 |
| P09668 | 3 | 4.44E-06 | Pro-cathepsin H OS=Homo sapiens OX=9606 GN=CTSH PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A087X0D5, E9PKT6 |
| E9PKT6 | 3 | 8.31E-06 | Pro-cathepsin H (Fragment) OS=Homo sapiens OX=9606 GN=CTSH PE=1 SV=1 |
| A0A087X0D5 | 3 | 4.61E-06 | Pro-cathepsin H OS=Homo sapiens OX=9606 GN=CTSH PE=1 SV=1 |
| Q8NBJ7-3 | 3 | 5.56E-06 | Isoform 3 of Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 |
| H7C3B2 | 3 | 6.19E-06 | Inactive C-alpha-formylglycine-generating enzyme 2 (Fragment) OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=1 |
| C9JL30 | 3 | 6.43E-06 | Inactive C-alpha-formylglycine-generating enzyme 2 (Fragment) OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=9 |
| C9J660 | 3 | 5.35E-06 | Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=1 |
| F8WA42 | 3 | 5.26E-06 | Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9J660, Q8NBJ7-3, J3KQJ1, A8MXB9, H7C3B2, Q8NBJ7, C9JL30, Q8NBJ7-2 |
| J3KRC4 | 3 | 1.24E-06 | 5'(3')-deoxyribonucleotidase, cytosolic type OS=Homo sapiens OX=9606 GN=NT5C PE=1 SV=1 |
| Q8TCD5-2 | 3 | 1.93E-06 | Isoform 2 of 5'(3')-deoxyribonucleotidase, cytosolic type OS=Homo sapiens OX=9606 GN=NT5C |
| Q8TCD5 | 3 | 1.12E-06 | 5'(3')-deoxyribonucleotidase, cytosolic type OS=Homo sapiens OX=9606 GN=NT5C PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: J3KRC4, Q8TCD5-2 |
| H3BQS5 | 3 | 5.34E-05 | Dipeptidase (Fragment) OS=Homo sapiens OX=9606 GN=DPEP1 PE=1 SV=1 |
| H3BP43 | 3 | 5.14E-05 | Dipeptidase (Fragment) OS=Homo sapiens OX=9606 GN=DPEP1 PE=1 SV=1 |
| E9PL10 | 3 | 5.01E-05 | Transcription factor BTF3 OS=Homo sapiens OX=9606 GN=BTF3L4 PE=1 SV=1 |
| E9PS65 | 3 | 6.69E-05 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| E9PM13 | 3 | 6.65E-05 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=8 |
| F8VU34 | 2 | 3.31E-06 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8VWQ5 | 2 | 3.57E-06 | Citrate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8W0J2 | 2 | 6.27E-06 | Citrate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| Reverse\_H7C112 | 2 | 7.39E-06 |  |
| Reverse\_Q6PCT2-3 | 2 | 6.51E-06 |  |
| Reverse\_H3BPZ0 | 2 | 6.42E-06 |  |
| Reverse\_Q6PCT2-2 | 2 | 6.65E-06 |  |
| Q99576 | 3 | 8.99E-05 | TSC22 domain family protein 3 OS=Homo sapiens OX=9606 GN=TSC22D3 PE=1 SV=2 |
| Q99576-3 | 3 | 6.03E-05 | Isoform 2 of TSC22 domain family protein 3 OS=Homo sapiens OX=9606 GN=TSC22D3 |
| Q99576-4 | 3 | 9.88E-05 | Isoform 3 of TSC22 domain family protein 3 OS=Homo sapiens OX=9606 GN=TSC22D3 |
| Q5JRJ0 | 3 | 1.10E-04 | TSC22 domain family protein 3 OS=Homo sapiens OX=9606 GN=TSC22D3 PE=1 SV=1 |
| E7EWD5 | 3 | 9.13E-05 | TSC22 domain family protein 3 OS=Homo sapiens OX=9606 GN=TSC22D3 PE=1 SV=1 |
| Q9UIL1 | 3 | 4.32E-06 | Short coiled-coil protein OS=Homo sapiens OX=9606 GN=SCOC PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UIL1-2, Q9UIL1-3, A0A0C4DGB0 |
| A0A0C4DGB0 | 3 | 8.38E-06 | Short coiled-coil protein OS=Homo sapiens OX=9606 GN=SCOC PE=1 SV=1 |
| Q9UIL1-2 | 3 | 5.63E-06 | Isoform 2 of Short coiled-coil protein OS=Homo sapiens OX=9606 GN=SCOC |
| Q9UIL1-3 | 3 | 5.68E-06 | Isoform 3 of Short coiled-coil protein OS=Homo sapiens OX=9606 GN=SCOC |
| P01593 | 3 | 9.75E-06 | Immunoglobulin kappa variable 1D-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P01594, A0A2Q2TTZ9 |
| P01594 | 3 | 9.75E-06 | Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1-33 PE=1 SV=2 |
| A0A2Q2TTZ9 | 3 | 1.06E-05 | Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1D-33 PE=1 SV=1 |
| Q9P1F3 | 2 | 4.44E-05 | Costars family protein ABRACL OS=Homo sapiens OX=9606 GN=ABRACL PE=1 SV=1 |
| Reverse\_E9PNU7 | 2 | 1.06E-05 |  |
| Reverse\_Q15743 | 2 | 9.84E-06 | ; Additional IDs concatenated into MaxParsimony group: Reverse\_E9PNU7, Q9P1F3 |
| H3BRV9 | 3 | 9.35E-05 | Nuclear transport factor 2 (Fragment) OS=Homo sapiens OX=9606 GN=NUTF2 PE=1 SV=1 |
| Q9H008 | 3 | 5.46E-06 | Phospholysine phosphohistidine inorganic pyrophosphate phosphatase OS=Homo sapiens OX=9606 GN=LHPP PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5T1Z0, Q9H008-2 |
| Q5T1Z0 | 3 | 6.96E-06 | Phospholysine phosphohistidine inorganic pyrophosphate phosphatase OS=Homo sapiens OX=9606 GN=LHPP PE=1 SV=1 |
| Q9H008-2 | 3 | 7.02E-06 | Isoform 2 of Phospholysine phosphohistidine inorganic pyrophosphate phosphatase OS=Homo sapiens OX=9606 GN=LHPP |
| O15511-2 | 3 | 8.35E-05 | Isoform 2 of Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens OX=9606 GN=ARPC5; Additional IDs concatenated into MaxParsimony group: O15511 |
| E9PBW4 | 3 | 0.00030899 | Hemoglobin subunit gamma-2 OS=Homo sapiens OX=9606 GN=HBG2 PE=1 SV=2 |
| A0A0J9YYA3 | 3 | 2.25E-04 | Hemoglobin subunit gamma-1 OS=Homo sapiens OX=9606 GN=HBG2 PE=1 SV=1 |
| Q96PQ5 | 2 | 1.87E-05 | Putative protein phosphatase inhibitor 2-like protein 1 OS=Homo sapiens OX=9606 GN=PPP1R2P1 PE=5 SV=1 |
| P37840 | 3 | 5.64E-05 | Alpha-synuclein OS=Homo sapiens OX=9606 GN=SNCA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E7EPV7, P37840-2, P37840-3, H6UYS7, D6RA31 |
| P37840-3 | 3 | 4.86E-05 | Isoform 2-5 of Alpha-synuclein OS=Homo sapiens OX=9606 GN=SNCA |
| E7EPV7 | 3 | 6.87E-05 | Alpha-synuclein OS=Homo sapiens OX=9606 GN=SNCA PE=1 SV=1 |
| P37840-2 | 3 | 7.05E-05 | Isoform 2-4 of Alpha-synuclein OS=Homo sapiens OX=9606 GN=SNCA |
| H6UYS7 | 3 | 6.24E-05 | Alpha-synuclein OS=Homo sapiens OX=9606 GN=SNCA PE=1 SV=1 |
| contaminant\_KERATIN16 | 2 | 4.78E-06 |  |
| P19013 | 2 | 4.78E-06 | Keratin, type II cytoskeletal 4 OS=Homo sapiens OX=9606 GN=KRT4 PE=1 SV=4 |
| A0A1B0GV01 | 3 | 6.28E-04 | Cathepsin D (Fragment) OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| P62851 | 2 | 1.66E-05 | 40S ribosomal protein S25 OS=Homo sapiens OX=9606 GN=RPS25 PE=1 SV=1 |
| Q9NZD4 | 2 | 1.29E-05 | Alpha-hemoglobin-stabilizing protein OS=Homo sapiens OX=9606 GN=AHSP PE=1 SV=1 |
| O95295 | 2 | 4.73E-06 | SNARE-associated protein Snapin OS=Homo sapiens OX=9606 GN=SNAPIN PE=1 SV=1 |
| O75629 | 2 | 1.96E-06 | Protein CREG1 OS=Homo sapiens OX=9606 GN=CREG1 PE=1 SV=1 |
| P06280 | 2 | 2.97E-06 | Alpha-galactosidase A OS=Homo sapiens OX=9606 GN=GLA PE=1 SV=1 |
| Q14696 | 2 | 5.56E-06 | LRP chaperone MESD OS=Homo sapiens OX=9606 GN=MESD PE=1 SV=2 |
| E9PR95 | 2 | 1.59E-05 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=8 |
| E9PIP1 | 2 | 7.06E-06 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| E9PLC5 | 2 | 1.21E-05 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| A0A1W2PRB8 | 2 | 5.42E-07 | Mediator of RNA polymerase II transcription subunit 17 OS=Homo sapiens OX=9606 GN=MED17 PE=3 SV=1 |
| E9PSC3 | 2 | 1.27E-05 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=8 |
| E9PLB3 | 2 | 8.10E-06 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| E9PQS1 | 2 | 5.59E-06 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| E9PPB5 | 2 | 6.53E-06 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| Q8WUW1-2 | 2 | 2.56E-05 | Isoform 2 of Protein BRICK1 OS=Homo sapiens OX=9606 GN=BRK1; Additional IDs concatenated into MaxParsimony group: Q8WUW1 |
| Q8WUW1 | 2 | 3.62E-05 | Protein BRICK1 OS=Homo sapiens OX=9606 GN=BRK1 PE=1 SV=1 |
| Reverse\_P16050 | 2 | 2.02E-05 |  |
| Reverse\_P16050-2 | 2 | 2.14E-05 |  |
| K7ENU8 | 2 | 4.95E-06 | Basal cell adhesion molecule (Fragment) OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=2 |
| Reverse\_Q13439-3 | 2 | 1.66E-07 |  |
| Reverse\_Q13439 | 2 | 1.66E-07 |  |
| Reverse\_Q13439-5 | 2 | 1.65E-07 | ; Additional IDs concatenated into MaxParsimony group: Reverse\_Q13439, Reverse\_Q13439-4, Reverse\_Q13439-3, Reverse\_H0Y6I0, Reverse\_C9JHJ5 |
| Reverse\_Q13439-4 | 2 | 1.66E-07 |  |
| Reverse\_H0Y6I0 | 2 | 1.76E-07 |  |
| Reverse\_C9JHJ5 | 2 | 6.33E-07 |  |
| Q6UXI9-4 | 2 | 2.95E-06 | Isoform 4 of Nephronectin OS=Homo sapiens OX=9606 GN=NPNT |
| Q6UXI9-5 | 2 | 3.12E-06 | Isoform 5 of Nephronectin OS=Homo sapiens OX=9606 GN=NPNT |
| Q6UXI9-2 | 2 | 3.28E-06 | Isoform 2 of Nephronectin OS=Homo sapiens OX=9606 GN=NPNT |
| C9J7B5 | 2 | 6.81E-06 | Eukaryotic translation initiation factor 5A OS=Homo sapiens OX=9606 GN=EIF5A2 PE=1 SV=1 |
| Q9GZV4 | 2 | 4.85E-06 | Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens OX=9606 GN=EIF5A2 PE=1 SV=3 |
| F8WCJ1 | 2 | 7.07E-06 | Eukaryotic translation initiation factor 5A OS=Homo sapiens OX=9606 GN=EIF5A2 PE=1 SV=1 |
| C9J4W5 | 2 | 6.45E-06 | Eukaryotic translation initiation factor 5A (Fragment) OS=Homo sapiens OX=9606 GN=EIF5A2 PE=1 SV=1 |
| E9PS44 | 2 | 1.69E-05 | Interferon-induced transmembrane protein 3 OS=Homo sapiens OX=9606 GN=IFITM3 PE=1 SV=1 |
| H7BYV1 | 2 | 1.82E-05 | Interferon-induced transmembrane protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=IFITM2 PE=4 SV=1 |
| Q01629 | 2 | 1.02E-05 | Interferon-induced transmembrane protein 2 OS=Homo sapiens OX=9606 GN=IFITM2 PE=1 SV=2 |
| Q01628 | 2 | 1.43E-05 | Interferon-induced transmembrane protein 3 OS=Homo sapiens OX=9606 GN=IFITM3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q01629, P13164, E9PS44, E9PQN9, H7BYV1 |
| P13164 | 2 | 1.08E-05 | Interferon-induced transmembrane protein 1 OS=Homo sapiens OX=9606 GN=IFITM1 PE=1 SV=3 |
| E9PQN9 | 2 | 1.20E-05 | Interferon-induced transmembrane protein 2 OS=Homo sapiens OX=9606 GN=IFITM2 PE=1 SV=1 |
| Q5JTJ3-3 | 2 | 2.92E-05 | Isoform 3 of Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens OX=9606 GN=COA6 |
| Q5JTJ3 | 2 | 1.85E-05 | Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens OX=9606 GN=COA6 PE=1 SV=1 |
| X6R5Z6 | 2 | 1.49E-05 | Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens OX=9606 GN=COA6 PE=1 SV=1 |
| Q5JTJ3-2 | 2 | 1.48E-05 | Isoform 2 of Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens OX=9606 GN=COA6; Additional IDs concatenated into MaxParsimony group: X6R5Z6, Q5JTJ3, Q5JTJ3-3 |
| P78310 | 2 | 2.30E-06 | Coxsackievirus and adenovirus receptor OS=Homo sapiens OX=9606 GN=CXADR PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P78310-7 |
| P78310-7 | 2 | 2.59E-06 | Isoform 7 of Coxsackievirus and adenovirus receptor OS=Homo sapiens OX=9606 GN=CXADR |
| B1AH72 | 2 | 4.67E-06 | Parvalbumin alpha OS=Homo sapiens OX=9606 GN=PVALB PE=1 SV=1 |
| H0Y3U0 | 2 | 3.44E-06 | Parvalbumin alpha (Fragment) OS=Homo sapiens OX=9606 GN=PVALB PE=1 SV=1 |
| B8ZZ19 | 2 | 3.61E-06 | Parvalbumin alpha (Fragment) OS=Homo sapiens OX=9606 GN=PVALB PE=1 SV=1 |
| P20472 | 2 | 3.31E-06 | Parvalbumin alpha OS=Homo sapiens OX=9606 GN=PVALB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H0Y3U0, B8ZZ19, B1AH72 |
| C9JCK5 | 2 | 9.80E-07 | Proteasome endopeptidase complex OS=Homo sapiens OX=9606 GN=PSMA2 PE=1 SV=1 |
| K7ENX5 | 2 | 1.44E-05 | Alpha-N-acetylglucosaminidase (Fragment) OS=Homo sapiens OX=9606 GN=NAGLU PE=1 SV=1 |
| B7ZBH1 | 2 | 3.83E-05 | Eukaryotic translation initiation factor 6 (Fragment) OS=Homo sapiens OX=9606 GN=EIF6 PE=1 SV=1 |

1&2 – List of the proteins

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Replicate Count** | **Total Signal** | **Description** |
| Q3SXM5 | 6 | 0.000138877 | Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens OX=9606 GN=HSDL1 PE=1 SV=3 |
| Q5BJH7-4 | 4 | 2.71E-05 | Isoform 4 of Protein YIF1B OS=Homo sapiens OX=9606 GN=YIF1B |
| Q5BJH7-5 | 4 | 2.69E-05 | Isoform 5 of Protein YIF1B OS=Homo sapiens OX=9606 GN=YIF1B |
| Q5BJH7-2 | 4 | 2.79E-05 | Isoform 2 of Protein YIF1B OS=Homo sapiens OX=9606 GN=YIF1B |
| Q5BJH7-3 | 4 | 2.54E-05 | Isoform 3 of Protein YIF1B OS=Homo sapiens OX=9606 GN=YIF1B |
| Q5BJH7 | 4 | 2.51E-05 | Protein YIF1B OS=Homo sapiens OX=9606 GN=YIF1B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5BJH7-3, Q5BJH7-6, Q5BJH7-5, Q5BJH7-4, Q5BJH7-2, K7EPQ7, K7ERY2, K7ERQ0, K7EJQ6 |
| Q5BJH7-6 | 4 | 2.64E-05 | Isoform 6 of Protein YIF1B OS=Homo sapiens OX=9606 GN=YIF1B |
| K7EPQ7 | 4 | 3.18E-05 | Protein YIF1B OS=Homo sapiens OX=9606 GN=YIF1B PE=1 SV=1 |
| K7ERQ0 | 4 | 4.11E-05 | Protein YIF1B (Fragment) OS=Homo sapiens OX=9606 GN=YIF1B PE=1 SV=1 |
| K7EJQ6 | 4 | 7.66E-05 | Protein YIF1B (Fragment) OS=Homo sapiens OX=9606 GN=YIF1B PE=1 SV=1 |
| K7ERY2 | 4 | 3.42E-05 | Protein YIF1B (Fragment) OS=Homo sapiens OX=9606 GN=YIF1B PE=1 SV=1 |
| Q5STU3 | 5 | 5.45E-05 | Spliceosome RNA helicase DDX39B OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=2 |
| A0A140T9X3 | 5 | 7.13E-05 | Spliceosome RNA helicase DDX39B (Fragment) OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1 |
| P61160-2 | 5 | 6.92E-05 | Isoform 2 of Actin-related protein 2 OS=Homo sapiens OX=9606 GN=ACTR2; Additional IDs concatenated into MaxParsimony group: P61160 |
| P61160 | 5 | 7.00E-05 | Actin-related protein 2 OS=Homo sapiens OX=9606 GN=ACTR2 PE=1 SV=1 |
| O43390-4 | 5 | 7.17E-05 | Isoform 4 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR |
| B7Z645 | 5 | 5.80E-05 | Synaptotagmin binding, cytoplasmic RNA interacting protein, isoform CRA\_b OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=1 |
| U3KQ84 | 6 | 0.000195298 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit (Fragment) OS=Homo sapiens OX=9606 GN=DDOST PE=1 SV=8 |
| A0A0C4DGS1 | 6 | 6.94E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens OX=9606 GN=DDOST PE=1 SV=1 |
| P39656 | 6 | 6.68E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens OX=9606 GN=DDOST PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A0C4DGS1, P39656-3, P39656-2, U3KQ84 |
| P39656-3 | 6 | 6.82E-05 | Isoform 3 of Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens OX=9606 GN=DDOST |
| P39656-2 | 6 | 7.13E-05 | Isoform 2 of Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens OX=9606 GN=DDOST |
| F2Z2S8 | 6 | 0.000371932 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| E9PJH4 | 6 | 0.0003705 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| E9PK82 | 6 | 0.000332871 | 40S ribosomal protein S3 (Fragment) OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| H0YF32 | 6 | 0.000350123 | 40S ribosomal protein S3 (Fragment) OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| H0YCJ7 | 6 | 0.000322341 | 40S ribosomal protein S3 (Fragment) OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| E9PQ96 | 6 | 0.000468215 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| O14828 | 4 | 3.36E-05 | Secretory carrier-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=SCAMP3 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O14828-2 |
| H3BP76 | 6 | 0.001018229 | Major vault protein (Fragment) OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=1 |
| P30711-2 | 6 | 0.000123408 | Isoform 2 of Glutathione S-transferase theta-1 OS=Homo sapiens OX=9606 GN=GSTT1 |
| A0A0G2JRQ5 | 6 | 7.30E-05 | Glutathione S-transferase theta-1 OS=Homo sapiens OX=9606 GN=GSTT1 PE=1 SV=1 |
| P30711 | 6 | 6.87E-05 | Glutathione S-transferase theta-1 OS=Homo sapiens OX=9606 GN=GSTT1 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A0G2JRQ5, P30711-2 |
| Q53TN4 | 6 | 7.99E-05 | Cytochrome b reductase 1 OS=Homo sapiens OX=9606 GN=CYBRD1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q53TN4-3 |
| Q53TN4-3 | 6 | 0.000100266 | Isoform 3 of Cytochrome b reductase 1 OS=Homo sapiens OX=9606 GN=CYBRD1 |
| A0A2R8YDT8 | 6 | 6.05E-05 | Peroxisomal multifunctional enzyme type 2 (Fragment) OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=1 |
| E7ER27 | 6 | 2.01E-05 | Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=3 |
| A0A2R8YF45 | 6 | 5.84E-05 | Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=1 |
| A0A2R8YEG2 | 6 | 0.000128964 | Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=1 |
| A0A2R8YD50 | 6 | 1.41E-05 | Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=1 |
| P51659 | 6 | 1.36E-05 | Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A0A2R8YD50, E7ER27, A0A2R8YF45, A0A2R8YDT8, A0A2R8YEG2 |
| E9PS78 | 6 | 0.155397747 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| A0A1P0AYU5 | 5 | 3.06E-05 | Sideroflexin OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0A0MS41, Q9BWM7, S4R3N9 |
| S4R3N9 | 5 | 5.62E-05 | Sideroflexin-3 OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=1 |
| A0A0A0MS41 | 5 | 3.10E-05 | Sideroflexin OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=1 |
| Q9BWM7 | 5 | 3.10E-05 | Sideroflexin-3 OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=3 |
| Q5JRS2 | 5 | 0.000119604 | Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=1 |
| Q5JRS1 | 5 | 0.000161777 | Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=1 |
| Q5JRS3 | 5 | 0.000143525 | Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=1 |
| Q53QV2 | 5 | 0.000145248 | Protein LBH OS=Homo sapiens OX=9606 GN=LBH PE=1 SV=1 |
| B5MCP4 | 5 | 0.000137397 | Protein LBH OS=Homo sapiens OX=9606 GN=LBH PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q53QV2, B5MBX5 |
| B5MBX5 | 5 | 0.000173308 | Protein LBH OS=Homo sapiens OX=9606 GN=LBH PE=1 SV=1 |

1&3 – List of the proteins

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Replicate Count** | **Total Signal** | **Description** |
| C9J7U9 | 5 | 8.12E-05 | Secernin-1 (Fragment) OS=Homo sapiens OX=9606 GN=SCRN1 PE=1 SV=1 |
| C9K052 | 5 | 4.67E-05 | Secernin-1 (Fragment) OS=Homo sapiens OX=9606 GN=SCRN1 PE=1 SV=1 |
| B8ZZP4 | 5 | 8.18E-05 | Secernin-1 OS=Homo sapiens OX=9606 GN=SCRN1 PE=1 SV=1 |
| P98161-3 | 4 | 2.22E-06 | Isoform 3 of Polycystin-1 OS=Homo sapiens OX=9606 GN=PKD1 |
| H3BV77 | 4 | 1.57E-05 | Polycystin-1 (Fragment) OS=Homo sapiens OX=9606 GN=PKD1 PE=1 SV=1 |
| P98161-2 | 4 | 2.23E-06 | Isoform 2 of Polycystin-1 OS=Homo sapiens OX=9606 GN=PKD1 |
| H3BTE0 | 4 | 8.52E-06 | Polycystin-1 (Fragment) OS=Homo sapiens OX=9606 GN=PKD1 PE=1 SV=1 |
| P98161 | 4 | 2.22E-06 | Polycystin-1 OS=Homo sapiens OX=9606 GN=PKD1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P98161-3, P98161-2, H3BTE0, H3BV77 |
| P13646-3 | 6 | 0.000694148 | Isoform 3 of Keratin, type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 |
| K7EMD9 | 6 | 0.001766923 | Keratin, type I cytoskeletal 13 (Fragment) OS=Homo sapiens OX=9606 GN=KRT13 PE=1 SV=1 |
| contaminant\_KERATIN04 | 5 | 0.000100538 |  |
| K7ERE3 | 6 | 0.000702512 | Keratin, type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 PE=1 SV=1 |
| Q2M2I5 | 6 | 0.000541937 | Keratin, type I cytoskeletal 24 OS=Homo sapiens OX=9606 GN=KRT24 PE=1 SV=1 |
| P13646 | 6 | 0.000636555 | Keratin, type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 PE=1 SV=4 |
| P13646-2 | 6 | 0.000821246 | Isoform 2 of Keratin, type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 |
| Q01546 | 6 | 0.00013504 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens OX=9606 GN=KRT76 PE=1 SV=2 |
| H0YID6 | 5 | 0.000563851 | Keratin, type II cytoskeletal 79 (Fragment) OS=Homo sapiens OX=9606 GN=KRT79 PE=1 SV=1 |
| contaminant\_KERATIN14 | 5 | 0.00010517 |  |
| P12035 | 5 | 0.000106844 | Keratin, type II cytoskeletal 3 OS=Homo sapiens OX=9606 GN=KRT3 PE=1 SV=3 |
| contaminant\_KERATIN15 | 5 | 0.000106675 |  |
| F8W0C6 | 5 | 0.000233542 | Keratin, type II cytoskeletal 5 (Fragment) OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=8 |

2&3 – List of the proteins

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Replicate Count** | **Total Signal** | **Description** |
| P62854 | 6 | 0.000102958 | 40S ribosomal protein S26 OS=Homo sapiens OX=9606 GN=RPS26 PE=1 SV=3 |
| Q9C005 | 6 | 0.000286784 | Protein dpy-30 homolog OS=Homo sapiens OX=9606 GN=DPY30 PE=1 SV=1 |
| Q8WXC6 | 6 | 0.000227804 | COP9 signalosome complex subunit 9 OS=Homo sapiens OX=9606 GN=COPS9 PE=1 SV=3 |
| F8WCH0 | 6 | 0.044033171 | Actin, gamma-enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=1 |
| S4R457 | 5 | 0.000506928 | Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1 |
| A0A0J9YXB8 | 6 | 0.015340757 | Prosaposin (Fragment) OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=1 |
| V9GZ17 | 6 | 0.000124891 | Tubulin alpha-8 chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA8 PE=1 SV=1 |
| H0YHX9 | 6 | 0.000193552 | Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 |
| E9PAV3 | 6 | 2.18E-05 | Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PAV3-2, Q13765, H0YHX9, F8W0W4, F8VZJ2 |
| F8VZJ2 | 6 | 0.000303137 | Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 |
| E9PAV3-2 | 6 | 4.89E-05 | Isoform skNAC-2 of Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens OX=9606 GN=NACA |
| F8W0W4 | 6 | 0.000208215 | Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 |
| Q13765 | 6 | 0.000191752 | Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 |
| P26373 | 6 | 0.00013637 | 60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RPL13 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P26373-2 |
| P26373-2 | 6 | 0.00011543 | Isoform 2 of 60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RPL13 |
| E5RIW3 | 6 | 0.002255111 | Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=1 |
| O75347-2 | 6 | 0.000910899 | Isoform 2 of Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA |
| E5RHG6 | 6 | 0.001208794 | Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: O75347-2, E5RJD8, O75347, E5RIW3 |
| O75347 | 6 | 0.001753975 | Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=3 |
| E5RJD8 | 6 | 0.001591843 | Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=1 |
| Q9Y639-5 | 6 | 3.55E-05 | Isoform 5 of Neuroplastin OS=Homo sapiens OX=9606 GN=NPTN |
| Q9Y639 | 6 | 3.51E-05 | Neuroplastin OS=Homo sapiens OX=9606 GN=NPTN PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9Y639-5, Q9Y639-4, Q9UFM8, Q9Y639-1, Q9Y639-3, H3BQ94 |
| Q9UFM8 | 6 | 4.54E-05 | Neuroplastin (Fragment) OS=Homo sapiens OX=9606 GN=NPTN PE=1 SV=2 |
| Q9Y639-1 | 6 | 4.96E-05 | Isoform 1 of Neuroplastin OS=Homo sapiens OX=9606 GN=NPTN |
| Q9Y639-4 | 6 | 4.15E-05 | Isoform 4 of Neuroplastin OS=Homo sapiens OX=9606 GN=NPTN |
| H3BQ94 | 6 | 9.20E-05 | Neuroplastin (Fragment) OS=Homo sapiens OX=9606 GN=NPTN PE=1 SV=1 |
| Q9Y639-3 | 6 | 5.03E-05 | Isoform 3 of Neuroplastin OS=Homo sapiens OX=9606 GN=NPTN |
| Q96A08 | 6 | 0.005229379 | Histone H2B type 1-A OS=Homo sapiens OX=9606 GN=HIST1H2BA PE=1 SV=3 |
| O95741-2 | 6 | 1.80E-05 | Isoform 2 of Copine-6 OS=Homo sapiens OX=9606 GN=CPNE6; Additional IDs concatenated into MaxParsimony group: Q96A23-2, Q96A23, O95741 |
| Q96A23 | 6 | 1.34E-05 | Copine-4 OS=Homo sapiens OX=9606 GN=CPNE4 PE=1 SV=1 |
| O95741 | 6 | 1.98E-05 | Copine-6 OS=Homo sapiens OX=9606 GN=CPNE6 PE=1 SV=3 |
| Q96A23-2 | 6 | 1.29E-05 | Isoform 2 of Copine-4 OS=Homo sapiens OX=9606 GN=CPNE4 |
| Q8TBX8 | 6 | 7.76E-06 | Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens OX=9606 GN=PIP4K2C PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q8TBX8-3, F8VU68, F8VNT5 |
| F8VU68 | 6 | 1.91E-05 | Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens OX=9606 GN=PIP4K2C PE=1 SV=1 |
| Q8TBX8-3 | 6 | 8.11E-06 | Isoform 3 of Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens OX=9606 GN=PIP4K2C |
| F8VNT5 | 6 | 1.82E-05 | Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma (Fragment) OS=Homo sapiens OX=9606 GN=PIP4K2C PE=1 SV=1 |
| P07910-3 | 6 | 0.000283389 | Isoform 3 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC |
| A0A0G2JNQ3 | 6 | 7.54E-05 | Heterogeneous nuclear ribonucleoprotein C-like 2 OS=Homo sapiens OX=9606 GN=HNRNPCL2 PE=4 SV=1 |
| G3V2H6 | 6 | 0.00017936 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| B7ZW38 | 6 | 7.54E-05 | Heterogeneous nuclear ribonucleoprotein C-like 3 OS=Homo sapiens OX=9606 GN=HNRNPCL3 PE=2 SV=1 |
| O60812 | 6 | 7.54E-05 | Heterogeneous nuclear ribonucleoprotein C-like 1 OS=Homo sapiens OX=9606 GN=HNRNPCL1 PE=1 SV=1 |
| B2RXH8 | 6 | 7.54E-05 | Heterogeneous nuclear ribonucleoprotein C-like 2 OS=Homo sapiens OX=9606 GN=HNRNPCL2 PE=1 SV=1 |
| G3V4M8 | 6 | 0.000167119 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| P0DMR1 | 6 | 7.54E-05 | Heterogeneous nuclear ribonucleoprotein C-like 4 OS=Homo sapiens OX=9606 GN=HNRNPCL4 PE=3 SV=1 |
| A0A0G2JPF8 | 6 | 7.54E-05 | Heterogeneous nuclear ribonucleoprotein C-like 4 OS=Homo sapiens OX=9606 GN=HNRNPCL4 PE=4 SV=1 |
| A0A0C4DFV9 | 6 | 0.00034184 | Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=1 |
| P0DME0 | 6 | 0.000195927 | Protein SETSIP OS=Homo sapiens OX=9606 GN=SETSIP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087X027, Q01105, Q01105-2, Q01105-4, A0A0C4DFV9, Q01105-3 |
| A0A087X027 | 6 | 0.000202637 | Protein SETSIP OS=Homo sapiens OX=9606 GN=SETSIP PE=1 SV=1 |
| Q01105-4 | 6 | 0.000339289 | Isoform 4 of Protein SET OS=Homo sapiens OX=9606 GN=SET |
| Q01105 | 6 | 0.00031355 | Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=3 |
| Q01105-2 | 6 | 0.000328265 | Isoform 2 of Protein SET OS=Homo sapiens OX=9606 GN=SET |
| Q01105-3 | 6 | 0.00034313 | Isoform 3 of Protein SET OS=Homo sapiens OX=9606 GN=SET |
| H3BLU7 | 6 | 9.84E-05 | Aflatoxin B1 aldehyde reductase member 2 (Fragment) OS=Homo sapiens OX=9606 GN=AKR7A2 PE=1 SV=1 |
| O43488 | 6 | 8.61E-05 | Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens OX=9606 GN=AKR7A2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H3BLU7 |
| E9PBF6 | 5 | 0.00019278 | Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=1 |
| P20700 | 5 | 0.000129304 | Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PBF6, A0A0D9SFE5, A0A0D9SFY5 |
| P22304 | 6 | 5.29E-05 | Iduronate 2-sulfatase OS=Homo sapiens OX=9606 GN=IDS PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B3KWA1 |
| B3KWA1 | 5 | 4.24E-05 | Iduronate 2-sulfatase (Hunter syndrome), isoform CRA\_e OS=Homo sapiens OX=9606 GN=IDS PE=2 SV=1 |
| Q6IAA8 | 6 | 4.90E-05 | Ragulator complex protein LAMTOR1 OS=Homo sapiens OX=9606 GN=LAMTOR1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F5H3Y3, F5GX19, F5H479, H0YFI1 |
| Q14011 | 6 | 0.000339024 | Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| K7EJV5 | 6 | 0.000399487 | Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| K7ER40 | 6 | 0.000242463 | Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=8 |
| K7ELT6 | 6 | 0.000310712 | Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| Q14011-2 | 6 | 0.000159491 | Isoform 2 of Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP |
| K7ENX8 | 6 | 0.000524327 | Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=2 |
| D6W5Y5 | 6 | 0.000141233 | Cold inducible RNA binding protein, isoform CRA\_c OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q14011-2, K7EQR7, K7ER40, Q14011, K7EPM4, K7EMY9, K7EJV1, K7ELT6, K7EJV5, K7ELV6, K7ENX8 |
| K7EMY9 | 6 | 0.000263812 | Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| K7EJV1 | 6 | 0.00028342 | Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=6 |
| K7EPM4 | 6 | 0.000249679 | Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| K7EQR7 | 6 | 0.000207654 | Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| K7ELV6 | 6 | 0.000471305 | Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=2 |
| F8W9N7 | 6 | 0.000200993 | F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=1 |
| P52907 | 6 | 0.000156645 | F-actin-capping protein subunit alpha-1 OS=Homo sapiens OX=9606 GN=CAPZA1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P47755, F8W9N7, A0A0D9SET8, P47755-2, C9JUG7 |
| P47755-2 | 6 | 0.00020333 | Isoform 2 of F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 |
| P47755 | 6 | 0.000122282 | F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=3 |
| A0A0D9SET8 | 6 | 0.000200993 | F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=1 |
| C9JUG7 | 6 | 0.00023954 | F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=1 |
| P07711 | 6 | 0.000105713 | Cathepsin L1 OS=Homo sapiens OX=9606 GN=CTSL PE=1 SV=2 |
| Q5T8F0 | 6 | 0.000156455 | Cathepsin L1 OS=Homo sapiens OX=9606 GN=CTSL PE=1 SV=1 |
| O60911 | 6 | 0.000105396 | Cathepsin L2 OS=Homo sapiens OX=9606 GN=CTSV PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P07711, Q5T8F0 |
| K7EJT5 | 6 | 0.000536069 | 60S ribosomal protein L22 (Fragment) OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=1 |
| P35268 | 6 | 0.000196838 | 60S ribosomal protein L22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: K7ERI7, K7EMH1, K7ELC4, K7EKS7, K7EP65, K7EJT5 |
| K7ELC4 | 6 | 0.000318927 | 60S ribosomal protein L22 (Fragment) OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=1 |
| K7EKS7 | 6 | 0.000475382 | 60S ribosomal protein L22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=1 |
| K7EMH1 | 6 | 0.000283093 | 60S ribosomal protein L22 (Fragment) OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=1 |
| K7EP65 | 6 | 0.000524901 | 60S ribosomal protein L22 (Fragment) OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=1 |
| K7ERI7 | 6 | 0.000265213 | 60S ribosomal protein L22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=1 |
| H7BY16 | 6 | 0.000136522 | Nucleolin (Fragment) OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=8 |
| P19338 | 6 | 0.000109696 | Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H7BY16 |
| H3BR68 | 6 | 0.000272715 | Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1 |
| P30044-4 | 6 | 0.000603297 | Isoform 4 of Peroxiredoxin-5, mitochondrial OS=Homo sapiens OX=9606 GN=PRDX5 |
| A0A0S2Z4J7 | 6 | 0.000235745 | Glutathione synthetase isoform 2 OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8Y6Y6 | 6 | 0.000384177 | Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8YF34 | 6 | 0.000233815 | Glutathione synthetase (Fragment) OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8Y446 | 6 | 0.000250954 | Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8Y4V9 | 6 | 0.000320808 | Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8Y2X9 | 6 | 0.000648299 | Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8Y790 | 6 | 0.000277842 | Glutathione synthetase (Fragment) OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| Q15714 | 6 | 0.000207513 | TSC22 domain family protein 1 OS=Homo sapiens OX=9606 GN=TSC22D1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q15714-3, Q15714-2, A0A087X0H8 |
| A0A087X0H8 | 6 | 0.00240788 | TSC22 domain family protein 1 OS=Homo sapiens OX=9606 GN=TSC22D1 PE=1 SV=1 |
| Q15714-2 | 6 | 0.001490841 | Isoform 2 of TSC22 domain family protein 1 OS=Homo sapiens OX=9606 GN=TSC22D1 |
| Q15714-3 | 6 | 0.000367472 | Isoform 3 of TSC22 domain family protein 1 OS=Homo sapiens OX=9606 GN=TSC22D1 |
| D6RBL5 | 6 | 0.000792686 | Annexin OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=1 |
| P46783 | 6 | 7.91E-05 | 40S ribosomal protein S10 OS=Homo sapiens OX=9606 GN=RPS10 PE=1 SV=1 |
| Q9NQ39 | 6 | 7.42E-05 | Putative 40S ribosomal protein S10-like OS=Homo sapiens OX=9606 GN=RPS10P5 PE=5 SV=1; Additional IDs concatenated into MaxParsimony group: P46783 |
| O15400 | 6 | 5.38E-05 | Syntaxin-7 OS=Homo sapiens OX=9606 GN=STX7 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: O15400-2 |
| O15400-2 | 6 | 5.87E-05 | Isoform 2 of Syntaxin-7 OS=Homo sapiens OX=9606 GN=STX7 |
| P16949-2 | 6 | 0.003753435 | Isoform 2 of Stathmin OS=Homo sapiens OX=9606 GN=STMN1; Additional IDs concatenated into MaxParsimony group: P16949, A2A2D0 |
| P16949 | 6 | 0.004981104 | Stathmin OS=Homo sapiens OX=9606 GN=STMN1 PE=1 SV=3 |
| A2A2D0 | 6 | 0.007683502 | Stathmin (Fragment) OS=Homo sapiens OX=9606 GN=STMN1 PE=1 SV=8 |
| Q5W0X3 | 6 | 0.000273408 | Peptidylprolyl isomerase OS=Homo sapiens OX=9606 GN=FKBP1A PE=1 SV=1 |
| Q1JUQ5 | 6 | 0.000306098 | Peptidylprolyl isomerase OS=Homo sapiens OX=9606 GN=FKBP1A PE=1 SV=1 |
| P62942 | 6 | 0.00026075 | Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens OX=9606 GN=FKBP1A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5W0X3, Q1JUQ5 |
| Q96RQ9-2 | 6 | 8.34E-05 | Isoform 2 of L-amino-acid oxidase OS=Homo sapiens OX=9606 GN=IL4I1; Additional IDs concatenated into MaxParsimony group: Q96RQ9 |
| Q96RQ9 | 6 | 8.67E-05 | L-amino-acid oxidase OS=Homo sapiens OX=9606 GN=IL4I1 PE=1 SV=1 |
| H3BM89 | 5 | 7.57E-05 | 60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=1 |
| P36578 | 5 | 7.30E-05 | 60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: H3BM89 |
| R4GMQ5 | 6 | 0.004238664 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| V9GZ37 | 6 | 0.000339664 | Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1 |
| D6RDP7 | 6 | 7.88E-05 | Calnexin (Fragment) OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=1 |
| D6RAU8 | 6 | 9.88E-05 | Calnexin (Fragment) OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=1 |
| D6RAQ8 | 6 | 0.000123751 | Calnexin (Fragment) OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=1 |
| H0Y9Q7 | 6 | 8.03E-05 | Calnexin (Fragment) OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=1 |
| D6RB85 | 6 | 9.20E-05 | Calnexin (Fragment) OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=1 |
| D6RD16 | 6 | 9.18E-05 | Calnexin OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=1 |
| D6RHJ3 | 6 | 0.000112926 | Calnexin (Fragment) OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=8 |
| P27797 | 6 | 0.000240774 | Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1 |
| Q07960 | 6 | 6.82E-05 | Rho GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=ARHGAP1 PE=1 SV=1 |
| Q9NS69 | 6 | 0.000200455 | Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens OX=9606 GN=TOMM22 PE=1 SV=3 |
| O95674 | 5 | 0.000109032 | Phosphatidate cytidylyltransferase 2 OS=Homo sapiens OX=9606 GN=CDS2 PE=1 SV=1 |
| O95747 | 6 | 0.000103449 | Serine/threonine-protein kinase OSR1 OS=Homo sapiens OX=9606 GN=OXSR1 PE=1 SV=1 |
| Q9BS26 | 6 | 1.55E-05 | Endoplasmic reticulum resident protein 44 OS=Homo sapiens OX=9606 GN=ERP44 PE=1 SV=1 |
| P48741 | 6 | 0.000434229 | Putative heat shock 70 kDa protein 7 OS=Homo sapiens OX=9606 GN=HSPA7 PE=5 SV=2 |
| E9PPY6 | 6 | 0.00158078 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| E9PK54 | 6 | 0.001207857 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=8 |
| E9PQK7 | 6 | 0.001241785 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| E9PQQ4 | 6 | 0.001292618 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| E9PN25 | 6 | 0.001553914 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| G3V226 | 6 | 0.013506946 | Calmodulin-1 OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1 |
| H0Y4K8 | 6 | 3.29E-05 | Fibronectin (Fragment) OS=Homo sapiens OX=9606 GN=FN1 PE=1 SV=1 |
| O00764-3 | 6 | 0.000529954 | Isoform 3 of Pyridoxal kinase OS=Homo sapiens OX=9606 GN=PDXK |
| A0A2R8YFE2 | 6 | 0.001776157 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 |
| K7ELW0 | 6 | 0.00265412 | Protein/nucleic acid deglycase DJ-1 OS=Homo sapiens OX=9606 GN=PARK7 PE=1 SV=1 |
| Q99497 | 6 | 0.002462116 | Protein/nucleic acid deglycase DJ-1 OS=Homo sapiens OX=9606 GN=PARK7 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: K7ELW0 |
| A0A0C4DGV4 | 6 | 0.00073966 | Hepatitis B virus x interacting protein OS=Homo sapiens OX=9606 GN=LAMTOR5 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O43504, E9PLX3, R4GMU8 |
| E9PLX3 | 6 | 0.001421791 | Ragulator complex protein LAMTOR5 OS=Homo sapiens OX=9606 GN=LAMTOR5 PE=1 SV=1 |
| O43504 | 6 | 0.001406167 | Ragulator complex protein LAMTOR5 OS=Homo sapiens OX=9606 GN=LAMTOR5 PE=1 SV=1 |
| R4GMU8 | 6 | 0.001619762 | Ragulator complex protein LAMTOR5 OS=Homo sapiens OX=9606 GN=LAMTOR5 PE=1 SV=1 |
| P30613 | 6 | 9.59E-05 | Pyruvate kinase PKLR OS=Homo sapiens OX=9606 GN=PKLR PE=1 SV=2 |
| P30613-2 | 6 | 0.000101402 | Isoform L-type of Pyruvate kinase PKLR OS=Homo sapiens OX=9606 GN=PKLR |
| P60174-1 | 6 | 0.003015701 | Isoform 2 of Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 |
| P60174-4 | 6 | 0.003728467 | Isoform 4 of Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 |
| U3KPZ0 | 6 | 0.003669831 | Triosephosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=1 |
| P60174 | 6 | 0.002625558 | Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P60174-1, P60174-4, U3KPZ0, U3KQF3 |
| U3KQF3 | 6 | 0.003474612 | Triosephosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=1 |
| A0A087WV01 | 6 | 0.000329894 | Elongation factor 1-alpha OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1 |
| G8JLB6 | 6 | 8.74E-05 | Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P31943, E9PCY7, H0YB39, P55795, P52597, H0YBD7, H0YBG7 |
| P52597 | 6 | 8.04E-05 | Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens OX=9606 GN=HNRNPF PE=1 SV=3 |
| P55795 | 5 | 6.97E-05 | Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNPH2 PE=1 SV=1 |
| H0YB39 | 6 | 0.000148974 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| E9PCY7 | 6 | 9.62E-05 | Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| H0YBD7 | 6 | 0.000201938 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=8 |
| H0YBG7 | 6 | 0.000203842 | Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 |
| P31943 | 6 | 9.19E-05 | Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=4 |
| Q6UWU2-2 | 6 | 8.39E-06 | Isoform 2 of Beta-galactosidase-1-like protein OS=Homo sapiens OX=9606 GN=GLB1L |
| Q6UWU2 | 6 | 7.23E-06 | Beta-galactosidase-1-like protein OS=Homo sapiens OX=9606 GN=GLB1L PE=2 SV=1 |
| Q93084-7 | 6 | 1.12E-05 | Isoform SERCA3F of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3 |
| Q93084-5 | 6 | 1.10E-05 | Isoform SERCA3E of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3; Additional IDs concatenated into MaxParsimony group: Q93084-6, Q93084, Q93084-7, Q93084-3, Q93084-2, Q93084-4 |
| Q93084 | 6 | 1.11E-05 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3 PE=1 SV=2 |
| Q93084-2 | 6 | 1.16E-05 | Isoform SERCA3A of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3 |
| Q93084-3 | 6 | 1.13E-05 | Isoform SERCA3C of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3 |
| Q93084-4 | 6 | 1.16E-05 | Isoform SERCA3G of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3 |
| Q93084-6 | 6 | 1.11E-05 | Isoform SERCA3D of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3 |
| Q16543 | 6 | 5.50E-05 | Hsp90 co-chaperone Cdc37 OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: K7EL68 |
| K7EL68 | 6 | 8.67E-05 | Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1 |
| F5GZI0 | 6 | 0.000410145 | 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| Q9ULU8-5 | 6 | 0.000225661 | Isoform 5 of Calcium-dependent secretion activator 1 OS=Homo sapiens OX=9606 GN=CADPS |
| E9PIA8 | 6 | 0.000348208 | Palmitoyl-protein thioesterase 1 (Fragment) OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=10 |
| P50897 | 6 | 0.000548871 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1 |
| A0A286YFL8 | 6 | 0.000348703 | Palmitoyl-protein thioesterase 1 (Fragment) OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1 |
| A0A286YFF7 | 6 | 0.000501356 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A286YFL8, P50897, A0A2C9F2P4, A0A286YFE3, Q5T0S4, E9PK48, E9PIA8 |
| A0A2C9F2P4 | 6 | 0.00055067 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1 |
| E9PK48 | 6 | 0.00027675 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1 |
| Q5T0S4 | 6 | 0.000399401 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=2 |
| A0A286YFE3 | 6 | 0.00037419 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1 |
| P10809-2 | 6 | 0.000265849 | Isoform 2 of 60 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 |
| C9J0S9 | 6 | 4.28E-05 | 60 kDa heat shock protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=1 |
| C9JL25 | 6 | 0.000121037 | 60 kDa heat shock protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=1 |
| C9JCQ4 | 6 | 0.000186441 | 60 kDa heat shock protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=1 |
| C9JL19 | 6 | 0.00021115 | 60 kDa heat shock protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=1 |
| Q58FF6 | 6 | 0.00013271 | Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens OX=9606 GN=HSP90AB4P PE=5 SV=1 |
| Q58FF7 | 6 | 0.000128198 | Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens OX=9606 GN=HSP90AB3P PE=5 SV=1 |
| F8W026 | 6 | 0.000555349 | Endoplasmin (Fragment) OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=8 |
| P08238 | 6 | 0.000153352 | Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4 |
| Q58FF8 | 6 | 0.000144971 | Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens OX=9606 GN=HSP90AB2P PE=1 SV=2 |
| Q13409-5 | 6 | 0.00010129 | Isoform 2E of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 |
| Q13409 | 6 | 0.000103664 | Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q13409-5, Q13409-2, Q13409-7, Q13409-3, Q13409-6 |
| Q13409-7 | 6 | 0.000104981 | Isoform 3 of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 |
| Q13409-3 | 6 | 0.000108068 | Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 |
| Q13409-2 | 6 | 0.000104648 | Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 |
| Q13409-6 | 6 | 0.000105601 | Isoform 2F of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 |
| A0A2R8YG06 | 6 | 2.49E-05 | Catenin beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| H0YLC7 | 6 | 5.29E-05 | Fumarylacetoacetase (Fragment) OS=Homo sapiens OX=9606 GN=FAH PE=1 SV=1 |
| P16930 | 6 | 9.80E-05 | Fumarylacetoacetase OS=Homo sapiens OX=9606 GN=FAH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H0YLC7 |
| O60664-2 | 6 | 8.13E-05 | Isoform 2 of Perilipin-3 OS=Homo sapiens OX=9606 GN=PLIN3 |
| Q14568 | 6 | 0.00014456 | Heat shock protein HSP 90-alpha A2 OS=Homo sapiens OX=9606 GN=HSP90AA2P PE=1 SV=2 |
| G3V2J8 | 6 | 0.000233536 | Heat shock protein HSP 90-alpha (Fragment) OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=1 |
| A6NL93 | 6 | 0.001537034 | Non-histone chromosomal protein HMG-14 OS=Homo sapiens OX=9606 GN=HMGN1 PE=1 SV=1 |
| A6NEL0 | 6 | 0.001308896 | Non-histone chromosomal protein HMG-14 OS=Homo sapiens OX=9606 GN=HMGN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P05114, A6NL93 |
| P05114 | 6 | 0.00151832 | Non-histone chromosomal protein HMG-14 OS=Homo sapiens OX=9606 GN=HMGN1 PE=1 SV=3 |
| Q9Y2B9 | 5 | 0.000127784 | cAMP-dependent protein kinase inhibitor gamma OS=Homo sapiens OX=9606 GN=PKIG PE=2 SV=1; Additional IDs concatenated into MaxParsimony group: Q5H937 |
| Q5H937 | 5 | 0.000151744 | cAMP-dependent protein kinase inhibitor gamma OS=Homo sapiens OX=9606 GN=PKIG PE=1 SV=1 |
| D6RFI0 | 6 | 4.57E-05 | Sideroflexin-1 (Fragment) OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=8 |
| Q9H9B4 | 6 | 3.04E-05 | Sideroflexin-1 OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: D6RFI0, S4R2X2, D6RDG7, D6RAE9, H0Y9J5 |
| H0Y9J5 | 6 | 0.000373273 | Sideroflexin-1 (Fragment) OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=1 |
| D6RAE9 | 6 | 0.000146643 | Sideroflexin-1 OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=1 |
| D6RDG7 | 6 | 6.12E-05 | Sideroflexin-1 (Fragment) OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=1 |
| S4R2X2 | 6 | 4.98E-05 | Sideroflexin-1 OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=1 |
| Q96S82 | 6 | 2.46E-05 | Ubiquitin-like protein 7 OS=Homo sapiens OX=9606 GN=UBL7 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H3BSQ2, H3BSE0 |
| H3BSE0 | 6 | 8.21E-05 | Ubiquitin-like protein 7 (Fragment) OS=Homo sapiens OX=9606 GN=UBL7 PE=1 SV=1 |
| H3BSQ2 | 6 | 5.14E-05 | Ubiquitin-like protein 7 (Fragment) OS=Homo sapiens OX=9606 GN=UBL7 PE=1 SV=1 |
| P13861 | 6 | 0.000184082 | cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR2A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P13861-2, C9J830 |
| C9J830 | 6 | 0.000571589 | cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment) OS=Homo sapiens OX=9606 GN=PRKAR2A PE=1 SV=1 |
| P13861-2 | 6 | 0.000194684 | Isoform 2 of cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR2A |
| J3KQ18 | 6 | 0.001131069 | D-dopachrome decarboxylase OS=Homo sapiens OX=9606 GN=DDT PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P30046, H7C342 |
| H7C342 | 5 | 0.000243383 | D-dopachrome decarboxylase (Fragment) OS=Homo sapiens OX=9606 GN=DDT PE=1 SV=1 |
| P30046 | 6 | 0.001265263 | D-dopachrome decarboxylase OS=Homo sapiens OX=9606 GN=DDT PE=1 SV=3 |
| Q7Z4H3 | 5 | 4.34E-05 | HD domain-containing protein 2 OS=Homo sapiens OX=9606 GN=HDDC2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q7Z4H3-2 |
| Q7Z4H3-2 | 5 | 5.21E-05 | Isoform 2 of HD domain-containing protein 2 OS=Homo sapiens OX=9606 GN=HDDC2 |
| Q8WVC2 | 6 | 0.001239989 | 40S ribosomal protein S21 OS=Homo sapiens OX=9606 GN=RPS21 PE=1 SV=1 |
| P63220 | 6 | 0.00121011 | 40S ribosomal protein S21 OS=Homo sapiens OX=9606 GN=RPS21 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q8WVC2 |
| H0YC77 | 6 | 0.000809083 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=1 |
| C9JIZ0 | 6 | 0.000367964 | LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae), isoform CRA\_a OS=Homo sapiens OX=9606 GN=LSM8 PE=1 SV=1 |
| Q5TGM0 | 5 | 1.05E-05 | Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens OX=9606 GN=VTA1 PE=1 SV=1 |
| Q9NP79 | 5 | 8.53E-06 | Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens OX=9606 GN=VTA1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5TGM0 |
| Q8N129 | 6 | 0.000128367 | Protein canopy homolog 4 OS=Homo sapiens OX=9606 GN=CNPY4 PE=2 SV=1 |
| Q02818 | 6 | 9.89E-05 | Nucleobindin-1 OS=Homo sapiens OX=9606 GN=NUCB1 PE=1 SV=4 |
| P49411 | 6 | 5.33E-05 | Elongation factor Tu, mitochondrial OS=Homo sapiens OX=9606 GN=TUFM PE=1 SV=2 |
| P54802 | 6 | 7.15E-05 | Alpha-N-acetylglucosaminidase OS=Homo sapiens OX=9606 GN=NAGLU PE=1 SV=2 |
| Q9BXV9 | 6 | 0.000526057 | EKC/KEOPS complex subunit GON7 OS=Homo sapiens OX=9606 GN=GON7 PE=1 SV=2 |
| E9PF18 | 5 | 5.12E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q16836-2, Q16836-3, A0A0D9SFP2, A0A0A0MSE2, Q16836, A0A1W2PQV5, A0A1W2PRT2, A0A1W2PP40, A0A1W2PQ55 |
| Q16836-3 | 5 | 6.03E-05 | Isoform 3 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH |
| A0A1W2PRT2 | 5 | 8.72E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| Q16836 | 5 | 6.36E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=3 |
| A0A0D9SFP2 | 5 | 6.28E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| A0A1W2PQV5 | 5 | 7.43E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| Q16836-2 | 5 | 5.12E-05 | Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH |
| A0A0A0MSE2 | 5 | 6.30E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=2 |
| H0YI37 | 6 | 9.72E-05 | ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=1 |
| F5H4C6 | 6 | 0.000274035 | N-acetylglucosamine-6-sulfatase (Fragment) OS=Homo sapiens OX=9606 GN=GNS PE=1 SV=8 |
| K7ERC6 | 6 | 0.000460607 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=9 |
| A0A0J9YYH3 | 6 | 0.000302568 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| A0A0J9YX90 | 6 | 0.000306394 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| A0A0J9YXP8 | 6 | 0.000319503 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| K7EQ48 | 6 | 0.000195013 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=3 |
| A0A2R8Y6C7 | 6 | 0.000270971 | Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| P04632 | 6 | 4.95E-05 | Calpain small subunit 1 OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1 |
| S4R3F9 | 6 | 0.000103465 | Calpain small subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1 |
| A0A075B7C0 | 6 | 6.73E-05 | Calpain small subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1 |
| K7ELJ7 | 6 | 4.77E-05 | Calpain small subunit 1 OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1 |
| K7EM73 | 6 | 7.93E-05 | Calpain small subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1 |
| K7EIV0 | 6 | 6.77E-05 | Calpain small subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=2 |
| A0A0C4DGQ5 | 6 | 4.12E-05 | Calpain small subunit 1 OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: K7ELJ7, P04632, A0A075B7C0, K7EIV0, K7EM73, S4R3F9 |
| J3KSZ5 | 6 | 0.000106346 | L-xylulose reductase (Fragment) OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=1 |
| J3QL34 | 6 | 8.64E-05 | L-xylulose reductase (Fragment) OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=1 |
| J3QS45 | 6 | 0.000152074 | L-xylulose reductase (Fragment) OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=1 |
| J3KRZ4 | 6 | 0.00017271 | L-xylulose reductase (Fragment) OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=1 |
| F8VZU9 | 6 | 0.002175434 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| F8VXL3 | 6 | 0.004130402 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| H0YI43 | 6 | 0.002560741 | Myosin light polypeptide 6 (Fragment) OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| J3KND3 | 6 | 0.003409396 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| B7Z6Z4 | 6 | 0.00217743 | cDNA FLJ56329, highly similar to Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| F8VPF3 | 6 | 0.003189728 | Myosin light polypeptide 6 (Fragment) OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| G8JLA2 | 6 | 0.003409396 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| G3V1Y7 | 6 | 0.002848985 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| F8W1R7 | 6 | 0.003573988 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| P60660-2 | 6 | 0.003431975 | Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 |
| G3V1V0 | 6 | 0.003218809 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| P60660 | 6 | 0.003431975 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: B7Z6Z4, F8W180, G3V1V0, J3KND3, G8JLA2, P60660-2, F8W1R7, F8VPF3, G3V1Y7, F8VZU9, H0YI43, F8VXL3 |
| F8W180 | 6 | 0.001143213 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| A0A087X2E9 | 6 | 0.00118746 | Glutathione S-transferase P (Fragment) OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=1 |
| J3KSW7 | 6 | 0.0002674 | Serine/arginine-rich-splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=1 |
| J3QQV5 | 6 | 0.00030031 | Serine/arginine-rich-splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=1 |
| A0A1B0GVC9 | 6 | 0.001833882 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GV88 | 6 | 0.005531226 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| M0R0I5 | 6 | 0.000278138 | Far upstream element-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=1 |
| A0A2R8Y4L2 | 5 | 3.29E-05 | Heterogeneous nuclear ribonucleoprotein A1 pseudogene 48 OS=Homo sapiens OX=9606 GN=HNRNPA1P48 PE=4 SV=1 |
| H0YH80 | 5 | 3.91E-05 | Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=1 |
| D6R9Q9 | 5 | 6.97E-05 | Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=1 |
| Q16643-2 | 5 | 4.33E-05 | Isoform 2 of Drebrin OS=Homo sapiens OX=9606 GN=DBN1 |
| Q16643 | 5 | 4.46E-05 | Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4 |
| Q16643-3 | 5 | 4.16E-05 | Isoform 3 of Drebrin OS=Homo sapiens OX=9606 GN=DBN1; Additional IDs concatenated into MaxParsimony group: Q16643-2, Q16643, D6R9Q9 |
| P04062-3 | 6 | 0.000303948 | Isoform 3 of Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA |
| E7EQG2 | 6 | 3.41E-05 | Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=1 |
| Q14240 | 6 | 3.03E-05 | Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=2 |
| Q14240-2 | 6 | 3.02E-05 | Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2; Additional IDs concatenated into MaxParsimony group: Q14240, P60842, E7EQG2 |
| P60842 | 6 | 2.16E-05 | Eukaryotic initiation factor 4A-I OS=Homo sapiens OX=9606 GN=EIF4A1 PE=1 SV=1 |
| E9PNS3 | 6 | 6.33E-05 | Toll-interacting protein OS=Homo sapiens OX=9606 GN=TOLLIP PE=1 SV=1 |
| Q9H0E2 | 6 | 0.00015955 | Toll-interacting protein OS=Homo sapiens OX=9606 GN=TOLLIP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F2Z2Y8, E9PNS3 |
| F2Z2Y8 | 6 | 0.000205242 | Toll-interacting protein OS=Homo sapiens OX=9606 GN=TOLLIP PE=1 SV=1 |
| Q5TEC6 | 6 | 0.005335398 | Histone H3 OS=Homo sapiens OX=9606 GN=HIST2H3PS2 PE=1 SV=1 |
| B4DEB1 | 6 | 0.006180034 | Histone H3 OS=Homo sapiens OX=9606 GN=H3F3A PE=1 SV=1 |
| K7EP01 | 6 | 0.004045293 | Histone H3.3 OS=Homo sapiens OX=9606 GN=H3F3B PE=1 SV=1 |
| Q6NXT2 | 6 | 0.005510324 | Histone H3.3C OS=Homo sapiens OX=9606 GN=H3F3C PE=1 SV=3 |
| P84243 | 6 | 0.00769794 | Histone H3.3 OS=Homo sapiens OX=9606 GN=H3F3A PE=1 SV=2 |
| K7EK07 | 6 | 0.007931211 | Histone H3 (Fragment) OS=Homo sapiens OX=9606 GN=H3F3B PE=1 SV=1 |
| P68431 | 6 | 0.00769794 | Histone H3.1 OS=Homo sapiens OX=9606 GN=HIST1H3A PE=1 SV=2 |
| Q16695 | 6 | 0.00769794 | Histone H3.1t OS=Homo sapiens OX=9606 GN=HIST3H3 PE=1 SV=3 |
| K7EMV3 | 6 | 0.008262437 | Histone H3 OS=Homo sapiens OX=9606 GN=H3F3B PE=1 SV=1 |
| K7ES00 | 6 | 0.005034067 | Histone H3.3 (Fragment) OS=Homo sapiens OX=9606 GN=H3F3B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5TEC6, P84243, P68431, Q16695, Q71DI3, Q6NXT2, K7EK07, B4DEB1, K7EP01, K7EMV3 |
| Q71DI3 | 6 | 0.00769794 | Histone H3.2 OS=Homo sapiens OX=9606 GN=HIST2H3A PE=1 SV=3 |
| Q14247-3 | 6 | 0.000160309 | Isoform 3 of Src substrate cortactin OS=Homo sapiens OX=9606 GN=CTTN |
| Q14247 | 6 | 0.000152802 | Src substrate cortactin OS=Homo sapiens OX=9606 GN=CTTN PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q14247-3 |
| H0YF90 | 5 | 4.76E-05 | Cation-dependent mannose-6-phosphate receptor (Fragment) OS=Homo sapiens OX=9606 GN=M6PR PE=1 SV=1 |
| P20645 | 5 | 3.47E-05 | Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=M6PR PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F5GX30, H0YF90 |
| F5GX30 | 5 | 3.69E-05 | Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=M6PR PE=1 SV=2 |
| A0A2R8YFZ7 | 5 | 9.33E-06 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1 |
| Q14204 | 6 | 1.30E-05 | Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: A0A2R8YFZ7 |
| A8MUD9 | 5 | 3.05E-05 | 60S ribosomal protein L7 OS=Homo sapiens OX=9606 GN=RPL7 PE=1 SV=1 |
| P18124 | 5 | 4.57E-05 | 60S ribosomal protein L7 OS=Homo sapiens OX=9606 GN=RPL7 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A8MUD9 |
| H0YMD9 | 6 | 0.000546598 | Annexin A2 (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YKL9 | 6 | 0.00032299 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YKZ7 | 6 | 0.000298562 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YMT9 | 6 | 0.000267134 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YMM1 | 6 | 0.000353727 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YKX9 | 6 | 0.000265141 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YMW4 | 6 | 0.000243348 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YKV8 | 6 | 0.000438628 | Annexin A2 (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YLV6 | 6 | 0.000269158 | Annexin OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| O00533-2 | 6 | 1.80E-05 | Isoform 2 of Neural cell adhesion molecule L1-like protein OS=Homo sapiens OX=9606 GN=CHL1; Additional IDs concatenated into MaxParsimony group: O00533, A0A087X0M8 |
| O00533 | 6 | 1.83E-05 | Neural cell adhesion molecule L1-like protein OS=Homo sapiens OX=9606 GN=CHL1 PE=1 SV=4 |
| A0A087X0M8 | 6 | 1.89E-05 | Neural cell adhesion molecule L1-like protein OS=Homo sapiens OX=9606 GN=CHL1 PE=1 SV=1 |
| A0A0D9SFH4 | 4 | 8.33E-05 | Spectrin alpha chain, non-erythrocytic 1 (Fragment) OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=1 |
| A0A0J9YWK4 | 6 | 0.082383387 | Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=1 |
| P04196 | 6 | 3.43E-06 | Histidine-rich glycoprotein OS=Homo sapiens OX=9606 GN=HRG PE=1 SV=1 |
| Q9Y6W5 | 6 | 4.71E-05 | Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens OX=9606 GN=WASF2 PE=1 SV=3 |
| P35270 | 6 | 1.70E-05 | Sepiapterin reductase OS=Homo sapiens OX=9606 GN=SPR PE=1 SV=1 |
| P51397 | 6 | 0.000341635 | Death-associated protein 1 OS=Homo sapiens OX=9606 GN=DAP PE=1 SV=3 |
| Q92820 | 6 | 9.64E-05 | Gamma-glutamyl hydrolase OS=Homo sapiens OX=9606 GN=GGH PE=1 SV=2 |
| Q9BUW7 | 6 | 0.000337786 | UPF0184 protein C9orf16 OS=Homo sapiens OX=9606 GN=C9orf16 PE=1 SV=1 |
| A0A087WZE9 | 6 | 0.000728838 | High mobility group nucleosome-binding domain-containing protein 3 OS=Homo sapiens OX=9606 GN=HMGN3 PE=1 SV=1 |
| P01019 | 6 | 1.75E-05 | Angiotensinogen OS=Homo sapiens OX=9606 GN=AGT PE=1 SV=1 |
| P35754 | 6 | 9.43E-05 | Glutaredoxin-1 OS=Homo sapiens OX=9606 GN=GLRX PE=1 SV=2 |
| Q9Y333 | 6 | 5.59E-05 | U6 snRNA-associated Sm-like protein LSm2 OS=Homo sapiens OX=9606 GN=LSM2 PE=1 SV=1 |
| P02649 | 6 | 3.32E-05 | Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1 |
| Q9P2B2 | 6 | 8.48E-05 | Prostaglandin F2 receptor negative regulator OS=Homo sapiens OX=9606 GN=PTGFRN PE=1 SV=2 |
| Q8N1G4 | 5 | 3.11E-05 | Leucine-rich repeat-containing protein 47 OS=Homo sapiens OX=9606 GN=LRRC47 PE=1 SV=1 |
| P61457 | 6 | 0.001476691 | Pterin-4-alpha-carbinolamine dehydratase OS=Homo sapiens OX=9606 GN=PCBD1 PE=1 SV=2 |
| P62328 | 6 | 0.0005934 | Thymosin beta-4 OS=Homo sapiens OX=9606 GN=TMSB4X PE=1 SV=2 |
| Q9H1K0 | 5 | 6.73E-06 | Rabenosyn-5 OS=Homo sapiens OX=9606 GN=RBSN PE=1 SV=2 |
| P48745 | 6 | 0.000241565 | Protein NOV homolog OS=Homo sapiens OX=9606 GN=NOV PE=1 SV=1 |
| P63313 | 5 | 0.004915309 | Thymosin beta-10 OS=Homo sapiens OX=9606 GN=TMSB10 PE=1 SV=2 |
| Q9UHP9 | 6 | 0.000101784 | Small muscular protein OS=Homo sapiens OX=9606 GN=SMPX PE=2 SV=3 |
| P51580 | 5 | 1.07E-05 | Thiopurine S-methyltransferase OS=Homo sapiens OX=9606 GN=TPMT PE=1 SV=1 |
| P00492 | 6 | 7.66E-05 | Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=HPRT1 PE=1 SV=2 |
| Q9P0R6 | 6 | 0.000253298 | GSK3B-interacting protein OS=Homo sapiens OX=9606 GN=GSKIP PE=1 SV=2 |
| P80108 | 6 | 1.47E-05 | Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens OX=9606 GN=GPLD1 PE=1 SV=3 |
| P04004 | 6 | 7.80E-05 | Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1 |
| Q9BXX0 | 6 | 2.35E-05 | EMILIN-2 OS=Homo sapiens OX=9606 GN=EMILIN2 PE=1 SV=3 |
| P53999 | 6 | 0.000112986 | Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens OX=9606 GN=SUB1 PE=1 SV=3 |
| Q9NSA3 | 6 | 5.36E-05 | Beta-catenin-interacting protein 1 OS=Homo sapiens OX=9606 GN=CTNNBIP1 PE=1 SV=1 |
| Q92520 | 6 | 1.14E-05 | Protein FAM3C OS=Homo sapiens OX=9606 GN=FAM3C PE=1 SV=1 |
| P12074 | 6 | 4.71E-05 | Cytochrome c oxidase subunit 6A1, mitochondrial OS=Homo sapiens OX=9606 GN=COX6A1 PE=1 SV=4 |
| P09669 | 6 | 0.000588105 | Cytochrome c oxidase subunit 6C OS=Homo sapiens OX=9606 GN=COX6C PE=1 SV=2 |
| P13010 | 6 | 0.000155832 | X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1 SV=3 |
| O75368 | 6 | 0.000811843 | SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens OX=9606 GN=SH3BGRL PE=1 SV=1 |
| O75531 | 6 | 0.00032501 | Barrier-to-autointegration factor OS=Homo sapiens OX=9606 GN=BANF1 PE=1 SV=1 |
| P26885 | 6 | 4.71E-05 | Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Homo sapiens OX=9606 GN=FKBP2 PE=1 SV=2 |
| O60220 | 6 | 0.000223923 | Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens OX=9606 GN=TIMM8A PE=1 SV=1 |
| Q9Y3C8 | 4 | 4.94E-05 | Ubiquitin-fold modifier-conjugating enzyme 1 OS=Homo sapiens OX=9606 GN=UFC1 PE=1 SV=3 |
| Q14118 | 6 | 1.48E-05 | Dystroglycan OS=Homo sapiens OX=9606 GN=DAG1 PE=1 SV=2 |
| Q9UMX5 | 6 | 0.000362699 | Neudesin OS=Homo sapiens OX=9606 GN=NENF PE=1 SV=1 |
| Q9UHV9 | 6 | 0.000109993 | Prefoldin subunit 2 OS=Homo sapiens OX=9606 GN=PFDN2 PE=1 SV=1 |
| P15090 | 5 | 0.00013549 | Fatty acid-binding protein, adipocyte OS=Homo sapiens OX=9606 GN=FABP4 PE=1 SV=3 |
| Q09666 | 6 | 1.38E-05 | Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens OX=9606 GN=AHNAK PE=1 SV=2 |
| P07099 | 6 | 4.26E-05 | Epoxide hydrolase 1 OS=Homo sapiens OX=9606 GN=EPHX1 PE=1 SV=1 |
| Q92797 | 6 | 1.43E-05 | Symplekin OS=Homo sapiens OX=9606 GN=SYMPK PE=1 SV=2 |
| P98179 | 5 | 0.000125442 | RNA-binding protein 3 OS=Homo sapiens OX=9606 GN=RBM3 PE=1 SV=1 |
| P30050 | 5 | 0.000105062 | 60S ribosomal protein L12 OS=Homo sapiens OX=9606 GN=RPL12 PE=1 SV=1 |
| P10606 | 6 | 0.000493092 | Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens OX=9606 GN=COX5B PE=1 SV=2 |
| Q9NX55 | 5 | 0.000126712 | Huntingtin-interacting protein K OS=Homo sapiens OX=9606 GN=HYPK PE=1 SV=2 |
| O14907 | 6 | 3.79E-05 | Tax1-binding protein 3 OS=Homo sapiens OX=9606 GN=TAX1BP3 PE=1 SV=2 |
| P14854 | 6 | 0.003401823 | Cytochrome c oxidase subunit 6B1 OS=Homo sapiens OX=9606 GN=COX6B1 PE=1 SV=2 |
| P56385 | 6 | 0.000944759 | ATP synthase subunit e, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5ME PE=1 SV=2 |
| A6NGN9 | 6 | 2.30E-05 | IgLON family member 5 OS=Homo sapiens OX=9606 GN=IGLON5 PE=2 SV=4 |
| O14561 | 6 | 0.000316389 | Acyl carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFAB1 PE=1 SV=3 |
| Q9UBI6 | 6 | 0.000192179 | Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens OX=9606 GN=GNG12 PE=1 SV=3 |
| Q9NVA4 | 5 | 1.22E-05 | Transmembrane protein 184C OS=Homo sapiens OX=9606 GN=TMEM184C PE=1 SV=2 |
| P28070 | 6 | 0.00014624 | Proteasome subunit beta type-4 OS=Homo sapiens OX=9606 GN=PSMB4 PE=1 SV=4 |
| P14550 | 6 | 8.24E-06 | Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens OX=9606 GN=AKR1A1 PE=1 SV=3 |
| Q9BS18 | 6 | 3.27E-05 | Anaphase-promoting complex subunit 13 OS=Homo sapiens OX=9606 GN=ANAPC13 PE=1 SV=1 |
| Q14126 | 4 | 1.45E-06 | Desmoglein-2 OS=Homo sapiens OX=9606 GN=DSG2 PE=1 SV=2 |
| O00299 | 6 | 0.000493622 | Chloride intracellular channel protein 1 OS=Homo sapiens OX=9606 GN=CLIC1 PE=1 SV=4 |
| P62310 | 6 | 0.00129045 | U6 snRNA-associated Sm-like protein LSm3 OS=Homo sapiens OX=9606 GN=LSM3 PE=1 SV=2 |
| P62072 | 6 | 0.000440424 | Mitochondrial import inner membrane translocase subunit Tim10 OS=Homo sapiens OX=9606 GN=TIMM10 PE=1 SV=1 |
| O76024 | 5 | 1.20E-05 | Wolframin OS=Homo sapiens OX=9606 GN=WFS1 PE=1 SV=2 |
| P51884 | 6 | 5.88E-06 | Lumican OS=Homo sapiens OX=9606 GN=LUM PE=1 SV=2 |
| Q9HCJ6 | 6 | 0.000143908 | Synaptic vesicle membrane protein VAT-1 homolog-like OS=Homo sapiens OX=9606 GN=VAT1L PE=1 SV=2 |
| Q9H223 | 5 | 1.88E-05 | EH domain-containing protein 4 OS=Homo sapiens OX=9606 GN=EHD4 PE=1 SV=1 |
| P62266 | 5 | 1.92E-05 | 40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3 |
| P06727 | 6 | 0.000473369 | Apolipoprotein A-IV OS=Homo sapiens OX=9606 GN=APOA4 PE=1 SV=3 |
| P11717 | 6 | 1.83E-05 | Cation-independent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=IGF2R PE=1 SV=3 |
| Q9UQ35 | 5 | 9.08E-06 | Serine/arginine repetitive matrix protein 2 OS=Homo sapiens OX=9606 GN=SRRM2 PE=1 SV=2 |
| Q96HQ2 | 6 | 4.55E-05 | CDKN2AIP N-terminal-like protein OS=Homo sapiens OX=9606 GN=CDKN2AIPNL PE=1 SV=1 |
| P25311 | 6 | 0.000313773 | Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=2 |
| P11766 | 5 | 1.38E-05 | Alcohol dehydrogenase class-3 OS=Homo sapiens OX=9606 GN=ADH5 PE=1 SV=4 |
| P16444 | 6 | 8.16E-05 | Dipeptidase 1 OS=Homo sapiens OX=9606 GN=DPEP1 PE=1 SV=3 |
| P62306 | 6 | 0.000389076 | Small nuclear ribonucleoprotein F OS=Homo sapiens OX=9606 GN=SNRPF PE=1 SV=1 |
| Q01459 | 5 | 1.50E-05 | Di-N-acetylchitobiase OS=Homo sapiens OX=9606 GN=CTBS PE=1 SV=1 |
| Q5JS37 | 5 | 9.57E-06 | NHL repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=NHLRC3 PE=2 SV=1 |
| Q9BPX5 | 5 | 1.17E-05 | Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens OX=9606 GN=ARPC5L PE=1 SV=1 |
| P05198 | 6 | 2.50E-05 | Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens OX=9606 GN=EIF2S1 PE=1 SV=3 |
| Q99584 | 6 | 0.000616617 | Protein S100-A13 OS=Homo sapiens OX=9606 GN=S100A13 PE=1 SV=1 |
| P09874 | 5 | 5.89E-06 | Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4 |
| Q96CT7 | 5 | 1.61E-05 | Coiled-coil domain-containing protein 124 OS=Homo sapiens OX=9606 GN=CCDC124 PE=1 SV=1 |
| Q9H444 | 6 | 1.20E-05 | Charged multivesicular body protein 4b OS=Homo sapiens OX=9606 GN=CHMP4B PE=1 SV=1 |
| P01023 | 6 | 2.56E-05 | Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3 |
| P62701 | 5 | 5.64E-05 | 40S ribosomal protein S4, X isoform OS=Homo sapiens OX=9606 GN=RPS4X PE=1 SV=2 |
| P36405 | 5 | 8.71E-06 | ADP-ribosylation factor-like protein 3 OS=Homo sapiens OX=9606 GN=ARL3 PE=1 SV=2 |
| P27482 | 6 | 0.011007394 | Calmodulin-like protein 3 OS=Homo sapiens OX=9606 GN=CALML3 PE=1 SV=2 |
| U3KPS5 | 6 | 0.001774575 | Triosephosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=8 |
| P02008 | 6 | 0.007503342 | Hemoglobin subunit zeta OS=Homo sapiens OX=9606 GN=HBZ PE=1 SV=2 |
| H7BZJ3 | 6 | 0.000172568 | Protein disulfide-isomerase A3 (Fragment) OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=1 |
| Q8TCE1 | 6 | 0.000181154 | Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1 |
| P01008 | 6 | 0.000325486 | Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q8TCE1 |
| K7EN27 | 6 | 0.001625257 | Protein/nucleic acid deglycase DJ-1 (Fragment) OS=Homo sapiens OX=9606 GN=PARK7 PE=1 SV=1 |
| E5RIX8 | 6 | 0.000828809 | Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=1 |
| A0A087WU08 | 6 | 0.000425105 | Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1 |
| P00739 | 6 | 0.000175487 | Haptoglobin-related protein OS=Homo sapiens OX=9606 GN=HPR PE=2 SV=2 |
| J3KTC3 | 6 | 0.000239277 | Haptoglobin-related protein OS=Homo sapiens OX=9606 GN=HPR PE=1 SV=1 |
| H0Y300 | 6 | 0.000333597 | Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P00738, J3QR68, A0A0C4DGL8, J3QLC9, P00738-2, A0A087WU08, P00739-2, P00739, A0A0A0MRD9, H3BS21, J3KRH2, J3KTC3 |
| J3KRH2 | 6 | 0.000125168 | Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1 |
| J3QLC9 | 6 | 0.000340514 | Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1 |
| A0A0A0MRD9 | 6 | 0.000117701 | Haptoglobin-related protein OS=Homo sapiens OX=9606 GN=HPR PE=1 SV=1 |
| A0A0C4DGL8 | 6 | 0.000424927 | Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1 |
| P00738 | 6 | 0.000363177 | Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1 |
| H3BS21 | 6 | 0.000322156 | Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1 |
| J3QR68 | 6 | 0.000364975 | Haptoglobin (Fragment) OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1 |
| P00738-2 | 6 | 0.000371181 | Isoform 2 of Haptoglobin OS=Homo sapiens OX=9606 GN=HP |
| P00739-2 | 6 | 0.000158622 | Isoform 2 of Haptoglobin-related protein OS=Homo sapiens OX=9606 GN=HPR |
| E9PNH1 | 5 | 0.000120677 | Neutral alpha-glucosidase AB (Fragment) OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=1 |
| E9PKU7 | 6 | 5.13E-05 | Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=1 |
| G5E9U5 | 6 | 0.000107901 | Rab GDP dissociation inhibitor OS=Homo sapiens OX=9606 GN=GDI1 PE=1 SV=1 |
| A0A0J9YXH9 | 6 | 0.000368169 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| K7ENA0 | 6 | 0.000306594 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=8 |
| K7ERK8 | 6 | 0.000352277 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=2 |
| K7ELR7 | 6 | 0.000367529 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| A0A0J9YXM3 | 6 | 0.000305027 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| K7EPY4 | 6 | 0.000415488 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=8 |
| K7EIL4 | 6 | 0.000422124 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=2 |
| K7EP41 | 6 | 0.000430264 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| A0A2R8YF08 | 6 | 0.000370064 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| P04217-2 | 6 | 0.000110429 | Isoform 2 of Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG |
| M0R009 | 6 | 9.12E-05 | Alpha-1B-glycoprotein (Fragment) OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=8 |
| P04217 | 6 | 0.00013627 | Alpha-1B-glycoprotein OS=Homo sapiens OX=9606 GN=A1BG PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: M0R009, P04217-2 |
| E5RI98 | 6 | 0.000723229 | Nucleophosmin (Fragment) OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=1 |
| E5RGW4 | 6 | 0.00108318 | Nucleophosmin (Fragment) OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=1 |
| P01024 | 6 | 2.04E-05 | Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0QXZ3 |
| Q15843 | 6 | 0.000941666 | NEDD8 OS=Homo sapiens OX=9606 GN=NEDD8 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PL57, S4R3E9, E9PS38, F8VSA6 |
| E9PS38 | 6 | 0.001019817 | NEDD8-MDP1 readthrough OS=Homo sapiens OX=9606 GN=NEDD8-MDP1 PE=4 SV=2 |
| F8VSA6 | 6 | 0.001366555 | NEDD8 OS=Homo sapiens OX=9606 GN=NEDD8 PE=4 SV=1 |
| E9PL57 | 6 | 0.000414711 | NEDD8-MDP1 readthrough (Fragment) OS=Homo sapiens OX=9606 GN=NEDD8-MDP1 PE=4 SV=1 |
| S4R3E9 | 6 | 0.000813426 | NEDD8-MDP1 readthrough OS=Homo sapiens OX=9606 GN=NEDD8-MDP1 PE=4 SV=1 |
| A0A286YFF3 | 6 | 0.000289362 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YFK5 | 6 | 0.000125723 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YF34 | 6 | 0.000574217 | D-3-phosphoglycerate dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| E7EMU4 | 6 | 0.000122207 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7EQU2 | 6 | 0.000141363 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7ERR6 | 6 | 9.35E-05 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7EUM4 | 6 | 9.49E-05 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7EV09 | 6 | 0.000104609 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=8 |
| E7ET01 | 6 | 0.000123556 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7ETL8 | 6 | 0.000116169 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E9PGG1 | 6 | 0.000118158 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7ERH4 | 6 | 8.61E-05 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7EU01 | 6 | 7.33E-05 | Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7ESD3 | 6 | 0.000139852 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| E7EQL5 | 6 | 8.57E-05 | Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=1 |
| P13591-5 | 6 | 6.70E-05 | Isoform 5 of Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 |
| A0A087WTE4 | 6 | 6.78E-05 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| H7BYX6 | 6 | 7.11E-05 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=2 |
| A0A087WWD4 | 6 | 0.000122282 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087WV75, A0A087WX77, P13591, P13591-1, A0A087WTF6, A0A087WTE4, P13591-3, P13591-4, H7BYX6, P13591-5, A0A087WWJ5, A0A0D9SF98, P13591-6, A0A087WVU1, A0A087X1V2, A0A0C4DGS4, A0A087WZS4 |
| P13591-4 | 6 | 7.10E-05 | Isoform 4 of Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 |
| A0A0D9SF30 | 6 | 0.000161333 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| A0A087X1V2 | 6 | 8.92E-05 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=6 |
| A0A087WWJ5 | 6 | 0.000208787 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| A0A0D9SF98 | 6 | 0.000217559 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| A0A0C4DGS4 | 6 | 8.55E-05 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| A0A087WVU1 | 6 | 6.93E-05 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| A0A087WX77 | 6 | 0.000125987 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| A0A087WTF6 | 6 | 0.000127473 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| A0A087WZS4 | 6 | 5.20E-05 | Neural cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=6 |
| P13591-6 | 6 | 7.72E-05 | Isoform 6 of Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 |
| A0A087WV75 | 6 | 0.000122282 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=1 |
| P13591-3 | 6 | 6.78E-05 | Isoform 3 of Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 |
| P13591 | 6 | 0.000125987 | Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 PE=1 SV=3 |
| P13591-1 | 6 | 0.000127473 | Isoform 2 of Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=NCAM1 |
| H3BUH9 | 6 | 0.000423572 | Glycine cleavage system H protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=GCSH PE=1 SV=2 |
| P23434 | 6 | 0.000289408 | Glycine cleavage system H protein, mitochondrial OS=Homo sapiens OX=9606 GN=GCSH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H3BUH9, A0A1W2PQV2 |
| A0A1W2PQV2 | 6 | 0.000500675 | Glycine cleavage system H protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=GCSH PE=1 SV=1 |
| P22392-2 | 6 | 0.000416166 | Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens OX=9606 GN=NME2 |
| F6XY72 | 5 | 0.000309141 | HCG2001850, isoform CRA\_c OS=Homo sapiens OX=9606 GN=NME2 PE=1 SV=2 |
| P22392 | 6 | 0.000665621 | Nucleoside diphosphate kinase B OS=Homo sapiens OX=9606 GN=NME2 PE=1 SV=1 |
| O60361 | 6 | 0.000526374 | Putative nucleoside diphosphate kinase OS=Homo sapiens OX=9606 GN=NME2P1 PE=5 SV=1 |
| E5RHP0 | 6 | 0.000471179 | Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 PE=3 SV=1 |
| E7ERL0 | 6 | 0.000628993 | Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 PE=1 SV=1 |
| P15531-2 | 6 | 0.000733618 | Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 |
| P15531 | 6 | 0.000854279 | Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 PE=1 SV=1 |
| J3KPD9 | 6 | 0.000443808 | NME1-NME2 readthrough OS=Homo sapiens OX=9606 GN=NME1-NME2 PE=1 SV=1 |
| C9K028 | 5 | 0.000422493 | Nucleoside diphosphate kinase A (Fragment) OS=Homo sapiens OX=9606 GN=NME1 PE=1 SV=1 |
| Q32Q12 | 6 | 0.000380535 | Nucleoside diphosphate kinase OS=Homo sapiens OX=9606 GN=NME1-NME2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P22392-2, P15531, J3KPD9, P22392, E7ERL0, O60361, E5RHP0, F6XY72, C9K028 |
| Q13423 | 6 | 3.19E-05 | NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: D6RAI5, D6RHU2, E9PCX7, D6RCR6 |
| D6RAI5 | 5 | 7.94E-05 | NAD(P) transhydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=1 |
| D6RHU2 | 5 | 8.66E-05 | NAD(P) transhydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=1 |
| P55084-2 | 6 | 7.32E-05 | Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=HADHB |
| F5GZQ3 | 6 | 6.73E-05 | Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=1 |
| P55084 | 6 | 6.98E-05 | Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P55084-2, F5GZQ3, B5MD38, C9JE81, C9JEY0, C9K0M0 |
| Q14103-2 | 6 | 0.000107305 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens OX=9606 GN=HNRNPD |
| H0Y8G5 | 6 | 0.000138672 | Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=8 |
| Q14103 | 6 | 0.000110362 | Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q14103-3, D6RAF8, Q14103-2, Q14103-4, H0Y8G5, H0YA96, D6RF44, D6RD83, A0A087WUK2, O14979-2, O14979-3, D6RBQ9 |
| D6RAF8 | 6 | 0.000177279 | Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1 |
| D6RF44 | 6 | 0.000320755 | Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=8 |
| H0YA96 | 6 | 0.000171689 | Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1 |
| Q14103-3 | 6 | 0.000128035 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens OX=9606 GN=HNRNPD |
| Q14103-4 | 6 | 0.000125626 | Isoform 4 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens OX=9606 GN=HNRNPD |
| K7EJB9 | 6 | 0.000374008 | Calreticulin (Fragment) OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1 |
| K7EL50 | 6 | 0.000369728 | Calreticulin (Fragment) OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1 |
| D6RB45 | 6 | 0.000599372 | Matrin-3 (Fragment) OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| D6R9F3 | 6 | 0.00036116 | Matrin-3 (Fragment) OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| D6R8Z5 | 6 | 0.000263275 | Matrin-3 (Fragment) OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| D6RCM3 | 6 | 0.00028455 | Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| A0A1B0GX04 | 6 | 0.00036585 | Matrin-3 (Fragment) OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| D6RBS2 | 6 | 0.000323798 | Matrin-3 (Fragment) OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| D6REK4 | 6 | 0.000281705 | Matrin-3 (Fragment) OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| O00264-2 | 6 | 0.000250162 | Isoform 2 of Membrane-associated progesterone receptor component 1 OS=Homo sapiens OX=9606 GN=PGRMC1 |
| O00264 | 6 | 0.000223533 | Membrane-associated progesterone receptor component 1 OS=Homo sapiens OX=9606 GN=PGRMC1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O00264-2 |
| M0R1M5 | 4 | 6.15E-05 | 40S ribosomal protein S16 (Fragment) OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=1 |
| M0QX76 | 4 | 0.000104542 | 40S ribosomal protein S16 (Fragment) OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=1 |
| O43390-3 | 6 | 3.88E-05 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR |
| E5RH81 | 6 | 0.001264555 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=8 |
| H0YBE2 | 6 | 0.000819055 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| E5RHP7 | 6 | 0.001013774 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| E5RFE7 | 6 | 0.000940651 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| P00915 | 6 | 0.001013242 | Carbonic anhydrase 1 OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E5RHP7, E5RH81, E5RFE7, H0YBE2, E5RG43, E5RIF9, E5RJI8, E5RJF6, E5RG81 |
| E5RJI8 | 6 | 0.00095023 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=8 |
| E5RG81 | 6 | 0.00092947 | Carbonic anhydrase 1 OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| E5RJF6 | 6 | 0.001115188 | Carbonic anhydrase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CA1 PE=1 SV=1 |
| A0A1W2PNM1 | 5 | 7.36E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| A0A1W2PQC2 | 5 | 9.49E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| A0A1W2PQ78 | 5 | 3.87E-05 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=1 |
| A0A087WYB4 | 6 | 0.000192354 | Stomatin-like protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=STOML2 PE=1 SV=1 |
| Q9UJZ1 | 6 | 0.000169592 | Stomatin-like protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=STOML2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UJZ1-2, A0A087WYB4, F2Z2I8 |
| Q9UJZ1-2 | 6 | 0.00019413 | Isoform 2 of Stomatin-like protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=STOML2 |
| Q7Z3Y9 | 4 | 2.12E-05 | Keratin, type I cytoskeletal 26 OS=Homo sapiens OX=9606 GN=KRT26 PE=1 SV=2 |
| O14983-3 | 5 | 3.09E-06 | Isoform 3 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Homo sapiens OX=9606 GN=ATP2A1 |
| O14983-2 | 5 | 2.70E-06 | Isoform SERCA1A of Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Homo sapiens OX=9606 GN=ATP2A1 |
| O14983 | 5 | 2.68E-06 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Homo sapiens OX=9606 GN=ATP2A1 PE=1 SV=1 |
| Q04760-2 | 6 | 0.00015558 | Isoform 2 of Lactoylglutathione lyase OS=Homo sapiens OX=9606 GN=GLO1 |
| Q04760 | 6 | 0.000142897 | Lactoylglutathione lyase OS=Homo sapiens OX=9606 GN=GLO1 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: Q04760-2 |
| O14737-2 | 6 | 0.000155272 | Isoform 2 of Programmed cell death protein 5 OS=Homo sapiens OX=9606 GN=PDCD5 |
| O14737 | 6 | 0.000209013 | Programmed cell death protein 5 OS=Homo sapiens OX=9606 GN=PDCD5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O14737-2, K7ESJ4, K7EQA1, X6R2P6, Q3HM38 |
| K7EQA1 | 6 | 0.000160591 | Programmed cell death protein 5 OS=Homo sapiens OX=9606 GN=PDCD5 PE=1 SV=1 |
| K7ESJ4 | 6 | 0.000308155 | Programmed cell death protein 5 OS=Homo sapiens OX=9606 GN=PDCD5 PE=1 SV=1 |
| P35613-4 | 6 | 0.000364598 | Isoform 4 of Basigin OS=Homo sapiens OX=9606 GN=BSG |
| R4GMX5 | 6 | 0.000636724 | Basigin (Fragment) OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=1 |
| A0A087X2B5 | 6 | 0.000338201 | Basigin (Fragment) OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=1 |
| I3L192 | 6 | 0.00033428 | Basigin (Fragment) OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=8 |
| P35613-2 | 6 | 0.000277853 | Isoform 2 of Basigin OS=Homo sapiens OX=9606 GN=BSG |
| P35613-3 | 6 | 0.000424673 | Isoform 3 of Basigin OS=Homo sapiens OX=9606 GN=BSG |
| P35613 | 6 | 0.000194136 | Basigin OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P35613-2, A0A087X2B5, P35613-4, A0A087WUV8, P35613-3, I3L192, R4GMX5, R4GN83 |
| A0A087WUV8 | 6 | 0.000395463 | Basigin OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=1 |
| H0YLK8 | 6 | 4.27E-05 | Clusterin (Fragment) OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1 |
| E7ERK6 | 6 | 6.21E-05 | Clusterin (Fragment) OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1 |
| P10909-5 | 6 | 5.05E-05 | Isoform 5 of Clusterin OS=Homo sapiens OX=9606 GN=CLU |
| P10909 | 6 | 5.17E-05 | Clusterin OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1 |
| H0YC35 | 6 | 6.95E-05 | Clusterin (Fragment) OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1 |
| P10909-4 | 6 | 5.58E-05 | Isoform 4 of Clusterin OS=Homo sapiens OX=9606 GN=CLU |
| H0YAS8 | 6 | 7.53E-05 | Clusterin (Fragment) OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1 |
| P10909-2 | 6 | 4.63E-05 | Isoform 2 of Clusterin OS=Homo sapiens OX=9606 GN=CLU; Additional IDs concatenated into MaxParsimony group: P10909-5, P10909, P10909-4, P10909-3, H0YC35, H0YAS8, H0YLK8, E7ERK6 |
| P10909-3 | 6 | 4.97E-05 | Isoform 3 of Clusterin OS=Homo sapiens OX=9606 GN=CLU |
| D6REB5 | 6 | 0.000102603 | Alpha-L-iduronidase OS=Homo sapiens OX=9606 GN=IDUA PE=1 SV=1 |
| P35475-2 | 6 | 7.05E-05 | Isoform 2 of Alpha-L-iduronidase OS=Homo sapiens OX=9606 GN=IDUA; Additional IDs concatenated into MaxParsimony group: P35475, D6REB5, H0Y9B3, D6R9D5, D6RBD5 |
| D6R9D5 | 6 | 9.76E-05 | Alpha-L-iduronidase (Fragment) OS=Homo sapiens OX=9606 GN=IDUA PE=1 SV=1 |
| P35475 | 6 | 8.19E-05 | Alpha-L-iduronidase OS=Homo sapiens OX=9606 GN=IDUA PE=1 SV=2 |
| D6RBD5 | 6 | 0.000124224 | Alpha-L-iduronidase (Fragment) OS=Homo sapiens OX=9606 GN=IDUA PE=1 SV=1 |
| H0Y9B3 | 6 | 0.000119651 | Alpha-L-iduronidase (Fragment) OS=Homo sapiens OX=9606 GN=IDUA PE=1 SV=1 |
| D6RHJ5 | 6 | 5.29E-05 | Receptor of-activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| J3KPE3 | 6 | 3.82E-05 | Receptor of-activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| D6RAC2 | 6 | 3.07E-05 | Receptor of-activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| P63244 | 6 | 4.46E-05 | Receptor of activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: D6RHH4, D6R9L0, J3KPE3, D6R9Z1, H0YAF8, D6RFZ9, D6RFX4, E9PD14, D6RAU2, H0Y8W2, D6RAC2, H0YAM7, H0Y8R5, D6RF23, D6RHJ5 |
| D6RHH4 | 6 | 6.07E-05 | Receptor of-activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| H0Y8R5 | 6 | 3.30E-05 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| H0YAF8 | 6 | 5.27E-05 | Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| D6RF23 | 6 | 4.50E-05 | Receptor of-activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=1 |
| Q8NC51-4 | 6 | 4.96E-05 | Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1 |
| Q8NC51-2 | 6 | 4.77E-05 | Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1 |
| Q8NC51 | 6 | 4.70E-05 | Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8NC51-2, Q8NC51-3, Q8NC51-4 |
| Q8NC51-3 | 6 | 4.88E-05 | Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1 |
| F8VV56 | 6 | 0.001555578 | CD63 antigen OS=Homo sapiens OX=9606 GN=CD63 PE=1 SV=1 |
| P08962 | 6 | 0.000947726 | CD63 antigen OS=Homo sapiens OX=9606 GN=CD63 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F8VWK8, P08962-2, F8W022, P08962-3, F8VV56, F8VNT9 |
| P08962-2 | 6 | 0.001049111 | Isoform 2 of CD63 antigen OS=Homo sapiens OX=9606 GN=CD63 |
| F8VNT9 | 6 | 0.000881183 | CD63 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD63 PE=1 SV=1 |
| F8W022 | 6 | 0.001049111 | Tetraspanin (Fragment) OS=Homo sapiens OX=9606 GN=CD63 PE=1 SV=1 |
| P08962-3 | 6 | 0.00144589 | Isoform 3 of CD63 antigen OS=Homo sapiens OX=9606 GN=CD63 |
| F8VWK8 | 6 | 0.001039442 | Tetraspanin (Fragment) OS=Homo sapiens OX=9606 GN=CD63 PE=1 SV=1 |
| Q92499-2 | 5 | 1.11E-05 | Isoform 2 of ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 |
| Q92499 | 6 | 1.76E-05 | ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F1T0B3, A0A087X2G1, Q92499-3, Q92499-2 |
| F1T0B3 | 6 | 1.97E-05 | ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=1 |
| Q92499-3 | 6 | 2.12E-05 | Isoform 3 of ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 |
| A0A087X2G1 | 6 | 1.97E-05 | ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=1 |
| P45974 | 5 | 8.46E-06 | Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P45974-2 |
| P45974-2 | 5 | 8.69E-06 | Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 |
| F8VNW4 | 6 | 0.000168916 | Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 |
| F8W1N5 | 6 | 0.000352107 | Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 |
| Q6BCY4 | 6 | 8.55E-05 | NADH-cytochrome b5 reductase 2 OS=Homo sapiens OX=9606 GN=CYB5R2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q6BCY4-2, E9PQW2, E9PMI2, E9PIV9, E9PRM4 |
| E9PQW2 | 6 | 0.000100081 | NADH-cytochrome b5 reductase 2 (Fragment) OS=Homo sapiens OX=9606 GN=CYB5R2 PE=1 SV=1 |
| E9PMI2 | 6 | 0.000110616 | NADH-cytochrome b5 reductase 2 (Fragment) OS=Homo sapiens OX=9606 GN=CYB5R2 PE=1 SV=1 |
| E9PRM4 | 5 | 9.33E-05 | NADH-cytochrome b5 reductase 2 (Fragment) OS=Homo sapiens OX=9606 GN=CYB5R2 PE=1 SV=1 |
| Q6BCY4-2 | 6 | 9.96E-05 | Isoform 2 of NADH-cytochrome b5 reductase 2 OS=Homo sapiens OX=9606 GN=CYB5R2 |
| E9PIV9 | 6 | 0.000129557 | NADH-cytochrome b5 reductase 2 (Fragment) OS=Homo sapiens OX=9606 GN=CYB5R2 PE=1 SV=1 |
| Q01469 | 5 | 0.000104064 | Fatty acid-binding protein 5 OS=Homo sapiens OX=9606 GN=FABP5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: I6L8B7 |
| J3KS60 | 5 | 0.000519892 | Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDIA PE=1 SV=1 |
| J3KRY1 | 5 | 0.000192089 | Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGDIA PE=1 SV=1 |
| J3KRE2 | 6 | 0.000652378 | Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDIA PE=1 SV=1 |
| P52565-2 | 5 | 0.000298938 | Isoform 2 of Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDIA |
| J3KTF8 | 6 | 0.000436045 | Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGDIA PE=1 SV=8 |
| J3QQX2 | 6 | 0.000358114 | Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDIA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P52565, J3KTF8, J3KRE2, J3KRY1, P52565-2, J3KS60 |
| P52565 | 6 | 0.000412533 | Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDIA PE=1 SV=3 |
| F5H4J1 | 5 | 1.29E-06 | Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=8 |
| A0A087WY61 | 5 | 2.06E-06 | Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=1 |
| Q14980-2 | 5 | 3.14E-06 | Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 |
| F5H6Y5 | 5 | 1.59E-06 | Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=1 |
| Q14980-3 | 5 | 2.50E-06 | Isoform 3 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 |
| Q14980 | 5 | 3.11E-06 | Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q14980-2, A0A087WY61, H0YFY6, Q14980-3, Q14980-4, Q14980-5, F5H4J1, F5H6Y5 |
| Q14980-4 | 5 | 2.52E-06 | Isoform 4 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 |
| E5RJ86 | 4 | 3.38E-05 | Armadillo repeat-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ARMC1 PE=1 SV=1 |
| E5RHK3 | 4 | 5.21E-05 | Armadillo repeat-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ARMC1 PE=1 SV=1 |
| Q9NVT9 | 4 | 3.52E-05 | Armadillo repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=ARMC1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NVT9-2, E5RJ86, E5RHK3, E9PR92 |
| E9PR92 | 4 | 6.29E-05 | Armadillo repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=ARMC1 PE=1 SV=1 |
| Q9HCH3 | 6 | 7.34E-06 | Copine-5 OS=Homo sapiens OX=9606 GN=CPNE5 PE=1 SV=2 |
| E7ENV7 | 6 | 7.89E-06 | Copine-8 OS=Homo sapiens OX=9606 GN=CPNE8 PE=1 SV=2 |
| Q9UBL6 | 6 | 6.88E-06 | Copine-7 OS=Homo sapiens OX=9606 GN=CPNE7 PE=1 SV=1 |
| Q8IYJ1 | 6 | 7.87E-06 | Copine-9 OS=Homo sapiens OX=9606 GN=CPNE9 PE=1 SV=3 |
| Q9HCH3-2 | 6 | 1.45E-05 | Isoform 2 of Copine-5 OS=Homo sapiens OX=9606 GN=CPNE5 |
| Q96FN4-2 | 6 | 9.76E-06 | Isoform 2 of Copine-2 OS=Homo sapiens OX=9606 GN=CPNE2 |
| Q86YQ8 | 6 | 7.72E-06 | Copine-8 OS=Homo sapiens OX=9606 GN=CPNE8 PE=1 SV=2 |
| Q9UBL6-2 | 6 | 7.80E-06 | Isoform 2 of Copine-7 OS=Homo sapiens OX=9606 GN=CPNE7 |
| O75131 | 6 | 1.42E-05 | Copine-3 OS=Homo sapiens OX=9606 GN=CPNE3 PE=1 SV=1 |
| Q96FN4 | 6 | 7.95E-06 | Copine-2 OS=Homo sapiens OX=9606 GN=CPNE2 PE=1 SV=3 |
| Q86YQ8-2 | 6 | 1.87E-05 | Isoform 2 of Copine-8 OS=Homo sapiens OX=9606 GN=CPNE8 |
| E9PPJ0 | 6 | 3.62E-05 | Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=1 |
| E9PIL8 | 6 | 0.000133114 | Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=8 |
| E9PJ04 | 6 | 8.78E-05 | Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=8 |
| E9PJT3 | 6 | 0.000113473 | Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=1 |
| Q13435 | 6 | 3.55E-05 | Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PPJ0, H0YCG1, E9PJ04, E9PJT3, E9PIL8 |
| H0YCG1 | 6 | 8.00E-05 | Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=1 |
| E5RG13 | 6 | 7.44E-05 | Inositol monophosphatase 1 (Fragment) OS=Homo sapiens OX=9606 GN=IMPA1 PE=1 SV=1 |
| E5RIP7 | 6 | 6.33E-05 | Inositol-1-monophosphatase (Fragment) OS=Homo sapiens OX=9606 GN=IMPA1 PE=1 SV=8 |
| H0YBL1 | 6 | 4.30E-05 | Inositol-1-monophosphatase (Fragment) OS=Homo sapiens OX=9606 GN=IMPA1 PE=1 SV=1 |
| P29218 | 6 | 6.90E-05 | Inositol monophosphatase 1 OS=Homo sapiens OX=9606 GN=IMPA1 PE=1 SV=1 |
| P29218-3 | 6 | 5.69E-05 | Isoform 3 of Inositol monophosphatase 1 OS=Homo sapiens OX=9606 GN=IMPA1; Additional IDs concatenated into MaxParsimony group: P29218, H0YBL1, E5RIP7, E5RG13 |
| Q13404-1 | 6 | 0.000349802 | Isoform 1 of Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens OX=9606 GN=UBE2V1 |
| Q13404 | 6 | 0.000525893 | Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens OX=9606 GN=UBE2V1 PE=1 SV=2 |
| I3L0A0 | 6 | 0.000208936 | HCG2044781 OS=Homo sapiens OX=9606 GN=TMEM189-UBE2V1 PE=4 SV=1 |
| Q13404-8 | 6 | 0.000736251 | Isoform 6 of Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens OX=9606 GN=UBE2V1 |
| E5RIF1 | 6 | 0.00148666 | Ubiquitin-conjugating enzyme E2 variant 2 (Fragment) OS=Homo sapiens OX=9606 GN=UBE2V2 PE=4 SV=1 |
| D6RG00 | 6 | 0.00086861 | HCG2018358, isoform CRA\_d OS=Homo sapiens OX=9606 GN=UBE2V1 PE=4 SV=2 |
| Q13404-2 | 6 | 0.000454743 | Isoform 2 of Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens OX=9606 GN=UBE2V1 |
| Q13404-7 | 6 | 0.000454743 | Isoform 5 of Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens OX=9606 GN=UBE2V1 |
| Q15819 | 6 | 0.000639898 | Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens OX=9606 GN=UBE2V2 PE=1 SV=4 |
| H0YBX6 | 6 | 0.000602502 | Ubiquitin-conjugating enzyme E2 variant 2 (Fragment) OS=Homo sapiens OX=9606 GN=UBE2V2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q15819, I3L0A0, Q13404-1, Q13404-2, Q13404-7, Q13404, Q13404-8, D6RG00, E5RIF1 |
| Q13310 | 6 | 0.000190938 | Polyadenylate-binding protein 4 OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1 |
| E7ERJ7 | 6 | 0.000203583 | Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| A0A087WTT1 | 6 | 0.000235563 | Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| B1ANR0 | 6 | 0.000199942 | Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1 |
| Q13310-3 | 6 | 0.000186309 | Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens OX=9606 GN=PABPC4; Additional IDs concatenated into MaxParsimony group: Q13310, P11940, Q13310-2, B1ANR0, E7ERJ7, E7EQV3, H0Y5F5, P11940-2, A0A087WTT1, H0Y6X6, H0YB75, H0YAS6, H0YAS7, H0YER0, Q9H361, H0YC10 |
| H0YER0 | 6 | 0.001808296 | Polyadenylate-binding protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1 |
| H0Y5F5 | 6 | 0.000223571 | Polyadenylate-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1 |
| Q13310-2 | 6 | 0.000194872 | Isoform 2 of Polyadenylate-binding protein 4 OS=Homo sapiens OX=9606 GN=PABPC4 |
| E7EQV3 | 6 | 0.000208061 | Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| P11940-2 | 6 | 0.000224797 | Isoform 2 of Polyadenylate-binding protein 1 OS=Homo sapiens OX=9606 GN=PABPC1 |
| H0YAS7 | 6 | 0.000904148 | Polyadenylate-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| H0YB75 | 6 | 0.000671935 | Polyadenylate-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| Q9H361 | 5 | 0.000192314 | Polyadenylate-binding protein 3 OS=Homo sapiens OX=9606 GN=PABPC3 PE=1 SV=2 |
| P11940 | 6 | 0.00019334 | Polyadenylate-binding protein 1 OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=2 |
| H0Y6X6 | 6 | 0.000630585 | Polyadenylate-binding protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1 |
| H0YC10 | 5 | 0.002889283 | Polyadenylate-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| H0YAS6 | 6 | 0.000727598 | Polyadenylate-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| Q9BY67-4 | 6 | 0.000113238 | Isoform 4 of Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1 |
| Q9BY67 | 6 | 0.000116056 | Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1 PE=1 SV=2 |
| A0A087X1W8 | 6 | 0.000124507 | Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1 PE=1 SV=1 |
| X5DQS5 | 6 | 0.000115794 | Cell adhesion molecule 1 isoform C (Fragment) OS=Homo sapiens OX=9606 GN=CADM1 PE=1 SV=1 |
| A0A0A0MTJ8 | 6 | 0.000124205 | Cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=CADM1 PE=1 SV=1 |
| Q9BY67-2 | 6 | 0.000133509 | Isoform 2 of Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1 |
| A0A087X0T8 | 6 | 0.000128493 | Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1 PE=1 SV=1 |
| F5H125 | 6 | 0.00018332 | Cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=CADM1 PE=1 SV=1 |
| H0YG94 | 6 | 0.000177469 | Cell adhesion molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=CADM1 PE=1 SV=8 |
| Q9BY67-5 | 6 | 0.000123905 | Isoform 5 of Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1 |
| Q9BY67-3 | 6 | 0.00010891 | Isoform 3 of Cell adhesion molecule 1 OS=Homo sapiens OX=9606 GN=CADM1; Additional IDs concatenated into MaxParsimony group: Q9BY67-4, X5DQS5, Q9BY67, Q9BY67-5, A0A0A0MTJ8, A0A087X1W8, A0A087X0T8, Q9BY67-2, H0YG94, F5H125 |
| P30740-2 | 6 | 4.72E-05 | Isoform 2 of Leukocyte elastase inhibitor OS=Homo sapiens OX=9606 GN=SERPINB1 |
| P30740 | 6 | 2.84E-05 | Leukocyte elastase inhibitor OS=Homo sapiens OX=9606 GN=SERPINB1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P30740-2 |
| F8WBY4 | 6 | 6.10E-05 | Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens OX=9606 GN=ATP1B3 PE=1 SV=1 |
| P54709 | 6 | 1.28E-05 | Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens OX=9606 GN=ATP1B3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F8WBY4, H7C547 |
| H7C547 | 6 | 6.24E-05 | Sodium/potassium-transporting ATPase subunit beta-3 (Fragment) OS=Homo sapiens OX=9606 GN=ATP1B3 PE=1 SV=1 |
| Q3ZCW2 | 6 | 3.77E-05 | Galectin-related protein OS=Homo sapiens OX=9606 GN=LGALSL PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: U3KQ88 |
| U3KQ88 | 6 | 1.04E-05 | Galectin (Fragment) OS=Homo sapiens OX=9606 GN=LGALSL PE=1 SV=1 |
| P60866 | 6 | 0.0001755 | 40S ribosomal protein S20 OS=Homo sapiens OX=9606 GN=RPS20 PE=1 SV=1 |
| E5RIP1 | 6 | 0.000328396 | 40S ribosomal protein S20 OS=Homo sapiens OX=9606 GN=RPS20 PE=1 SV=1 |
| P60866-2 | 6 | 0.000147074 | Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens OX=9606 GN=RPS20; Additional IDs concatenated into MaxParsimony group: P60866, G3XAN0, E5RJX2, E5RIP1 |
| E5RJX2 | 6 | 0.000247643 | 40S ribosomal protein S20 OS=Homo sapiens OX=9606 GN=RPS20 PE=1 SV=1 |
| P47985 | 6 | 6.77E-05 | Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRFS1 PE=1 SV=2 |
| P0C7P4 | 6 | 6.55E-05 | Putative cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo sapiens OX=9606 GN=UQCRFS1P1 PE=5 SV=1; Additional IDs concatenated into MaxParsimony group: P47985 |
| Q9H6Z4 | 4 | 8.59E-06 | Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=1 |
| Q9H6Z4-3 | 4 | 9.77E-06 | Isoform 3 of Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3 |
| B7Z7F3 | 4 | 1.10E-05 | cDNA FLJ58549, highly similar to Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=1 |
| Q9H6Z4-2 | 4 | 9.67E-06 | Isoform 2 of Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3; Additional IDs concatenated into MaxParsimony group: B7Z7F3, Q9H6Z4, Q9H6Z4-3, K7ESQ0 |
| H0YHG0 | 6 | 4.74E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F8VZQ9, P82979 |
| F8VZQ9 | 6 | 0.000116398 | SAP domain-containing ribonucleoprotein OS=Homo sapiens OX=9606 GN=SARNP PE=1 SV=1 |
| P82979 | 6 | 0.000118061 | SAP domain-containing ribonucleoprotein OS=Homo sapiens OX=9606 GN=SARNP PE=1 SV=3 |
| H0YDW7 | 6 | 3.61E-05 | CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=2 |
| P16070-10 | 6 | 1.76E-05 | Isoform 10 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-14 | 6 | 2.19E-05 | Isoform 14 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| H0YD17 | 6 | 3.78E-05 | CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=8 |
| P16070-16 | 6 | 1.30E-05 | Isoform 16 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-6 | 6 | 1.24E-05 | Isoform 6 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-15 | 6 | 2.94E-05 | Isoform 15 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-7 | 6 | 1.21E-05 | Isoform 7 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| H0YCV9 | 6 | 3.12E-05 | CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=2 |
| P16070 | 6 | 1.17E-05 | CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P16070-5, P16070-7, P16070-3, P16070-4, P16070-6, P16070-17, P16070-9, P16070-8, P16070-16, P16070-10, P16070-11, P16070-13, P16070-14, P16070-12, P16070-18, H0Y5E4, P16070-15, H0Y2P0, H0YCV9, H0YDW7, H0YD17, H0YD13, H0YDX6, E9PKC6 |
| H0Y5E4 | 6 | 2.94E-05 | CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=1 |
| P16070-5 | 6 | 1.18E-05 | Isoform 5 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| H0YD13 | 6 | 4.20E-05 | CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=2 |
| H0YDX6 | 6 | 4.73E-05 | CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=2 |
| H0Y2P0 | 6 | 3.02E-05 | CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=1 |
| P16070-12 | 6 | 2.40E-05 | Isoform 12 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-18 | 6 | 2.55E-05 | Isoform 18 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-17 | 6 | 1.25E-05 | Isoform 17 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-9 | 6 | 1.28E-05 | Isoform 9 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-13 | 6 | 2.04E-05 | Isoform 13 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-3 | 6 | 1.22E-05 | Isoform 3 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-4 | 6 | 1.24E-05 | Isoform 4 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-8 | 6 | 1.28E-05 | Isoform 8 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| P16070-11 | 6 | 2.02E-05 | Isoform 11 of CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 |
| U3KQE2 | 5 | 4.77E-05 | Calpain small subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1 |
| P63027 | 6 | 0.000128428 | Vesicle-associated membrane protein 2 OS=Homo sapiens OX=9606 GN=VAMP2 PE=1 SV=3 |
| K7ENK9 | 6 | 0.000182892 | Vesicle-associated membrane protein 2 OS=Homo sapiens OX=9606 GN=VAMP2 PE=4 SV=1 |
| L7N2F9 | 6 | 0.000123121 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1; Additional IDs concatenated into MaxParsimony group: F8WCA0, P63027, J3QRU4, Q15836, K7EKX0, K7ENK9 |
| K7EKX0 | 6 | 0.000172731 | Vesicle-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=VAMP3 PE=4 SV=1 |
| F8WCA0 | 6 | 0.000126252 | Vesicle-associated membrane protein 2 OS=Homo sapiens OX=9606 GN=VAMP2 PE=4 SV=1 |
| J3QRU4 | 6 | 0.000131838 | Vesicle-associated membrane protein 2 OS=Homo sapiens OX=9606 GN=VAMP2 PE=4 SV=2 |
| Q15836 | 6 | 0.000156965 | Vesicle-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=VAMP3 PE=1 SV=3 |
| P04179 | 6 | 0.000983311 | Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens OX=9606 GN=SOD2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: F5GYZ5, F5H4R2, P04179-4, P04179-3, F5H3C5 |
| F5H4R2 | 6 | 0.001190642 | Superoxide dismutase (Fragment) OS=Homo sapiens OX=9606 GN=SOD2 PE=1 SV=1 |
| F5H3C5 | 6 | 0.001962951 | Superoxide dismutase (Fragment) OS=Homo sapiens OX=9606 GN=SOD2 PE=1 SV=1 |
| F5GYZ5 | 6 | 0.001146776 | Superoxide dismutase (Fragment) OS=Homo sapiens OX=9606 GN=SOD2 PE=1 SV=1 |
| P04179-3 | 6 | 0.001326376 | Isoform 3 of Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens OX=9606 GN=SOD2 |
| P04179-4 | 6 | 0.001240313 | Isoform 4 of Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens OX=9606 GN=SOD2 |
| Q8NCW5 | 6 | 3.43E-05 | NAD(P)H-hydrate epimerase OS=Homo sapiens OX=9606 GN=NAXE PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8NCW5-2 |
| Q8NCW5-2 | 6 | 5.34E-05 | Isoform 2 of NAD(P)H-hydrate epimerase OS=Homo sapiens OX=9606 GN=NAXE |
| O60716-7 | 6 | 1.12E-05 | Isoform 1C of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-29 | 6 | 1.69E-05 | Isoform 4A of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-13 | 6 | 1.17E-05 | Isoform 2A of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-32 | 6 | 1.75E-05 | Isoform 4 of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-14 | 6 | 1.16E-05 | Isoform 2B of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-4 | 6 | 1.09E-05 | Isoform 1BC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-22 | 6 | 1.23E-05 | Isoform 3B of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-19 | 6 | 1.23E-05 | Isoform 3AC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716 | 6 | 1.07E-05 | Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O60716-2, O60716-4, O60716-6, O60716-3, C9JZR2, O60716-5, O60716-7, O60716-9, O60716-8, O60716-10, O60716-12, O60716-14, O60716-11, O60716-13, O60716-17, O60716-15, O60716-18, O60716-16, O60716-20, O60716-22, O60716-19, O60716-21, O60716-23, O60716-24, O60716-25, O60716-26, O60716-28, O60716-30, O60716-27, O60716-29, O60716-31, O60716-32, E9PKY0, H0YC95 |
| H0YC95 | 6 | 7.48E-05 | Catenin delta-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNND1 PE=1 SV=1 |
| O60716-3 | 6 | 1.10E-05 | Isoform 1AC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-17 | 6 | 1.19E-05 | Isoform 3ABC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-12 | 6 | 1.16E-05 | Isoform 2BC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-2 | 6 | 1.07E-05 | Isoform 1AB of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-21 | 6 | 1.24E-05 | Isoform 3A of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-24 | 6 | 1.27E-05 | Isoform 3 of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-28 | 6 | 1.65E-05 | Isoform 4BC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-25 | 6 | 1.60E-05 | Isoform 4ABC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-27 | 6 | 1.67E-05 | Isoform 4AC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-15 | 6 | 1.19E-05 | Isoform 2C of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-11 | 6 | 1.17E-05 | Isoform 2AC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-8 | 6 | 1.13E-05 | Isoform 1 of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-16 | 6 | 1.20E-05 | Isoform 2 of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-31 | 6 | 1.73E-05 | Isoform 4C of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-18 | 6 | 1.20E-05 | Isoform 3AB of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-6 | 6 | 1.10E-05 | Isoform 1B of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-30 | 6 | 1.67E-05 | Isoform 4B of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-23 | 6 | 1.26E-05 | Isoform 3C of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-10 | 6 | 1.14E-05 | Isoform 2AB of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-9 | 6 | 1.13E-05 | Isoform 2ABC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-26 | 6 | 1.61E-05 | Isoform 4AB of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| C9JZR2 | 6 | 1.10E-05 | Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 PE=1 SV=2 |
| O60716-5 | 6 | 1.11E-05 | Isoform 1A of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| O60716-20 | 6 | 1.22E-05 | Isoform 3BC of Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 |
| P40855 | 6 | 7.66E-06 | Peroxisomal biogenesis factor 19 OS=Homo sapiens OX=9606 GN=PEX19 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B7Z8B3 |
| B7Z8B3 | 6 | 1.23E-05 | cDNA FLJ52177, highly similar to Peroxisomal biogenesis factor 19 OS=Homo sapiens OX=9606 GN=PEX19 PE=1 SV=1 |
| F8VV59 | 5 | 8.04E-06 | Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| H0YHC3 | 5 | 1.33E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| P55209-2 | 6 | 1.24E-05 | Isoform 2 of Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 |
| P55209-3 | 5 | 8.14E-06 | Isoform 3 of Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 |
| P55209 | 6 | 1.17E-05 | Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0YIV4, F5H4R6, F8W0J6, P55209-2, B7Z9C2, F8VV59, P55209-3, F8VY35, F8VUX1, F8VXI6, F8W118, F8W020, H0YHC3, F8VRJ2 |
| F8VXI6 | 6 | 2.12E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| F8W118 | 5 | 1.26E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| F5H4R6 | 6 | 1.19E-05 | Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| F8W020 | 6 | 2.20E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| H0YIV4 | 6 | 1.19E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| F8VRJ2 | 5 | 2.21E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| F8VUX1 | 6 | 1.93E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| F8VY35 | 6 | 1.73E-05 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| B7Z9C2 | 5 | 7.53E-06 | cDNA FLJ58569, highly similar to Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| F8W0J6 | 6 | 1.20E-05 | Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| P21266 | 5 | 0.000127107 | Glutathione S-transferase Mu 3 OS=Homo sapiens OX=9606 GN=GSTM3 PE=1 SV=3 |
| E9PHN6 | 6 | 0.000194138 | Glutathione S-transferase OS=Homo sapiens OX=9606 GN=GSTM2 PE=1 SV=1 |
| E9PLF1 | 6 | 0.000254888 | Glutathione S-transferase Mu 2 (Fragment) OS=Homo sapiens OX=9606 GN=GSTM2 PE=1 SV=2 |
| P28161 | 6 | 0.000171874 | Glutathione S-transferase Mu 2 OS=Homo sapiens OX=9606 GN=GSTM2 PE=1 SV=2 |
| P28161-2 | 6 | 0.000196171 | Isoform 2 of Glutathione S-transferase Mu 2 OS=Homo sapiens OX=9606 GN=GSTM2 |
| A0A0A0MTN3 | 5 | 0.000134901 | Glutathione S-transferase OS=Homo sapiens OX=9606 GN=GSTM3 PE=1 SV=1 |
| F6XZQ7 | 6 | 0.000170312 | Glutathione S-transferase OS=Homo sapiens OX=9606 GN=GSTM2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P28161, E9PHN6, P28161-2, E9PHN7, E9PLF1, P21266, P46439, Q5T8R1, A0A0A0MTN3, Q5T8Q9 |
| E9PHN7 | 6 | 0.000207009 | Glutathione S-transferase Mu 2 OS=Homo sapiens OX=9606 GN=GSTM2 PE=1 SV=2 |
| Q9H910-3 | 5 | 3.83E-05 | Isoform 3 of Jupiter microtubule associated homolog 2 OS=Homo sapiens OX=9606 GN=JPT2; Additional IDs concatenated into MaxParsimony group: H3BMV3, Q9H910, A6NGP5, Q9H910-2, H3BU16, H3BTV5, H3BMT0, B4E1P3, H3BMM8 |
| H3BU16 | 5 | 5.00E-05 | Jupiter microtubule-associated homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=JPT2 PE=1 SV=1 |
| H3BMV3 | 5 | 4.39E-05 | Jupiter microtubule-associated homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=JPT2 PE=1 SV=1 |
| H3BMT0 | 5 | 7.26E-05 | Jupiter microtubule-associated homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=JPT2 PE=1 SV=1 |
| A6NGP5 | 5 | 4.69E-05 | Jupiter microtubule-associated homolog 2 OS=Homo sapiens OX=9606 GN=JPT2 PE=1 SV=2 |
| Q9H910 | 5 | 4.39E-05 | Jupiter microtubule associated homolog 2 OS=Homo sapiens OX=9606 GN=JPT2 PE=1 SV=1 |
| Q9H910-2 | 5 | 4.80E-05 | Isoform 2 of Jupiter microtubule associated homolog 2 OS=Homo sapiens OX=9606 GN=JPT2 |
| H3BTV5 | 5 | 7.19E-05 | Jupiter microtubule-associated homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=JPT2 PE=1 SV=1 |
| E9PQY2 | 6 | 0.000248429 | Prefoldin subunit 4 OS=Homo sapiens OX=9606 GN=PFDN4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NQP4 |
| Q9NQP4 | 6 | 0.000252137 | Prefoldin subunit 4 OS=Homo sapiens OX=9606 GN=PFDN4 PE=1 SV=1 |
| Q99471 | 4 | 2.19E-06 | Prefoldin subunit 5 OS=Homo sapiens OX=9606 GN=PFDN5 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H3BPF6, Q99471-2 |
| H3BPF6 | 4 | 2.22E-06 | Prefoldin subunit 5 (Fragment) OS=Homo sapiens OX=9606 GN=PFDN5 PE=1 SV=1 |
| Q99471-2 | 4 | 5.11E-06 | Isoform 2 of Prefoldin subunit 5 OS=Homo sapiens OX=9606 GN=PFDN5 |
| A0A2R8Y4Q3 | 6 | 5.66E-06 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| A0A2R8Y5G3 | 6 | 1.84E-05 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| O60313 | 6 | 4.45E-06 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=3 |
| A0A2R8YGE5 | 6 | 6.43E-06 | Dynamin-like 120 kDa protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| A0A2R8YDM2 | 6 | 4.42E-06 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| O60313-2 | 6 | 4.28E-06 | Isoform 2 of Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1; Additional IDs concatenated into MaxParsimony group: C9JMB8, A0A2R8YDM2, A0A2R8YE78, O60313, A0A2R8YGE5, A0A2R8YD53, A0A2R8Y4Q3, A0A2R8Y4G4, A0A2R8Y5G3, C9JY58 |
| C9JMB8 | 6 | 4.39E-06 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=2 |
| C9JY58 | 6 | 2.78E-05 | Dynamin-like 120 kDa protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| A0A2R8YD53 | 6 | 6.77E-06 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| A0A2R8YE78 | 6 | 4.43E-06 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| A0A2R8Y4G4 | 6 | 1.02E-05 | Dynamin-like 120 kDa protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 |
| Q15056-2 | 6 | 1.21E-05 | Isoform Short of Eukaryotic translation initiation factor 4H OS=Homo sapiens OX=9606 GN=EIF4H |
| Q15056 | 6 | 1.11E-05 | Eukaryotic translation initiation factor 4H OS=Homo sapiens OX=9606 GN=EIF4H PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: Q15056-2 |
| B4DUD2 | 6 | 2.13E-05 | Protein lifeguard 3 OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=1 |
| Q969X1 | 6 | 1.47E-05 | Protein lifeguard 3 OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: B4DUD2, C9JWV9, C9JW19, C9IZ27, F8WDY4, C9IYT2, C9JEN3 |
| C9IYT2 | 6 | 4.28E-05 | Protein lifeguard 3 (Fragment) OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=1 |
| C9JEN3 | 6 | 4.32E-05 | Protein lifeguard 3 (Fragment) OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=1 |
| C9JW19 | 6 | 2.74E-05 | Protein lifeguard 3 (Fragment) OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=1 |
| F8WDY4 | 6 | 3.27E-05 | Protein lifeguard 3 OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=1 |
| C9IZ27 | 6 | 3.05E-05 | Protein lifeguard 3 (Fragment) OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=8 |
| C9JWV9 | 6 | 2.68E-05 | Protein lifeguard 3 (Fragment) OS=Homo sapiens OX=9606 GN=TMBIM1 PE=1 SV=1 |
| Q04637-3 | 6 | 2.50E-06 | Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 |
| E7EX73 | 6 | 2.72E-06 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| Q04637-8 | 6 | 2.44E-06 | Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 |
| C9J6B6 | 6 | 5.16E-06 | Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| Q04637-5 | 6 | 2.72E-06 | Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 |
| Q04637 | 6 | 2.44E-06 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=4 |
| C9K073 | 6 | 4.49E-06 | Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| C9J2Z7 | 6 | 4.69E-06 | Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=8 |
| Q04637-4 | 6 | 2.58E-06 | Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 |
| E9PGM1 | 6 | 2.58E-06 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| E7EUU4 | 6 | 2.50E-06 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| C9JF13 | 6 | 4.32E-06 | Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1 |
| Q04637-9 | 6 | 2.43E-06 | Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1; Additional IDs concatenated into MaxParsimony group: Q04637-8, Q04637, E7EUU4, Q04637-3, E9PGM1, Q04637-4, E7EX73, Q04637-5, C9JF13, C9K073, C9J2Z7, C9J6B6, C9JHW9, F8WCF2 |
| Q8TAA3-2 | 6 | 1.08E-05 | Isoform 2 of Proteasome subunit alpha-type 8 OS=Homo sapiens OX=9606 GN=PSMA8 |
| Q8TAA3-5 | 6 | 9.17E-06 | Isoform 3 of Proteasome subunit alpha-type 8 OS=Homo sapiens OX=9606 GN=PSMA8 |
| H0Y586 | 6 | 2.85E-05 | Proteasome endopeptidase complex (Fragment) OS=Homo sapiens OX=9606 GN=PSMA7 PE=1 SV=1 |
| O14818-4 | 6 | 1.54E-05 | Isoform 3 of Proteasome subunit alpha type-7 OS=Homo sapiens OX=9606 GN=PSMA7 |
| Q8TAA3 | 6 | 8.95E-06 | Proteasome subunit alpha-type 8 OS=Homo sapiens OX=9606 GN=PSMA8 PE=2 SV=3; Additional IDs concatenated into MaxParsimony group: Q8TAA3-5, O14818, A0A087WYS6, Q8TAA3-2, H0Y586, O14818-2, O14818-4 |
| O14818 | 6 | 2.15E-05 | Proteasome subunit alpha type-7 OS=Homo sapiens OX=9606 GN=PSMA7 PE=1 SV=1 |
| O14818-2 | 6 | 3.00E-05 | Isoform 2 of Proteasome subunit alpha type-7 OS=Homo sapiens OX=9606 GN=PSMA7 |
| A0A087WYS6 | 6 | 1.02E-05 | Proteasome endopeptidase complex OS=Homo sapiens OX=9606 GN=PSMA8 PE=1 SV=1 |
| Q9H4G4 | 6 | 0.000189591 | Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens OX=9606 GN=GLIPR2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q5VZR0, A0A087WUM5 |
| Q5VZR0 | 6 | 0.000228101 | Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens OX=9606 GN=GLIPR2 PE=1 SV=1 |
| E9PR30 | 6 | 0.000435062 | 40S ribosomal protein S30 OS=Homo sapiens OX=9606 GN=FAU PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P62861 |
| P62861 | 6 | 0.000722645 | 40S ribosomal protein S30 OS=Homo sapiens OX=9606 GN=FAU PE=1 SV=1 |
| A6PVN8 | 6 | 4.13E-05 | Serine/threonine-protein phosphatase 2A activator (Fragment) OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| C9IZ76 | 6 | 4.04E-05 | Serine/threonine-protein phosphatase 2A activator (Fragment) OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| Q15257-2 | 6 | 3.18E-05 | Isoform 1 of Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA |
| Q15257 | 6 | 2.87E-05 | Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A6PVN5, Q15257-2, Q15257-3, F6WIT2, A6PVN9, Q5T948, Q5T949, A6PVN6, C9IZ76, A6PVN8, A6PVN7 |
| A6PVN6 | 6 | 3.03E-05 | Serine/threonine-protein phosphatase 2A activator (Fragment) OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| Q5T948 | 6 | 2.52E-05 | Serine/threonine-protein phosphatase 2A activator (Fragment) OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=8 |
| A6PVN5 | 6 | 3.13E-05 | Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| A6PVN7 | 6 | 7.32E-05 | Serine/threonine-protein phosphatase 2A activator (Fragment) OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| Q15257-3 | 6 | 3.50E-05 | Isoform 3 of Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA |
| A6PVN9 | 6 | 2.13E-05 | Serine/threonine-protein phosphatase 2A activator (Fragment) OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| F6WIT2 | 6 | 3.21E-05 | Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| Q5T949 | 6 | 2.55E-05 | Serine/threonine-protein phosphatase 2A activator (Fragment) OS=Homo sapiens OX=9606 GN=PTPA PE=1 SV=1 |
| Q52LJ0-2 | 6 | 2.27E-05 | Isoform 2 of Protein FAM98B OS=Homo sapiens OX=9606 GN=FAM98B; Additional IDs concatenated into MaxParsimony group: Q52LJ0 |
| Q52LJ0 | 6 | 2.97E-05 | Protein FAM98B OS=Homo sapiens OX=9606 GN=FAM98B PE=1 SV=1 |
| Q9H0W9-4 | 4 | 4.23E-05 | Isoform 4 of Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 |
| E9PJU8 | 4 | 4.62E-05 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| A0A087WT99 | 5 | 4.57E-05 | Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| Q9H0W9 | 5 | 3.72E-05 | Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9H0W9-2, Q9H0W9-3, A0A087WT99, Q9H0W9-4, E9PJU8 |
| Q9H0W9-2 | 5 | 3.95E-05 | Isoform 2 of Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 |
| Q9H0W9-3 | 5 | 4.42E-05 | Isoform 3 of Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 |
| Q9UMS0 | 4 | 7.99E-06 | NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Homo sapiens OX=9606 GN=NFU1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UMS0-3 |
| Q9UMS0-3 | 4 | 8.82E-06 | Isoform 3 of NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Homo sapiens OX=9606 GN=NFU1 |
| A0A182DWF5 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A182DWE9 | 5 | 2.64E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| Q95IE3 | 5 | 2.56E-05 | HLA class II histocompatibility antigen, DRB1-12 beta chain OS=Homo sapiens OX=9606 GN=HLA-DRB1 PE=1 SV=1 |
| Q5EP54 | 5 | 2.64E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A0G2JJV3 | 5 | 2.98E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| P04440 | 5 | 2.64E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A182DWG2 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T966 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9T0 | 5 | 3.04E-05 | HLA class II histocompatibility antigen, DQ beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQB1 PE=1 SV=1 |
| A0A140T8Z3 | 5 | 2.98E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| B4DJG1 | 5 | 5.00E-05 | HLA class II histocompatibility antigen, DQ beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQB1 PE=1 SV=1 |
| A0A182DWF4 | 5 | 2.98E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T928 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9Q1 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| Q5Y7D3 | 5 | 2.61E-05 | HLA class II histocompatibility antigen, DQ beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQB1 PE=1 SV=1 |
| A0A0G2JII1 | 5 | 2.98E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9S8 | 5 | 2.53E-05 | HLA class II histocompatibility antigen, DQ beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQB1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q95IE3, P20039, Q5Y7A7, P01911, P01912, Q5Y7D3, A0A182DWE9, Q5EP54, P04440, A0A140T9Y0, A0A140T9I3, H0Y5P2, A0A140T9Y2, A0A182DWF5, A0A140T9P7, A0A140T928, A0A140T9Q1, A0A182DWG2, A0A140T966, A0A140T915, A0A140T9P1, A0A140T976, A0A140T9A5, A0A140T8Z7, H0Y7G7, A0A182DWF4, A0A140T9T6, A0A0G2JJV3, A0A140T8Z3, A0A0G2JII1, A0A140T9T0, A0A140T8Z1, B4DJG1 |
| A0A140T9Y2 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| P01912 | 5 | 2.56E-05 | HLA class II histocompatibility antigen, DRB1-3 chain OS=Homo sapiens OX=9606 GN=HLA-DRB1 PE=1 SV=2 |
| A0A140T8Z7 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9A5 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| H0Y5P2 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9I3 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9P1 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T976 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| P01911 | 5 | 2.56E-05 | HLA class II histocompatibility antigen, DRB1-15 beta chain OS=Homo sapiens OX=9606 GN=HLA-DRB1 PE=1 SV=2 |
| A0A140T915 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9Y0 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T8Z1 | 5 | 3.04E-05 | HLA class II histocompatibility antigen, DQ beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQB1 PE=1 SV=1 |
| A0A140T9T6 | 5 | 2.98E-05 | HLA class II histocompatibility antigen, DP beta 1 chain OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| Q5Y7A7 | 5 | 2.56E-05 | HLA class II histocompatibility antigen, DRB1-13 beta chain OS=Homo sapiens OX=9606 GN=HLA-DRB1 PE=1 SV=1 |
| P20039 | 5 | 2.56E-05 | HLA class II histocompatibility antigen, DRB1-11 beta chain OS=Homo sapiens OX=9606 GN=HLA-DRB1 PE=1 SV=1 |
| H0Y7G7 | 5 | 2.97E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| A0A140T9P7 | 5 | 2.89E-05 | HLA class II histocompatibility antigen, DP beta 1 chain (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DPB1 PE=1 SV=1 |
| F5GX23 | 5 | 3.62E-05 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=1 |
| F5H169 | 5 | 5.06E-05 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=1 |
| J3KN29 | 5 | 2.92E-05 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=1 |
| F5H5V4 | 5 | 4.23E-05 | 26S proteasome non-ATPase regulatory subunit 9 (Fragment) OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=1 |
| F5H7X1 | 5 | 7.62E-05 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=1 |
| O00233-2 | 5 | 3.10E-05 | Isoform p27-S of 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 |
| O00233 | 5 | 2.90E-05 | 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: J3KN29, O00233-2, F5GX23, F5H5V4, F5H169, F5H7X1 |
| Q99538-2 | 5 | 3.75E-06 | Isoform 2 of Legumain OS=Homo sapiens OX=9606 GN=LGMN |
| G3V4E4 | 5 | 6.32E-06 | Legumain OS=Homo sapiens OX=9606 GN=LGMN PE=1 SV=1 |
| Q99538-3 | 5 | 3.79E-06 | Isoform 3 of Legumain OS=Homo sapiens OX=9606 GN=LGMN |
| G3V2T4 | 5 | 1.04E-05 | Legumain (Fragment) OS=Homo sapiens OX=9606 GN=LGMN PE=1 SV=1 |
| H0YJN9 | 5 | 1.55E-05 | Legumain (Fragment) OS=Homo sapiens OX=9606 GN=LGMN PE=1 SV=1 |
| Q99538 | 5 | 3.26E-06 | Legumain OS=Homo sapiens OX=9606 GN=LGMN PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q99538-2, Q99538-3, G3V4E4, G3V2T4, H0YJN9 |
| A0A075B6H7 | 5 | 6.26E-05 | Immunoglobulin kappa variable 3-7 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGKV3-7 PE=1 SV=1 |
| A0A0C4DH55 | 5 | 6.10E-05 | Immunoglobulin kappa variable 3D-7 OS=Homo sapiens OX=9606 GN=IGKV3D-7 PE=3 SV=5; Additional IDs concatenated into MaxParsimony group: A0A075B6H7, A0A0C4DH90, P01624 |
| P01624 | 5 | 6.31E-05 | Immunoglobulin kappa variable 3-15 OS=Homo sapiens OX=9606 GN=IGKV3-15 PE=1 SV=2 |
| A0A0C4DH90 | 5 | 6.26E-05 | Immunoglobulin kappa variable 3/OR2-268 (non-functional) (Fragment) OS=Homo sapiens OX=9606 GN=IGKV3OR2-268 PE=4 SV=5 |
| P17980 | 5 | 4.34E-06 | 26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: R4GNH3, E9PM69, E9PKD5 |
| E9PM69 | 5 | 4.80E-06 | 26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=1 |
| E9PKD5 | 5 | 6.13E-06 | 26S proteasome regulatory subunit 6A (Fragment) OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=2 |
| R4GNH3 | 5 | 4.50E-06 | 26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=1 |
| F2Z388 | 6 | 7.20E-05 | 60S ribosomal protein L35 OS=Homo sapiens OX=9606 GN=RPL35 PE=1 SV=1 |
| P42766 | 6 | 5.62E-05 | 60S ribosomal protein L35 OS=Homo sapiens OX=9606 GN=RPL35 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F2Z388 |
| C9JEU5 | 6 | 1.73E-05 | Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1 |
| P02679-2 | 6 | 1.76E-05 | Isoform Gamma-A of Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG |
| P02679 | 6 | 1.70E-05 | Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=3 |
| C9JC84 | 6 | 1.67E-05 | Fibrinogen gamma chain OS=Homo sapiens OX=9606 GN=FGG PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P02679, C9JEU5, P02679-2 |
| A0A2R8Y6H2 | 6 | 7.14E-06 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1 |
| A0A2R8Y706 | 6 | 1.07E-05 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1 |
| A0A2R8Y5T0 | 5 | 1.18E-05 | Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1 |
| P13637-2 | 6 | 3.90E-05 | Isoform 2 of Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens OX=9606 GN=ATP1A3 |
| A0A2R8YEY8 | 6 | 3.95E-05 | Sodium/potassium-transporting ATPase subunit alpha OS=Homo sapiens OX=9606 PE=3 SV=1 |
| P20648 | 6 | 1.40E-05 | Potassium-transporting ATPase alpha chain 1 OS=Homo sapiens OX=9606 GN=ATP4A PE=2 SV=5 |
| H0Y7C1 | 6 | 1.37E-05 | Sodium/potassium-transporting ATPase subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=ATP1A2 PE=1 SV=1 |
| P13637 | 6 | 3.94E-05 | Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens OX=9606 GN=ATP1A3 PE=1 SV=3 |
| P50993 | 6 | 2.86E-05 | Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens OX=9606 GN=ATP1A2 PE=1 SV=1 |
| P13637-3 | 6 | 3.89E-05 | Isoform 3 of Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens OX=9606 GN=ATP1A3 |
| M0QXF2 | 6 | 7.72E-05 | Sodium/potassium-transporting ATPase subunit alpha-3 (Fragment) OS=Homo sapiens OX=9606 GN=ATP1A3 PE=1 SV=2 |
| M0R116 | 6 | 4.06E-05 | Sodium/potassium-transporting ATPase subunit alpha OS=Homo sapiens OX=9606 GN=ATP1A3 PE=1 SV=1 |
| A0A0A0MT26 | 6 | 3.26E-05 | Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens OX=9606 GN=ATP1A3 PE=1 SV=1 |
| B1AKY9 | 6 | 2.89E-05 | Sodium/potassium-transporting ATPase subunit alpha OS=Homo sapiens OX=9606 GN=ATP1A2 PE=1 SV=1 |
| C9J5G3 | 6 | 0.002675038 | Limbic system-associated membrane protein (Fragment) OS=Homo sapiens OX=9606 GN=LSAMP PE=1 SV=1 |
| H0YCY8 | 6 | 0.001151492 | Dipeptidyl peptidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CTSC PE=1 SV=8 |
| I3L3T3 | 6 | 0.000457443 | N-sulphoglucosamine sulphohydrolase (Fragment) OS=Homo sapiens OX=9606 GN=SGSH PE=1 SV=1 |
| Q5JR01 | 6 | 0.000135129 | Elongation factor 1-alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1 |
| A0A2R8YDN5 | 6 | 0.000182139 | Elongation factor 1-alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1 |
| A0A2R8Y660 | 6 | 0.000137193 | Elongation factor 1-alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1 |
| A6PW80 | 6 | 0.000184846 | Elongation factor 1-alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=EEF1A1 PE=4 SV=8 |
| A0A2R8Y488 | 6 | 0.00012054 | Elongation factor 1-alpha 2 (Fragment) OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1 |
| J3KSR8 | 6 | 0.000272322 | Serine/arginine-rich-splicing factor 1 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=1 |
| H0YKN4 | 6 | 0.000428846 | Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YNB8 | 6 | 0.000629582 | Annexin A2 (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YLE2 | 6 | 0.0003817 | Annexin A2 (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| Q99623-2 | 5 | 9.15E-05 | Isoform 2 of Prohibitin-2 OS=Homo sapiens OX=9606 GN=PHB2 |
| J3KPX7 | 5 | 0.000107934 | Prohibitin-2 OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=2 |
| F5GY37 | 5 | 0.000118489 | Prohibitin-2 OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=1 |
| F5GWA7 | 5 | 8.88E-05 | Prohibitin-2 (Fragment) OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=1 |
| F5H0C5 | 5 | 6.02E-05 | Prohibitin-2 OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=1 |
| Q99623 | 5 | 0.000107573 | Prohibitin-2 OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: J3KPX7, F5GY37, Q99623-2, F5GWA7, F5H3X6, F5H0C5, F5H2D2 |
| P16401 | 5 | 0.000233818 | Histone H1.5 OS=Homo sapiens OX=9606 GN=HIST1H1B PE=1 SV=3 |
| C9J4G9 | 6 | 8.33E-06 | Beta-galactosidase (Fragment) OS=Homo sapiens OX=9606 GN=GLB1 PE=1 SV=1 |
| Q13263-2 | 6 | 4.38E-05 | Isoform 2 of Transcription intermediary factor 1-beta OS=Homo sapiens OX=9606 GN=TRIM28 |
| M0R0K9 | 6 | 7.17E-05 | Transcription intermediary factor 1-beta (Fragment) OS=Homo sapiens OX=9606 GN=TRIM28 PE=1 SV=1 |
| Q13263 | 6 | 3.95E-05 | Transcription intermediary factor 1-beta OS=Homo sapiens OX=9606 GN=TRIM28 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: Q13263-2, M0R0K9 |
| I3L3P5 | 6 | 3.73E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=1 |
| H7BZ94 | 6 | 6.74E-05 | Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=2 |
| I3L398 | 6 | 7.68E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=1 |
| P07237 | 6 | 6.65E-05 | Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H7BZ94, H0Y3Z3, I3L398, I3L312, I3NI03, I3L4M2, I3L3P5, I3L0S0, I3L3U6 |
| I3L312 | 6 | 4.30E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=2 |
| I3NI03 | 5 | 5.72E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=1 |
| H0Y3Z3 | 6 | 8.39E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=1 |
| I3L4M2 | 5 | 6.34E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=1 |
| I3L3U6 | 5 | 1.77E-05 | Protein disulfide-isomerase (Fragment) OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=1 |
| P24844-2 | 6 | 0.000978177 | Isoform 2 of Myosin regulatory light polypeptide 9 OS=Homo sapiens OX=9606 GN=MYL9 |
| P24844 | 6 | 0.000727261 | Myosin regulatory light polypeptide 9 OS=Homo sapiens OX=9606 GN=MYL9 PE=1 SV=4 |
| J3KTJ1 | 6 | 0.000276662 | Myosin regulatory light chain 12A (Fragment) OS=Homo sapiens OX=9606 GN=MYL12A PE=1 SV=1 |
| P01860 | 6 | 0.000430297 | Immunoglobulin heavy constant gamma 3 OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=2 |
| A0A0A0MS07 | 6 | 0.001060155 | Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1 |
| P01857 | 6 | 0.000950279 | Immunoglobulin heavy constant gamma 1 OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1 |
| P01859 | 6 | 0.000467791 | Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2 |
| A0A0A0MS08 | 6 | 0.000785945 | Immunoglobulin heavy constant gamma 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P01857, A0A0A0MS07, contaminant\_NRL\_1MCOH, A0A286YES1, P01860, P01859, A0A286YFJ8, P01861 |
| contaminant\_NRL\_1MCOH | 6 | 0.000731974 | Immunoglobulin g1 (igg1) (mcg) with a hinge deletion, chain H... |
| A0A286YEY4 | 6 | 0.000386076 | Immunoglobulin heavy constant gamma 2 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=1 |
| P01861 | 6 | 0.000141074 | Immunoglobulin heavy constant gamma 4 OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1 |
| A0A286YES1 | 6 | 0.000363726 | Immunoglobulin heavy constant gamma 3 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG3 PE=1 SV=1 |
| A0A286YFJ8 | 6 | 0.000116493 | Immunoglobulin heavy constant gamma 4 (Fragment) OS=Homo sapiens OX=9606 GN=IGHG4 PE=1 SV=1 |
| A0A087X243 | 6 | 0.000207275 | Glutathione S-transferase P (Fragment) OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=1 |
| A0A0X1KG78 | 6 | 0.000264534 | Calcyphosine, isoform CRA\_d OS=Homo sapiens OX=9606 GN=CAPS PE=1 SV=1 |
| Q13938-3 | 6 | 0.000404965 | Isoform 2 of Calcyphosin OS=Homo sapiens OX=9606 GN=CAPS |
| Q13938 | 6 | 0.000451046 | Calcyphosin OS=Homo sapiens OX=9606 GN=CAPS PE=1 SV=1 |
| K7ES72 | 6 | 0.000489585 | Calcyphosin (Fragment) OS=Homo sapiens OX=9606 GN=CAPS PE=1 SV=2 |
| K7EL21 | 6 | 0.000309992 | Calcyphosine, isoform CRA\_b OS=Homo sapiens OX=9606 GN=CAPS PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q13938, A0A0X1KG78, Q13938-3, K7ES72 |
| F8WDB3 | 6 | 7.69E-05 | ADP-ribosylation factor 4 OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=1 |
| P18085 | 6 | 2.62E-05 | ADP-ribosylation factor 4 OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=3 |
| F5H0C7 | 6 | 4.77E-05 | ADP-ribosylation factor 3 (Fragment) OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=1 |
| F5H1V1 | 6 | 0.000113405 | ADP-ribosylation factor 3 (Fragment) OS=Homo sapiens OX=9606 GN=ARF3 PE=4 SV=1 |
| C9JPM4 | 6 | 3.71E-05 | ADP-ribosylation factor 4 (Fragment) OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=1 |
| F5H6T5 | 6 | 9.07E-05 | ADP-ribosylation factor 3 (Fragment) OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=1 |
| Q06323-2 | 6 | 0.00038737 | Isoform 2 of Proteasome activator complex subunit 1 OS=Homo sapiens OX=9606 GN=PSME1; Additional IDs concatenated into MaxParsimony group: Q06323, Q06323-3, H0YLU2 |
| Q06323 | 6 | 0.000388925 | Proteasome activator complex subunit 1 OS=Homo sapiens OX=9606 GN=PSME1 PE=1 SV=1 |
| Q06323-3 | 6 | 0.000415633 | Isoform 3 of Proteasome activator complex subunit 1 OS=Homo sapiens OX=9606 GN=PSME1 |
| H0YLU2 | 6 | 0.000192766 | Proteasome activator complex subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=PSME1 PE=1 SV=1 |
| H0YE29 | 6 | 7.63E-05 | Rho GTPase-activating protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGAP1 PE=1 SV=1 |
| P42785-2 | 6 | 0.000167562 | Isoform 2 of Lysosomal Pro-X carboxypeptidase OS=Homo sapiens OX=9606 GN=PRCP; Additional IDs concatenated into MaxParsimony group: P42785, E9PIG4, E9PKN6, E9PQN3, E9PNJ1, E9PL85, E9PQB5, E9PNF7, E9PLY4, E9PL49 |
| P42785 | 6 | 0.000174656 | Lysosomal Pro-X carboxypeptidase OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1 |
| E9PLY4 | 6 | 9.64E-05 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=8 |
| E9PIG4 | 6 | 9.31E-05 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=8 |
| E9PNJ1 | 6 | 6.06E-05 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=8 |
| E9PNF7 | 6 | 8.52E-05 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1 |
| E9PL49 | 6 | 0.000221128 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1 |
| E9PQN3 | 6 | 0.000118598 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1 |
| E9PKN6 | 6 | 0.000113039 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1 |
| E9PL85 | 6 | 0.000147643 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=8 |
| E9PQB5 | 6 | 0.000149679 | Lysosomal Pro-X carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1 |
| B9A067 | 6 | 4.49E-05 | MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=2 |
| Q16891-4 | 6 | 4.21E-05 | Isoform 4 of MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT |
| H7C463 | 6 | 3.40E-05 | MICOS complex subunit MIC60 (Fragment) OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=1 |
| Q16891-3 | 6 | 2.87E-05 | Isoform 3 of MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT |
| Q16891-2 | 6 | 4.27E-05 | Isoform 2 of MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT |
| Q16891 | 6 | 4.21E-05 | MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q16891-4, Q16891-2, B9A067, C9J406, Q16891-3, H7C463 |
| C9J406 | 6 | 4.84E-05 | MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=1 |
| Q9NRN5-3 | 6 | 0.000235439 | Isoform 3 of Olfactomedin-like protein 3 OS=Homo sapiens OX=9606 GN=OLFML3 |
| Q9NRN5-2 | 5 | 5.36E-05 | Isoform 2 of Olfactomedin-like protein 3 OS=Homo sapiens OX=9606 GN=OLFML3 |
| Q9NRN5 | 6 | 0.000166431 | Olfactomedin-like protein 3 OS=Homo sapiens OX=9606 GN=OLFML3 PE=2 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NRN5-3, Q9NRN5-2, B4DNG0 |
| B4DNG0 | 5 | 6.00E-05 | cDNA FLJ58142, highly similar to Olfactomedin-like protein 3 OS=Homo sapiens OX=9606 GN=OLFML3 PE=1 SV=1 |
| Q6IPX3-2 | 6 | 0.000216705 | Isoform 2 of Transcription elongation factor A protein-like 6 OS=Homo sapiens OX=9606 GN=TCEAL6 |
| Q969E4 | 6 | 0.000370994 | Transcription elongation factor A protein-like 3 OS=Homo sapiens OX=9606 GN=TCEAL3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5H9L2, Q6IPX3, Q6IPX3-2 |
| Q6IPX3 | 6 | 0.000216612 | Transcription elongation factor A protein-like 6 OS=Homo sapiens OX=9606 GN=TCEAL6 PE=2 SV=1 |
| Q5H9L2 | 6 | 0.000220965 | Transcription elongation factor A protein-like 5 OS=Homo sapiens OX=9606 GN=TCEAL5 PE=1 SV=1 |
| H0Y865 | 6 | 0.000401743 | TSC22 domain family protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=TSC22D2 PE=1 SV=1 |
| O75157-2 | 6 | 0.00011275 | Isoform 2 of TSC22 domain family protein 2 OS=Homo sapiens OX=9606 GN=TSC22D2 |
| O75157 | 6 | 0.000109281 | TSC22 domain family protein 2 OS=Homo sapiens OX=9606 GN=TSC22D2 PE=1 SV=3 |
| F5GX11 | 6 | 0.00016599 | Proteasome endopeptidase complex OS=Homo sapiens OX=9606 GN=PSMA1 PE=1 SV=1 |
| P25786 | 6 | 0.000150212 | Proteasome subunit alpha type-1 OS=Homo sapiens OX=9606 GN=PSMA1 PE=1 SV=1 |
| P25786-2 | 6 | 0.000146861 | Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens OX=9606 GN=PSMA1; Additional IDs concatenated into MaxParsimony group: P25786, F5GX11 |
| O00461 | 6 | 5.68E-05 | Golgi integral membrane protein 4 OS=Homo sapiens OX=9606 GN=GOLIM4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F8W785 |
| F8W785 | 6 | 5.92E-05 | Golgi integral membrane protein 4 OS=Homo sapiens OX=9606 GN=GOLIM4 PE=1 SV=1 |
| Q9UIJ7-2 | 6 | 0.000113852 | Isoform 2 of GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens OX=9606 GN=AK3 |
| Q9UIJ7-3 | 6 | 0.000126146 | Isoform 3 of GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens OX=9606 GN=AK3 |
| Q9UIJ7 | 6 | 0.000130231 | GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens OX=9606 GN=AK3 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: Q9UIJ7-3, Q9UIJ7-2 |
| P09496-3 | 6 | 0.000566847 | Isoform 3 of Clathrin light chain A OS=Homo sapiens OX=9606 GN=CLTA |
| P09496-4 | 6 | 0.000581635 | Isoform 4 of Clathrin light chain A OS=Homo sapiens OX=9606 GN=CLTA |
| F8WF69 | 6 | 0.000483877 | Clathrin light chain OS=Homo sapiens OX=9606 GN=CLTA PE=1 SV=1 |
| P09496 | 6 | 0.000539419 | Clathrin light chain A OS=Homo sapiens OX=9606 GN=CLTA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P09496-3, P09496-4, P09496-2, F8WF69, C9J8P9, P09496-5 |
| P09496-5 | 6 | 0.00010307 | Isoform 5 of Clathrin light chain A OS=Homo sapiens OX=9606 GN=CLTA |
| P09496-2 | 6 | 0.000613651 | Isoform Non-brain of Clathrin light chain A OS=Homo sapiens OX=9606 GN=CLTA |
| C9J8P9 | 6 | 8.73E-05 | Clathrin light chain OS=Homo sapiens OX=9606 GN=CLTA PE=1 SV=1 |
| Q9UHG3-2 | 6 | 3.43E-05 | Isoform 2 of Prenylcysteine oxidase 1 OS=Homo sapiens OX=9606 GN=PCYOX1 |
| Q9UHG3 | 6 | 2.91E-05 | Prenylcysteine oxidase 1 OS=Homo sapiens OX=9606 GN=PCYOX1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9UHG3-2, F8W8W4, C9K055, C9JM55 |
| F8W8W4 | 5 | 4.63E-05 | Prenylcysteine oxidase 1 OS=Homo sapiens OX=9606 GN=PCYOX1 PE=1 SV=1 |
| C9JM55 | 5 | 8.80E-05 | Prenylcysteine oxidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=PCYOX1 PE=1 SV=1 |
| C9K055 | 5 | 6.48E-05 | Prenylcysteine oxidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=PCYOX1 PE=1 SV=1 |
| K7EIF7 | 6 | 0.00012786 | Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| K7ENN6 | 6 | 0.000201884 | Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=2 |
| K7EQX4 | 6 | 0.000239737 | Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| K7EQL0 | 6 | 9.71E-05 | Cold-inducible RNA-binding protein OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 |
| H7C1X2 | 6 | 1.06E-05 | Glutathione hydrolase 5 proenzyme (Fragment) OS=Homo sapiens OX=9606 GN=GGT5 PE=1 SV=1 |
| P36269-3 | 6 | 1.34E-05 | Isoform 3 of Glutathione hydrolase 5 proenzyme OS=Homo sapiens OX=9606 GN=GGT5; Additional IDs concatenated into MaxParsimony group: P36269, P36269-2, H7C1X2 |
| P36269 | 6 | 1.34E-05 | Glutathione hydrolase 5 proenzyme OS=Homo sapiens OX=9606 GN=GGT5 PE=1 SV=2 |
| P36269-2 | 6 | 1.42E-05 | Isoform 2 of Glutathione hydrolase 5 proenzyme OS=Homo sapiens OX=9606 GN=GGT5 |
| A8MTM1 | 6 | 8.72E-05 | Carbonyl reductase [NADPH] 1 OS=Homo sapiens OX=9606 GN=CBR1 PE=1 SV=1 |
| P16152-2 | 6 | 0.000111952 | Isoform 2 of Carbonyl reductase [NADPH] 1 OS=Homo sapiens OX=9606 GN=CBR1 |
| E9PQ63 | 6 | 0.000108807 | Carbonyl reductase [NADPH] 1 OS=Homo sapiens OX=9606 GN=CBR1 PE=1 SV=1 |
| P16152 | 6 | 0.000110606 | Carbonyl reductase [NADPH] 1 OS=Homo sapiens OX=9606 GN=CBR1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A8MTM1, E9PQ63, P16152-2, O75828 |
| O75828 | 6 | 4.17E-05 | Carbonyl reductase [NADPH] 3 OS=Homo sapiens OX=9606 GN=CBR3 PE=1 SV=3 |
| P99999 | 6 | 0.000156921 | Cytochrome c OS=Homo sapiens OX=9606 GN=CYCS PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9JFR7 |
| C9JFR7 | 6 | 0.000163136 | Cytochrome c (Fragment) OS=Homo sapiens OX=9606 GN=CYCS PE=1 SV=1 |
| Q16890-2 | 6 | 0.000234512 | Isoform 2 of Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 |
| Q16890-4 | 6 | 0.000331075 | Isoform 4 of Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 |
| Q16890-5 | 6 | 0.000219675 | Isoform 5 of Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 |
| E9PPQ1 | 6 | 0.000201273 | Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 PE=1 SV=1 |
| Q16890 | 6 | 0.000188447 | Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 PE=1 SV=1 |
| E9PNK6 | 6 | 0.000231585 | Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 PE=1 SV=1 |
| J3KNE7 | 6 | 0.000183938 | Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q16890, E9PPQ1, Q16890-5, E9PNK6, Q16890-2, Q16890-3, Q16890-4, E9PNQ9 |
| Q16890-3 | 6 | 0.000257784 | Isoform 3 of Tumor protein D53 OS=Homo sapiens OX=9606 GN=TPD52L1 |
| E9PNQ9 | 6 | 0.000318955 | Tumor protein D53 (Fragment) OS=Homo sapiens OX=9606 GN=TPD52L1 PE=1 SV=1 |
| H7C003 | 4 | 3.32E-06 | Protein phosphatase 1 regulatory subunit 7 (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1 |
| B5MBZ8 | 5 | 3.27E-05 | Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1 |
| Q15435 | 5 | 2.49E-05 | Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q15435-3, B5MBZ8, C9JRC4, H7C003, Q15435-2, C9J177, C9JD73, Q15435-4, Q15435-5 |
| Q15435-3 | 5 | 3.20E-05 | Isoform 3 of Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 |
| C9JD73 | 4 | 3.95E-06 | Protein phosphatase 1 regulatory subunit 7 (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1 |
| B7Z7D2 | 6 | 7.05E-05 | cDNA FLJ51131, highly similar to Lysosomal acid phosphatase (EC 3.1.3.2) OS=Homo sapiens OX=9606 GN=ACP2 PE=1 SV=1 |
| P11117 | 6 | 7.01E-05 | Lysosomal acid phosphatase OS=Homo sapiens OX=9606 GN=ACP2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: E9PHY0, E9PQY3, B7Z7D2, E9PP23 |
| E9PP23 | 4 | 3.04E-05 | Lysosomal acid phosphatase (Fragment) OS=Homo sapiens OX=9606 GN=ACP2 PE=1 SV=1 |
| E9PHY0 | 6 | 8.24E-05 | Lysosomal acid phosphatase OS=Homo sapiens OX=9606 GN=ACP2 PE=1 SV=1 |
| E9PQY3 | 6 | 6.98E-05 | Lysosomal acid phosphatase OS=Homo sapiens OX=9606 GN=ACP2 PE=1 SV=1 |
| F8WEF0 | 5 | 9.63E-05 | Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=1 |
| P31939 | 5 | 1.39E-05 | Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: F8WEF0, P31939-2 |
| P31939-2 | 5 | 1.16E-05 | Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC |
| A0A0C4DGL3 | 6 | 7.40E-05 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=DUT PE=1 SV=1 |
| H0YKI0 | 6 | 5.96E-05 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=DUT PE=1 SV=1 |
| P33316-2 | 6 | 0.000107305 | Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=DUT |
| P33316 | 6 | 6.98E-05 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=DUT PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: H0YKC5, H0YNW5, P33316-2, H0YKI0, H0YNJ9, A0A0C4DGL3, H0YMM5 |
| H0YKC5 | 6 | 7.96E-05 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=DUT PE=1 SV=1 |
| H0YNJ9 | 6 | 9.42E-05 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=DUT PE=1 SV=1 |
| H0YNW5 | 6 | 0.000105377 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=DUT PE=1 SV=1 |
| H0YMM5 | 6 | 0.000101232 | Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=DUT PE=1 SV=1 |
| F2Z393 | 6 | 0.000149212 | Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=1 SV=1 |
| E9PM01 | 6 | 0.000324442 | Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=1 SV=1 |
| P37837 | 6 | 0.0001408 | Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F2Z393, E9PKI8, E9PM01 |
| E9PKI8 | 6 | 0.000174431 | Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=1 SV=1 |
| A0A0J9YYJ0 | 6 | 0.000187452 | Protein canopy homolog 4 (Fragment) OS=Homo sapiens OX=9606 GN=CNPY4 PE=1 SV=1 |
| P53004 | 6 | 2.76E-05 | Biliverdin reductase A OS=Homo sapiens OX=9606 GN=BLVRA PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9J1E1 |
| P00390-4 | 6 | 1.19E-05 | Isoform 3 of Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSR |
| P00390-2 | 6 | 1.17E-05 | Isoform Cytoplasmic of Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSR |
| P00390 | 6 | 1.07E-05 | Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSR PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P00390-3, P00390-2, P00390-4, P00390-5, H0YC68, A0A2R8YF59 |
| P00390-3 | 6 | 1.13E-05 | Isoform 2 of Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSR |
| P00390-5 | 6 | 1.27E-05 | Isoform 4 of Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSR |
| A0A2R8YDH4 | 6 | 2.80E-05 | Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 PE=3 SV=1; Additional IDs concatenated into MaxParsimony group: A0A1B0GTW1, Q9UDY2-7, Q9UDY2, Q9UDY2-3, Q9UDY2-6, Q9UDY2-2, Q9UDY2-4, Q9UDY2-5, B1AN86, U3KQJ2 |
| Q9UDY2 | 6 | 3.10E-05 | Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=2 |
| Q9UDY2-3 | 6 | 3.16E-05 | Isoform C1 of Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 |
| B1AN86 | 6 | 0.000215895 | Tight junction protein ZO-2 (Fragment) OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=1 |
| Q9UDY2-2 | 6 | 3.36E-05 | Isoform A2 of Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 |
| Q9UDY2-5 | 6 | 3.53E-05 | Isoform A3 of Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 |
| A0A1B0GTW1 | 6 | 2.96E-05 | Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=1 |
| Q9UDY2-6 | 6 | 3.19E-05 | Isoform 6 of Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 |
| Q9UDY2-4 | 6 | 3.44E-05 | Isoform C2 of Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 |
| U3KQJ2 | 6 | 0.000259396 | Tight junction protein ZO-2 (Fragment) OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=1 |
| Q9UDY2-7 | 6 | 3.02E-05 | Isoform 7 of Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 |
| A0A024QZ42 | 6 | 1.80E-05 | HCG1985580, isoform CRA\_c OS=Homo sapiens OX=9606 GN=PDCD6 PE=1 SV=1 |
| O75340-2 | 6 | 1.25E-05 | Isoform 2 of Programmed cell death protein 6 OS=Homo sapiens OX=9606 GN=PDCD6 |
| O75340 | 6 | 1.24E-05 | Programmed cell death protein 6 OS=Homo sapiens OX=9606 GN=PDCD6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O75340-2, A0A024QZ42 |
| P07108-2 | 6 | 0.000716806 | Isoform 2 of Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI |
| A0A0A0MTI5 | 6 | 0.000521314 | Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI PE=1 SV=1 |
| P07108 | 6 | 0.000856872 | Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI PE=1 SV=2 |
| P07108-4 | 6 | 0.00057789 | Isoform 4 of Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI |
| P07108-3 | 6 | 0.000847135 | Isoform 3 of Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI |
| P07108-5 | 6 | 0.000503702 | Isoform 5 of Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI; Additional IDs concatenated into MaxParsimony group: A0A0A0MTI5, P07108-4, P07108-2, B8ZWD1, P07108-3, P07108 |
| B8ZWD1 | 6 | 0.000768535 | Acyl-CoA-binding protein OS=Homo sapiens OX=9606 GN=DBI PE=1 SV=1 |
| H3BPK3 | 6 | 4.32E-05 | Hydroxyacylglutathione hydrolase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HAGH PE=1 SV=1 |
| H3BPQ4 | 6 | 3.88E-05 | Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=HAGH PE=1 SV=1 |
| Q16775 | 6 | 3.35E-05 | Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=HAGH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q16775-2, H3BPQ4, H3BPK3, Q16775-3, H3BQW8 |
| Q16775-2 | 6 | 3.97E-05 | Isoform 2 of Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=HAGH |
| H0YN88 | 5 | 9.17E-06 | 40S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=1 |
| A0A075B716 | 5 | 6.53E-06 | 40S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=1 |
| H3BNC9 | 6 | 6.33E-06 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=3 SV=2; Additional IDs concatenated into MaxParsimony group: P08708, A0A075B716, H0YN88 |
| P08708 | 6 | 2.74E-05 | 40S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=2 |
| S4R3G0 | 6 | 8.83E-05 | Serine/arginine-rich-splicing factor 9 OS=Homo sapiens OX=9606 GN=SRSF9 PE=1 SV=1 |
| H0YIB4 | 6 | 9.64E-05 | Serine/arginine-rich-splicing factor 9 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF9 PE=1 SV=8 |
| Q13242 | 6 | 4.75E-05 | Serine/arginine-rich splicing factor 9 OS=Homo sapiens OX=9606 GN=SRSF9 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: S4R3G0, H0YIB4 |
| Q6UXV4 | 6 | 8.97E-05 | MICOS complex subunit MIC27 OS=Homo sapiens OX=9606 GN=APOOL PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087WYF7, A0A087WUX8 |
| A0A087WUX8 | 6 | 9.14E-05 | MICOS complex subunit OS=Homo sapiens OX=9606 GN=APOOL PE=1 SV=1 |
| A0A087WYF7 | 6 | 8.97E-05 | MICOS complex subunit OS=Homo sapiens OX=9606 GN=APOOL PE=1 SV=1 |
| A0A0B4J1R2 | 6 | 1.78E-05 | Acyl-CoA synthetase short-chain family member 3, mitochondrial OS=Homo sapiens OX=9606 GN=ACSS3 PE=1 SV=1 |
| Q9H6R3-2 | 6 | 1.49E-05 | Isoform 2 of Acyl-CoA synthetase short-chain family member 3, mitochondrial OS=Homo sapiens OX=9606 GN=ACSS3 |
| Q9H6R3 | 6 | 1.78E-05 | Acyl-CoA synthetase short-chain family member 3, mitochondrial OS=Homo sapiens OX=9606 GN=ACSS3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0B4J1R2, Q9H6R3-2 |
| P55287-2 | 5 | 4.40E-06 | Isoform 2 of Cadherin-11 OS=Homo sapiens OX=9606 GN=CDH11 |
| H3BUU9 | 6 | 1.90E-05 | Cadherin-11 OS=Homo sapiens OX=9606 GN=CDH11 PE=1 SV=1 |
| P55287 | 6 | 1.64E-05 | Cadherin-11 OS=Homo sapiens OX=9606 GN=CDH11 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H3BUU9, P55287-2 |
| B4DHE8 | 5 | 5.25E-06 | cDNA FLJ56904, highly similar to RNA-binding protein Musashi homolog 2 OS=Homo sapiens OX=9606 GN=MSI2 PE=1 SV=1 |
| Q96DH6-2 | 5 | 6.78E-06 | Isoform 2 of RNA-binding protein Musashi homolog 2 OS=Homo sapiens OX=9606 GN=MSI2 |
| J3KTC1 | 5 | 1.22E-05 | RNA-binding protein Musashi homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=MSI2 PE=1 SV=8 |
| Q96DH6 | 5 | 5.19E-06 | RNA-binding protein Musashi homolog 2 OS=Homo sapiens OX=9606 GN=MSI2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B4DHE8, Q96DH6-2, J3KTC1, J3QKT5 |
| J3QKT5 | 5 | 1.72E-05 | RNA-binding protein Musashi homolog 2 OS=Homo sapiens OX=9606 GN=MSI2 PE=1 SV=1 |
| H0YC44 | 6 | 5.41E-05 | Tumor protein D52 (Fragment) OS=Homo sapiens OX=9606 GN=TPD52 PE=4 SV=1 |
| P55327-8 | 6 | 5.31E-05 | Isoform 8 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 |
| H0YC42 | 6 | 2.88E-05 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=2; Additional IDs concatenated into MaxParsimony group: P55327-3, P55327-6, P55327-5, P55327-7, P55327, P55327-4, P55327-2, P55327-8, H0YC44, E5RFR7 |
| E5RFR7 | 6 | 7.22E-05 | Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 PE=1 SV=1 |
| B4DUC8 | 5 | 9.56E-06 | S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP PE=1 SV=1 |
| Q13126-4 | 5 | 1.02E-05 | Isoform 4 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP |
| A0A2R8Y4K0 | 5 | 9.84E-06 | S-methyl-5'-thioadenosine phosphorylase (Fragment) OS=Homo sapiens OX=9606 GN=MTAP PE=4 SV=1 |
| F8WES2 | 5 | 4.66E-05 | S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP PE=4 SV=1 |
| Q13126 | 5 | 1.01E-05 | S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP PE=1 SV=2 |
| Q13126-3 | 5 | 8.59E-06 | Isoform 3 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP |
| Q13126-7 | 5 | 1.20E-05 | Isoform 7 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP |
| Q13126-6 | 5 | 9.79E-06 | Isoform 6 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP |
| F2Z2F3 | 5 | 2.01E-05 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |
| Q13126-2 | 5 | 8.29E-06 | Isoform 2 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP; Additional IDs concatenated into MaxParsimony group: Q13126-3, Q13126-5, B4DUC8, Q13126-6, Q13126, Q13126-4, J3QSB7, Q13126-7, F2Z2F3, A0A2R8Y4K0, F8WES2 |
| Q13126-5 | 5 | 9.41E-06 | Isoform 5 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP |
| J3QSB7 | 5 | 1.19E-05 | Purine nucleoside phosphorylase OS=Homo sapiens OX=9606 GN=MTAP PE=1 SV=1 |
| O60238-2 | 5 | 0.000225959 | Isoform 2 of BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like OS=Homo sapiens OX=9606 GN=BNIP3L |
| H0YBC7 | 5 | 0.00021863 | BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like (Fragment) OS=Homo sapiens OX=9606 GN=BNIP3L PE=1 SV=1 |
| O60238 | 5 | 0.000184688 | BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like OS=Homo sapiens OX=9606 GN=BNIP3L PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0YBC7, O60238-2 |
| Q9UJ70 | 5 | 5.60E-05 | N-acetyl-D-glucosamine kinase OS=Homo sapiens OX=9606 GN=NAGK PE=1 SV=4 |
| H0YE82 | 5 | 3.78E-05 | N-acetyl-D-glucosamine kinase (Fragment) OS=Homo sapiens OX=9606 GN=NAGK PE=1 SV=2 |
| Q9UJ70-2 | 5 | 4.94E-05 | Isoform 2 of N-acetyl-D-glucosamine kinase OS=Homo sapiens OX=9606 GN=NAGK; Additional IDs concatenated into MaxParsimony group: Q9UJ70, H7C3G9, H0YEB7, H7C1L7, C9JEV6, H0YE82 |
| C9JEV6 | 5 | 1.08E-05 | N-acetyl-D-glucosamine kinase OS=Homo sapiens OX=9606 GN=NAGK PE=1 SV=3 |
| H7C1L7 | 5 | 0.000121238 | N-acetyl-D-glucosamine kinase OS=Homo sapiens OX=9606 GN=NAGK PE=1 SV=2 |
| H7C3G9 | 5 | 5.67E-05 | N-acetyl-D-glucosamine kinase OS=Homo sapiens OX=9606 GN=NAGK PE=1 SV=2 |
| H0YEB7 | 5 | 0.000105917 | N-acetyl-D-glucosamine kinase (Fragment) OS=Homo sapiens OX=9606 GN=NAGK PE=1 SV=1 |
| A0A1B0GV49 | 6 | 1.97E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| A0A1B0GTG2 | 6 | 1.73E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| A0A1B0GW77 | 6 | 1.68E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A1B0GW82, P49419, A0A1B0GTG2, A0A1B0GUA1, P49419-2, A0A1B0GTJ4, A0A1B0GTY9, P49419-4, A0A1B0GV49, A0A1B0GUY0, A0A0J9YWF7, H0YHM6, F8VVF2, A0A1B0GVU0 |
| P49419 | 6 | 1.72E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=5 |
| P49419-2 | 6 | 1.82E-05 | Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 |
| A0A1B0GUY0 | 6 | 2.67E-05 | Alpha-aminoadipic semialdehyde dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| P49419-4 | 6 | 1.95E-05 | Isoform 4 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 |
| A0A1B0GUA1 | 6 | 1.78E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| A0A1B0GTJ4 | 6 | 1.86E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| A0A1B0GTY9 | 6 | 1.94E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| A0A0J9YWF7 | 6 | 3.16E-05 | Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| A0A1B0GW82 | 6 | 1.70E-05 | Alpha-aminoadipic semialdehyde dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 |
| O43598-2 | 5 | 4.19E-05 | Isoform 2 of 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 OS=Homo sapiens OX=9606 GN=DNPH1 |
| O43598 | 6 | 4.26E-05 | 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 OS=Homo sapiens OX=9606 GN=DNPH1 PE=1 SV=1 |
| H0Y8X4 | 6 | 3.05E-05 | 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 (Fragment) OS=Homo sapiens OX=9606 GN=DNPH1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O43598, O43598-2 |
| B1AHM7 | 6 | 4.18E-05 | Fibulin-1 (Fragment) OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=1 |
| P23142-2 | 6 | 1.03E-05 | Isoform A of Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 |
| P23142-4 | 6 | 8.51E-06 | Isoform C of Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 |
| B1AHL2 | 6 | 8.06E-06 | Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P23142, P23142-4, P23142-3, P23142-2, B1AHM9, H7C1M6, B1AHM7 |
| P23142 | 6 | 8.48E-06 | Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=4 |
| P23142-3 | 6 | 9.67E-06 | Isoform B of Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 |
| B1AHM9 | 6 | 3.08E-05 | Fibulin-1 (Fragment) OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=1 |
| H7C1M6 | 6 | 3.18E-05 | Fibulin-1 (Fragment) OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=1 |
| O60888 | 6 | 6.19E-05 | Protein CutA OS=Homo sapiens OX=9606 GN=CUTA PE=1 SV=2 |
| C9IZG4 | 5 | 6.06E-05 | Protein CutA OS=Homo sapiens OX=9606 GN=CUTA PE=1 SV=1 |
| O60888-2 | 6 | 5.59E-05 | Isoform A of Protein CutA OS=Homo sapiens OX=9606 GN=CUTA; Additional IDs concatenated into MaxParsimony group: O60888, O60888-3, C9IZG4 |
| O60888-3 | 6 | 7.10E-05 | Isoform C of Protein CutA OS=Homo sapiens OX=9606 GN=CUTA |
| Q9NY33-2 | 6 | 5.67E-06 | Isoform 2 of Dipeptidyl peptidase 3 OS=Homo sapiens OX=9606 GN=DPP3 |
| G3V1D3 | 6 | 4.99E-06 | Dipeptidyl peptidase 3 OS=Homo sapiens OX=9606 GN=DPP3 PE=1 SV=1 |
| G3V180 | 6 | 4.98E-06 | Dipeptidyl peptidase 3 OS=Homo sapiens OX=9606 GN=DPP3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: G3V1D3, Q9NY33, Q9NY33-4, Q9NY33-2 |
| Q9NY33 | 6 | 5.11E-06 | Dipeptidyl peptidase 3 OS=Homo sapiens OX=9606 GN=DPP3 PE=1 SV=2 |
| Q9NY33-4 | 6 | 5.33E-06 | Isoform 4 of Dipeptidyl peptidase 3 OS=Homo sapiens OX=9606 GN=DPP3 |
| C9JFV4 | 6 | 4.03E-06 | Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens OX=9606 GN=PELP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8IZL8 |
| Q8IZL8 | 6 | 4.21E-06 | Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens OX=9606 GN=PELP1 PE=1 SV=2 |
| C9J6N5 | 6 | 3.24E-05 | Protein FAM107B (Fragment) OS=Homo sapiens OX=9606 GN=FAM107B PE=1 SV=8 |
| C9JW51 | 6 | 3.13E-05 | Protein FAM107B (Fragment) OS=Homo sapiens OX=9606 GN=FAM107B PE=1 SV=1 |
| C9JQ40 | 6 | 3.18E-05 | Protein FAM107B (Fragment) OS=Homo sapiens OX=9606 GN=FAM107B PE=1 SV=1 |
| Q9H098-2 | 6 | 1.31E-05 | Isoform 2 of Protein FAM107B OS=Homo sapiens OX=9606 GN=FAM107B; Additional IDs concatenated into MaxParsimony group: Q9H098, A0A1C7CYX8, C9JW51, C9JQ40, C9J6N5 |
| Q9H098 | 6 | 3.06E-05 | Protein FAM107B OS=Homo sapiens OX=9606 GN=FAM107B PE=1 SV=1 |
| A0A1C7CYX8 | 6 | 3.09E-05 | Protein FAM107B (Fragment) OS=Homo sapiens OX=9606 GN=FAM107B PE=1 SV=1 |
| P61086 | 5 | 6.96E-05 | Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens OX=9606 GN=UBE2K PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P61086-3, D6RDM7 |
| D6RDM7 | 5 | 0.000113108 | Ubiquitin-conjugating enzyme E2 K (Fragment) OS=Homo sapiens OX=9606 GN=UBE2K PE=1 SV=1 |
| P61086-3 | 5 | 8.86E-05 | Isoform 3 of Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens OX=9606 GN=UBE2K |
| G3V4P8 | 5 | 2.13E-05 | Glia maturation factor beta (Fragment) OS=Homo sapiens OX=9606 GN=GMFB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P60983 |
| P60983 | 5 | 2.25E-05 | Glia maturation factor beta OS=Homo sapiens OX=9606 GN=GMFB PE=1 SV=2 |
| H3BVD1 | 6 | 1.17E-05 | Mothers against decapentaplegic homolog (Fragment) OS=Homo sapiens OX=9606 GN=SMAD3 PE=1 SV=1 |
| P84022-3 | 6 | 7.81E-06 | Isoform 3 of Mothers against decapentaplegic homolog 3 OS=Homo sapiens OX=9606 GN=SMAD3 |
| Q15796-2 | 6 | 5.72E-06 | Isoform Short of Mothers against decapentaplegic homolog 2 OS=Homo sapiens OX=9606 GN=SMAD2 |
| H0YMP2 | 6 | 3.97E-05 | Mothers against decapentaplegic homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=SMAD3 PE=4 SV=1 |
| O15198 | 6 | 5.35E-06 | Mothers against decapentaplegic homolog 9 OS=Homo sapiens OX=9606 GN=SMAD9 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q15796, Q15796-2, B7Z5N5, O15198-2, P84022, P84022-2, P84022-3, K7EJX0, H3BVD1, H3BP09, H0YL71, H0YMP2 |
| Q15796 | 6 | 5.35E-06 | Mothers against decapentaplegic homolog 2 OS=Homo sapiens OX=9606 GN=SMAD2 PE=1 SV=1 |
| H0YL71 | 6 | 2.72E-05 | Mothers against decapentaplegic homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=SMAD3 PE=4 SV=1 |
| O15198-2 | 6 | 5.81E-06 | Isoform B of Mothers against decapentaplegic homolog 9 OS=Homo sapiens OX=9606 GN=SMAD9 |
| P84022-2 | 6 | 6.56E-06 | Isoform 2 of Mothers against decapentaplegic homolog 3 OS=Homo sapiens OX=9606 GN=SMAD3 |
| H3BP09 | 6 | 2.19E-05 | Mothers against decapentaplegic homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=SMAD3 PE=1 SV=1 |
| P84022 | 6 | 5.88E-06 | Mothers against decapentaplegic homolog 3 OS=Homo sapiens OX=9606 GN=SMAD3 PE=1 SV=1 |
| B7Z5N5 | 6 | 5.80E-06 | Mothers against decapentaplegic homolog OS=Homo sapiens OX=9606 GN=SMAD2 PE=1 SV=1 |
| K7EJX0 | 6 | 1.15E-05 | Mothers against decapentaplegic homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=SMAD2 PE=1 SV=1 |
| P67775 | 5 | 5.79E-06 | Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens OX=9606 GN=PPP2CA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P62714, P67775-2, H0YBN9 |
| H0YBN9 | 5 | 3.44E-05 | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (Fragment) OS=Homo sapiens OX=9606 GN=PPP2CB PE=4 SV=1 |
| P67775-2 | 5 | 7.02E-06 | Isoform 2 of Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens OX=9606 GN=PPP2CA |
| P62714 | 5 | 5.79E-06 | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens OX=9606 GN=PPP2CB PE=1 SV=1 |
| A0A087X0Q4 | 6 | 7.56E-05 | Immunoglobulin kappa variable 2-40 OS=Homo sapiens OX=9606 GN=IGKV2-40 PE=1 SV=1 |
| A0A075B6S2 | 6 | 6.56E-05 | Immunoglobulin kappa variable 2D-29 OS=Homo sapiens OX=9606 GN=IGKV2D-29 PE=3 SV=1 |
| P01614 | 6 | 6.50E-05 | Immunoglobulin kappa variable 2D-40 OS=Homo sapiens OX=9606 GN=IGKV2D-40 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A087WW87, A0A075B6S2, P01615, P06310, A2NJV5, A0A0A0MRZ7, A0A075B6P5, A0A075B6S6, A0A087X0Q4 |
| P01615 | 6 | 6.56E-05 | Immunoglobulin kappa variable 2D-28 OS=Homo sapiens OX=9606 GN=IGKV2D-28 PE=1 SV=2 |
| P06310 | 6 | 6.56E-05 | Immunoglobulin kappa variable 2-30 OS=Homo sapiens OX=9606 GN=IGKV2-30 PE=3 SV=2 |
| A2NJV5 | 6 | 6.56E-05 | Immunoglobulin kappa variable 2-29 OS=Homo sapiens OX=9606 GN=IGKV2-29 PE=3 SV=2 |
| A0A0A0MRZ7 | 6 | 6.56E-05 | Immunoglobulin kappa variable 2D-26 OS=Homo sapiens OX=9606 GN=IGKV2D-26 PE=3 SV=1 |
| A0A075B6P5 | 6 | 6.56E-05 | Immunoglobulin kappa variable 2-28 OS=Homo sapiens OX=9606 GN=IGKV2-28 PE=3 SV=1 |
| A0A075B6S6 | 6 | 6.56E-05 | Immunoglobulin kappa variable 2D-30 OS=Homo sapiens OX=9606 GN=IGKV2D-30 PE=3 SV=1 |
| A0A087WW87 | 6 | 6.50E-05 | Immunoglobulin kappa variable 2-40 OS=Homo sapiens OX=9606 GN=IGKV2-40 PE=3 SV=2 |
| C9JJ34 | 6 | 0.000128358 | Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1 |
| F6WQW2 | 6 | 0.000135275 | Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P43487, P43487-2, C9JDM3, C9JJ34 |
| C9JDM3 | 6 | 0.000126802 | Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=8 |
| P43487-2 | 6 | 0.000188032 | Isoform 2 of Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 |
| P43487 | 6 | 0.000187097 | Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1 |
| Q9NTK5 | 5 | 1.14E-06 | Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=2 |
| Q9NTK5-3 | 5 | 1.63E-06 | Isoform 3 of Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 |
| C9JTK6 | 5 | 1.83E-06 | Obg-like ATPase 1 (Fragment) OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=1 |
| J3KQ32 | 5 | 1.09E-06 | Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NTK5, Q9NTK5-3, C9JTK6 |
| Q9Y5J7 | 5 | 0.00028545 | Mitochondrial import inner membrane translocase subunit Tim9 OS=Homo sapiens OX=9606 GN=TIMM9 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: G3V502, A0A1W2PQS5, A0A1W2PRH9 |
| P55058-3 | 5 | 5.04E-06 | Isoform 3 of Phospholipid transfer protein OS=Homo sapiens OX=9606 GN=PLTP |
| P55058 | 6 | 9.45E-06 | Phospholipid transfer protein OS=Homo sapiens OX=9606 GN=PLTP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P55058-2, P55058-4, P55058-3 |
| P55058-4 | 5 | 4.65E-06 | Isoform 4 of Phospholipid transfer protein OS=Homo sapiens OX=9606 GN=PLTP |
| P55058-2 | 5 | 4.55E-06 | Isoform 2 of Phospholipid transfer protein OS=Homo sapiens OX=9606 GN=PLTP |
| P28482 | 5 | 3.03E-05 | Mitogen-activated protein kinase 1 OS=Homo sapiens OX=9606 GN=MAPK1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P28482-2 |
| P28482-2 | 5 | 3.45E-05 | Isoform 2 of Mitogen-activated protein kinase 1 OS=Homo sapiens OX=9606 GN=MAPK1 |
| E9PBK7 | 5 | 9.05E-06 | Mitogen-activated protein kinase OS=Homo sapiens OX=9606 GN=MAPK3 PE=1 SV=1 |
| E9PRH7 | 5 | 2.07E-05 | Mitogen-activated protein kinase 3 (Fragment) OS=Homo sapiens OX=9606 GN=MAPK3 PE=1 SV=1 |
| H0YEX6 | 5 | 2.33E-05 | Mitogen-activated protein kinase 3 (Fragment) OS=Homo sapiens OX=9606 GN=MAPK3 PE=1 SV=1 |
| P27361-2 | 5 | 8.40E-06 | Isoform 2 of Mitogen-activated protein kinase 3 OS=Homo sapiens OX=9606 GN=MAPK3 |
| B3KR49 | 5 | 1.06E-05 | Mitogen-activated protein kinase 3, isoform CRA\_b OS=Homo sapiens OX=9606 GN=MAPK3 PE=1 SV=1 |
| P27361 | 5 | 7.43E-06 | Mitogen-activated protein kinase 3 OS=Homo sapiens OX=9606 GN=MAPK3 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P27361-2, E9PBK7, B3KR49, E9PRH7, H0YEX6 |
| Q9P260-2 | 6 | 4.12E-07 | Isoform 2 of LisH domain and HEAT repeat-containing protein KIAA1468 OS=Homo sapiens OX=9606 GN=KIAA1468; Additional IDs concatenated into MaxParsimony group: A0A2R8Y566, Q9P260, A0A075B785 |
| A0A2R8Y566 | 6 | 4.23E-07 | RAB11-binding and LisH domain, coiled-coil and HEAT repeat-containing OS=Homo sapiens OX=9606 GN=RELCH PE=1 SV=1 |
| A0A075B785 | 6 | 5.06E-07 | RAB11-binding and LisH domain, coiled-coil and HEAT repeat-containing OS=Homo sapiens OX=9606 GN=RELCH PE=1 SV=7 |
| Q9P260 | 6 | 4.23E-07 | LisH domain and HEAT repeat-containing protein KIAA1468 OS=Homo sapiens OX=9606 GN=KIAA1468 PE=1 SV=2 |
| Q9H0N5 | 6 | 0.000567565 | Pterin-4-alpha-carbinolamine dehydratase 2 OS=Homo sapiens OX=9606 GN=PCBD2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: H0YA52 |
| H0YA52 | 6 | 0.000620029 | Pterin-4-alpha-carbinolamine dehydratase 2 (Fragment) OS=Homo sapiens OX=9606 GN=PCBD2 PE=1 SV=1 |
| P13693 | 6 | 0.000104749 | Translationally-controlled tumor protein OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1 |
| A0A0B4J2C3 | 6 | 9.15E-05 | Translationally-controlled tumor protein OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5W0H4, P13693 |
| Q5W0H4 | 6 | 9.58E-05 | Translationally-controlled tumor protein OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1 |
| A0A0J9YW37 | 4 | 1.52E-05 | Microtubule-associated protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1 |
| H0Y2V1 | 6 | 2.23E-05 | Microtubule-associated protein (Fragment) OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1 |
| H7C456 | 6 | 9.00E-05 | Microtubule-associated protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=2 |
| A0A0J9YVV8 | 4 | 2.80E-05 | Microtubule-associated protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1 |
| H7C4C5 | 6 | 2.22E-05 | Microtubule-associated protein (Fragment) OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1 |
| F8W9U4 | 6 | 1.24E-05 | Microtubule-associated protein OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1 |
| P27816-7 | 4 | 2.15E-05 | Isoform 7 of Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 |
| P27816-4 | 6 | 1.26E-05 | Isoform 4 of Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 |
| P27816-5 | 6 | 4.69E-05 | Isoform 5 of Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 |
| A0A2R8YDY1 | 6 | 0.002248975 | Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=1 |
| E7EV34 | 6 | 8.34E-05 | Tripeptidyl-peptidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=3 |
| E5RGX5 | 6 | 0.001910886 | Stathmin OS=Homo sapiens OX=9606 GN=STMN2 PE=1 SV=1 |
| Q93045-2 | 6 | 0.001716732 | Isoform 2 of Stathmin-2 OS=Homo sapiens OX=9606 GN=STMN2 |
| Q93045 | 6 | 0.001793457 | Stathmin-2 OS=Homo sapiens OX=9606 GN=STMN2 PE=1 SV=3 |
| B0QZK8 | 6 | 9.84E-05 | Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1 |
| X6RGJ2 | 6 | 0.000113325 | Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1 |
| Q5SSJ5 | 6 | 7.29E-05 | Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: X6RGJ2, Q5SSJ5-2, Q5SSJ5-3, B0QZK4, Q5SWC8, Q5SSJ5-5, B0QZK8, B0QZK9 |
| Q5SSJ5-2 | 6 | 5.46E-05 | Isoform 2 of Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 |
| Q5SSJ5-5 | 6 | 9.18E-05 | Isoform 4 of Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 |
| B0QZK4 | 6 | 0.000100786 | Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1 |
| B0QZK9 | 6 | 0.000162737 | Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=8 |
| Q5SWC8 | 6 | 7.46E-05 | Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1 |
| Q14847 | 5 | 0.000290484 | LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 PE=1 SV=2 |
| Q14847-2 | 5 | 0.000234725 | Isoform 2 of LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1; Additional IDs concatenated into MaxParsimony group: Q14847, Q14847-3, C9J9W2, J3KSN1 |
| C9J9W2 | 5 | 0.000456725 | LIM and SH3 domain protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=LASP1 PE=1 SV=1 |
| Q14847-3 | 5 | 0.000369836 | Isoform 3 of LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 |
| P35241 | 6 | 1.17E-05 | Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1 |
| P35241-4 | 5 | 1.10E-05 | Isoform 4 of Radixin OS=Homo sapiens OX=9606 GN=RDX |
| P26038 | 6 | 4.08E-05 | Moesin OS=Homo sapiens OX=9606 GN=MSN PE=1 SV=3 |
| A0A2R8Y7M3 | 6 | 1.27E-05 | Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1 |
| P35241-5 | 6 | 1.13E-05 | Isoform 5 of Radixin OS=Homo sapiens OX=9606 GN=RDX |
| A0A2R8Y5S7 | 6 | 1.15E-05 | Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1 |
| I3L1I0 | 6 | 0.000431117 | Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=GLOD4 PE=1 SV=1 |
| Q9HC38 | 6 | 0.0003112 | Glyoxalase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GLOD4 PE=1 SV=1 |
| F6TLX2 | 6 | 0.000194035 | Glyoxalase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GLOD4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9HC38, Q9HC38-2, I3L3Q4, I3L1I0, Q9HC38-3 |
| Q9HC38-2 | 6 | 0.000326864 | Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GLOD4 |
| Q9HC38-3 | 6 | 0.000115356 | Isoform 3 of Glyoxalase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GLOD4 |
| I3L3Q4 | 6 | 0.000199675 | Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=GLOD4 PE=1 SV=1 |
| H3BTD4 | 6 | 0.00011658 | Beta-hexosaminidase subunit alpha OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=1 |
| H3BS10 | 6 | 0.000122047 | Beta-hexosaminidase OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=1 |
| H3BU85 | 6 | 0.000136743 | Beta-hexosaminidase subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=1 |
| P06865 | 6 | 0.000117433 | Beta-hexosaminidase subunit alpha OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=2 |
| H3BP20 | 6 | 0.000115041 | Beta-hexosaminidase OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P06865, H3BS10, H3BTD4, H3BU85, P06865-2 |
| P06865-2 | 6 | 8.69E-05 | Isoform 2 of Beta-hexosaminidase subunit alpha OS=Homo sapiens OX=9606 GN=HEXA |
| Q5URX0 | 6 | 0.000140301 | Beta-hexosaminidase subunit beta OS=Homo sapiens OX=9606 GN=HEXB PE=1 SV=1 |
| P07686 | 6 | 8.66E-05 | Beta-hexosaminidase subunit beta OS=Homo sapiens OX=9606 GN=HEXB PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q5URX0, H0Y9B6, H0YA83 |
| H0Y9B6 | 6 | 0.000166086 | Beta-hexosaminidase subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=HEXB PE=1 SV=1 |
| H0YA83 | 6 | 0.00017945 | Beta-hexosaminidase subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=HEXB PE=1 SV=1 |
| A0A286YFL6 | 4 | 0.00046286 | Palmitoyl-protein thioesterase 1 (Fragment) OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1 |
| P50897-2 | 6 | 0.000612892 | Isoform 2 of Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 |
| E9PSE5 | 6 | 0.0006359 | Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1 |
| A0A0C4DGP4 | 6 | 0.000137382 | Glucosidase 2 subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=1 |
| E9PQZ1 | 5 | 2.13E-05 | Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| P29692-4 | 5 | 1.93E-05 | Isoform 4 of Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D |
| H0YE72 | 5 | 3.07E-05 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| P24752-2 | 5 | 5.30E-05 | Isoform 2 of Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 |
| E9PRQ6 | 5 | 6.09E-05 | Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 PE=1 SV=1 |
| P24752 | 6 | 3.75E-05 | Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P24752-2, E9PRQ6, H0YEL7 |
| H0Y4U1 | 6 | 4.02E-05 | Tensin-1 OS=Homo sapiens OX=9606 GN=TNS1 PE=1 SV=1 |
| A0A2R8Y4T1 | 6 | 2.44E-05 | Tensin-1 OS=Homo sapiens OX=9606 GN=TNS1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9HBL0, E9PF55, E9PGF5, A0A087WWW7, H0Y4U1 |
| Q9HBL0 | 6 | 2.61E-05 | Tensin-1 OS=Homo sapiens OX=9606 GN=TNS1 PE=1 SV=2 |
| E9PF55 | 6 | 2.64E-05 | Tensin-1 OS=Homo sapiens OX=9606 GN=TNS1 PE=1 SV=1 |
| E9PGF5 | 6 | 2.65E-05 | Tensin-1 OS=Homo sapiens OX=9606 GN=TNS1 PE=1 SV=1 |
| A0A087WWW7 | 6 | 3.32E-05 | Tensin-1 OS=Homo sapiens OX=9606 GN=TNS1 PE=1 SV=1 |
| Q8TAV4 | 5 | 3.57E-05 | Stomatin-like protein 3 OS=Homo sapiens OX=9606 GN=STOML3 PE=2 SV=1 |
| P27105-2 | 6 | 0.000131613 | Isoform 2 of Erythrocyte band 7 integral membrane protein OS=Homo sapiens OX=9606 GN=STOM |
| F8VSL7 | 5 | 6.58E-05 | Erythrocyte band 7 integral membrane protein OS=Homo sapiens OX=9606 GN=STOM PE=1 SV=1 |
| Q8TAV4-2 | 5 | 3.69E-05 | Isoform 2 of Stomatin-like protein 3 OS=Homo sapiens OX=9606 GN=STOML3 |
| P27105 | 6 | 0.000109848 | Erythrocyte band 7 integral membrane protein OS=Homo sapiens OX=9606 GN=STOM PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P27105-2, Q8TAV4, Q8TAV4-2, F8VSL7 |
| P0DOY2 | 6 | 0.000568196 | Immunoglobulin lambda constant 2 OS=Homo sapiens OX=9606 GN=IGLC2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P0DOY3, A0A0B4J231, B9A064, P0CF74, A0M8Q6, P0CG04 |
| A0A0B4J231 | 6 | 0.000183173 | Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=1 SV=1 |
| contaminant\_NRL\_1MCOL | 6 | 0.000182325 | Immunoglobulin g1 (igg1) (mcg) with a hinge deletion, chain L... |
| A0M8Q6 | 6 | 0.000253947 | Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3 |
| B9A064 | 6 | 0.000184029 | Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens OX=9606 GN=IGLL5 PE=2 SV=2 |
| P0DOY3 | 6 | 0.000568196 | Immunoglobulin lambda constant 3 OS=Homo sapiens OX=9606 GN=IGLC3 PE=1 SV=1 |
| P0CF74 | 6 | 0.000383061 | Immunoglobulin lambda constant 6 OS=Homo sapiens OX=9606 GN=IGLC6 PE=1 SV=1 |
| P0CG04 | 6 | 0.000199455 | Immunoglobulin lambda constant 1 OS=Homo sapiens OX=9606 GN=IGLC1 PE=1 SV=1 |
| A0A0A0MRJ6 | 6 | 9.97E-05 | Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=1 |
| P22061 | 6 | 0.000125124 | Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=4 |
| C9J0F2 | 6 | 8.24E-05 | Protein-L-isoaspartate(D-aspartate) O-methyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=1 |
| P22061-2 | 6 | 0.000124576 | Isoform 2 of Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 |
| F6S8N6 | 6 | 0.000113613 | Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=1 |
| H7BY58 | 6 | 9.93E-05 | Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0A0MRJ6, F6S8N6, P22061-2, P22061, C9J0F2 |
| H0Y4Y4 | 6 | 4.29E-05 | EF-hand domain-containing protein D2 (Fragment) OS=Homo sapiens OX=9606 GN=EFHD2 PE=1 SV=1 |
| Q96C19 | 6 | 6.31E-05 | EF-hand domain-containing protein D2 OS=Homo sapiens OX=9606 GN=EFHD2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0Y4Y4 |
| P42166 | 6 | 4.99E-05 | Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P42167, G5E972, P42167-2, P42167-3, H0YJH7 |
| P42167-3 | 6 | 0.000139711 | Isoform Zeta of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO |
| P42167 | 6 | 7.63E-05 | Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2 |
| P42167-2 | 6 | 0.00010043 | Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO |
| G5E972 | 6 | 8.37E-05 | Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=1 |
| P13797-3 | 5 | 2.39E-05 | Isoform 3 of Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 |
| C9JAM8 | 4 | 2.29E-05 | Plastin-1 (Fragment) OS=Homo sapiens OX=9606 GN=PLS1 PE=1 SV=1 |
| P13797-2 | 5 | 2.27E-05 | Isoform 2 of Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 |
| Q14651 | 4 | 9.70E-06 | Plastin-1 OS=Homo sapiens OX=9606 GN=PLS1 PE=1 SV=2 |
| A0A0A0MSQ0 | 5 | 2.27E-05 | Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=1 |
| P13796 | 4 | 9.99E-06 | Plastin-2 OS=Homo sapiens OX=9606 GN=LCP1 PE=1 SV=6 |
| P13797 | 5 | 2.66E-05 | Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P13797-2, A0A0A0MSQ0, P13797-3, Q14651, P13796, Reverse\_Q9HC44, C9JAM8, U3KQI3, F2Z2Z9 |
| D6RDK6 | 6 | 8.02E-05 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| D6RBN5 | 6 | 6.59E-05 | OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1 |
| Q9NX40 | 6 | 0.000209643 | OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: D6RBN5, D6RDK6, Q9NX40-4, Q9NX40-3, Q9NX40-2, D6RIT9, D6RG39, D6RC55, D6RA54, D6RDI5, D6RBC5, D6R918, D6RF07 |
| P02790 | 6 | 8.02E-05 | Hemopexin OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9BS19 |
| Q9BS19 | 6 | 0.000139442 | HPX protein OS=Homo sapiens OX=9606 GN=HPX PE=1 SV=1 |
| P78417-2 | 6 | 8.87E-05 | Isoform 2 of Glutathione S-transferase omega-1 OS=Homo sapiens OX=9606 GN=GSTO1 |
| Q5TA01 | 6 | 6.39E-05 | Glutathione S-transferase omega-1 (Fragment) OS=Homo sapiens OX=9606 GN=GSTO1 PE=1 SV=1 |
| Q5TA02 | 6 | 0.000144675 | Glutathione S-transferase omega-1 (Fragment) OS=Homo sapiens OX=9606 GN=GSTO1 PE=1 SV=1 |
| P78417 | 6 | 0.000148873 | Glutathione S-transferase omega-1 OS=Homo sapiens OX=9606 GN=GSTO1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P78417-3, P78417-2, Q5TA02, Q5TA01 |
| P78417-3 | 6 | 0.000135845 | Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens OX=9606 GN=GSTO1 |
| Q5T0R3 | 5 | 3.64E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1 |
| Q01518-2 | 6 | 2.14E-05 | Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAP1 |
| Q01518 | 6 | 2.13E-05 | Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: Q01518-2, Q5T0R9, Q5T0R1, Q5T0R2, Q5T0R3, Q5T0R4, Q5T0R5, Q5T0R6, Q5T0R7 |
| Q5T0R1 | 5 | 3.43E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1 |
| Q5T0R6 | 5 | 4.19E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1 |
| Q5T0R5 | 5 | 4.12E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=8 |
| Q5T0R4 | 5 | 3.67E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=8 |
| Q5T0R7 | 5 | 4.24E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1 |
| Q5T0R2 | 5 | 3.55E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1 |
| Q5T0R9 | 5 | 2.82E-05 | Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=8 |
| B1AH49 | 6 | 2.37E-05 | 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens OX=9606 GN=MPST PE=1 SV=1 |
| P25325 | 6 | 2.55E-05 | 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens OX=9606 GN=MPST PE=1 SV=3 |
| P25325-2 | 6 | 2.38E-05 | Isoform 2 of 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens OX=9606 GN=MPST; Additional IDs concatenated into MaxParsimony group: P25325, B1AH49 |
| F8VZG5 | 6 | 0.000134464 | Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1 |
| F8VPP1 | 5 | 0.000326418 | Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1 |
| P54819-2 | 6 | 9.39E-05 | Isoform 2 of Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 |
| F8VY04 | 5 | 8.30E-05 | Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1 |
| F8W1A4 | 6 | 9.39E-05 | Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1 |
| P54819-3 | 6 | 0.000107838 | Isoform 3 of Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 |
| P54819 | 6 | 9.11E-05 | Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P54819-2, F8W1A4, P54819-3, F8VZG5, P54819-5, P54819-6, F8VY04, G3V213, P54819-4, F8VPP1 |
| P54819-4 | 6 | 4.51E-05 | Isoform 4 of Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 |
| P54819-5 | 6 | 9.58E-05 | Isoform 5 of Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 |
| G3V213 | 6 | 0.000161265 | Adenylate kinase 2, isoform CRA\_a OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1 |
| P54819-6 | 6 | 3.07E-05 | Isoform 6 of Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 |
| Q12905 | 5 | 2.23E-05 | Interleukin enhancer-binding factor 2 OS=Homo sapiens OX=9606 GN=ILF2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: B4DY09, X6R6Z1, A0A0A0MRL0 |
| X6R6Z1 | 5 | 3.81E-05 | Interleukin enhancer-binding factor 2 (Fragment) OS=Homo sapiens OX=9606 GN=ILF2 PE=1 SV=1 |
| B4DY09 | 5 | 2.47E-05 | cDNA FLJ51660, highly similar to Interleukin enhancer-binding factor 2 OS=Homo sapiens OX=9606 GN=ILF2 PE=1 SV=1 |
| P11171-5 | 6 | 5.17E-05 | Isoform 5 of Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 |
| P11171-3 | 6 | 6.04E-05 | Isoform 3 of Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 |
| A0A2R8YD30 | 6 | 5.91E-05 | Erythrocyte membrane protein band 4.1 (Elliptocytosis 1, RH-linked), isoform CRA\_e OS=Homo sapiens OX=9606 GN=EPB41 PE=1 SV=1 |
| P11171-4 | 6 | 6.58E-05 | Isoform 4 of Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 |
| A0A2R8Y7Y3 | 6 | 6.44E-05 | Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 PE=1 SV=1 |
| Q4VB86 | 6 | 6.22E-05 | EPB41 protein OS=Homo sapiens OX=9606 GN=EPB41 PE=1 SV=2 |
| A0A2U3TZH6 | 6 | 4.76E-05 | Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 PE=4 SV=1 |
| P11171-6 | 6 | 6.84E-05 | Isoform 6 of Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 |
| P11171-2 | 6 | 4.82E-05 | Isoform 2 of Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 |
| P11171 | 6 | 4.63E-05 | Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A2U3TZH6, P11171-2, P11171-5, A0A2R8YD30, P11171-3, Q4VB86, A0A2R8Y7Y3, P11171-4, P11171-6, A0A2R8Y783 |
| B8ZZT4 | 6 | 0.000167609 | Vesicle-associated membrane protein 8 OS=Homo sapiens OX=9606 GN=VAMP8 PE=1 SV=1 |
| Q9BV40 | 6 | 0.000165933 | Vesicle-associated membrane protein 8 OS=Homo sapiens OX=9606 GN=VAMP8 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B8ZZT4 |
| E9PFE6 | 5 | 5.64E-05 | Prostatic acid phosphatase (Fragment) OS=Homo sapiens OX=9606 GN=ACPP PE=1 SV=1 |
| P15309 | 5 | 2.41E-05 | Prostatic acid phosphatase OS=Homo sapiens OX=9606 GN=ACPP PE=1 SV=3 |
| P15309-3 | 5 | 1.28E-05 | Isoform 3 of Prostatic acid phosphatase OS=Homo sapiens OX=9606 GN=ACPP |
| P15309-2 | 5 | 2.23E-05 | Isoform 2 of Prostatic acid phosphatase OS=Homo sapiens OX=9606 GN=ACPP; Additional IDs concatenated into MaxParsimony group: P15309, E9PFE6, P15309-3 |
| C9JZW3 | 6 | 3.03E-05 | Elongation factor 1-beta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1B2 PE=1 SV=1 |
| P24534 | 6 | 2.94E-05 | Elongation factor 1-beta OS=Homo sapiens OX=9606 GN=EEF1B2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: C9JZW3, F2Z2G2, F8WF65 |
| F8WF65 | 6 | 0.000128468 | Elongation factor 1-beta OS=Homo sapiens OX=9606 GN=EEF1B2 PE=1 SV=1 |
| F2Z2G2 | 6 | 5.48E-05 | Elongation factor 1-beta OS=Homo sapiens OX=9606 GN=EEF1B2 PE=1 SV=1 |
| B2RPK0 | 6 | 9.15E-05 | Putative high mobility group protein B1-like 1 OS=Homo sapiens OX=9606 GN=HMGB1P1 PE=5 SV=1 |
| Q5T7C4 | 6 | 0.000133093 | High mobility group protein B1 OS=Homo sapiens OX=9606 GN=HMGB1 PE=1 SV=1 |
| P09429 | 6 | 9.78E-05 | High mobility group protein B1 OS=Homo sapiens OX=9606 GN=HMGB1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: B2RPK0, Q5T7C4 |
| A0A0C4DH25 | 6 | 8.87E-05 | Immunoglobulin kappa variable 3D-20 OS=Homo sapiens OX=9606 GN=IGKV3D-20 PE=3 SV=1 |
| P01619 | 6 | 0.000133178 | Immunoglobulin kappa variable 3-20 OS=Homo sapiens OX=9606 GN=IGKV3-20 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A0C4DH25 |
| Q92530 | 6 | 3.74E-05 | Proteasome inhibitor PI31 subunit OS=Homo sapiens OX=9606 GN=PSMF1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5QPM7, F5H4Z3, H0Y555 |
| F5H4Z3 | 6 | 7.98E-05 | Proteasome inhibitor PI31 subunit (Fragment) OS=Homo sapiens OX=9606 GN=PSMF1 PE=1 SV=2 |
| Q5QPM7 | 6 | 3.85E-05 | Proteasome inhibitor PI31 subunit OS=Homo sapiens OX=9606 GN=PSMF1 PE=1 SV=2 |
| H0Y555 | 6 | 9.47E-05 | Proteasome inhibitor PI31 subunit (Fragment) OS=Homo sapiens OX=9606 GN=PSMF1 PE=1 SV=1 |
| Q9NR28 | 6 | 4.33E-05 | Diablo homolog, mitochondrial OS=Homo sapiens OX=9606 GN=DIABLO PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NR28-3, Q9NR28-2, A0A024RBT2 |
| Q9NR28-2 | 6 | 5.56E-05 | Isoform 2 of Diablo homolog, mitochondrial OS=Homo sapiens OX=9606 GN=DIABLO |
| A0A024RBT2 | 6 | 6.23E-05 | Diablo homolog, mitochondrial OS=Homo sapiens OX=9606 GN=DIABLO PE=1 SV=1 |
| Q9NR28-3 | 6 | 5.31E-05 | Isoform 3 of Diablo homolog, mitochondrial OS=Homo sapiens OX=9606 GN=DIABLO |
| Q00325 | 6 | 3.88E-05 | Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q00325-2, F8VVM2, F8VWQ0, F8VWR4, F8VZL5 |
| F8VVM2 | 6 | 4.44E-05 | Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=1 |
| F8VZL5 | 5 | 1.06E-05 | Phosphate carrier protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=1 |
| F8VWR4 | 5 | 1.05E-05 | Phosphate carrier protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=1 |
| Q00325-2 | 6 | 3.98E-05 | Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 |
| F8VWQ0 | 5 | 1.26E-05 | Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=1 |
| Q16626 | 6 | 6.79E-05 | Male-enhanced antigen 1 OS=Homo sapiens OX=9606 GN=MEA1 PE=1 SV=2 |
| A0A2R8Y6W5 | 6 | 6.68E-05 | Male-enhanced antigen 1 OS=Homo sapiens OX=9606 GN=MEA1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q16626, A0A2R8Y7W8 |
| A0A2R8Y7W8 | 6 | 7.30E-05 | Male-enhanced antigen 1 OS=Homo sapiens OX=9606 GN=MEA1 PE=1 SV=1 |
| H0Y9V9 | 6 | 4.39E-05 | 60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=2 |
| H0Y9R4 | 6 | 5.51E-05 | 60S ribosomal protein L9 (Fragment) OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=2 |
| D6RAN4 | 6 | 2.74E-05 | 60S ribosomal protein L9 (Fragment) OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=8 |
| A0A2R8Y5Y7 | 6 | 2.25E-05 | 60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P32969, D6RAN4, H0Y9V9, H0Y9R4 |
| P32969 | 6 | 2.58E-05 | 60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1 |
| E7ERF2 | 5 | 1.62E-05 | T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 |
| P17987 | 5 | 1.48E-05 | T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E7ERF2, F5H136, F5H676, F5GZI8, F5H726 |
| F5H136 | 5 | 5.16E-05 | T-complex protein 1 subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 |
| F5GZI8 | 5 | 6.98E-05 | T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 |
| F5H676 | 5 | 6.32E-05 | T-complex protein 1 subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 |
| F5H726 | 5 | 7.70E-05 | T-complex protein 1 subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 |
| P00450 | 6 | 1.05E-05 | Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PFZ2, H7C5R1 |
| H7C5R1 | 6 | 1.29E-05 | Ceruloplasmin (Fragment) OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1 |
| E9PFZ2 | 6 | 8.13E-06 | Ceruloplasmin OS=Homo sapiens OX=9606 GN=CP PE=1 SV=1 |
| Q9UJ68-2 | 6 | 4.94E-05 | Isoform 2 of Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens OX=9606 GN=MSRA |
| Q9UJ68-4 | 6 | 4.28E-05 | Isoform 4 of Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens OX=9606 GN=MSRA |
| Q9UJ68-5 | 6 | 3.92E-05 | Isoform 5 of Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens OX=9606 GN=MSRA |
| Q9UJ68 | 6 | 3.56E-05 | Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens OX=9606 GN=MSRA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UJ68-5, Q9UJ68-4, Q9UJ68-3, Q9UJ68-2 |
| Q9UJ68-3 | 6 | 4.35E-05 | Isoform 3 of Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens OX=9606 GN=MSRA |
| E9PBU7 | 4 | 1.06E-05 | Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1 |
| O00560 | 6 | 2.11E-05 | Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O00560-3, G5EA09, O00560-2, E9PBU7, B4DHN5 |
| G5EA09 | 5 | 8.60E-06 | Syndecan binding protein (Syntenin), isoform CRA\_a OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1 |
| O00560-2 | 5 | 9.21E-06 | Isoform 2 of Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP |
| O00560-3 | 6 | 2.16E-05 | Isoform 3 of Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP |
| B4DHN5 | 4 | 1.08E-05 | cDNA FLJ55055, moderately similar to Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1 |
| Q9UK76-3 | 6 | 0.000180815 | Isoform 3 of Jupiter microtubule associated homolog 1 OS=Homo sapiens OX=9606 GN=JPT1 |
| Q9UK76 | 6 | 0.000129211 | Jupiter microtubule associated homolog 1 OS=Homo sapiens OX=9606 GN=JPT1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9UK76-3, Q9UK76-2, J3KT51, J3KSH8 |
| J3KT51 | 6 | 0.000178192 | Jupiter microtubule-associated homolog 1 OS=Homo sapiens OX=9606 GN=JPT1 PE=1 SV=1 |
| Q9UK76-2 | 6 | 0.000102387 | Isoform 2 of Jupiter microtubule associated homolog 1 OS=Homo sapiens OX=9606 GN=JPT1 |
| J3KSH8 | 6 | 0.000195285 | Jupiter microtubule-associated homolog 1 (Fragment) OS=Homo sapiens OX=9606 GN=JPT1 PE=1 SV=8 |
| P52655 | 6 | 8.52E-06 | Transcription initiation factor IIA subunit 1 OS=Homo sapiens OX=9606 GN=GTF2A1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: J3KNC0 |
| J3KNC0 | 6 | 5.43E-05 | Transcription initiation factor IIA subunit 1 OS=Homo sapiens OX=9606 GN=GTF2A1 PE=1 SV=1 |
| Q9P121-3 | 5 | 6.27E-06 | Isoform 3 of Neurotrimin OS=Homo sapiens OX=9606 GN=NTM |
| Q9P121 | 5 | 5.76E-06 | Neurotrimin OS=Homo sapiens OX=9606 GN=NTM PE=1 SV=1 |
| F8VTR5 | 5 | 1.04E-05 | Neurotrimin (Fragment) OS=Homo sapiens OX=9606 GN=NTM PE=1 SV=1 |
| Q9P121-2 | 5 | 5.76E-06 | Isoform 2 of Neurotrimin OS=Homo sapiens OX=9606 GN=NTM |
| Q9P121-4 | 5 | 5.58E-06 | Isoform 4 of Neurotrimin OS=Homo sapiens OX=9606 GN=NTM; Additional IDs concatenated into MaxParsimony group: Q9P121, Q9P121-2, Q9P121-3, F8VTR5 |
| H3BN72 | 6 | 0.000113542 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens OX=9606 GN=COX4I1 PE=1 SV=1 |
| Q86WV2 | 6 | 0.000146763 | COX4I1 protein OS=Homo sapiens OX=9606 GN=COX4I1 PE=1 SV=1 |
| H3BNI5 | 5 | 0.000178926 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=COX4I1 PE=1 SV=1 |
| P13073 | 6 | 8.47E-05 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens OX=9606 GN=COX4I1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H3BNV9, H3BN72, Q86WV2, H3BNI5 |
| H3BNV9 | 6 | 0.000102923 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens OX=9606 GN=COX4I1 PE=1 SV=1 |
| F5GXS0 | 5 | 8.12E-07 | Complement C4-B OS=Homo sapiens OX=9606 GN=C4B PE=1 SV=1 |
| A0A140TA49 | 5 | 8.12E-07 | Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=1 |
| P0C0L4-2 | 5 | 8.12E-07 | Isoform 2 of Complement C4-A OS=Homo sapiens OX=9606 GN=C4A |
| A0A140TA44 | 5 | 8.12E-07 | Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=1 |
| P0C0L4 | 5 | 7.91E-07 | Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P0C0L5, A0A0G2JPR0, F5GXS0, A0A140TA49, P0C0L4-2, A0A140TA44, A0A140TA32, A0A0G2JL54, A0A140TA29 |
| A0A140TA32 | 5 | 8.12E-07 | Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=1 |
| A0A0G2JL54 | 5 | 8.12E-07 | Complement C4-B OS=Homo sapiens OX=9606 GN=C4B\_2 PE=1 SV=1 |
| P0C0L5 | 5 | 7.91E-07 | Complement C4-B OS=Homo sapiens OX=9606 GN=C4B PE=1 SV=2 |
| A0A0G2JPR0 | 5 | 7.91E-07 | Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=1 |
| A0A140TA29 | 5 | 8.12E-07 | Complement C4-B OS=Homo sapiens OX=9606 GN=C4B PE=1 SV=1 |
| P25713 | 6 | 0.000437733 | Metallothionein-3 OS=Homo sapiens OX=9606 GN=MT3 PE=1 SV=1 |
| H3BQX6 | 6 | 0.00036748 | Metallothionein OS=Homo sapiens OX=9606 GN=MT3 PE=1 SV=1 |
| H3BPK2 | 6 | 0.000263415 | Metallothionein-3 OS=Homo sapiens OX=9606 GN=MT3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H3BQX6, P25713 |
| P12931-2 | 5 | 5.64E-06 | Isoform 2 of Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens OX=9606 GN=SRC; Additional IDs concatenated into MaxParsimony group: P12931 |
| P12931 | 5 | 5.70E-06 | Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens OX=9606 GN=SRC PE=1 SV=3 |
| C9JA05 | 5 | 0.000162526 | Immunoglobulin J chain (Fragment) OS=Homo sapiens OX=9606 GN=JCHAIN PE=1 SV=1 |
| D6RHJ6 | 5 | 7.25E-05 | Immunoglobulin J chain (Fragment) OS=Homo sapiens OX=9606 GN=JCHAIN PE=1 SV=1 |
| D6RD17 | 5 | 7.25E-05 | Immunoglobulin J chain (Fragment) OS=Homo sapiens OX=9606 GN=JCHAIN PE=1 SV=8 |
| P01591 | 5 | 7.16E-05 | Immunoglobulin J chain OS=Homo sapiens OX=9606 GN=JCHAIN PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: D6RHJ6, D6RD17, C9JA05 |
| Q9UHA4 | 6 | 3.67E-05 | Ragulator complex protein LAMTOR3 OS=Homo sapiens OX=9606 GN=LAMTOR3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UHA4-2 |
| Q9UHA4-2 | 6 | 3.89E-05 | Isoform 2 of Ragulator complex protein LAMTOR3 OS=Homo sapiens OX=9606 GN=LAMTOR3 |
| Q9UIQ6-2 | 6 | 6.46E-06 | Isoform 2 of Leucyl-cystinyl aminopeptidase OS=Homo sapiens OX=9606 GN=LNPEP |
| Q9UIQ6-3 | 6 | 6.49E-06 | Isoform 3 of Leucyl-cystinyl aminopeptidase OS=Homo sapiens OX=9606 GN=LNPEP |
| Q9UIQ6 | 6 | 6.99E-06 | Leucyl-cystinyl aminopeptidase OS=Homo sapiens OX=9606 GN=LNPEP PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9UIQ6-2, Q9UIQ6-3 |
| A0A0C4DFM8 | 5 | 1.32E-05 | Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=1 |
| Q7Z406-6 | 5 | 3.34E-06 | Isoform 6 of Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 |
| Q5BKV1 | 6 | 5.80E-05 | MYH9 protein OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=1 |
| Q7Z406 | 5 | 3.35E-06 | Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=2 |
| B1AH99 | 6 | 0.000122752 | Myosin-9 (Fragment) OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=1 |
| Q7Z406-2 | 5 | 3.28E-06 | Isoform 2 of Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 |
| P13611-4 | 6 | 0.000193435 | Isoform V3 of Versican core protein OS=Homo sapiens OX=9606 GN=VCAN |
| E9PF17 | 6 | 0.000116626 | Versican core protein OS=Homo sapiens OX=9606 GN=VCAN PE=1 SV=2 |
| P13611-3 | 6 | 0.000113217 | Isoform V2 of Versican core protein OS=Homo sapiens OX=9606 GN=VCAN |
| Q86W61 | 6 | 0.000351436 | VCAN protein OS=Homo sapiens OX=9606 GN=VCAN PE=1 SV=1 |
| P40926 | 6 | 0.000404367 | Malate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P40926-2, G3XAL0 |
| G3XAL0 | 6 | 0.000571346 | Malate dehydrogenase OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=1 |
| P40926-2 | 6 | 0.000387396 | Isoform 2 of Malate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 |
| R4GN98 | 6 | 0.017964922 | Protein S100 (Fragment) OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1 |
| P06703 | 6 | 0.017470271 | Protein S100-A6 OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: R4GN98 |
| Q71UI9-5 | 6 | 0.010590045 | Isoform 5 of Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AFV |
| H0YB91 | 6 | 5.96E-05 | Iduronate 2-sulfatase (Fragment) OS=Homo sapiens OX=9606 GN=IDS PE=1 SV=1 |
| P22304-2 | 6 | 4.44E-05 | Isoform 2 of Iduronate 2-sulfatase OS=Homo sapiens OX=9606 GN=IDS |
| P22304-3 | 6 | 4.60E-05 | Isoform 3 of Iduronate 2-sulfatase OS=Homo sapiens OX=9606 GN=IDS |
| O60597 | 6 | 3.53E-05 | Iduronate 2-sulfatase OS=Homo sapiens OX=9606 GN=IDS PE=1 SV=1 |
| G3V595 | 6 | 8.28E-05 | Alpha-1-antichymotrypsin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=3 |
| P01011-2 | 6 | 9.91E-05 | Isoform 2 of Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 |
| C9IZA5 | 6 | 3.15E-05 | Transitional endoplasmic reticulum ATPase (Fragment) OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=1 |
| C9JUP7 | 6 | 4.38E-05 | Transitional endoplasmic reticulum ATPase (Fragment) OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=1 |
| P55072 | 6 | 3.56E-05 | Transitional endoplasmic reticulum ATPase OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: C9IZA5, C9JUP7 |
| B4DJC3 | 5 | 9.43E-05 | Histone H2A OS=Homo sapiens OX=9606 GN=H2AFY PE=1 SV=1 |
| O75367 | 6 | 9.83E-05 | Core histone macro-H2A.1 OS=Homo sapiens OX=9606 GN=H2AFY PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: O75367-3, O75367-2, D6RCF2, B4DJC3 |
| O75367-2 | 6 | 9.91E-05 | Isoform 1 of Core histone macro-H2A.1 OS=Homo sapiens OX=9606 GN=H2AFY |
| D6RCF2 | 6 | 0.000165728 | Histone H2A OS=Homo sapiens OX=9606 GN=H2AFY PE=1 SV=1 |
| O75367-3 | 6 | 9.85E-05 | Isoform 3 of Core histone macro-H2A.1 OS=Homo sapiens OX=9606 GN=H2AFY |
| Q00839-2 | 6 | 8.94E-05 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU |
| Q00839 | 6 | 8.73E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6; Additional IDs concatenated into MaxParsimony group: Q00839-2, A0A1W2PPS1, A0A1X7SBS1, A0A1W2PP35, Q5RI18, A0A1W2PPH7, A0A1W2PPL4, A0A1W2PP34, A0A1W2PQL0, A0A1W2PQ74, A0A1W2PRZ7 |
| A0A1X7SBS1 | 6 | 9.68E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PP35 | 6 | 4.16E-05 | Heterogeneous nuclear ribonucleoprotein U (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A0A1W2PPS1 | 6 | 8.96E-05 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| E9PQA1 | 6 | 0.000142529 | Chromosome 11 open reading frame 58 OS=Homo sapiens OX=9606 GN=C11orf58 PE=1 SV=1 |
| E9PRZ9 | 6 | 0.000400133 | Chromosome 11 open reading frame 58 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf58 PE=1 SV=1 |
| O00193 | 6 | 0.000275416 | Small acidic protein OS=Homo sapiens OX=9606 GN=SMAP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PM92, E9PRZ9, E9PQA1 |
| E9PM92 | 6 | 0.000307449 | Chromosome 11 open reading frame 58 OS=Homo sapiens OX=9606 GN=C11orf58 PE=1 SV=2 |
| F8VRV7 | 6 | 0.000220766 | Dynactin subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=8 |
| Q13561-3 | 6 | 8.92E-05 | Isoform 3 of Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 |
| Q13561-2 | 6 | 8.86E-05 | Isoform 2 of Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2; Additional IDs concatenated into MaxParsimony group: Q13561-3, Q13561, F8W1I6, F8VW18, H0YI98, F8VRV7, H0YHL1, F8W0U6 |
| F8VW18 | 6 | 0.000124783 | Dynactin subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=1 |
| F8W0U6 | 6 | 0.00066466 | Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=1 |
| Q13561 | 6 | 8.97E-05 | Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=4 |
| F8W1I6 | 6 | 0.000112834 | Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=1 |
| P20810-5 | 6 | 4.64E-05 | Isoform 5 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| P20810-9 | 6 | 4.68E-05 | Isoform 9 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| E7EVY3 | 6 | 4.82E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| E7EQ12 | 6 | 6.83E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| P20810-7 | 6 | 4.54E-05 | Isoform 7 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| A0A0C4DGB5 | 6 | 4.65E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| E9PCH5 | 6 | 5.21E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| P20810-3 | 6 | 5.94E-05 | Isoform 3 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| P20810 | 6 | 4.95E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=4 |
| E7EQA0 | 6 | 5.26E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| P20810-6 | 6 | 4.43E-05 | Isoform 6 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST; Additional IDs concatenated into MaxParsimony group: P20810-7, P20810-10, P20810-5, A0A0C4DGB5, P20810-9, P20810, P20810-2, B7Z574, E7EVY3, P20810-8, E9PCH5, P20810-4, E7ES10, E9PDE4, P20810-3, H0Y9H6, H0Y7F0, H0YD33, E7EQA0, A0A0A0MR45, E7EQ12, F8W7E0, H0YA91, A0A0C4DGD1 |
| H0Y7F0 | 6 | 8.04E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| H0Y9H6 | 6 | 7.19E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| P20810-8 | 6 | 5.11E-05 | Isoform 8 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| F8W7E0 | 6 | 3.16E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| H0YD33 | 6 | 4.67E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| E9PDE4 | 6 | 5.51E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| P20810-2 | 6 | 5.05E-05 | Isoform 2 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| B7Z574 | 6 | 5.05E-05 | cDNA FLJ56123, highly similar to Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| P20810-10 | 6 | 4.56E-05 | Isoform 10 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| P20810-4 | 6 | 5.26E-05 | Isoform 4 of Calpastatin OS=Homo sapiens OX=9606 GN=CAST |
| E7ES10 | 6 | 5.46E-05 | Calpastatin (Fragment) OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| A0A0A0MR45 | 6 | 4.88E-05 | Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=1 |
| Q5T205 | 6 | 0.000149219 | Nicastrin (Fragment) OS=Homo sapiens OX=9606 GN=NCSTN PE=1 SV=1 |
| H0Y3Z4 | 6 | 0.000103414 | Nicastrin (Fragment) OS=Homo sapiens OX=9606 GN=NCSTN PE=1 SV=9 |
| E9PPI5 | 6 | 9.49E-05 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=1 |
| P30154-4 | 6 | 1.42E-05 | Isoform 4 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B |
| P30153 | 6 | 4.25E-05 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: B3KQV6, E9PH38, P30154-2, P30154, P30154-4, P30154-5, C9J9C1, E9PHZ6, E9PNM7, E9PPI5 |
| E9PH38 | 6 | 0.000115207 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Fragment) OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=2 |
| C9J9C1 | 6 | 1.30E-05 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Fragment) OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=2 |
| P30154 | 6 | 1.31E-05 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=3 |
| P30154-5 | 6 | 1.66E-05 | Isoform 5 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B |
| P30154-2 | 6 | 1.18E-05 | Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B |
| E9PHZ6 | 6 | 5.83E-05 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=1 |
| B3KQV6 | 6 | 3.97E-05 | cDNA FLJ33169 fis, clone ADRGL2000384, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=1 |
| E9PNM7 | 6 | 2.82E-05 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform (Fragment) OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=1 |
| P35244 | 6 | 0.000128698 | Replication protein A 14 kDa subunit OS=Homo sapiens OX=9606 GN=RPA3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B5MC59 |
| B5MC59 | 6 | 0.000189907 | Replication protein A 14 kDa subunit OS=Homo sapiens OX=9606 GN=RPA3 PE=1 SV=1 |
| H3BQB1 | 6 | 0.000195008 | Adenine phosphoribosyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=1 |
| H3BSW3 | 6 | 0.000286922 | Adenine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=1 |
| P07741-2 | 6 | 0.000235755 | Isoform 2 of Adenine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=APRT |
| P07741 | 6 | 0.000175507 | Adenine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H3BQB1, H3BQF1, P07741-2, H3BQZ9, H3BSW3 |
| H3BQF1 | 6 | 0.000194579 | Adenine phosphoribosyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=8 |
| H3BQZ9 | 6 | 0.000136402 | Adenine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=1 |
| F5H018 | 5 | 0.000133641 | GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=8 |
| J3KQE5 | 5 | 0.000113081 | GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B5MDF5, P62826, F5H018, H0YFC6, B4DV51 |
| B5MDF5 | 5 | 0.000113566 | GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=1 |
| P62826 | 5 | 0.000122504 | GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=3 |
| H0YFC6 | 5 | 0.000217907 | GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=1 |
| Q9BRX8 | 6 | 3.43E-05 | Redox-regulatory protein FAM213A OS=Homo sapiens OX=9606 GN=FAM213A PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q9BRX8-2 |
| Q9BRX8-2 | 6 | 3.60E-05 | Isoform 2 of Redox-regulatory protein FAM213A OS=Homo sapiens OX=9606 GN=FAM213A |
| A4D2B0 | 6 | 6.08E-05 | Metallo-beta-lactamase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MBLAC1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JAV3 |
| C9JAV3 | 6 | 0.000141387 | Metallo-beta-lactamase domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=MBLAC1 PE=1 SV=1 |
| E5RHW4 | 6 | 1.82E-05 | Erlin-2 (Fragment) OS=Homo sapiens OX=9606 GN=ERLIN2 PE=1 SV=1 |
| O94905 | 6 | 1.81E-05 | Erlin-2 OS=Homo sapiens OX=9606 GN=ERLIN2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E5RHW4, O75477, B0QZ43 |
| H3BRB0 | 5 | 4.83E-05 | Ataxin-2-like protein (Fragment) OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=2 |
| Q8WWM7-9 | 5 | 8.25E-06 | Isoform 9 of Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L |
| Q8WWM7 | 5 | 2.37E-05 | Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8WWM7-3, H3BUF6, Q8WWM7-9, Q8WWM7-2, A0A0C4DGL7, H3BRB0, Q8WWM7-8, Q8WWM7-4, Q8WWM7-5, Q8WWM7-6 |
| A0A0C4DGL7 | 5 | 4.82E-05 | Ataxin-2-like protein (Fragment) OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=1 |
| Q8WWM7-3 | 5 | 7.98E-06 | Isoform 3 of Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L |
| Q8WWM7-2 | 5 | 8.25E-06 | Isoform 2 of Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L |
| H3BUF6 | 5 | 8.20E-06 | Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=1 |
| O60763-2 | 5 | 3.67E-06 | Isoform 2 of General vesicular transport factor p115 OS=Homo sapiens OX=9606 GN=USO1; Additional IDs concatenated into MaxParsimony group: O60763 |
| O60763 | 5 | 3.71E-06 | General vesicular transport factor p115 OS=Homo sapiens OX=9606 GN=USO1 PE=1 SV=2 |
| P18859 | 6 | 0.000920909 | ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5J PE=1 SV=1 |
| P18859-2 | 6 | 0.000857398 | Isoform 2 of ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5J; Additional IDs concatenated into MaxParsimony group: P18859 |
| H0YMU3 | 5 | 4.46E-05 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1 |
| P50213 | 5 | 2.13E-05 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0YL72, H0YMU3, H0YLI6, H0YKD0, P50213-2, H0YM64 |
| H0YL72 | 5 | 2.36E-05 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1 |
| H0YKD0 | 5 | 7.17E-05 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1 |
| H0YLI6 | 5 | 5.83E-05 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1 |
| H0YM64 | 5 | 0.000139047 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1 |
| E9PLL6 | 6 | 0.000148892 | 60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=1 |
| E9PJD9 | 6 | 0.000176707 | 60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=1 |
| E9PLX7 | 6 | 0.00011604 | 60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=1 |
| P46776 | 6 | 0.000108651 | 60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PLL6, E9PJD9, E9PLX7 |
| Q99574 | 6 | 3.74E-06 | Neuroserpin OS=Homo sapiens OX=9606 GN=SERPINI1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H7C5T9 |
| Q9UM22-3 | 6 | 2.82E-05 | Isoform 3 of Mammalian ependymin-related protein 1 OS=Homo sapiens OX=9606 GN=EPDR1 |
| Q9UM22 | 6 | 0.000119906 | Mammalian ependymin-related protein 1 OS=Homo sapiens OX=9606 GN=EPDR1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UM22-3, D6RIH7, Q9UM22-2 |
| D6RIH7 | 6 | 3.71E-05 | Mammalian ependymin-related protein 1 OS=Homo sapiens OX=9606 GN=EPDR1 PE=1 SV=1 |
| Q9UM22-2 | 6 | 0.00024734 | Isoform 2 of Mammalian ependymin-related protein 1 OS=Homo sapiens OX=9606 GN=EPDR1 |
| H3BPE7 | 6 | 2.51E-05 | RNA-binding protein FUS OS=Homo sapiens OX=9606 GN=FUS PE=1 SV=1 |
| P35637-2 | 6 | 2.52E-05 | Isoform Short of RNA-binding protein FUS OS=Homo sapiens OX=9606 GN=FUS |
| A0A075B7D9 | 6 | 2.94E-05 | TATA-binding protein-associated factor 2N OS=Homo sapiens OX=9606 GN=TAF15 PE=1 SV=1 |
| Q92804 | 6 | 2.23E-05 | TATA-binding protein-associated factor 2N OS=Homo sapiens OX=9606 GN=TAF15 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q92804-2, H3BPE7, P35637, P35637-2, A0A075B7D9 |
| P35637 | 6 | 2.51E-05 | RNA-binding protein FUS OS=Homo sapiens OX=9606 GN=FUS PE=1 SV=1 |
| Q92804-2 | 6 | 2.24E-05 | Isoform Short of TATA-binding protein-associated factor 2N OS=Homo sapiens OX=9606 GN=TAF15 |
| A0A0G2JMH6 | 6 | 2.20E-05 | HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens OX=9606 GN=HLA-DRA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P01903, Q30118, A0A0G2JH46, Q5Y7H0, P01906, A0A140TA34, Q08AS3, A0A1W2PP70 |
| Q5Y7H0 | 6 | 1.04E-05 | HLA class II histocompatibility antigen, DQ alpha 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQA1 PE=1 SV=1 |
| Q30118 | 6 | 2.44E-05 | HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens OX=9606 GN=HLA-DRA PE=1 SV=1 |
| A0A1W2PP70 | 6 | 1.39E-05 | HLA class II histocompatibility antigen, DQ alpha 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQA1 PE=1 SV=1 |
| Q08AS3 | 6 | 1.04E-05 | HLA class II histocompatibility antigen, DQ alpha 1 chain OS=Homo sapiens OX=9606 GN=HLA-DQA1 PE=1 SV=1 |
| P01906 | 6 | 1.04E-05 | HLA class II histocompatibility antigen, DQ alpha 2 chain OS=Homo sapiens OX=9606 GN=HLA-DQA2 PE=1 SV=2 |
| A0A0G2JH46 | 6 | 2.44E-05 | HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens OX=9606 GN=HLA-DRA PE=1 SV=1 |
| A0A140TA34 | 6 | 1.04E-05 | HLA class II histocompatibility antigen, DQ alpha 2 chain OS=Homo sapiens OX=9606 GN=HLA-DQA2 PE=3 SV=1 |
| P01903 | 6 | 2.20E-05 | HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens OX=9606 GN=HLA-DRA PE=1 SV=1 |
| P11177-3 | 6 | 2.15E-05 | Isoform 3 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=PDHB |
| P11177 | 6 | 2.04E-05 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=PDHB PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P11177-3, P11177-2, C9J634, F8WF02 |
| P11177-2 | 6 | 2.15E-05 | Isoform 2 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=PDHB |
| B0YIW2 | 6 | 0.000151833 | Apolipoprotein C-III variant 1 OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P02656 |
| P02656 | 6 | 0.000179439 | Apolipoprotein C-III OS=Homo sapiens OX=9606 GN=APOC3 PE=1 SV=1 |
| Q9NUQ9 | 5 | 3.61E-06 | Protein FAM49B OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E5RI16, E5RJL8, E5RIR8, E5RJE1, E5RGI7, E5RHU5, E5RFS4, E5RK61 |
| E5RGI7 | 5 | 1.50E-05 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=8 |
| E5RI16 | 5 | 7.55E-06 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 |
| E5RK61 | 5 | 1.86E-05 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 |
| E5RFS4 | 5 | 1.80E-05 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 |
| E5RJL8 | 5 | 1.17E-05 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 |
| E5RHU5 | 5 | 1.72E-05 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 |
| E5RIR8 | 5 | 1.19E-05 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 |
| E5RJE1 | 5 | 1.26E-05 | Protein FAM49B (Fragment) OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 |
| P05164-2 | 5 | 2.01E-06 | Isoform H14 of Myeloperoxidase OS=Homo sapiens OX=9606 GN=MPO |
| P05164 | 5 | 1.76E-06 | Myeloperoxidase OS=Homo sapiens OX=9606 GN=MPO PE=1 SV=1 |
| J3QSF7 | 5 | 1.52E-05 | Myeloperoxidase (Fragment) OS=Homo sapiens OX=9606 GN=MPO PE=1 SV=8 |
| P05164-3 | 5 | 1.69E-06 | Isoform H7 of Myeloperoxidase OS=Homo sapiens OX=9606 GN=MPO; Additional IDs concatenated into MaxParsimony group: P05164, P05164-2, J3QSF7 |
| P52566 | 5 | 2.53E-05 | Rho GDP-dissociation inhibitor 2 OS=Homo sapiens OX=9606 GN=ARHGDIB PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: F5H3P3, F5H6Q0, F5H2R5 |
| F5H2R5 | 5 | 5.77E-05 | Rho GDP-dissociation inhibitor 2 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGDIB PE=1 SV=1 |
| F5H3P3 | 5 | 3.21E-05 | Rho GDP-dissociation inhibitor 2 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGDIB PE=1 SV=8 |
| F5H6Q0 | 5 | 4.53E-05 | Rho GDP-dissociation inhibitor 2 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGDIB PE=1 SV=1 |
| Q9NPJ3-2 | 5 | 4.13E-05 | Isoform 2 of Acyl-coenzyme A thioesterase 13 OS=Homo sapiens OX=9606 GN=ACOT13 |
| Q9NPJ3 | 5 | 3.46E-05 | Acyl-coenzyme A thioesterase 13 OS=Homo sapiens OX=9606 GN=ACOT13 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NPJ3-2 |
| P55145 | 6 | 5.04E-05 | Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens OX=9606 GN=MANF PE=1 SV=3 |
| A8K878 | 6 | 4.96E-05 | Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens OX=9606 GN=MANF PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P55145, H7C2D6 |
| H7C2D6 | 5 | 7.70E-05 | Mesencephalic astrocyte-derived neurotrophic factor (Fragment) OS=Homo sapiens OX=9606 GN=MANF PE=1 SV=1 |
| O43464 | 5 | 5.56E-06 | Serine protease HTRA2, mitochondrial OS=Homo sapiens OX=9606 GN=HTRA2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: O43464-3, A0A0C4DG44, O43464-2 |
| A0A0C4DG44 | 5 | 6.02E-06 | Serine protease HTRA2, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HTRA2 PE=1 SV=1 |
| O43464-2 | 5 | 7.05E-06 | Isoform 2 of Serine protease HTRA2, mitochondrial OS=Homo sapiens OX=9606 GN=HTRA2 |
| O43464-3 | 5 | 5.84E-06 | Isoform 3 of Serine protease HTRA2, mitochondrial OS=Homo sapiens OX=9606 GN=HTRA2 |
| K7ERZ6 | 6 | 0.000840244 | Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| K7ES75 | 6 | 0.001063615 | Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| K7EJD3 | 6 | 0.000536936 | Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| K7EN99 | 6 | 0.000828302 | Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| A0A2R8Y6G0 | 6 | 4.21E-05 | Catenin beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| G3V2D6 | 5 | 0.000265073 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V5V7 | 5 | 0.000214902 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| A0A087WVQ6 | 6 | 0.00041361 | Clathrin heavy chain OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q00610, Q00610-2, J3KS13, P53675, P53675-2, A0A087WX41, K7EJJ5 |
| Q00610-2 | 6 | 0.000423704 | Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens OX=9606 GN=CLTC |
| Q00610 | 6 | 0.000414597 | Clathrin heavy chain 1 OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=5 |
| O60784-2 | 6 | 9.78E-05 | Isoform 2 of Target of Myb protein 1 OS=Homo sapiens OX=9606 GN=TOM1 |
| O60784-4 | 6 | 0.000104785 | Isoform 4 of Target of Myb protein 1 OS=Homo sapiens OX=9606 GN=TOM1 |
| O60784 | 6 | 0.000122381 | Target of Myb protein 1 OS=Homo sapiens OX=9606 GN=TOM1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: O60784-3, O60784-2, O60784-4, Q6ZVM7-5, Q6ZVM7-3, Q6ZVM7-2, B7Z2U2, F5H3S6, B0QY01, Q6ZVM7-4 |
| O60784-3 | 6 | 0.000134701 | Isoform 3 of Target of Myb protein 1 OS=Homo sapiens OX=9606 GN=TOM1 |
| A0A087WUA0 | 6 | 3.52E-05 | Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA PE=1 SV=1 |
| Q5SYQ9 | 5 | 3.82E-05 | Retinal dehydrogenase 1 OS=Homo sapiens OX=9606 GN=ALDH1A1 PE=1 SV=1 |
| Q5SYQ8 | 5 | 3.69E-05 | Retinal dehydrogenase 1 (Fragment) OS=Homo sapiens OX=9606 GN=ALDH1A1 PE=1 SV=1 |
| Q5SYQ7 | 5 | 4.33E-05 | Retinal dehydrogenase 1 (Fragment) OS=Homo sapiens OX=9606 GN=ALDH1A1 PE=1 SV=1 |
| Q8NHV4-3 | 6 | 5.09E-05 | Isoform 3 of Protein NEDD1 OS=Homo sapiens OX=9606 GN=NEDD1; Additional IDs concatenated into MaxParsimony group: Q8NHV4, Q8NHV4-2 |
| Q8NHV4-2 | 6 | 5.39E-05 | Isoform 2 of Protein NEDD1 OS=Homo sapiens OX=9606 GN=NEDD1 |
| Q8NHV4 | 6 | 5.15E-05 | Protein NEDD1 OS=Homo sapiens OX=9606 GN=NEDD1 PE=1 SV=1 |
| H0YK49 | 6 | 8.07E-05 | Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ETFA PE=1 SV=1 |
| H0YL12 | 6 | 8.24E-05 | Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ETFA PE=1 SV=8 |
| P13804-2 | 6 | 6.93E-05 | Isoform 2 of Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ETFA |
| H0YNX6 | 6 | 7.27E-05 | Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ETFA PE=1 SV=1 |
| H0YKF0 | 6 | 6.74E-05 | Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ETFA PE=1 SV=1 |
| H0YLU7 | 6 | 6.43E-05 | Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ETFA PE=1 SV=1 |
| P13804 | 6 | 5.91E-05 | Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ETFA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P13804-2, H0YL12, H0YLU7, H0YKF0, H0YNX6, H0YK49 |
| P61224-3 | 6 | 0.000112524 | Isoform 3 of Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B |
| F5H0B7 | 6 | 0.000168428 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| P62834 | 6 | 9.58E-05 | Ras-related protein Rap-1A OS=Homo sapiens OX=9606 GN=RAP1A PE=1 SV=1 |
| F5H004 | 6 | 0.000137296 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| P01112 | 6 | 5.32E-05 | GTPase HRas OS=Homo sapiens OX=9606 GN=HRAS PE=1 SV=1 |
| B7ZB78 | 6 | 4.94E-05 | cDNA, FLJ79442, highly similar to Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5H500 | 6 | 0.000163426 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5H7Y6 | 6 | 9.74E-05 | Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5H4H0 | 4 | 0.000210086 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=4 SV=1 |
| A6NIZ1 | 6 | 7.33E-05 | Ras-related protein Rap-1b-like protein OS=Homo sapiens OX=9606 PE=2 SV=1 |
| A0A075B6Q0 | 6 | 0.000127953 | Ras-related protein Rap-1A (Fragment) OS=Homo sapiens OX=9606 GN=RAP1A PE=1 SV=1 |
| E7ESV4 | 6 | 0.000111061 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5GYH7 | 4 | 0.000190267 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5GX62 | 6 | 0.000125443 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| P01116-2 | 6 | 5.35E-05 | Isoform 2B of GTPase KRas OS=Homo sapiens OX=9606 GN=KRAS |
| F5H6R7 | 6 | 0.000142923 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5H491 | 4 | 0.000108432 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5GZG1 | 6 | 4.82E-05 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8 |
| P01112-2 | 6 | 5.92E-05 | Isoform 2 of GTPase HRas OS=Homo sapiens OX=9606 GN=HRAS |
| P01111 | 6 | 5.32E-05 | GTPase NRas OS=Homo sapiens OX=9606 GN=NRAS PE=1 SV=1 |
| P61224-4 | 6 | 7.68E-05 | Isoform 4 of Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B |
| P01116 | 6 | 5.32E-05 | GTPase KRas OS=Homo sapiens OX=9606 GN=KRAS PE=1 SV=1 |
| F5GWU8 | 4 | 0.00011591 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| F5H077 | 4 | 0.000120049 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=8 |
| F5H823 | 6 | 5.66E-05 | Ras-related protein Rap-1b (Fragment) OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| P61224 | 6 | 0.000100905 | Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P61224-3, P62834, A6NIZ1, F5H7Y6, E7ESV4, F5GX62, F5H004, F5H6R7, P61224-4, P61224-2, F5GYB5, A0A075B6Q0, F5H500, F5H0B7, F5GZG1, B7ZB78, F5H823, F5H491, F5GWU8, F5H077, F5GYH7, F5H4H0, P01112, P01111, P01116-2, P01112-2, F8WBC0 |
| F5GYB5 | 6 | 0.000121367 | Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1 |
| P61224-2 | 6 | 0.000101225 | Isoform 2 of Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B |
| C9JKZ2 | 6 | 3.15E-05 | Nucleobindin-1 (Fragment) OS=Homo sapiens OX=9606 GN=NUCB1 PE=1 SV=8 |
| H7BZI1 | 6 | 4.14E-05 | Nucleobindin-1 (Fragment) OS=Homo sapiens OX=9606 GN=NUCB1 PE=1 SV=1 |
| P30626 | 6 | 0.000167068 | Sorcin OS=Homo sapiens OX=9606 GN=SRI PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P30626-2, P30626-3, C9J0K6, B4DHQ6 |
| P30626-3 | 6 | 0.000183775 | Isoform 3 of Sorcin OS=Homo sapiens OX=9606 GN=SRI |
| P30626-2 | 6 | 0.000180762 | Isoform 2 of Sorcin OS=Homo sapiens OX=9606 GN=SRI |
| C9J0K6 | 6 | 0.000213416 | Sorcin OS=Homo sapiens OX=9606 GN=SRI PE=1 SV=1 |
| M0QXK4 | 6 | 0.000212097 | 40S ribosomal protein S19 (Fragment) OS=Homo sapiens OX=9606 GN=RPS19 PE=1 SV=1 |
| P39019 | 6 | 0.000184979 | 40S ribosomal protein S19 OS=Homo sapiens OX=9606 GN=RPS19 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0R140, M0QYF7, M0QXK4, M0R2L9 |
| M0QYF7 | 6 | 0.000161194 | 40S ribosomal protein S19 (Fragment) OS=Homo sapiens OX=9606 GN=RPS19 PE=1 SV=1 |
| M0R140 | 6 | 0.000158033 | 40S ribosomal protein S19 (Fragment) OS=Homo sapiens OX=9606 GN=RPS19 PE=1 SV=1 |
| M0R2L9 | 6 | 0.000227033 | 40S ribosomal protein S19 (Fragment) OS=Homo sapiens OX=9606 GN=RPS19 PE=1 SV=1 |
| P15121 | 6 | 0.000119095 | Aldose reductase OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: E9PCX2, E9PEF9 |
| E9PEF9 | 6 | 0.000232074 | Aldose reductase OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1 SV=1 |
| E9PCX2 | 6 | 9.00E-05 | Aldose reductase OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1 SV=1 |
| C9JV77 | 6 | 0.000220983 | Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1 |
| P02765 | 6 | 0.000221586 | Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHSG PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JV77 |
| B4DQU5 | 6 | 4.75E-05 | cDNA FLJ57160, highly similar to Ras-related protein Rab-11A OS=Homo sapiens OX=9606 GN=RAB11A PE=1 SV=1 |
| P62491 | 6 | 0.000137033 | Ras-related protein Rab-11A OS=Homo sapiens OX=9606 GN=RAB11A PE=1 SV=3 |
| Q15907-2 | 6 | 0.000165358 | Isoform 2 of Ras-related protein Rab-11B OS=Homo sapiens OX=9606 GN=RAB11B |
| H3BSC1 | 6 | 0.00014949 | Ras-related protein Rab-11A OS=Homo sapiens OX=9606 GN=RAB11A PE=1 SV=1 |
| Q15907 | 6 | 0.000135776 | Ras-related protein Rab-11B OS=Homo sapiens OX=9606 GN=RAB11B PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P62491, H3BSC1, Q15907-2, P62491-2, H3BMH2, B4DQU5 |
| P62491-2 | 6 | 0.000190962 | Isoform 2 of Ras-related protein Rab-11A OS=Homo sapiens OX=9606 GN=RAB11A |
| H3BMH2 | 6 | 0.000190962 | Ras-related protein Rab-11A (Fragment) OS=Homo sapiens OX=9606 GN=RAB11A PE=4 SV=1 |
| P37802 | 6 | 0.000220443 | Transgelin-2 OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=3 |
| X6RJP6 | 6 | 0.000222007 | Transgelin-2 (Fragment) OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=1 |
| P37802-2 | 6 | 0.0001994 | Isoform 2 of Transgelin-2 OS=Homo sapiens OX=9606 GN=TAGLN2; Additional IDs concatenated into MaxParsimony group: P37802, X6RJP6 |
| B8ZZ43 | 6 | 7.69E-05 | Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA\_b OS=Homo sapiens OX=9606 GN=CBX3 PE=1 SV=1 |
| S4R2Y4 | 6 | 7.26E-05 | Chromobox protein homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=CBX3 PE=1 SV=1 |
| J3KS05 | 6 | 2.19E-05 | Chromobox protein homolog 1 (Fragment) OS=Homo sapiens OX=9606 GN=CBX1 PE=1 SV=8 |
| K7ELA4 | 6 | 2.74E-05 | Chromobox protein homolog 1 OS=Homo sapiens OX=9606 GN=CBX1 PE=1 SV=1 |
| C9JMM0 | 6 | 0.000125225 | Chromobox protein homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=CBX3 PE=1 SV=1 |
| B5MD17 | 6 | 2.25E-05 | Chromobox protein homolog 1 (Fragment) OS=Homo sapiens OX=9606 GN=CBX1 PE=1 SV=1 |
| Q13185 | 6 | 6.86E-05 | Chromobox protein homolog 3 OS=Homo sapiens OX=9606 GN=CBX3 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: S4R2Y4, B8ZZ43, C9JMM0, P83916, J3KS05, B5MD17, K7ELA4 |
| P83916 | 6 | 2.05E-05 | Chromobox protein homolog 1 OS=Homo sapiens OX=9606 GN=CBX1 PE=1 SV=1 |
| A6NP24 | 6 | 4.94E-05 | Quinone oxidoreductase (Fragment) OS=Homo sapiens OX=9606 GN=CRYZ PE=1 SV=1 |
| Q08257-3 | 6 | 5.01E-05 | Isoform 3 of Quinone oxidoreductase OS=Homo sapiens OX=9606 GN=CRYZ |
| C9JH92 | 6 | 5.82E-05 | Quinone oxidoreductase (Fragment) OS=Homo sapiens OX=9606 GN=CRYZ PE=1 SV=1 |
| Q08257 | 6 | 4.50E-05 | Quinone oxidoreductase OS=Homo sapiens OX=9606 GN=CRYZ PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q08257-3, A6NP24, C9JH92, Q08257-2 |
| Q5JYX0 | 6 | 2.49E-05 | Cell division control protein 42 homolog (Fragment) OS=Homo sapiens OX=9606 GN=CDC42 PE=1 SV=1 |
| P60953 | 6 | 8.37E-05 | Cell division control protein 42 homolog OS=Homo sapiens OX=9606 GN=CDC42 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P15153, P63000, P60953-1, B1AH80, B1AH77, Q5JYX0, J3QLK0, J3KSC4, B1AH78 |
| P60953-1 | 6 | 1.78E-05 | Isoform 1 of Cell division control protein 42 homolog OS=Homo sapiens OX=9606 GN=CDC42 |
| P50991 | 5 | 2.11E-05 | T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P50991-2 |
| P50991-2 | 5 | 2.24E-05 | Isoform 2 of T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 |
| P14866 | 5 | 3.09E-05 | Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0QXS5, P14866-2, M0QYT0, M0R1W6, M0QYL7, M0R076 |
| M0R076 | 5 | 4.75E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 |
| M0QYT0 | 5 | 1.69E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 |
| P14866-2 | 5 | 1.19E-05 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL |
| M0QXS5 | 5 | 1.98E-05 | Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=1 |
| E7ENQ8 | 6 | 4.31E-05 | Phosphoglucomutase-2 OS=Homo sapiens OX=9606 GN=PGM2 PE=1 SV=1 |
| E9PD70 | 6 | 9.76E-05 | Phosphoglucomutase-2 OS=Homo sapiens OX=9606 GN=PGM2 PE=1 SV=1 |
| Q96G03 | 6 | 1.88E-05 | Phosphoglucomutase-2 OS=Homo sapiens OX=9606 GN=PGM2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: E7ENQ8, E9PD70 |
| Q04837 | 5 | 0.000128743 | Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=SSBP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E7EUY5, A0A0G2JLD8, C9K0U8 |
| A0A0G2JLD8 | 5 | 0.000139301 | Single-stranded DNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SSBP1 PE=1 SV=1 |
| E7EUY5 | 5 | 0.000138269 | Single-stranded DNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SSBP1 PE=1 SV=1 |
| C9K0U8 | 5 | 0.000154267 | Single-stranded DNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SSBP1 PE=1 SV=1 |
| B4DEH8 | 6 | 0.000300726 | Polyadenylate-binding protein 2 OS=Homo sapiens OX=9606 GN=PABPN1 PE=1 SV=1 |
| H0YJH9 | 6 | 0.000479642 | Polyadenylate-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=PABPN1 PE=1 SV=1 |
| Q86U42 | 6 | 0.000165105 | Polyadenylate-binding protein 2 OS=Homo sapiens OX=9606 GN=PABPN1 PE=1 SV=3 |
| G3V4T2 | 6 | 0.000283832 | Polyadenylate-binding protein 2 OS=Homo sapiens OX=9606 GN=PABPN1 PE=1 SV=1 |
| Q92843-2 | 6 | 0.000151718 | Isoform 3 of Bcl-2-like protein 2 OS=Homo sapiens OX=9606 GN=BCL2L2; Additional IDs concatenated into MaxParsimony group: Q86U42, Q86U42-2, G3V4T2, B4DEH8, H0YJH9 |
| Q86U42-2 | 6 | 0.000170683 | Isoform 2 of Polyadenylate-binding protein 2 OS=Homo sapiens OX=9606 GN=PABPN1 |
| F5GX29 | 6 | 0.000123691 | Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=1 |
| H0YKE7 | 6 | 0.000128719 | Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=1 |
| H0YLY7 | 6 | 0.000150956 | Calcineurin B homologous protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=1 |
| Q99653 | 6 | 8.23E-05 | Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H0YNG9, F5GX29, H0YKE7, H0YLY7 |
| H0YNG9 | 6 | 0.000102808 | Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=1 |
| Q9HAT2 | 6 | 2.51E-05 | Sialate O-acetylesterase OS=Homo sapiens OX=9606 GN=SIAE PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9HAT2-2 |
| Q9HAT2-2 | 6 | 2.69E-05 | Isoform 2 of Sialate O-acetylesterase OS=Homo sapiens OX=9606 GN=SIAE |
| Q9UBQ7 | 5 | 2.56E-05 | Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens OX=9606 GN=GRHPR PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: U3KQ56 |
| Q9UI30 | 6 | 3.22E-05 | Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens OX=9606 GN=TRMT112 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F5GX77, F5GYQ2, Q9UI30-2 |
| Q9UI30-2 | 6 | 3.18E-05 | Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens OX=9606 GN=TRMT112 |
| F5GYQ2 | 6 | 4.97E-05 | Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens OX=9606 GN=TRMT112 PE=1 SV=1 |
| F5GX77 | 6 | 3.80E-05 | Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens OX=9606 GN=TRMT112 PE=1 SV=1 |
| F8W4S1 | 5 | 1.37E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| B4DJV2 | 5 | 1.38E-05 | Citrate synthase OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| F8VTT8 | 5 | 1.64E-05 | Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 |
| O75390 | 5 | 1.34E-05 | Citrate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: B4DJV2, A0A0C4DGI3, H0YH82, F8W4S1, F8W1S4, F8VTT8, F8VPA1, F8VPF9, H0YIC4, F8VX68, F8VRP1, F8VX07, F8VZK9, F8W642 |
| C9J8F3 | 6 | 2.72E-05 | Fructose-bisphosphate aldolase C (Fragment) OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=1 |
| J3QKP5 | 6 | 3.23E-05 | Fructose-bisphosphate aldolase C (Fragment) OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=2 |
| J3KSV6 | 6 | 3.32E-05 | Fructose-bisphosphate aldolase C (Fragment) OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=1 |
| J3QKK1 | 5 | 2.49E-05 | Fructose-bisphosphate aldolase C (Fragment) OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=1 |
| K7EKH5 | 6 | 1.50E-05 | Fructose-bisphosphate aldolase C (Fragment) OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=1 |
| A8MVZ9 | 6 | 2.40E-05 | Fructose-bisphosphate aldolase OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=1 |
| P09972 | 6 | 2.22E-05 | Fructose-bisphosphate aldolase C OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A8MVZ9, J3QKP5, J3KSV6, C9J8F3, K7EKH5, J3QKK1 |
| Q01844 | 5 | 6.50E-06 | RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1 |
| Q01844-4 | 4 | 8.14E-06 | Isoform 4 of RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 |
| Q01844-3 | 5 | 6.51E-06 | Isoform 3 of RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 |
| B0QYK0 | 5 | 6.89E-06 | RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1 |
| Q01844-6 | 5 | 7.10E-06 | Isoform 6 of RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 |
| Q01844-5 | 5 | 6.45E-06 | Isoform 5 of RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1; Additional IDs concatenated into MaxParsimony group: Q01844, Q01844-3, B0QYK0, Q01844-6, C9JGE3, A0A0D9SFL3, Q01844-2, Q01844-4, H7BY36 |
| A0A087WWI4 | 5 | 4.61E-06 | Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1 |
| Q9Y4L1 | 5 | 3.21E-06 | Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087X054, K7EQK2, A0A087WWI4, E9PJ21, Q9Y4L1-2 |
| E9PJ21 | 5 | 4.76E-06 | Hypoxia up-regulated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1 |
| Q9Y4L1-2 | 5 | 5.59E-06 | Isoform 2 of Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 |
| A0A087X054 | 5 | 3.43E-06 | Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1 |
| K7EQK2 | 5 | 4.61E-06 | Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1 |
| P13489 | 5 | 1.39E-05 | Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PIM9, E9PLZ3, E9PMJ3, E9PIK5, E9PMN0, E9PMA9 |
| E9PLZ3 | 5 | 2.89E-05 | Ribonuclease inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=1 |
| E9PIM9 | 5 | 2.81E-05 | Ribonuclease inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=1 |
| E9PMJ3 | 5 | 2.96E-05 | Ribonuclease inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=1 |
| E9PMA9 | 5 | 6.40E-05 | Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=1 |
| E9PIK5 | 5 | 2.72E-05 | Ribonuclease inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=1 |
| E9PMN0 | 5 | 2.93E-05 | Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=1 |
| O43768-4 | 5 | 7.70E-05 | Isoform 4 of Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA |
| O43768-2 | 5 | 9.21E-05 | Isoform 2 of Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA |
| O43768-3 | 5 | 7.87E-05 | Isoform 3 of Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA |
| O43768-9 | 5 | 8.11E-05 | Isoform 9 of Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA |
| Q5T5H1 | 5 | 5.77E-05 | Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O43768-4, A6NMQ3, O43768-3, O43768-9, O43768, A0A1W2PRU0, O43768-2, O43768-8 |
| A6NMQ3 | 5 | 7.70E-05 | Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA PE=1 SV=2 |
| O43768 | 5 | 8.91E-05 | Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA PE=1 SV=1 |
| A0A1W2PRU0 | 5 | 9.06E-05 | Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA PE=1 SV=1 |
| O43768-8 | 4 | 9.69E-05 | Isoform 8 of Alpha-endosulfine OS=Homo sapiens OX=9606 GN=ENSA |
| K7ER39 | 6 | 0.000320461 | Perilipin-3 (Fragment) OS=Homo sapiens OX=9606 GN=PLIN3 PE=1 SV=1 |
| F5GWF6 | 5 | 1.65E-05 | T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=2 |
| P78371-2 | 5 | 3.07E-05 | Isoform 2 of T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 |
| P78371 | 5 | 2.99E-05 | T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P78371-2, F5GWF6, F8VQ14 |
| F8VQ14 | 5 | 1.91E-05 | T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=1 |
| H0YFD6 | 6 | 1.83E-05 | Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P40939, A0A2R8Y4F5, A0A2R8YG21, A0A2R8Y688 |
| P40939 | 6 | 1.90E-05 | Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=2 |
| A0A2R8Y4F5 | 6 | 1.82E-05 | Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=1 |
| H0YDS0 | 6 | 4.12E-05 | Ubiquilin-1 (Fragment) OS=Homo sapiens OX=9606 GN=UBQLN1 PE=1 SV=1 |
| Q9BSJ8 | 6 | 5.50E-06 | Extended synaptotagmin-1 OS=Homo sapiens OX=9606 GN=ESYT1 PE=1 SV=1 |
| Q9BSJ8-2 | 6 | 5.45E-06 | Isoform 2 of Extended synaptotagmin-1 OS=Homo sapiens OX=9606 GN=ESYT1; Additional IDs concatenated into MaxParsimony group: Q9BSJ8 |
| P16930-2 | 6 | 0.000106773 | Isoform 2 of Fumarylacetoacetase OS=Homo sapiens OX=9606 GN=FAH |
| F8W1I5 | 6 | 0.001089114 | Myosin light chain 6B OS=Homo sapiens OX=9606 GN=MYL6B PE=1 SV=1 |
| P14649 | 6 | 0.000916322 | Myosin light chain 6B OS=Homo sapiens OX=9606 GN=MYL6B PE=1 SV=1 |
| A0A2U3U034 | 6 | 2.51E-05 | Arylsulfatase B OS=Homo sapiens OX=9606 GN=ARSB PE=4 SV=1 |
| P15848-2 | 6 | 6.90E-05 | Isoform 2 of Arylsulfatase B OS=Homo sapiens OX=9606 GN=ARSB |
| P15848 | 6 | 5.51E-05 | Arylsulfatase B OS=Homo sapiens OX=9606 GN=ARSB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P15848-2, A0A2U3U034 |
| Q13442 | 6 | 7.84E-05 | 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens OX=9606 GN=PDAP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F8WBW6 |
| P00387-2 | 6 | 5.99E-05 | Isoform 2 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens OX=9606 GN=CYB5R3 |
| P00387-3 | 6 | 4.99E-05 | Isoform 3 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens OX=9606 GN=CYB5R3; Additional IDs concatenated into MaxParsimony group: P00387, P00387-2, B1AHF3 |
| B1AHF3 | 6 | 9.29E-05 | NADH-cytochrome b5 reductase 3 (Fragment) OS=Homo sapiens OX=9606 GN=CYB5R3 PE=1 SV=1 |
| P00387 | 6 | 5.54E-05 | NADH-cytochrome b5 reductase 3 OS=Homo sapiens OX=9606 GN=CYB5R3 PE=1 SV=3 |
| P46108-2 | 6 | 2.37E-05 | Isoform Crk-I of Adapter molecule crk OS=Homo sapiens OX=9606 GN=CRK |
| P46108 | 6 | 1.71E-05 | Adapter molecule crk OS=Homo sapiens OX=9606 GN=CRK PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P46108-2, I3L297 |
| I3L297 | 5 | 1.75E-05 | Adapter molecule crk OS=Homo sapiens OX=9606 GN=CRK PE=1 SV=1 |
| P50502 | 6 | 7.99E-05 | Hsc70-interacting protein OS=Homo sapiens OX=9606 GN=ST13 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8NFI4, Q8IZP2, Q3KNR6, F6VDH7, H7C3I1 |
| H7C3I1 | 6 | 0.000138434 | Hsc70-interacting protein (Fragment) OS=Homo sapiens OX=9606 GN=ST13 PE=1 SV=1 |
| Q8NFI4 | 6 | 4.49E-05 | Putative protein FAM10A5 OS=Homo sapiens OX=9606 GN=ST13P5 PE=5 SV=1 |
| F6VDH7 | 6 | 0.000124761 | Hsc70-interacting protein (Fragment) OS=Homo sapiens OX=9606 GN=ST13 PE=1 SV=1 |
| Q8IZP2 | 6 | 8.42E-05 | Putative protein FAM10A4 OS=Homo sapiens OX=9606 GN=ST13P4 PE=5 SV=1 |
| Q3KNR6 | 6 | 9.58E-05 | Hsc70-interacting protein OS=Homo sapiens OX=9606 GN=ST13 PE=1 SV=1 |
| Q86VM9 | 6 | 2.40E-05 | Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18 PE=1 SV=2 |
| H3BPD0 | 6 | 0.000106596 | Zinc finger CCCH domain-containing protein 18 (Fragment) OS=Homo sapiens OX=9606 GN=ZC3H18 PE=1 SV=1 |
| Q86VM9-2 | 6 | 3.02E-05 | Isoform 2 of Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18 |
| E7ERS3 | 6 | 2.34E-05 | Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q86VM9, Q86VM9-2, H3BPD0 |
| O60493-2 | 5 | 1.23E-05 | Isoform 2 of Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 |
| O60493 | 6 | 2.72E-05 | Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 PE=1 SV=3 |
| Q9UMY4-2 | 6 | 3.92E-05 | Isoform 2 of Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 |
| Q9UMY4-3 | 6 | 4.02E-05 | Isoform 3 of Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 |
| O60493-4 | 6 | 3.15E-05 | Isoform 4 of Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 |
| A0A087X0R6 | 6 | 3.69E-05 | Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UMY4, Q9UMY4-2, Q9UMY4-3, O60493-4, O60493-2, O60493-3 |
| Q9UMY4 | 6 | 3.69E-05 | Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 PE=1 SV=3 |
| E9PAL7 | 6 | 2.28E-05 | Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 PE=1 SV=1 |
| P43307-2 | 6 | 2.56E-05 | Isoform 2 of Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 |
| C9J5W0 | 6 | 2.49E-05 | Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 PE=1 SV=1 |
| P43307 | 6 | 2.32E-05 | Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 PE=1 SV=3 |
| C9IZQ1 | 6 | 2.23E-05 | Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PAL7, P43307, C9J5W0, C9J3L8, P43307-2 |
| C9J3L8 | 6 | 2.50E-05 | Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 PE=1 SV=1 |
| F6U1T9 | 6 | 2.01E-05 | Calcineurin subunit B type 1 OS=Homo sapiens OX=9606 GN=PPP3R1 PE=1 SV=1 |
| D3YTA9 | 6 | 1.70E-05 | Calcineurin subunit B type 1 OS=Homo sapiens OX=9606 GN=PPP3R1 PE=1 SV=1 |
| H7BYZ3 | 6 | 9.71E-06 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1; Additional IDs concatenated into MaxParsimony group: D3YTA9, P63098, F6U1T9 |
| P63098 | 6 | 1.89E-05 | Calcineurin subunit B type 1 OS=Homo sapiens OX=9606 GN=PPP3R1 PE=1 SV=2 |
| P55884-2 | 6 | 1.23E-05 | Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens OX=9606 GN=EIF3B; Additional IDs concatenated into MaxParsimony group: P55884, C9JZG1 |
| C9JZG1 | 6 | 3.55E-05 | Eukaryotic translation initiation factor 3 subunit B (Fragment) OS=Homo sapiens OX=9606 GN=EIF3B PE=1 SV=1 |
| P55884 | 6 | 1.32E-05 | Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens OX=9606 GN=EIF3B PE=1 SV=3 |
| A0A087X1N8 | 5 | 1.32E-05 | Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A024QZX5, P35237, A0A2R8YD12 |
| A0A024QZX5 | 5 | 1.37E-05 | Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=1 |
| P35237 | 5 | 1.39E-05 | Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=3 |
| A0A2R8YD12 | 5 | 1.57E-05 | Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=1 |
| Q9GZX9 | 6 | 4.36E-05 | Twisted gastrulation protein homolog 1 OS=Homo sapiens OX=9606 GN=TWSG1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: J3QS03 |
| J3QS03 | 6 | 5.28E-05 | Twisted gastrulation protein homolog 1 OS=Homo sapiens OX=9606 GN=TWSG1 PE=1 SV=1 |
| P35080 | 4 | 1.32E-05 | Profilin-2 OS=Homo sapiens OX=9606 GN=PFN2 PE=1 SV=3 |
| C9J712 | 4 | 2.04E-05 | Profilin OS=Homo sapiens OX=9606 GN=PFN2 PE=1 SV=1 |
| C9J0J7 | 4 | 2.04E-05 | Profilin OS=Homo sapiens OX=9606 GN=PFN2 PE=1 SV=1 |
| P35080-2 | 4 | 1.32E-05 | Isoform IIb of Profilin-2 OS=Homo sapiens OX=9606 GN=PFN2 |
| G5E9Q6 | 4 | 9.86E-06 | Profilin OS=Homo sapiens OX=9606 GN=PFN2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P35080, P35080-2, C9J2N0, C9JQ45, C9J712, C9J0J7 |
| C9JQ45 | 4 | 1.68E-05 | Profilin OS=Homo sapiens OX=9606 GN=PFN2 PE=1 SV=1 |
| A0A0A0MRZ8 | 6 | 6.07E-05 | Immunoglobulin kappa variable 3D-11 OS=Homo sapiens OX=9606 GN=IGKV3D-11 PE=3 SV=6; Additional IDs concatenated into MaxParsimony group: P04433 |
| P04433 | 6 | 6.07E-05 | Immunoglobulin kappa variable 3-11 OS=Homo sapiens OX=9606 GN=IGKV3-11 PE=1 SV=1 |
| P32119-2 | 6 | 0.00042682 | Isoform 2 of Peroxiredoxin-2 OS=Homo sapiens OX=9606 GN=PRDX2 |
| Q13162 | 6 | 0.000126177 | Peroxiredoxin-4 OS=Homo sapiens OX=9606 GN=PRDX4 PE=1 SV=1 |
| H7C3T4 | 6 | 0.000212385 | Peroxiredoxin-4 (Fragment) OS=Homo sapiens OX=9606 GN=PRDX4 PE=1 SV=1 |
| H0YCD9 | 5 | 7.24E-05 | Src substrate cortactin (Fragment) OS=Homo sapiens OX=9606 GN=CTTN PE=1 SV=1 |
| Q14247-2 | 6 | 0.000114775 | Isoform 2 of Src substrate cortactin OS=Homo sapiens OX=9606 GN=CTTN |
| H0YEV2 | 5 | 0.000106008 | Src substrate cortactin (Fragment) OS=Homo sapiens OX=9606 GN=CTTN PE=1 SV=1 |
| P38117 | 6 | 0.000218012 | Electron transfer flavoprotein subunit beta OS=Homo sapiens OX=9606 GN=ETFB PE=1 SV=3 |
| M0QY67 | 6 | 8.25E-05 | Electron transfer flavoprotein subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=ETFB PE=1 SV=1 |
| P38117-2 | 6 | 0.000160673 | Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens OX=9606 GN=ETFB; Additional IDs concatenated into MaxParsimony group: P38117, M0QY67 |
| M0QX44 | 5 | 4.43E-05 | Amino acid transporter (Fragment) OS=Homo sapiens OX=9606 GN=SLC1A5 PE=1 SV=8 |
| A6NEC2-3 | 6 | 9.96E-05 | Isoform 3 of Puromycin-sensitive aminopeptidase-like protein OS=Homo sapiens OX=9606 GN=NPEPPSL1 |
| P55786 | 6 | 2.96E-05 | Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PLK3, P55786-2, A6NEC2, E9PP11, A6NEC2-3, E9PPD4, E9PJY4, E9PPZ2, H0YDG0, E9PJF9 |
| E9PJY4 | 6 | 0.000115173 | Puromycin-sensitive aminopeptidase (Fragment) OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=2 |
| E9PP11 | 6 | 9.15E-05 | Puromycin-sensitive aminopeptidase (Fragment) OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1 |
| H0YDG0 | 6 | 1.47E-05 | Puromycin-sensitive aminopeptidase (Fragment) OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1 |
| P55786-2 | 6 | 2.71E-05 | Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS |
| E9PLK3 | 6 | 2.97E-05 | Aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1 |
| E9PPD4 | 6 | 9.96E-05 | Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1 |
| A6NEC2 | 6 | 4.33E-05 | Puromycin-sensitive aminopeptidase-like protein OS=Homo sapiens OX=9606 GN=NPEPPSL1 PE=2 SV=3 |
| Q99436 | 6 | 0.000185884 | Proteasome subunit beta type-7 OS=Homo sapiens OX=9606 GN=PSMB7 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5TBG5, Q99436-2 |
| Q5TBG5 | 6 | 0.000176567 | Proteasome subunit beta type (Fragment) OS=Homo sapiens OX=9606 GN=PSMB7 PE=1 SV=1 |
| Q99436-2 | 6 | 0.00026112 | Isoform 2 of Proteasome subunit beta type-7 OS=Homo sapiens OX=9606 GN=PSMB7 |
| Q96KP4-2 | 6 | 1.71E-05 | Isoform 2 of Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 |
| Q96KP4 | 6 | 2.15E-05 | Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q96KP4-2, J3QKT2, J3QRH4 |
| F8VSD4 | 6 | 0.000861457 | Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens OX=9606 GN=UBE2N PE=1 SV=1 |
| F8VZ29 | 6 | 0.00102813 | Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens OX=9606 GN=UBE2N PE=1 SV=1 |
| F8VV71 | 6 | 0.000595086 | Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens OX=9606 GN=UBE2N PE=1 SV=1 |
| B5MCP9 | 5 | 6.46E-06 | 40S ribosomal protein S7 OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1 |
| P62081 | 6 | 4.48E-05 | 40S ribosomal protein S7 OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B5MCP9, A0A2R8Y623 |
| Q5JR95 | 5 | 0.003499839 | 40S ribosomal protein S8 OS=Homo sapiens OX=9606 GN=RPS8 PE=1 SV=1 |
| P62241 | 5 | 0.003163316 | 40S ribosomal protein S8 OS=Homo sapiens OX=9606 GN=RPS8 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5JR95 |
| G3V2K7 | 6 | 5.74E-05 | Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens OX=9606 GN=TMED10 PE=1 SV=1 |
| P49755 | 6 | 4.36E-05 | Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens OX=9606 GN=TMED10 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: G3V2K7 |
| Q15274 | 6 | 0.000162207 | Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens OX=9606 GN=QPRT PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: C9JCJ5 |
| C9JCJ5 | 6 | 0.000257901 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=10 |
| P48047 | 6 | 2.10E-05 | ATP synthase subunit O, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5O PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H7C0C1 |
| H7C0C1 | 6 | 8.93E-06 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=2 |
| Q8WZA9 | 6 | 8.03E-06 | Immunity-related GTPase family Q protein OS=Homo sapiens OX=9606 GN=IRGQ PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: M0QZP8 |
| C9JXI5 | 6 | 0.003198973 | Transmembrane protein 198 (Fragment) OS=Homo sapiens OX=9606 GN=TMEM198 PE=4 SV=1 |
| Q66K66 | 6 | 0.00201713 | Transmembrane protein 198 OS=Homo sapiens OX=9606 GN=TMEM198 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JXI5 |
| Q9BRL6 | 6 | 0.003269106 | Serine/arginine-rich splicing factor 8 OS=Homo sapiens OX=9606 GN=SRSF8 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9BRL6-2, Q01130, Q01130-2, J3KP15, J3QL05 |
| Q9BRL6-2 | 6 | 0.003352319 | Isoform 2 of Serine/arginine-rich splicing factor 8 OS=Homo sapiens OX=9606 GN=SRSF8 |
| Q16864-2 | 6 | 6.49E-05 | Isoform 2 of V-type proton ATPase subunit F OS=Homo sapiens OX=9606 GN=ATP6V1F; Additional IDs concatenated into MaxParsimony group: Q16864 |
| Q16864 | 6 | 8.01E-05 | V-type proton ATPase subunit F OS=Homo sapiens OX=9606 GN=ATP6V1F PE=1 SV=2 |
| Q9UBT2-2 | 6 | 3.82E-05 | Isoform 2 of SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 GN=UBA2 |
| U3KQ93 | 6 | 0.000125044 | SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 GN=UBA2 PE=1 SV=1 |
| Q9UBT2 | 6 | 5.07E-05 | SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 GN=UBA2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UBT2-2, U3KQ93 |
| Q9NY59-2 | 6 | 3.50E-05 | Isoform 2 of Sphingomyelin phosphodiesterase 3 OS=Homo sapiens OX=9606 GN=SMPD3 |
| Q9NY59 | 6 | 3.46E-05 | Sphingomyelin phosphodiesterase 3 OS=Homo sapiens OX=9606 GN=SMPD3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NY59-2, H3BS51 |
| H3BS51 | 6 | 3.40E-05 | Sphingomyelin phosphodiesterase 3 OS=Homo sapiens OX=9606 GN=SMPD3 PE=1 SV=1 |
| P23470-2 | 6 | 3.08E-06 | Isoform 2 of Receptor-type tyrosine-protein phosphatase gamma OS=Homo sapiens OX=9606 GN=PTPRG |
| P23470 | 6 | 3.02E-06 | Receptor-type tyrosine-protein phosphatase gamma OS=Homo sapiens OX=9606 GN=PTPRG PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P23470-2 |
| Q15293-2 | 6 | 1.12E-05 | Isoform 2 of Reticulocalbin-1 OS=Homo sapiens OX=9606 GN=RCN1 |
| E9PP27 | 6 | 5.42E-05 | Reticulocalbin-1 (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 |
| Q15293 | 6 | 1.73E-05 | Reticulocalbin-1 OS=Homo sapiens OX=9606 GN=RCN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q15293-2, E9PP27 |
| Q96K17 | 6 | 0.000107778 | Transcription factor BTF3 homolog 4 OS=Homo sapiens OX=9606 GN=BTF3L4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q96K17-2 |
| Q96K17-2 | 6 | 0.000161593 | Isoform 2 of Transcription factor BTF3 homolog 4 OS=Homo sapiens OX=9606 GN=BTF3L4 |
| Q7Z434 | 6 | 2.14E-05 | Mitochondrial antiviral-signaling protein OS=Homo sapiens OX=9606 GN=MAVS PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q7Z434-4 |
| Q7Z434-4 | 6 | 2.90E-05 | Isoform 4 of Mitochondrial antiviral-signaling protein OS=Homo sapiens OX=9606 GN=MAVS |
| O43493-4 | 6 | 2.33E-05 | Isoform 4 of Trans-Golgi network integral membrane protein 2 OS=Homo sapiens OX=9606 GN=TGOLN2 |
| O43493-6 | 6 | 3.14E-05 | Isoform 6 of Trans-Golgi network integral membrane protein 2 OS=Homo sapiens OX=9606 GN=TGOLN2 |
| O43493-5 | 6 | 1.97E-05 | Isoform 5 of Trans-Golgi network integral membrane protein 2 OS=Homo sapiens OX=9606 GN=TGOLN2 |
| O43493-3 | 6 | 1.95E-05 | Isoform TGN48 of Trans-Golgi network integral membrane protein 2 OS=Homo sapiens OX=9606 GN=TGOLN2 |
| O43493 | 6 | 1.84E-05 | Trans-Golgi network integral membrane protein 2 OS=Homo sapiens OX=9606 GN=TGOLN2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O43493-3, O43493-5, O43493-2, O43493-4, O43493-6 |
| O43493-2 | 6 | 2.02E-05 | Isoform TGN46 of Trans-Golgi network integral membrane protein 2 OS=Homo sapiens OX=9606 GN=TGOLN2 |
| P62318 | 5 | 2.79E-05 | Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens OX=9606 GN=SNRPD3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P62318-2 |
| P62318-2 | 5 | 2.93E-05 | Isoform 2 of Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens OX=9606 GN=SNRPD3 |
| Q16563-2 | 6 | 5.31E-05 | Isoform 2 of Synaptophysin-like protein 1 OS=Homo sapiens OX=9606 GN=SYPL1 |
| C9JYN0 | 6 | 5.71E-05 | Synaptophysin-like protein 1 OS=Homo sapiens OX=9606 GN=SYPL1 PE=1 SV=1 |
| A0A0U1RQT9 | 6 | 9.47E-05 | Synaptophysin-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=SYPL1 PE=1 SV=1 |
| Q16563 | 6 | 4.94E-05 | Synaptophysin-like protein 1 OS=Homo sapiens OX=9606 GN=SYPL1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q16563-2, C9JYN0, A0A0U1RQT9 |
| P15170-3 | 5 | 2.30E-05 | Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens OX=9606 GN=GSPT1; Additional IDs concatenated into MaxParsimony group: P15170-2 |
| P15170-2 | 5 | 2.31E-05 | Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens OX=9606 GN=GSPT1 |
| Q16270 | 6 | 4.52E-05 | Insulin-like growth factor-binding protein 7 OS=Homo sapiens OX=9606 GN=IGFBP7 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q16270-2 |
| Q16270-2 | 6 | 4.57E-05 | Isoform 2 of Insulin-like growth factor-binding protein 7 OS=Homo sapiens OX=9606 GN=IGFBP7 |
| P46821 | 6 | 3.68E-05 | Microtubule-associated protein 1B OS=Homo sapiens OX=9606 GN=MAP1B PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: D6RA32, E9PGC8, P78559-2, P78559, D6RGJ3, D6RCL2 |
| E9PGC8 | 6 | 1.88E-06 | Microtubule-associated protein 1A OS=Homo sapiens OX=9606 GN=MAP1A PE=1 SV=1 |
| P78559 | 6 | 2.04E-06 | Microtubule-associated protein 1A OS=Homo sapiens OX=9606 GN=MAP1A PE=1 SV=6 |
| P78559-2 | 6 | 2.04E-06 | Isoform 2 of Microtubule-associated protein 1A OS=Homo sapiens OX=9606 GN=MAP1A |
| H3BNX8 | 6 | 0.002087623 | Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens OX=9606 GN=COX5A PE=1 SV=1 |
| H3BT58 | 6 | 0.002528393 | Coactosin-like protein OS=Homo sapiens OX=9606 GN=COTL1 PE=1 SV=1 |
| Q14019 | 6 | 0.001757471 | Coactosin-like protein OS=Homo sapiens OX=9606 GN=COTL1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H3BT58 |
| M0R261 | 6 | 0.000223117 | 6-phosphogluconolactonase (Fragment) OS=Homo sapiens OX=9606 GN=PGLS PE=1 SV=1 |
| O95336 | 6 | 0.000217084 | 6-phosphogluconolactonase OS=Homo sapiens OX=9606 GN=PGLS PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0R261, M0R0U3, M0R1L2 |
| M0R0U3 | 6 | 0.000142802 | 6-phosphogluconolactonase OS=Homo sapiens OX=9606 GN=PGLS PE=1 SV=1 |
| M0R1L2 | 6 | 7.30E-05 | 6-phosphogluconolactonase (Fragment) OS=Homo sapiens OX=9606 GN=PGLS PE=1 SV=1 |
| D6RFI1 | 5 | 1.36E-05 | Drebrin (Fragment) OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=1 |
| D6R9W4 | 5 | 2.29E-06 | Drebrin (Fragment) OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=1 |
| E9PSF4 | 5 | 9.64E-05 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| Q9H0C2 | 5 | 0.000170315 | ADP/ATP translocase 4 OS=Homo sapiens OX=9606 GN=SLC25A31 PE=2 SV=1 |
| P05141 | 6 | 0.000281338 | ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC25A5 PE=1 SV=7; Additional IDs concatenated into MaxParsimony group: P12236, V9GYG0, Q9H0C2 |
| V9GYG0 | 5 | 0.000306554 | ADP/ATP translocase 1 OS=Homo sapiens OX=9606 GN=SLC25A4 PE=1 SV=1 |
| P12235 | 5 | 0.000261911 | ADP/ATP translocase 1 OS=Homo sapiens OX=9606 GN=SLC25A4 PE=1 SV=4 |
| V9GYM3 | 6 | 0.000896025 | Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P02652, V9GYG9, V9GYE3, V9GYS1, V9GYC1 |
| V9GYE3 | 6 | 0.002282276 | Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1 |
| P02652 | 6 | 0.001191714 | Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1 |
| V9GYG9 | 6 | 0.001254435 | Apolipoprotein A-II (Fragment) OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1 |
| V9GYS1 | 6 | 0.000846027 | Apolipoprotein A-II OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1 |
| V9GYC1 | 6 | 0.001051124 | Apolipoprotein A-II (Fragment) OS=Homo sapiens OX=9606 GN=APOA2 PE=1 SV=1 |
| M0QZR9 | 5 | 5.44E-05 | ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=1 |
| P55036 | 6 | 0.000100076 | 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens OX=9606 GN=PSMD4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0Y3Y9, Q5VWC4, A2A3N6, H0Y561 |
| H0Y3Y9 | 6 | 0.000195484 | 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens OX=9606 GN=PSMD4 PE=1 SV=1 |
| A2A3N6 | 6 | 8.02E-06 | Putative PIP5K1A and PSMD4-like protein OS=Homo sapiens OX=9606 GN=PIPSL PE=5 SV=1 |
| Q5VWC4 | 6 | 8.11E-05 | 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens OX=9606 GN=PSMD4 PE=1 SV=1 |
| K7ES59 | 6 | 1.10E-05 | Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=3 |
| K7ELW5 | 6 | 1.56E-05 | Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=2 |
| K7EKJ7 | 6 | 6.93E-06 | Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=7 |
| E7EUI7 | 6 | 0.000508379 | Protein phosphatase inhibitor 2 OS=Homo sapiens OX=9606 GN=PPP1R2 PE=1 SV=1 |
| Q6NXS1 | 6 | 9.20E-05 | Protein phosphatase inhibitor 2 family member B OS=Homo sapiens OX=9606 GN=PPP1R2B PE=1 SV=2 |
| P41236 | 6 | 0.000238612 | Protein phosphatase inhibitor 2 OS=Homo sapiens OX=9606 GN=PPP1R2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E7EMN6, E7EUI7, Q6NXS1 |
| E7EMN6 | 6 | 0.000265976 | Protein phosphatase inhibitor 2 (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R2 PE=1 SV=1 |
| C9J4S4 | 6 | 0.000105636 | Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 |
| C9J4V0 | 6 | 7.99E-05 | Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 |
| C9IZZ0 | 6 | 5.30E-05 | Ras-related protein Rab-7a (Fragment) OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 |
| C9J8S3 | 6 | 8.01E-05 | Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 |
| A0A286YEY1 | 5 | 2.55E-05 | Immunoglobulin heavy constant alpha 1 (Fragment) OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P01876, A0A0G2JMB2 |
| P01876 | 5 | 2.87E-05 | Immunoglobulin heavy constant alpha 1 OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=2 |
| E9PNJ4 | 6 | 6.80E-05 | Stromal interaction molecule 1 OS=Homo sapiens OX=9606 GN=STIM1 PE=1 SV=1 |
| Q13586 | 6 | 5.08E-05 | Stromal interaction molecule 1 OS=Homo sapiens OX=9606 GN=STIM1 PE=1 SV=3 |
| H0YDB2 | 6 | 8.60E-05 | Stromal interaction molecule 1 (Fragment) OS=Homo sapiens OX=9606 GN=STIM1 PE=1 SV=1 |
| G0XQ39 | 6 | 4.40E-05 | STIM1L OS=Homo sapiens OX=9606 GN=STIM1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q13586, E9PNJ4, H0YDB2 |
| H7C125 | 6 | 0.000100386 | Ras-related protein Rab-2A (Fragment) OS=Homo sapiens OX=9606 GN=RAB2A PE=1 SV=1 |
| P61019 | 6 | 5.85E-05 | Ras-related protein Rab-2A OS=Homo sapiens OX=9606 GN=RAB2A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P61019-2, Q8WUD1, E9PKL7, Q8WUD1-2, Q6PIK3, H7C125 |
| P61019-2 | 6 | 6.60E-05 | Isoform 2 of Ras-related protein Rab-2A OS=Homo sapiens OX=9606 GN=RAB2A |
| P62308 | 6 | 7.83E-05 | Small nuclear ribonucleoprotein G OS=Homo sapiens OX=9606 GN=SNRPG PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A8MWD9, F5H013, Q49AN9 |
| A8MWD9 | 6 | 7.83E-05 | Putative small nuclear ribonucleoprotein G-like protein 15 OS=Homo sapiens OX=9606 GN=SNRPGP15 PE=5 SV=2 |
| F5H013 | 6 | 8.75E-05 | Small nuclear ribonucleoprotein G OS=Homo sapiens OX=9606 GN=SNRPG PE=1 SV=1 |
| Q49AN9 | 6 | 9.30E-05 | SNRPG protein OS=Homo sapiens OX=9606 GN=SNRPG PE=1 SV=1 |
| D6RIE3 | 6 | 7.84E-05 | Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens OX=9606 GN=COX7A2 PE=1 SV=1 |
| D6R9C3 | 5 | 7.12E-05 | Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens OX=9606 GN=COX7A2 PE=1 SV=1 |
| D6RGV5 | 6 | 6.92E-05 | Cytochrome c oxidase subunit 7A2, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=COX7A2 PE=1 SV=1 |
| P14406 | 6 | 8.59E-05 | Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens OX=9606 GN=COX7A2 PE=1 SV=1 |
| H0UI06 | 6 | 6.20E-05 | Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens OX=9606 GN=COX7A2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: D6RGV5, D6RIE3, P14406, D6R9C3 |
| Q3LXA3 | 6 | 1.20E-05 | Triokinase/FMN cyclase OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q3LXA3-2, H0YCY6, I3L252 |
| A2AB88 | 5 | 1.70E-05 | Prefoldin subunit 6 OS=Homo sapiens OX=9606 GN=PFDN6 PE=1 SV=1 |
| O15212 | 6 | 6.27E-05 | Prefoldin subunit 6 OS=Homo sapiens OX=9606 GN=PFDN6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A2AB88 |
| Q14157-1 | 6 | 7.24E-06 | Isoform 2 of Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L |
| Q14157-4 | 6 | 7.29E-06 | Isoform 4 of Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L |
| F8W726 | 6 | 6.60E-06 | Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L PE=1 SV=2 |
| Q14157 | 6 | 6.55E-06 | Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L PE=1 SV=2 |
| Q14157-5 | 6 | 6.45E-06 | Isoform 5 of Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L; Additional IDs concatenated into MaxParsimony group: Q14157, F8W726, Q14157-3, Q14157-1, Q14157-4 |
| Q14157-3 | 6 | 6.66E-06 | Isoform 3 of Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L |
| Q9BRT3 | 6 | 0.00025026 | Migration and invasion enhancer 1 OS=Homo sapiens OX=9606 GN=MIEN1 PE=1 SV=1 |
| J3KTI2 | 6 | 0.000248102 | Migration and invasion enhancer 1 OS=Homo sapiens OX=9606 GN=MIEN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9BRT3 |
| M0R3G9 | 5 | 5.14E-05 | Phospholipase D3 (Fragment) OS=Homo sapiens OX=9606 GN=PLD3 PE=1 SV=1 |
| Q8IV08 | 5 | 1.09E-05 | Phospholipase D3 OS=Homo sapiens OX=9606 GN=PLD3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: M0R3G9 |
| O43157 | 4 | 8.88E-07 | Plexin-B1 OS=Homo sapiens OX=9606 GN=PLXNB1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O43157-2 |
| O43157-2 | 4 | 9.71E-07 | Isoform 2 of Plexin-B1 OS=Homo sapiens OX=9606 GN=PLXNB1 |
| P12111-3 | 6 | 1.66E-05 | Isoform 3 of Collagen alpha-3(VI) chain OS=Homo sapiens OX=9606 GN=COL6A3 |
| E7ENL6 | 6 | 1.02E-05 | Collagen alpha-3(VI) chain OS=Homo sapiens OX=9606 GN=COL6A3 PE=1 SV=2 |
| P12111-2 | 6 | 1.01E-05 | Isoform 2 of Collagen alpha-3(VI) chain OS=Homo sapiens OX=9606 GN=COL6A3 |
| C9JNG9 | 6 | 9.29E-06 | Collagen alpha-3(VI) chain (Fragment) OS=Homo sapiens OX=9606 GN=COL6A3 PE=1 SV=1 |
| P12111-4 | 6 | 1.02E-05 | Isoform 4 of Collagen alpha-3(VI) chain OS=Homo sapiens OX=9606 GN=COL6A3 |
| P12111 | 6 | 9.48E-06 | Collagen alpha-3(VI) chain OS=Homo sapiens OX=9606 GN=COL6A3 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: P12111-2, P12111-4, E7ENL6, P12111-5, P12111-3, C9JNG9 |
| P12111-5 | 6 | 1.71E-05 | Isoform 5 of Collagen alpha-3(VI) chain OS=Homo sapiens OX=9606 GN=COL6A3 |
| H7BYH4 | 6 | 0.004374703 | Superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD1 PE=1 SV=1 |
| G3XAP5 | 6 | 5.65E-05 | L-lactate dehydrogenase OS=Homo sapiens OX=9606 GN=LDHC PE=1 SV=1 |
| F5H155 | 6 | 6.05E-05 | L-lactate dehydrogenase OS=Homo sapiens OX=9606 GN=LDHC PE=1 SV=1 |
| F5H245 | 6 | 4.28E-05 | L-lactate dehydrogenase OS=Homo sapiens OX=9606 GN=LDHC PE=1 SV=1 |
| F5H5G7 | 6 | 7.44E-05 | L-lactate dehydrogenase OS=Homo sapiens OX=9606 GN=LDHC PE=1 SV=1 |
| P07864 | 6 | 4.10E-05 | L-lactate dehydrogenase C chain OS=Homo sapiens OX=9606 GN=LDHC PE=1 SV=4 |
| H3BR04 | 6 | 0.000469972 | Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1 |
| H3BMQ8 | 6 | 0.00050719 | Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1 |
| H3BU78 | 6 | 0.000167343 | Fructose-bisphosphate aldolase (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=2 |
| P36871 | 6 | 7.25E-05 | Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P36871-2, P36871-3 |
| P36871-3 | 6 | 6.24E-05 | Isoform 3 of Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 |
| P36871-2 | 6 | 5.44E-05 | Isoform 2 of Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 |
| A0A0U1RQJ0 | 5 | 0.000105727 | Probable ATP-dependent RNA helicase DDX17 (Fragment) OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=1 |
| A0A2R8Y6Q7 | 6 | 0.000175364 | Glutathione synthetase (Fragment) OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8Y7I7 | 6 | 0.000190178 | Glutathione synthetase (Fragment) OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| A0A2R8Y5T7 | 6 | 9.18E-05 | Glutathione synthetase (Fragment) OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| P20339-2 | 6 | 3.42E-05 | Isoform 2 of Ras-related protein Rab-5A OS=Homo sapiens OX=9606 GN=RAB5A |
| P20339 | 6 | 3.20E-05 | Ras-related protein Rab-5A OS=Homo sapiens OX=9606 GN=RAB5A PE=1 SV=2 |
| K7ERI8 | 6 | 5.55E-05 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |
| K7ERQ8 | 6 | 3.17E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1 |
| F8VWU4 | 6 | 7.56E-05 | Ras-related protein Rab-5C (Fragment) OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=8 |
| F8VUA5 | 6 | 5.98E-05 | Ras-related protein Rab-5B (Fragment) OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1 |
| P51148 | 6 | 9.63E-05 | Ras-related protein Rab-5C OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=2 |
| K7EIP6 | 6 | 0.000361657 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1 |
| K7ENY4 | 6 | 5.31E-05 | Ras-related protein Rab-5C (Fragment) OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=1 |
| P61020 | 6 | 3.50E-05 | Ras-related protein Rab-5B OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1 |
| P51148-2 | 6 | 8.36E-05 | Isoform 2 of Ras-related protein Rab-5C OS=Homo sapiens OX=9606 GN=RAB5C; Additional IDs concatenated into MaxParsimony group: P51148, K7ERQ8, P61020-2, K7ERI8, P20339, P20339-2, K7ENY4, F8VVK3, F8VUA5, F8VVZ0, F8VWU4, F8VWZ7, F8VSF8, F8VPW9, F8WD79, F8WCY6, K7EIP6 |
| F8VVZ0 | 6 | 6.88E-05 | Ras-related protein Rab-5B (Fragment) OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1 |
| P61020-2 | 6 | 4.32E-05 | Isoform 2 of Ras-related protein Rab-5B OS=Homo sapiens OX=9606 GN=RAB5B |
| F8VVK3 | 6 | 5.55E-05 | Ras-related protein Rab-5C (Fragment) OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=1 |
| P63241 | 6 | 0.0007126 | Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=2 |
| I3L504 | 6 | 0.000590002 | Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P63241-2, P63241, I3L397, Q6IS14 |
| I3L397 | 6 | 0.000751646 | Eukaryotic translation initiation factor 5A (Fragment) OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=8 |
| P63241-2 | 6 | 0.000596415 | Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A |
| Q6IS14 | 6 | 0.000691146 | Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens OX=9606 GN=EIF5AL1 PE=2 SV=2 |
| F8VZS0 | 6 | 2.74E-05 | 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| F8VPE8 | 6 | 6.28E-05 | 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| F8VW21 | 6 | 4.07E-05 | 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| F8VRK7 | 5 | 4.11E-05 | 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| G3V210 | 6 | 4.83E-05 | 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| Q8NHW5 | 6 | 4.77E-05 | 60S acidic ribosomal protein P0-like OS=Homo sapiens OX=9606 GN=RPLP0P6 PE=5 SV=1 |
| F8VU65 | 6 | 4.11E-05 | 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| F8VS58 | 5 | 5.29E-05 | 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| F8VQY6 | 5 | 4.51E-05 | 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| F8VWV4 | 5 | 5.28E-05 | 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| Q9NZB2-6 | 6 | 1.31E-05 | Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A; Additional IDs concatenated into MaxParsimony group: Q9NZB2, Q9NZB2-4, A0A0C4DG79 |
| Q9NZB2 | 6 | 1.34E-05 | Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A PE=1 SV=2 |
| Q9NZB2-4 | 6 | 1.40E-05 | Isoform D of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A |
| A0A0C4DG79 | 6 | 3.04E-05 | Constitutive coactivator of PPAR-gamma-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=FAM120A PE=1 SV=1 |
| H3BSS4 | 6 | 0.000272717 | Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1 |
| Q15366-6 | 6 | 0.000151271 | Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 |
| F8VRH0 | 6 | 0.000161435 | Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=2 |
| H3BRU6 | 6 | 0.000181424 | Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1 |
| Q15365 | 6 | 0.000162726 | Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q15366, Q15366-3, Q15366-6, Q15366-5, Q15366-4, Q15366-8, F8VZX2, Q15366-7, H3BRU6, H3BSS4, P57721, P57721-4, E9PFP8, P57721-5, P57721-3, P57721-2, J3QT27, F8VRH0, F8VXH9, F8W0G4 |
| Q15366-7 | 6 | 0.000171726 | Isoform 7 of Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 |
| Q15366 | 6 | 0.000149613 | Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1 |
| Q15366-8 | 6 | 0.000169592 | Isoform 8 of Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 |
| Q15366-5 | 6 | 0.000163011 | Isoform 5 of Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 |
| F8VZX2 | 6 | 0.000170121 | Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1 |
| Q15366-4 | 6 | 0.000164981 | Isoform 4 of Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 |
| Q15366-2 | 6 | 0.000149204 | Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 |
| Q15366-3 | 6 | 0.000150853 | Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 |
| P56537-2 | 6 | 4.13E-05 | Isoform 2 of Eukaryotic translation initiation factor 6 OS=Homo sapiens OX=9606 GN=EIF6 |
| A0A0U1RQV5 | 6 | 4.43E-05 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 |
| P56537 | 6 | 7.72E-05 | Eukaryotic translation initiation factor 6 OS=Homo sapiens OX=9606 GN=EIF6 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P56537-2, A0A0U1RQV5 |
| P22695 | 5 | 7.18E-06 | Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H3BRG4, H3BSJ9, H3BP04, H3BUI9, H3BUE4 |
| P30038-3 | 5 | 8.65E-06 | Isoform 3 of Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH4A1 |
| Q5TF55 | 5 | 1.47E-05 | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ALDH4A1 PE=1 SV=1 |
| P30038 | 5 | 1.02E-05 | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH4A1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P30038-3, P30038-2, Q5TF55 |
| P61106 | 6 | 5.01E-05 | Ras-related protein Rab-14 OS=Homo sapiens OX=9606 GN=RAB14 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: X6RFL8 |
| X6RFL8 | 6 | 5.95E-05 | Ras-related protein Rab-14 (Fragment) OS=Homo sapiens OX=9606 GN=RAB14 PE=1 SV=1 |
| P62316 | 5 | 9.41E-05 | Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens OX=9606 GN=SNRPD2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: K7ERG4 |
| K7ERG4 | 5 | 0.000142319 | Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens OX=9606 GN=SNRPD2 PE=1 SV=1 |
| P14136-3 | 6 | 0.0003817 | Isoform 3 of Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP |
| A0A1X7SBR3 | 6 | 0.000348544 | Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 |
| A0A1W2PRT3 | 6 | 0.00050464 | Glial fibrillary acidic protein (Fragment) OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 |
| P14136-2 | 6 | 0.0003756 | Isoform 2 of Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP |
| P14136 | 6 | 0.000380816 | Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 |
| A0A1W2PR46 | 6 | 0.000325768 | Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 |
| K7EMP8 | 6 | 0.000380816 | Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=2 |
| F8WEI7 | 4 | 0.003383535 | Galectin-1 OS=Homo sapiens OX=9606 GN=LGALS1 PE=1 SV=1 |
| P18669 | 6 | 0.000410639 | Phosphoglycerate mutase 1 OS=Homo sapiens OX=9606 GN=PGAM1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P15259, Q8N0Y7 |
| P15259 | 6 | 0.000233326 | Phosphoglycerate mutase 2 OS=Homo sapiens OX=9606 GN=PGAM2 PE=1 SV=3 |
| Q8N0Y7 | 6 | 0.000109488 | Probable phosphoglycerate mutase 4 OS=Homo sapiens OX=9606 GN=PGAM4 PE=3 SV=1 |
| P45880 | 6 | 0.000217641 | Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2 PE=1 SV=2 |
| Q5JSD2 | 5 | 8.26E-05 | Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=VDAC2 PE=1 SV=8 |
| P45880-1 | 6 | 0.000207076 | Isoform 1 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2; Additional IDs concatenated into MaxParsimony group: P45880, P45880-2, A0A0A0MR02, P21796, C9JI87, Q9Y277-2, Q9Y277, Q5JSD1, Q5JSD2, E5RHZ6, E5RJN6, E5RFP6, E5RK27 |
| Q5JSD1 | 5 | 7.85E-05 | Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=VDAC2 PE=1 SV=1 |
| P45880-2 | 6 | 0.0002261 | Isoform 2 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2 |
| A0A0A0MR02 | 6 | 0.000226902 | Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=VDAC2 PE=1 SV=1 |
| P23246-2 | 5 | 5.20E-05 | Isoform Short of Splicing factor, proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ |
| Q8WW12-2 | 6 | 0.000583576 | Isoform 2 of PEST proteolytic signal-containing nuclear protein OS=Homo sapiens OX=9606 GN=PCNP |
| Q8WW12 | 6 | 0.000512832 | PEST proteolytic signal-containing nuclear protein OS=Homo sapiens OX=9606 GN=PCNP PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8WW12-2, Q8WW12-3 |
| A0A087X0N3 | 5 | 1.68E-05 | Nucleolar protein 4-like OS=Homo sapiens OX=9606 GN=NOL4L PE=1 SV=1 |
| P08236-2 | 6 | 6.77E-05 | Isoform 2 of Beta-glucuronidase OS=Homo sapiens OX=9606 GN=GUSB |
| K7EQ17 | 5 | 2.04E-05 | Nucleolar protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=NOL4 PE=1 SV=1 |
| F2Z3L6 | 6 | 0.00018213 | Beta-glucuronidase OS=Homo sapiens OX=9606 GN=GUSB PE=1 SV=1 |
| O94818 | 5 | 1.79E-05 | Nucleolar protein 4 OS=Homo sapiens OX=9606 GN=NOL4 PE=1 SV=2 |
| F8WBK6 | 6 | 0.000195721 | Beta-glucuronidase OS=Homo sapiens OX=9606 GN=GUSB PE=1 SV=1 |
| P08236 | 6 | 6.24E-05 | Beta-glucuronidase OS=Homo sapiens OX=9606 GN=GUSB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P08236-2, P08236-3, F2Z3L6, F8WBK6, A0A087X0N3, O94818, O94818-3, K7EQ17, O94818-2, Q96MY1, O94818-4 |
| O94818-3 | 5 | 2.02E-05 | Isoform 3 of Nucleolar protein 4 OS=Homo sapiens OX=9606 GN=NOL4 |
| O94818-2 | 5 | 2.13E-05 | Isoform 2 of Nucleolar protein 4 OS=Homo sapiens OX=9606 GN=NOL4 |
| O94818-4 | 5 | 3.23E-05 | Isoform 4 of Nucleolar protein 4 OS=Homo sapiens OX=9606 GN=NOL4 |
| P08236-3 | 6 | 8.00E-05 | Isoform 3 of Beta-glucuronidase OS=Homo sapiens OX=9606 GN=GUSB |
| Q96MY1 | 5 | 2.62E-05 | Nucleolar protein 4-like OS=Homo sapiens OX=9606 GN=NOL4L PE=1 SV=2 |
| P36957-2 | 6 | 3.40E-05 | Isoform 2 of Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens OX=9606 GN=DLST |
| H0YJF9 | 6 | 0.000267845 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=DLST PE=1 SV=1 |
| G3V5M3 | 6 | 0.000238802 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens OX=9606 GN=DLST PE=1 SV=1 |
| G3V3F0 | 6 | 0.000190582 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens OX=9606 GN=DLST PE=1 SV=1 |
| Q86SW4 | 6 | 0.000104893 | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Homo sapiens OX=9606 GN=DLST PE=1 SV=1 |
| P36957 | 6 | 7.13E-05 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens OX=9606 GN=DLST PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P36957-2, Q86SW4, G3V3F0, G3V5M3, H0YJF9 |
| P30040-2 | 5 | 5.60E-05 | Isoform 2 of Endoplasmic reticulum resident protein 29 OS=Homo sapiens OX=9606 GN=ERP29 |
| F8VY02 | 6 | 3.97E-05 | Endoplasmic reticulum resident protein 29 OS=Homo sapiens OX=9606 GN=ERP29 PE=1 SV=1 |
| P30040 | 6 | 4.04E-05 | Endoplasmic reticulum resident protein 29 OS=Homo sapiens OX=9606 GN=ERP29 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: F8VY02, P30040-2 |
| H0YBY3 | 6 | 0.000450917 | Ganglioside GM2 activator (Fragment) OS=Homo sapiens OX=9606 GN=GM2A PE=1 SV=1 |
| E5RJD0 | 6 | 0.000321201 | Ganglioside GM2 activator (Fragment) OS=Homo sapiens OX=9606 GN=GM2A PE=1 SV=1 |
| P17900 | 6 | 0.000451046 | Ganglioside GM2 activator OS=Homo sapiens OX=9606 GN=GM2A PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: E5RJD0, H0YBY3 |
| P25788 | 6 | 0.000114399 | Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P25788-2, G3V4X5, H0YJ03, G3V5N4, G3V3W4 |
| G3V5N4 | 5 | 0.000110281 | Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=1 |
| P25788-2 | 6 | 0.000117628 | Isoform 2 of Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 |
| G3V3W4 | 5 | 0.000165421 | Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=1 |
| E9PCA1 | 5 | 3.02E-05 | T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1 |
| P48643-2 | 5 | 3.51E-05 | Isoform 2 of T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 |
| P48643 | 5 | 2.90E-05 | T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PCA1, B7ZAR1, E7ENZ3, P48643-2 |
| B7ZAR1 | 5 | 3.12E-05 | cDNA, FLJ79275, highly similar to T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1 |
| E7ENZ3 | 5 | 3.23E-05 | T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1 |
| O43301 | 6 | 4.10E-05 | Heat shock 70 kDa protein 12A OS=Homo sapiens OX=9606 GN=HSPA12A PE=1 SV=2 |
| K7ENF6 | 6 | 0.000184188 | Heat shock 70 kDa protein 12A (Fragment) OS=Homo sapiens OX=9606 GN=HSPA12A PE=1 SV=1 |
| A0A1B0GTF3 | 6 | 4.00E-05 | Heat shock 70 kDa protein 12A OS=Homo sapiens OX=9606 GN=HSPA12A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O43301, K7ENF6 |
| F8WEH5 | 6 | 4.47E-05 | Acylamino-acid-releasing enzyme OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=1 |
| P13798 | 6 | 7.78E-06 | Acylamino-acid-releasing enzyme OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=4 |
| C9JIF9 | 6 | 7.73E-06 | Acylamino-acid-releasing enzyme OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P13798, H7C1U0, H7C393, C9JLK2, F8WEH5 |
| H7C393 | 6 | 1.28E-05 | Acylamino-acid-releasing enzyme (Fragment) OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=1 |
| H0YDP7 | 5 | 2.79E-06 | 39S ribosomal protein L49, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=MRPL49 PE=1 SV=1 |
| Q13405 | 5 | 4.89E-06 | 39S ribosomal protein L49, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL49 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E9PNF1, H0YDP7, E9PI78 |
| Q5T1J5 | 6 | 0.00010074 | Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9, mitochondrial OS=Homo sapiens OX=9606 GN=CHCHD2P9 PE=5 SV=1; Additional IDs concatenated into MaxParsimony group: Q9Y6H1 |
| Q9Y6H1 | 6 | 0.00010074 | Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CHCHD2 PE=1 SV=1 |
| P09960-3 | 6 | 9.17E-06 | Isoform 3 of Leukotriene A-4 hydrolase OS=Homo sapiens OX=9606 GN=LTA4H |
| P09960-2 | 6 | 9.31E-06 | Isoform 2 of Leukotriene A-4 hydrolase OS=Homo sapiens OX=9606 GN=LTA4H |
| P09960 | 6 | 8.11E-06 | Leukotriene A-4 hydrolase OS=Homo sapiens OX=9606 GN=LTA4H PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P09960-2, P09960-4, P09960-3, B4DEH5 |
| P09960-4 | 6 | 7.93E-06 | Isoform 4 of Leukotriene A-4 hydrolase OS=Homo sapiens OX=9606 GN=LTA4H |
| M0QXB5 | 6 | 3.41E-05 | Persulfide dioxygenase ETHE1, mitochondrial OS=Homo sapiens OX=9606 GN=ETHE1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O95571, M0QY80 |
| M0QY80 | 6 | 9.33E-05 | Persulfide dioxygenase ETHE1, mitochondrial OS=Homo sapiens OX=9606 GN=ETHE1 PE=1 SV=1 |
| O95571 | 6 | 3.49E-05 | Persulfide dioxygenase ETHE1, mitochondrial OS=Homo sapiens OX=9606 GN=ETHE1 PE=1 SV=2 |
| E5RH77 | 6 | 0.000135079 | 40S ribosomal protein S14 OS=Homo sapiens OX=9606 GN=RPS14 PE=1 SV=1 |
| Q01082-2 | 6 | 1.43E-05 | Isoform Short of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTBN1 |
| Q01082 | 6 | 1.31E-05 | Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTBN1 PE=1 SV=2 |
| Q01082-3 | 6 | 1.43E-05 | Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTBN1 |
| A0A087WUZ3 | 6 | 1.31E-05 | Spectrin beta chain OS=Homo sapiens OX=9606 GN=SPTBN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q01082, Q01082-2, Q01082-3, F8W6C1 |
| P34932-2 | 5 | 6.06E-05 | Isoform 2 of Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 |
| P34932 | 5 | 1.37E-05 | Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A087WYC1, A0A087WTS8, P34932-2 |
| P30046-2 | 6 | 0.001268711 | Isoform 2 of D-dopachrome decarboxylase OS=Homo sapiens OX=9606 GN=DDT |
| B5MC82 | 6 | 0.000817784 | D-dopachrome decarboxylase OS=Homo sapiens OX=9606 GN=DDT PE=4 SV=2 |
| A6NHG4 | 6 | 0.001013075 | D-dopachrome decarboxylase-like protein OS=Homo sapiens OX=9606 GN=DDTL PE=2 SV=1 |
| G3V3D1 | 6 | 0.000236792 | NPC intracellular cholesterol transporter 2 (Fragment) OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E7EMS2, G3V3E8, P61916, J3KMY5, P61916-2, G3V2V8, H0YIZ1 |
| H0YIZ1 | 6 | 0.000145375 | NPC intracellular cholesterol transporter 2 (Fragment) OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1 |
| G3V3E8 | 6 | 0.000300753 | NPC intracellular cholesterol transporter 2 OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1 |
| E7EMS2 | 6 | 0.000260353 | NPC intracellular cholesterol transporter 2 OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1 |
| J3KMY5 | 6 | 0.000353588 | NPC intracellular cholesterol transporter 2 OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1 |
| G3V2V8 | 6 | 0.000428943 | NPC intracellular cholesterol transporter 2 (Fragment) OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1 |
| P61916 | 6 | 0.000346563 | NPC intracellular cholesterol transporter 2 OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1 |
| P61916-2 | 6 | 0.000418648 | Isoform 2 of NPC intracellular cholesterol transporter 2 OS=Homo sapiens OX=9606 GN=NPC2 |
| C9J4N6 | 5 | 8.73E-05 | Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment) OS=Homo sapiens OX=9606 GN=IDH1 PE=1 SV=1 |
| O75874 | 5 | 5.29E-05 | Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens OX=9606 GN=IDH1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9J4N6 |
| E9PNQ8 | 6 | 0.000685753 | Thy-1 membrane glycoprotein (Fragment) OS=Homo sapiens OX=9606 GN=THY1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P04216, E9PIM6, J3QRJ3 |
| P04216 | 6 | 0.00070279 | Thy-1 membrane glycoprotein OS=Homo sapiens OX=9606 GN=THY1 PE=1 SV=2 |
| E9PIM6 | 6 | 0.000744403 | Thy-1 membrane glycoprotein (Fragment) OS=Homo sapiens OX=9606 GN=THY1 PE=1 SV=8 |
| J3QRJ3 | 6 | 0.000283132 | Thy-1 membrane glycoprotein OS=Homo sapiens OX=9606 GN=THY1 PE=1 SV=1 |
| P13716-2 | 4 | 4.26E-06 | Isoform 2 of Delta-aminolevulinic acid dehydratase OS=Homo sapiens OX=9606 GN=ALAD; Additional IDs concatenated into MaxParsimony group: P13716 |
| P13716 | 4 | 4.63E-06 | Delta-aminolevulinic acid dehydratase OS=Homo sapiens OX=9606 GN=ALAD PE=1 SV=1 |
| E5RI76 | 5 | 7.06E-05 | Protein NDRG1 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| Q92597 | 6 | 4.37E-05 | Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q92597-2, Q92597-3, E5RIM2, E5RIV1, E5RK17, E5RGM5, E5RIR1, E5RH82, E7ESM1, E5RI76, E5RJY1, E5RJ98 |
| E7ESM1 | 6 | 4.71E-05 | Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| E5RK17 | 5 | 5.62E-05 | Protein NDRG1 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| E5RIV1 | 5 | 4.87E-05 | Protein NDRG1 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| Q92597-3 | 6 | 2.12E-05 | Isoform 3 of Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 |
| E5RGM5 | 5 | 5.69E-05 | Protein NDRG1 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| E5RIR1 | 5 | 5.94E-05 | Protein NDRG1 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| E5RH82 | 5 | 6.02E-05 | Protein NDRG1 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=8 |
| E5RJY1 | 6 | 6.44E-05 | Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| E5RIM2 | 5 | 4.35E-05 | Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| Q92597-2 | 6 | 2.02E-05 | Isoform 2 of Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 |
| E5RJ98 | 5 | 9.88E-05 | Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 |
| O95772-2 | 6 | 2.86E-05 | Isoform 2 of STARD3 N-terminal-like protein OS=Homo sapiens OX=9606 GN=STARD3NL |
| C9JPX5 | 6 | 3.15E-05 | STARD3 N-terminal-like protein (Fragment) OS=Homo sapiens OX=9606 GN=STARD3NL PE=1 SV=1 |
| O95772 | 6 | 2.78E-05 | STARD3 N-terminal-like protein OS=Homo sapiens OX=9606 GN=STARD3NL PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O95772-2, C9JKL2, C9JPX5 |
| C9JKL2 | 6 | 3.01E-05 | STARD3 N-terminal-like protein OS=Homo sapiens OX=9606 GN=STARD3NL PE=1 SV=1 |
| M0R174 | 6 | 0.000127333 | Lysosomal alpha-mannosidase (Fragment) OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=1 |
| P35609 | 6 | 1.13E-05 | Alpha-actinin-2 OS=Homo sapiens OX=9606 GN=ACTN2 PE=1 SV=1 |
| K7EP19 | 6 | 8.89E-05 | Alpha-actinin-4 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=1 |
| P35609-2 | 6 | 1.13E-05 | Isoform 2 of Alpha-actinin-2 OS=Homo sapiens OX=9606 GN=ACTN2 |
| Q08043 | 6 | 1.04E-05 | Alpha-actinin-3 OS=Homo sapiens OX=9606 GN=ACTN3 PE=1 SV=2 |
| D6RH00 | 6 | 0.000129707 | Alpha-actinin-3 OS=Homo sapiens OX=9606 GN=ACTN3 PE=1 SV=1 |
| F6THM6 | 5 | 1.14E-06 | Alpha-actinin-2 OS=Homo sapiens OX=9606 GN=ACTN2 PE=1 SV=1 |
| P04792 | 6 | 0.00068292 | Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F8WE04, C9J3N8 |
| C9J3N8 | 6 | 0.002241281 | Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=1 |
| F8WE04 | 6 | 0.000236 | Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=1 |
| Q9UNZ2-6 | 6 | 0.000173956 | Isoform 4 of NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C |
| P51572-2 | 6 | 0.000378426 | Isoform 2 of B-cell receptor-associated protein 31 OS=Homo sapiens OX=9606 GN=BCAP31; Additional IDs concatenated into MaxParsimony group: P51572, A0A2R8Y5M6, C9J0M4, C9JQ75, C9JSP1, C9JMD7 |
| A0A2R8Y5M6 | 6 | 0.000333012 | B-cell receptor-associated protein 31 OS=Homo sapiens OX=9606 GN=BCAP31 PE=1 SV=1 |
| C9J0M4 | 6 | 0.000232301 | B-cell receptor-associated protein 31 (Fragment) OS=Homo sapiens OX=9606 GN=BCAP31 PE=1 SV=1 |
| C9JMD7 | 6 | 0.000245351 | B-cell receptor-associated protein 31 (Fragment) OS=Homo sapiens OX=9606 GN=BCAP31 PE=1 SV=1 |
| P51572 | 6 | 0.000481493 | B-cell receptor-associated protein 31 OS=Homo sapiens OX=9606 GN=BCAP31 PE=1 SV=3 |
| C9JQ75 | 6 | 0.000233543 | B-cell receptor-associated protein 31 (Fragment) OS=Homo sapiens OX=9606 GN=BCAP31 PE=1 SV=1 |
| C9JSP1 | 6 | 0.000239959 | B-cell receptor-associated protein 31 (Fragment) OS=Homo sapiens OX=9606 GN=BCAP31 PE=1 SV=1 |
| Q8IWE2-2 | 6 | 5.54E-05 | Isoform 2 of Protein NOXP20 OS=Homo sapiens OX=9606 GN=FAM114A1 |
| Q8IWE2 | 6 | 7.43E-05 | Protein NOXP20 OS=Homo sapiens OX=9606 GN=FAM114A1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8IWE2-2, D6R9C9 |
| Q9Y5Z4-2 | 6 | 0.000157654 | Isoform 2 of Heme-binding protein 2 OS=Homo sapiens OX=9606 GN=HEBP2 |
| P05455 | 6 | 2.22E-05 | Lupus La protein OS=Homo sapiens OX=9606 GN=SSB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E7ERC4, E9PFL9, E9PGX9 |
| D6RB01 | 5 | 1.37E-05 | Soluble lamin-associated protein of 75 kDa OS=Homo sapiens OX=9606 GN=FAM169A PE=1 SV=1 |
| Q9Y6X4 | 5 | 1.25E-05 | Soluble lamin-associated protein of 75 kDa OS=Homo sapiens OX=9606 GN=FAM169A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: D6RB01 |
| C9JAX1 | 6 | 6.75E-05 | Frataxin, mitochondrial OS=Homo sapiens OX=9606 GN=FXN PE=1 SV=1 |
| A0A2R8Y5A1 | 6 | 2.81E-05 | Tight junction protein ZO-2 (Fragment) OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=1 |
| Q16595 | 6 | 4.34E-05 | Frataxin, mitochondrial OS=Homo sapiens OX=9606 GN=FXN PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9JAX1, H7C585, Q16595-3, A0A2R8Y5A1, Q16595-2 |
| Q16595-3 | 6 | 2.45E-05 | Isoform 3 of Frataxin, mitochondrial OS=Homo sapiens OX=9606 GN=FXN |
| Q16595-2 | 6 | 2.81E-05 | Isoform 2 of Frataxin, mitochondrial OS=Homo sapiens OX=9606 GN=FXN |
| H7C585 | 6 | 8.44E-05 | Frataxin, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=FXN PE=1 SV=1 |
| Q8NI22-2 | 6 | 0.00048768 | Isoform 2 of Multiple coagulation factor deficiency protein 2 OS=Homo sapiens OX=9606 GN=MCFD2 |
| Q8NI22-3 | 6 | 0.00036096 | Isoform 3 of Multiple coagulation factor deficiency protein 2 OS=Homo sapiens OX=9606 GN=MCFD2 |
| Q8NI22 | 6 | 0.000313986 | Multiple coagulation factor deficiency protein 2 OS=Homo sapiens OX=9606 GN=MCFD2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q8NI22-3, Q8NI22-2 |
| Q8N5J2-3 | 5 | 2.01E-05 | Isoform 3 of Ubiquitin carboxyl-terminal hydrolase MINDY-1 OS=Homo sapiens OX=9606 GN=MINDY1; Additional IDs concatenated into MaxParsimony group: Q8N5J2 |
| Q8N5J2 | 5 | 2.22E-05 | Ubiquitin carboxyl-terminal hydrolase MINDY-1 OS=Homo sapiens OX=9606 GN=MINDY1 PE=1 SV=2 |
| H0YIN6 | 6 | 3.36E-05 | Charged multivesicular body protein 4a OS=Homo sapiens OX=9606 GN=CHMP4A PE=1 SV=2 |
| Q9BY43-2 | 6 | 1.48E-05 | Isoform 2 of Charged multivesicular body protein 4a OS=Homo sapiens OX=9606 GN=CHMP4A; Additional IDs concatenated into MaxParsimony group: Q9BY43, H0YIN6 |
| Q9BY43 | 6 | 1.77E-05 | Charged multivesicular body protein 4a OS=Homo sapiens OX=9606 GN=CHMP4A PE=1 SV=3 |
| H0YL43 | 6 | 0.000142159 | Reticulocalbin-2 (Fragment) OS=Homo sapiens OX=9606 GN=RCN2 PE=1 SV=1 |
| Q8WZA0 | 6 | 0.00016022 | Protein LZIC OS=Homo sapiens OX=9606 GN=LZIC PE=1 SV=1 |
| Q8WZA0-2 | 6 | 0.000144274 | Isoform 2 of Protein LZIC OS=Homo sapiens OX=9606 GN=LZIC; Additional IDs concatenated into MaxParsimony group: Q8WZA0, K7ES95 |
| K7ES95 | 6 | 4.49E-05 | Protein LZIC (Fragment) OS=Homo sapiens OX=9606 GN=LZIC PE=1 SV=1 |
| H0YCG2 | 6 | 9.63E-05 | Lysosome-associated membrane glycoprotein 2 (Fragment) OS=Homo sapiens OX=9606 GN=LAMP2 PE=1 SV=1 |
| Q9H1E3-2 | 6 | 0.000538434 | Isoform 2 of Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens OX=9606 GN=NUCKS1 |
| Q9H1E3 | 6 | 0.000465039 | Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens OX=9606 GN=NUCKS1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9H1E3-2 |
| P50995 | 6 | 1.57E-05 | Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P50995-2 |
| P50995-2 | 6 | 1.68E-05 | Isoform 2 of Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 |
| J3KN42 | 6 | 0.00020248 | Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens OX=9606 GN=SLC25A24 PE=1 SV=1 |
| Q6NUK1 | 6 | 5.82E-05 | Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens OX=9606 GN=SLC25A24 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: J3KN42, H3BMI3, Q6NUK1-2 |
| H3BMI3 | 6 | 7.91E-05 | Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens OX=9606 GN=SLC25A24 PE=1 SV=1 |
| Q8TF09 | 6 | 0.000127222 | Dynein light chain roadblock-type 2 OS=Homo sapiens OX=9606 GN=DYNLRB2 PE=1 SV=1 |
| Q9NP97 | 6 | 0.000224157 | Dynein light chain roadblock-type 1 OS=Homo sapiens OX=9606 GN=DYNLRB1 PE=1 SV=3 |
| H3BQI1 | 6 | 9.77E-05 | Dynein light chain roadblock-type 2 OS=Homo sapiens OX=9606 GN=DYNLRB2 PE=1 SV=1 |
| B1AKR6 | 6 | 0.000145399 | Dynein light chain roadblock-type 1 OS=Homo sapiens OX=9606 GN=DYNLRB1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NP97, H3BQI1, Q8TF09 |
| G3V2U7 | 5 | 4.25E-05 | Acylphosphatase OS=Homo sapiens OX=9606 GN=ACYP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P07311 |
| P07311 | 5 | 5.54E-05 | Acylphosphatase-1 OS=Homo sapiens OX=9606 GN=ACYP1 PE=1 SV=2 |
| J3QR48 | 6 | 6.55E-05 | Importin subunit beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=8 |
| Q14974 | 6 | 1.19E-05 | Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q14974-2, J3KTM9, J3QR48 |
| Q9BYK1 | 6 | 0.000189276 | 40S ribosomal protein S21 OS=Homo sapiens OX=9606 GN=RPS21 PE=1 SV=1 |
| S4R3N1 | 6 | 0.001049879 | HSPE1-MOB4 readthrough OS=Homo sapiens OX=9606 GN=HSPE1-MOB4 PE=3 SV=1 |
| P54803-3 | 6 | 1.67E-06 | Isoform 3 of Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC |
| P54803-4 | 6 | 1.57E-05 | Isoform 4 of Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC |
| P54803-5 | 6 | 1.57E-05 | Isoform 5 of Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC |
| G3V4M2 | 6 | 0.000169091 | Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC PE=1 SV=1 |
| A0A087WX10 | 6 | 4.69E-05 | Galactocerebrosidase (Fragment) OS=Homo sapiens OX=9606 GN=GALC PE=1 SV=1 |
| P54803 | 6 | 2.93E-05 | Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P54803-4, P54803-3, A0A087WX10, G3V5E8, G3V4M2, P54803-5 |
| G3V5E8 | 6 | 8.98E-05 | Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC PE=1 SV=1 |
| P21926 | 6 | 0.000794782 | CD9 antigen OS=Homo sapiens OX=9606 GN=CD9 PE=1 SV=4 |
| A6NNI4 | 6 | 0.001139688 | Tetraspanin OS=Homo sapiens OX=9606 GN=CD9 PE=1 SV=1 |
| A0A2R8Y478 | 6 | 0.001139688 | Tetraspanin OS=Homo sapiens OX=9606 GN=CD9 PE=1 SV=1 |
| G8JLH6 | 6 | 0.000721954 | Tetraspanin OS=Homo sapiens OX=9606 GN=CD9 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P21926, A6NNI4, A0A2R8Y478 |
| D6RA00 | 6 | 2.06E-05 | Enolase-phosphatase E1 OS=Homo sapiens OX=9606 GN=ENOPH1 PE=1 SV=1 |
| Q9UHY7 | 6 | 2.23E-05 | Enolase-phosphatase E1 OS=Homo sapiens OX=9606 GN=ENOPH1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: D6RA00, A0A0C4DGY8 |
| A0A0C4DGY8 | 6 | 2.39E-05 | Enolase-phosphatase E1 OS=Homo sapiens OX=9606 GN=ENOPH1 PE=1 SV=1 |
| O14618 | 6 | 1.77E-05 | Copper chaperone for superoxide dismutase OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: J3KNF4, E9PK03, E9PP76 |
| J3KNF4 | 6 | 1.90E-05 | Copper chaperone for superoxide dismutase OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1 |
| E9PP76 | 5 | 5.19E-05 | Copper chaperone for superoxide dismutase (Fragment) OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1 |
| P23526 | 5 | 1.26E-05 | Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=AHCY PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P23526-2 |
| A0A1W2PS52 | 6 | 0.000503181 | Cystatin-B OS=Homo sapiens OX=9606 GN=CSTB PE=1 SV=1 |
| A0A1W2PQG6 | 6 | 0.000678419 | Cystatin-B (Fragment) OS=Homo sapiens OX=9606 GN=CSTB PE=1 SV=1 |
| P04080 | 6 | 0.000799986 | Cystatin-B OS=Homo sapiens OX=9606 GN=CSTB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A1W2PS52, A0A1W2PQG6 |
| Q6P587-3 | 6 | 8.41E-06 | Isoform 3 of Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens OX=9606 GN=FAHD1; Additional IDs concatenated into MaxParsimony group: Q6P587-2, Q6P587 |
| Q6P587-2 | 6 | 9.23E-06 | Isoform 2 of Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens OX=9606 GN=FAHD1 |
| Q6P587 | 6 | 9.31E-06 | Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens OX=9606 GN=FAHD1 PE=1 SV=2 |
| M0QYW8 | 6 | 7.78E-05 | L-amino-acid oxidase (Fragment) OS=Homo sapiens OX=9606 GN=IL4I1 PE=1 SV=1 |
| M0R1I1 | 6 | 7.89E-05 | Tubulin beta chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| U3KQQ1 | 6 | 0.000105516 | Gamma-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=1 |
| P38646 | 6 | 8.62E-05 | Stress-70 protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H0YBG6, H0Y8S0, D6RJI2, D6RA73 |
| H0Y8S0 | 6 | 7.87E-05 | Stress-70 protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=1 |
| C9JIG9 | 6 | 3.11E-05 | Serine/threonine-protein kinase OSR1 OS=Homo sapiens OX=9606 GN=OXSR1 PE=1 SV=1 |
| P28066-2 | 6 | 0.000181185 | Isoform 2 of Proteasome subunit alpha type-5 OS=Homo sapiens OX=9606 GN=PSMA5 |
| P28066 | 6 | 0.000345276 | Proteasome subunit alpha type-5 OS=Homo sapiens OX=9606 GN=PSMA5 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P28066-2 |
| H0Y9C7 | 6 | 4.63E-05 | N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase (Fragment) OS=Homo sapiens OX=9606 GN=AGA PE=1 SV=8 |
| B9A041 | 6 | 0.00016 | Malate dehydrogenase, cytoplasmic OS=Homo sapiens OX=9606 GN=MDH1 PE=1 SV=1 |
| P40925-2 | 6 | 0.000137143 | Isoform 2 of Malate dehydrogenase, cytoplasmic OS=Homo sapiens OX=9606 GN=MDH1 |
| B8ZZ51 | 6 | 0.000198817 | Malate dehydrogenase, cytoplasmic OS=Homo sapiens OX=9606 GN=MDH1 PE=1 SV=1 |
| B1AJQ6 | 6 | 5.72E-05 | Syntaxin-12 (Fragment) OS=Homo sapiens OX=9606 GN=STX12 PE=1 SV=2 |
| Q86Y82 | 6 | 4.66E-05 | Syntaxin-12 OS=Homo sapiens OX=9606 GN=STX12 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B1AJQ6 |
| Q9NYJ1 | 5 | 4.29E-05 | Cytochrome c oxidase assembly factor 4 homolog, mitochondrial OS=Homo sapiens OX=9606 GN=COA4 PE=1 SV=2 |
| Q9NYJ1-2 | 5 | 3.89E-05 | Isoform 2 of Cytochrome c oxidase assembly factor 4 homolog, mitochondrial OS=Homo sapiens OX=9606 GN=COA4; Additional IDs concatenated into MaxParsimony group: Q9NYJ1 |
| F8WF32 | 6 | 3.58E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1 |
| B7Z4L4 | 5 | 2.20E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1 |
| P04843 | 6 | 2.29E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B7Z4L4, F8WF32 |
| C9JRG0 | 6 | 0.005165809 | Hemoglobin subunit delta (Fragment) OS=Homo sapiens OX=9606 GN=HBD PE=1 SV=1 |
| Q5VU61 | 6 | 0.000620234 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=2 |
| H0YK20 | 6 | 0.000390036 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| K7EPV9 | 6 | 0.001329048 | Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| P06753-7 | 6 | 0.000473392 | Isoform 7 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 |
| H0YL42 | 6 | 0.000332252 | Tropomyosin alpha-1 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| A0A2R8YHD2 | 6 | 0.001417651 | Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| K7EMU5 | 6 | 0.001457867 | Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| U3KQK2 | 6 | 0.000769625 | Tropomyosin beta chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM2 PE=1 SV=1 |
| K7EPB9 | 6 | 0.002081877 | Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| P50990-2 | 5 | 3.32E-05 | Isoform 2 of T-complex protein 1 subunit theta OS=Homo sapiens OX=9606 GN=CCT8 |
| P50990 | 5 | 3.20E-05 | T-complex protein 1 subunit theta OS=Homo sapiens OX=9606 GN=CCT8 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P50990-2, P50990-3, H7C4C8, H7C2U0 |
| H7C4C8 | 5 | 2.88E-05 | T-complex protein 1 subunit theta (Fragment) OS=Homo sapiens OX=9606 GN=CCT8 PE=1 SV=1 |
| P50990-3 | 5 | 3.40E-05 | Isoform 3 of T-complex protein 1 subunit theta OS=Homo sapiens OX=9606 GN=CCT8 |
| P29373 | 6 | 0.001978026 | Cellular retinoic acid-binding protein 2 OS=Homo sapiens OX=9606 GN=CRABP2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5SYZ4 |
| Q5SYZ4 | 6 | 0.003325555 | Cellular retinoic acid-binding protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CRABP2 PE=1 SV=1 |
| Q9P0L0-2 | 6 | 5.88E-05 | Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens OX=9606 GN=VAPA; Additional IDs concatenated into MaxParsimony group: Q9P0L0, O95292, O95292-2, E5RK64, J3QKM9 |
| Q9P0L0 | 6 | 6.94E-05 | Vesicle-associated membrane protein-associated protein A OS=Homo sapiens OX=9606 GN=VAPA PE=1 SV=3 |
| J3QKM9 | 5 | 0.000154487 | Vesicle-associated membrane protein-associated protein A OS=Homo sapiens OX=9606 GN=VAPA PE=1 SV=1 |
| E5RK64 | 6 | 0.000150833 | Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens OX=9606 GN=VAPB PE=1 SV=1 |
| O95292-2 | 6 | 0.000108173 | Isoform 2 of Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens OX=9606 GN=VAPB |
| O95292 | 6 | 4.41E-05 | Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens OX=9606 GN=VAPB PE=1 SV=3 |
| Q9Y5L4 | 6 | 0.00017264 | Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens OX=9606 GN=TIMM13 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: K7EIT2 |
| Q9Y617-2 | 6 | 8.82E-05 | Isoform 2 of Phosphoserine aminotransferase OS=Homo sapiens OX=9606 GN=PSAT1 |
| Q9Y617 | 6 | 7.73E-05 | Phosphoserine aminotransferase OS=Homo sapiens OX=9606 GN=PSAT1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9Y617-2 |
| E9PP50 | 6 | 0.000207857 | Cofilin-1 (Fragment) OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=8 |
| E9PQB7 | 6 | 0.000270896 | Cofilin-1 (Fragment) OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=1 |
| E9PLJ3 | 6 | 0.000418345 | Cofilin-1 (Fragment) OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=1 |
| Q9Y281-3 | 6 | 6.49E-05 | Isoform 3 of Cofilin-2 OS=Homo sapiens OX=9606 GN=CFL2 |
| Q9Y281 | 6 | 5.82E-05 | Cofilin-2 OS=Homo sapiens OX=9606 GN=CFL2 PE=1 SV=1 |
| E9PS23 | 6 | 0.000288445 | Cofilin-1 (Fragment) OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=8 |
| P12955 | 5 | 9.09E-06 | Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P12955-2, P12955-3 |
| P12955-2 | 5 | 9.40E-06 | Isoform 2 of Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD |
| P12955-3 | 5 | 1.05E-05 | Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD |
| B5MCK8 | 6 | 2.31E-05 | Inactive glutathione hydrolase 2 OS=Homo sapiens OX=9606 GN=GGT2 PE=4 SV=2 |
| P36268-3 | 6 | 2.25E-05 | Isoform 3 of Inactive glutathione hydrolase 2 OS=Homo sapiens OX=9606 GN=GGT2; Additional IDs concatenated into MaxParsimony group: P36268, P19440, A6NGU5, B5MCK8, P36268-2, E7ET76, B5MC34, A0A0C4DG87, B5MD39, P19440-3, Q14390, B5MC36 |
| Q14390 | 6 | 3.60E-05 | Glutathione hydrolase light chain 2 OS=Homo sapiens OX=9606 GN=GGTLC2 PE=2 SV=4 |
| A0A0C4DG87 | 6 | 3.48E-05 | Glutathione hydrolase light chain 2 OS=Homo sapiens OX=9606 GN=GGTLC2 PE=4 SV=1 |
| B5MD39 | 6 | 3.48E-05 | Putative glutathione hydrolase light chain 3 OS=Homo sapiens OX=9606 GN=GGTLC3 PE=5 SV=1 |
| P36268 | 6 | 2.27E-05 | Inactive glutathione hydrolase 2 OS=Homo sapiens OX=9606 GN=GGT2 PE=1 SV=3 |
| P19440-3 | 6 | 3.48E-05 | Isoform 3 of Glutathione hydrolase 1 proenzyme OS=Homo sapiens OX=9606 GN=GGT1 |
| A6NGU5 | 6 | 2.10E-05 | Putative glutathione hydrolase 3 proenzyme OS=Homo sapiens OX=9606 GN=GGT3P PE=5 SV=2 |
| B5MC34 | 6 | 3.11E-05 | Glutathione hydrolase 1 proenzyme OS=Homo sapiens OX=9606 GN=GGT1 PE=1 SV=1 |
| B5MC36 | 6 | 3.60E-05 | Glutathione hydrolase 1 proenzyme OS=Homo sapiens OX=9606 GN=GGT1 PE=1 SV=1 |
| P19440 | 6 | 2.27E-05 | Glutathione hydrolase 1 proenzyme OS=Homo sapiens OX=9606 GN=GGT1 PE=1 SV=2 |
| P36268-2 | 6 | 2.31E-05 | Isoform 2 of Inactive glutathione hydrolase 2 OS=Homo sapiens OX=9606 GN=GGT2 |
| E7ET76 | 6 | 1.09E-05 | Glutathione hydrolase 1 proenzyme (Fragment) OS=Homo sapiens OX=9606 GN=GGT1 PE=1 SV=1 |
| A0A075B6K5 | 6 | 4.62E-05 | Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1 |
| P80748 | 6 | 4.54E-05 | Immunoglobulin lambda variable 3-21 OS=Homo sapiens OX=9606 GN=IGLV3-21 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A075B6K5 |
| Q92688 | 6 | 9.60E-05 | Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens OX=9606 GN=ANP32B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q92688-2, H0YN26, O43423, H7BZ09 |
| Q92688-2 | 6 | 0.000123531 | Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens OX=9606 GN=ANP32B |
| O43423 | 6 | 0.000171412 | Acidic leucine-rich nuclear phosphoprotein 32 family member C OS=Homo sapiens OX=9606 GN=ANP32C PE=2 SV=1 |
| H7BZ09 | 6 | 0.000899968 | Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32A PE=1 SV=1 |
| H0YN26 | 6 | 0.000715077 | Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32A PE=1 SV=1 |
| P39687 | 6 | 0.000586942 | Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32A PE=1 SV=1 |
| P34059 | 6 | 0.000185585 | N-acetylgalactosamine-6-sulfatase OS=Homo sapiens OX=9606 GN=GALNS PE=1 SV=1 |
| H3BP66 | 5 | 0.000468358 | N-acetylgalactosamine-6-sulfatase (Fragment) OS=Homo sapiens OX=9606 GN=GALNS PE=1 SV=1 |
| P54727-2 | 6 | 0.000194257 | Isoform 2 of UV excision repair protein RAD23 homolog B OS=Homo sapiens OX=9606 GN=RAD23B |
| P54727 | 6 | 0.000199812 | UV excision repair protein RAD23 homolog B OS=Homo sapiens OX=9606 GN=RAD23B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P54727-2, P54725-3, P54725-2, Q5W0S5 |
| P68402-3 | 5 | 1.69E-05 | Isoform 3 of Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens OX=9606 GN=PAFAH1B2 |
| P68402-4 | 5 | 1.11E-05 | Isoform 4 of Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens OX=9606 GN=PAFAH1B2 |
| J3KNE3 | 6 | 1.67E-05 | Platelet-activating factor acetylhydrolase IB subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=PAFAH1B2 PE=1 SV=1 |
| P68402-2 | 5 | 1.44E-05 | Isoform 2 of Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens OX=9606 GN=PAFAH1B2 |
| P68402 | 6 | 2.25E-05 | Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens OX=9606 GN=PAFAH1B2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P68402-4, J3KNE3, P68402-2, P68402-3 |
| Q9UNF1 | 6 | 4.52E-05 | Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGED2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UNF1-2, Q5H909 |
| Q9UNF1-2 | 6 | 5.61E-06 | Isoform 2 of Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGED2 |
| Q5H909 | 6 | 5.61E-06 | Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGED2 PE=1 SV=2 |
| F8W696 | 6 | 0.002900116 | Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1 |
| Q58FG0 | 6 | 7.93E-05 | Putative heat shock protein HSP 90-alpha A5 OS=Homo sapiens OX=9606 GN=HSP90AA5P PE=2 SV=1 |
| H0YIV0 | 6 | 0.000297125 | Endoplasmin (Fragment) OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1 |
| K7EKL3 | 6 | 0.000817643 | Granulins (Fragment) OS=Homo sapiens OX=9606 GN=GRN PE=1 SV=1 |
| P28799-3 | 6 | 0.000624119 | Isoform 3 of Granulins OS=Homo sapiens OX=9606 GN=GRN |
| K7EPL0 | 5 | 0.000237264 | Granulins (Fragment) OS=Homo sapiens OX=9606 GN=GRN PE=1 SV=1 |
| P28799-2 | 6 | 0.000819358 | Isoform 2 of Granulins OS=Homo sapiens OX=9606 GN=GRN |
| P28799 | 6 | 0.000622612 | Granulins OS=Homo sapiens OX=9606 GN=GRN PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P28799-2, K7EKL3, P28799-3, K7EMR1, K7EQ05, K7EPL0 |
| K7EQ05 | 6 | 5.45E-05 | Granulins OS=Homo sapiens OX=9606 GN=GRN PE=1 SV=1 |
| K7EMR1 | 6 | 0.000647951 | Granulins (Fragment) OS=Homo sapiens OX=9606 GN=GRN PE=1 SV=1 |
| A0A0C4DGK8 | 6 | 9.26E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| G3V2D9 | 6 | 0.000198805 | DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| G3V5D9 | 6 | 9.10E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=8 |
| G3V5Q1 | 6 | 8.40E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| G3V5M0 | 5 | 2.33E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| H7C4A8 | 5 | 2.52E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| G3V3C7 | 6 | 7.77E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| G3V359 | 5 | 2.20E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| G3V3M6 | 6 | 7.73E-05 | DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=1 |
| P27695 | 6 | 6.43E-05 | DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: G3V3M6, G3V5Q1, G3V3C7, A0A0C4DGK8, G3V359, G3V5M0, H7C4A8, G3V5D9, G3V2D9 |
| Q9NUJ1 | 6 | 1.22E-05 | Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens OX=9606 GN=ABHD10 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9NUJ1-2 |
| Q9NUJ1-2 | 6 | 2.50E-05 | Isoform 2 of Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens OX=9606 GN=ABHD10 |
| P17174 | 5 | 7.20E-06 | Aspartate aminotransferase, cytoplasmic OS=Homo sapiens OX=9606 GN=GOT1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P17174-2 |
| P22748 | 6 | 0.001174611 | Carbonic anhydrase 4 OS=Homo sapiens OX=9606 GN=CA4 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: K7EKY5, P22748-2, K7EIH9, K7ENI8 |
| K7EIH9 | 6 | 0.000612466 | Carbonic anhydrase 4 (Fragment) OS=Homo sapiens OX=9606 GN=CA4 PE=1 SV=1 |
| K7EKY5 | 6 | 0.001055572 | Carbonic anhydrase 4 (Fragment) OS=Homo sapiens OX=9606 GN=CA4 PE=1 SV=1 |
| K7ENI8 | 6 | 0.001373367 | Carbonic anhydrase 4 (Fragment) OS=Homo sapiens OX=9606 GN=CA4 PE=1 SV=1 |
| P22748-2 | 6 | 0.000885677 | Isoform 2 of Carbonic anhydrase 4 OS=Homo sapiens OX=9606 GN=CA4 |
| H0YLR3 | 6 | 0.000463515 | U2 small nuclear ribonucleoprotein A' (Fragment) OS=Homo sapiens OX=9606 GN=SNRPA1 PE=1 SV=1 |
| H0YMA0 | 6 | 0.000290513 | U2 small nuclear ribonucleoprotein A' (Fragment) OS=Homo sapiens OX=9606 GN=SNRPA1 PE=1 SV=1 |
| P09661 | 6 | 0.000161776 | U2 small nuclear ribonucleoprotein A' OS=Homo sapiens OX=9606 GN=SNRPA1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H0YMA0, H0YLR3 |
| E9PID8 | 6 | 7.29E-05 | Cleavage stimulation factor subunit 2 OS=Homo sapiens OX=9606 GN=CSTF2 PE=1 SV=1 |
| P33240 | 6 | 5.54E-05 | Cleavage stimulation factor subunit 2 OS=Homo sapiens OX=9606 GN=CSTF2 PE=1 SV=1 |
| E7EWR4 | 6 | 5.35E-05 | Cleavage stimulation factor subunit 2 OS=Homo sapiens OX=9606 GN=CSTF2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P33240, P33240-2, E9PID8, Q9H0L4, A0A0A0MT56 |
| A0A0A0MT56 | 6 | 4.16E-06 | Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=CSTF2 PE=1 SV=1 |
| P33240-2 | 6 | 5.70E-05 | Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens OX=9606 GN=CSTF2 |
| P49189 | 6 | 4.64E-05 | 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P49189-2 |
| P49189-2 | 6 | 4.25E-05 | Isoform 2 of 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1 |
| Q86VP6 | 6 | 1.23E-05 | Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q86VP6-2, A0A0C4DGH5 |
| Q86VP6-2 | 6 | 1.40E-05 | Isoform 2 of Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1 |
| A0A0C4DGH5 | 6 | 1.80E-05 | Cullin-associated NEDD8-dissociated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAND1 PE=1 SV=1 |
| Q03167-2 | 6 | 3.48E-06 | Isoform 2 of Transforming growth factor beta receptor type 3 OS=Homo sapiens OX=9606 GN=TGFBR3 |
| Q03167 | 6 | 3.48E-06 | Transforming growth factor beta receptor type 3 OS=Homo sapiens OX=9606 GN=TGFBR3 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q03167-2 |
| K7ENX2 | 6 | 0.000153857 | Synaptic vesicle membrane protein VAT-1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=1 |
| K7EM19 | 6 | 0.00015086 | Synaptic vesicle membrane protein VAT-1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=1 |
| Q99536-2 | 6 | 0.000239496 | Isoform 2 of Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens OX=9606 GN=VAT1 |
| K7ESA3 | 6 | 0.000135182 | Synaptic vesicle membrane protein VAT-1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=1 |
| K7ER81 | 6 | 0.000101501 | Synaptic vesicle membrane protein VAT-1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=1 |
| J3KTJ3 | 6 | 0.000233848 | 60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1 |
| Q05519 | 5 | 2.66E-05 | Serine/arginine-rich splicing factor 11 OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q05519-2, Q5T760 |
| Q5T760 | 5 | 3.31E-05 | Serine/arginine-rich-splicing factor 11 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1 |
| Q05519-2 | 5 | 2.66E-05 | Isoform 2 of Serine/arginine-rich splicing factor 11 OS=Homo sapiens OX=9606 GN=SRSF11 |
| O60831 | 4 | 1.28E-05 | PRA1 family protein 2 OS=Homo sapiens OX=9606 GN=PRAF2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A6NP52 |
| A6NP52 | 4 | 1.42E-05 | PRA1 family protein OS=Homo sapiens OX=9606 GN=PRAF2 PE=1 SV=1 |
| Q5SQT6 | 6 | 0.000239249 | Inorganic pyrophosphatase OS=Homo sapiens OX=9606 GN=PPA1 PE=1 SV=1 |
| Q15181 | 6 | 0.000175011 | Inorganic pyrophosphatase OS=Homo sapiens OX=9606 GN=PPA1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5SQT6 |
| P0CG29 | 6 | 1.92E-05 | Glutathione S-transferase theta-2 OS=Homo sapiens OX=9606 GN=GSTT2 PE=1 SV=1 |
| Q6ICJ4 | 6 | 2.04E-05 | Em:AP000351.3 protein OS=Homo sapiens OX=9606 GN=GSTT2B PE=1 SV=1 |
| A0A087WY67 | 6 | 1.93E-05 | Glutathione S-transferase theta-2 OS=Homo sapiens OX=9606 GN=GSTT2 PE=1 SV=1 |
| P0CG30 | 6 | 1.92E-05 | Glutathione S-transferase theta-2B OS=Homo sapiens OX=9606 GN=GSTT2B PE=1 SV=1 |
| P59768 | 6 | 0.000212032 | Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2 OS=Homo sapiens OX=9606 GN=GNG2 PE=1 SV=2 |
| G3V2N0 | 6 | 0.000136857 | Guanine nucleotide-binding protein subunit gamma OS=Homo sapiens OX=9606 GN=GNG2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: G3V3J9, P59768 |
| G3V3J9 | 6 | 0.000147591 | Guanine nucleotide-binding protein subunit gamma OS=Homo sapiens OX=9606 GN=GNG2 PE=1 SV=1 |
| Q4VY20 | 6 | 0.000908392 | 14-3-3 protein beta/alpha (Fragment) OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=1 |
| I3L0W5 | 6 | 0.000774491 | 14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1 |
| Q4VY19 | 6 | 0.00067221 | 14-3-3 protein beta/alpha (Fragment) OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=1 |
| A0A0J9YWZ2 | 6 | 0.000323014 | 14-3-3 protein beta/alpha (Fragment) OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=1 |
| A0A0J9YWE8 | 6 | 0.000451147 | 14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=1 |
| R4GMV4 | 6 | 0.002277568 | Dipeptidyl peptidase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DPP7 PE=1 SV=1 |
| R4GMU5 | 6 | 0.000374437 | Dipeptidyl peptidase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DPP7 PE=1 SV=1 |
| M0QXH0 | 6 | 0.000158834 | Thioredoxin, mitochondrial OS=Homo sapiens OX=9606 GN=TXN2 PE=1 SV=1 |
| Q99757 | 6 | 7.37E-05 | Thioredoxin, mitochondrial OS=Homo sapiens OX=9606 GN=TXN2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0QXH0, F8WDN2 |
| P37235 | 6 | 2.56E-05 | Hippocalcin-like protein 1 OS=Homo sapiens OX=9606 GN=HPCAL1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P84074, P61601 |
| P84074 | 6 | 2.56E-05 | Neuron-specific calcium-binding protein hippocalcin OS=Homo sapiens OX=9606 GN=HPCA PE=1 SV=2 |
| P61601 | 6 | 2.56E-05 | Neurocalcin-delta OS=Homo sapiens OX=9606 GN=NCALD PE=1 SV=2 |
| C9JB55 | 6 | 0.000316174 | Serotransferrin (Fragment) OS=Homo sapiens OX=9606 GN=TF PE=1 SV=8 |
| F8WEK9 | 6 | 0.000205695 | Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=1 |
| F8WCI6 | 6 | 0.000205705 | Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=1 |
| H7C5E8 | 6 | 0.001535437 | Serotransferrin (Fragment) OS=Homo sapiens OX=9606 GN=TF PE=1 SV=1 |
| P62937 | 6 | 0.00300749 | Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9J5S7, F8WE65, P62937-2, E5RIZ5 |
| C9J5S7 | 6 | 0.002934741 | Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=1 |
| P23284 | 6 | 0.000247183 | Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens OX=9606 GN=PPIB PE=1 SV=2 |
| P62937-2 | 6 | 0.00244175 | Isoform 2 of Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA |
| E5RIZ5 | 6 | 2.05E-05 | Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=1 |
| F8WE65 | 6 | 0.002959198 | Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=1 |
| P01700 | 4 | 3.36E-05 | Immunoglobulin lambda variable 1-47 OS=Homo sapiens OX=9606 GN=IGLV1-47 PE=1 SV=2 |
| H7BZF5 | 5 | 0.000689702 | Uncharacterized protein C2orf80 (Fragment) OS=Homo sapiens OX=9606 GN=C2orf80 PE=4 SV=1 |
| P00918 | 5 | 6.18E-05 | Carbonic anhydrase 2 OS=Homo sapiens OX=9606 GN=CA2 PE=1 SV=2 |
| Q9BT09 | 5 | 4.84E-05 | Protein canopy homolog 3 OS=Homo sapiens OX=9606 GN=CNPY3 PE=1 SV=1 |
| Q96DD7 | 5 | 5.37E-06 | Protein shisa-4 OS=Homo sapiens OX=9606 GN=SHISA4 PE=2 SV=3 |
| Q969L2 | 4 | 9.52E-05 | Protein MAL2 OS=Homo sapiens OX=9606 GN=MAL2 PE=1 SV=1 |
| C9J7D1 | 4 | 4.06E-05 | Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 |
| P04179-2 | 5 | 0.001041931 | Isoform 2 of Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens OX=9606 GN=SOD2 |
| A6NF51 | 5 | 1.67E-05 | 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=2 |
| O95861-2 | 5 | 1.50E-05 | Isoform 2 of 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1; Additional IDs concatenated into MaxParsimony group: O95861, A6NF51, O95861-3, F8VVW8, F8VRY7 |
| F8VVW8 | 5 | 3.51E-05 | 3'(2'),5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=2 |
| O95861 | 5 | 1.58E-05 | 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1 |
| P53990-6 | 4 | 1.35E-05 | Isoform 6 of IST1 homolog OS=Homo sapiens OX=9606 GN=IST1 |
| P53990-4 | 4 | 8.06E-06 | Isoform 4 of IST1 homolog OS=Homo sapiens OX=9606 GN=IST1 |
| P53990 | 4 | 8.10E-06 | IST1 homolog OS=Homo sapiens OX=9606 GN=IST1 PE=1 SV=1 |
| P53990-5 | 4 | 7.78E-06 | Isoform 5 of IST1 homolog OS=Homo sapiens OX=9606 GN=IST1; Additional IDs concatenated into MaxParsimony group: P53990-4, P53990, P53990-2, P53990-6 |
| P53990-2 | 4 | 8.81E-06 | Isoform 2 of IST1 homolog OS=Homo sapiens OX=9606 GN=IST1 |
| P16150 | 5 | 0.000131799 | Leukosialin OS=Homo sapiens OX=9606 GN=SPN PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JUK7 |
| D6RGY2 | 5 | 9.97E-05 | Calnexin (Fragment) OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=1 |
| Q15257-4 | 4 | 1.47E-05 | Isoform 4 of Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens OX=9606 GN=PTPA |
| A0A024R644 | 4 | 5.34E-06 | Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens OX=9606 GN=CLN5 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O75503, A0A0A0MRU5, A0A1B0GWI2, A0A1B0GV94, A0A1B0GUE8, A0A1B0GTV7, A0A1B0GTR6, A0A1C7CYZ2, A0A1B0GWJ7, A0A087WZY0, A0A1B0GTI0, A0A1B0GVL0, A0A1B0GU14 |
| A0A1B0GWI2 | 4 | 7.15E-06 | Ceroid-lipofuscinosis neuronal protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=CLN5 PE=1 SV=1 |
| O75503 | 4 | 6.07E-06 | Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens OX=9606 GN=CLN5 PE=1 SV=2 |
| A0A0A0MRU5 | 4 | 6.07E-06 | Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens OX=9606 GN=CLN5 PE=1 SV=1 |
| K7EPW7 | 5 | 3.58E-05 | Glucosidase 2 subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=1 |
| D6R9T5 | 4 | 1.96E-05 | OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=OCIAD1 PE=1 SV=2 |
| O00244 | 5 | 0.000508952 | Copper transport protein ATOX1 OS=Homo sapiens OX=9606 GN=ATOX1 PE=1 SV=1 |
| E5RGN3 | 5 | 0.000586589 | Copper transport protein ATOX1 OS=Homo sapiens OX=9606 GN=ATOX1 PE=1 SV=1 |
| E5RIM7 | 5 | 0.000474093 | Copper transport protein ATOX1 OS=Homo sapiens OX=9606 GN=ATOX1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O00244, E5RGN3 |
| K7ERT8 | 5 | 6.67E-05 | 60S ribosomal protein L23a (Fragment) OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1 |
| P62750 | 5 | 7.49E-05 | 60S ribosomal protein L23a OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1 |
| H7BY10 | 5 | 7.39E-05 | 60S ribosomal protein L23a (Fragment) OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1 |
| K7EMA7 | 5 | 0.00012067 | 60S ribosomal protein L23a OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1 |
| A8MUS3 | 5 | 6.02E-05 | 60S ribosomal protein L23a OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: K7ERT8, K7EJV9, H7BY10, P62750, K7EMA7 |
| K7EJV9 | 5 | 6.87E-05 | 60S ribosomal protein L23a (Fragment) OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1 |
| A0A087WY93 | 5 | 7.48E-05 | Alpha-1-antichymotrypsin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=1 |
| A0A1W2PP22 | 5 | 7.00E-05 | Heterogeneous nuclear ribonucleoprotein U (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=1 |
| A8MUH2 | 5 | 4.38E-05 | ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PF PE=1 SV=1 |
| E7EX17 | 4 | 2.63E-05 | Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P23588, P23588-2 |
| P23588-2 | 4 | 2.83E-05 | Isoform 2 of Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B |
| P23588 | 4 | 2.65E-05 | Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=2 |
| A6NFX8 | 4 | 3.51E-05 | ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UKK9, A6NJU6 |
| Q9UKK9 | 4 | 3.72E-05 | ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1 |
| P02774 | 4 | 2.05E-05 | Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC PE=1 SV=1 |
| P02774-2 | 4 | 2.76E-05 | Isoform 2 of Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC |
| P02774-3 | 4 | 1.97E-05 | Isoform 3 of Vitamin D-binding protein OS=Homo sapiens OX=9606 GN=GC; Additional IDs concatenated into MaxParsimony group: P02774, P02774-2 |
| Q5VU77 | 4 | 5.92E-06 | Ubiquitin-associated protein 2-like (Fragment) OS=Homo sapiens OX=9606 GN=UBAP2L PE=1 SV=1 |
| O75947-2 | 5 | 3.40E-05 | Isoform 2 of ATP synthase subunit d, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5H |
| O75947 | 5 | 6.06E-05 | ATP synthase subunit d, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5H PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O75947-2, F5H608 |
| F5H608 | 5 | 5.59E-05 | ATP synthase peripheral stalk subunit d OS=Homo sapiens OX=9606 GN=ATP5PD PE=1 SV=2 |
| P48735 | 4 | 1.01E-05 | Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens OX=9606 GN=IDH2 PE=1 SV=2 |
| P48735-2 | 4 | 1.15E-05 | Isoform 2 of Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens OX=9606 GN=IDH2 |
| A0A087X1G7 | 5 | 1.18E-05 | Selenoprotein F OS=Homo sapiens OX=9606 GN=SELENOF PE=1 SV=1 |
| A0A0J9YX89 | 5 | 2.19E-05 | Selenoprotein F (Fragment) OS=Homo sapiens OX=9606 GN=SELENOF PE=1 SV=1 |
| O60613 | 5 | 1.17E-05 | Selenoprotein F OS=Homo sapiens OX=9606 GN=SELENOF PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A087X1G7, A0A0J9YX89 |
| E7ETB4 | 5 | 3.54E-05 | Clusterin (Fragment) OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1 |
| H7C1L0 | 4 | 6.56E-06 | cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment) OS=Homo sapiens OX=9606 GN=PRKAR2A PE=1 SV=1 |

1&2&3 – List of the proteins

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Replicate Count** | **Total Signal** | **Description** |
| P30086 | 9 | 4.15E-03 | Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PEBP1 PE=1 SV=3 |
| P62805 | 9 | 1.57E-02 | Histone H4 OS=Homo sapiens OX=9606 GN=HIST1H4A PE=1 SV=2 |
| P30101 | 8 | 1.84E-04 | Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=4 |
| P53634 | 8 | 9.60E-04 | Dipeptidyl peptidase 1 OS=Homo sapiens OX=9606 GN=CTSC PE=1 SV=2 |
| P04066 | 9 | 6.74E-05 | Tissue alpha-L-fucosidase OS=Homo sapiens OX=9606 GN=FUCA1 PE=1 SV=4 |
| P14174 | 9 | 2.21E-03 | Macrophage migration inhibitory factor OS=Homo sapiens OX=9606 GN=MIF PE=1 SV=4 |
| P17050 | 8 | 6.44E-04 | Alpha-N-acetylgalactosaminidase OS=Homo sapiens OX=9606 GN=NAGA PE=1 SV=2 |
| Q07507 | 8 | 1.34E-04 | Dermatopontin OS=Homo sapiens OX=9606 GN=DPT PE=1 SV=2 |
| P35579 | 9 | 0.000101182 | Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4 |
| Q8TC26 | 9 | 0.000520372 | Transmembrane protein 163 OS=Homo sapiens OX=9606 GN=TMEM163 PE=2 SV=1 |
| P28072 | 9 | 0.00060178 | Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=4 |
| P30049 | 9 | 0.012305449 | ATP synthase subunit delta, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1D PE=1 SV=2 |
| P31949 | 9 | 0.007283838 | Protein S100-A11 OS=Homo sapiens OX=9606 GN=S100A11 PE=1 SV=2 |
| P00441 | 8 | 0.006255721 | Superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD1 PE=1 SV=2 |
| P30084 | 9 | 0.000865405 | Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=ECHS1 PE=1 SV=4 |
| P09382 | 9 | 0.028078242 | Galectin-1 OS=Homo sapiens OX=9606 GN=LGALS1 PE=1 SV=2 |
| P23246 | 9 | 0.000239267 | Splicing factor, proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2 |
| Q03252 | 8 | 0.000138495 | Lamin-B2 OS=Homo sapiens OX=9606 GN=LMNB2 PE=1 SV=4 |
| P29966 | 9 | 0.001481369 | Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens OX=9606 GN=MARCKS PE=1 SV=4 |
| P62857 | 9 | 0.0045491 | 40S ribosomal protein S28 OS=Homo sapiens OX=9606 GN=RPS28 PE=1 SV=1 |
| P10809 | 9 | 0.000590117 | 60 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=2 |
| Q9NZZ3 | 8 | 9.14E-05 | Charged multivesicular body protein 5 OS=Homo sapiens OX=9606 GN=CHMP5 PE=1 SV=1 |
| Q9UHG2 | 9 | 0.000711405 | ProSAAS OS=Homo sapiens OX=9606 GN=PCSK1N PE=1 SV=1 |
| P00352 | 9 | 0.000184448 | Retinal dehydrogenase 1 OS=Homo sapiens OX=9606 GN=ALDH1A1 PE=1 SV=2 |
| Q8TEA8 | 7 | 0.000103401 | D-aminoacyl-tRNA deacylase 1 OS=Homo sapiens OX=9606 GN=DTD1 PE=1 SV=2 |
| O95810 | 9 | 0.000216437 | Caveolae-associated protein 2 OS=Homo sapiens OX=9606 GN=CAVIN2 PE=1 SV=3 |
| P20933 | 8 | 0.000115822 | N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase OS=Homo sapiens OX=9606 GN=AGA PE=1 SV=2 |
| O75506 | 9 | 0.003875139 | Heat shock factor-binding protein 1 OS=Homo sapiens OX=9606 GN=HSBP1 PE=1 SV=1 |
| Q9BVC6 | 9 | 0.000146053 | Transmembrane protein 109 OS=Homo sapiens OX=9606 GN=TMEM109 PE=1 SV=1 |
| P49006 | 9 | 0.001903066 | MARCKS-related protein OS=Homo sapiens OX=9606 GN=MARCKSL1 PE=1 SV=2 |
| O15240 | 7 | 4.41E-05 | Neurosecretory protein VGF OS=Homo sapiens OX=9606 GN=VGF PE=1 SV=2 |
| Q9UBR2 | 9 | 0.002294333 | Cathepsin Z OS=Homo sapiens OX=9606 GN=CTSZ PE=1 SV=1 |
| P00403 | 7 | 0.00043159 | Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1 |
| P30041 | 8 | 0.000811644 | Peroxiredoxin-6 OS=Homo sapiens OX=9606 GN=PRDX6 PE=1 SV=3 |
| Q04941 | 9 | 0.002649084 | Proteolipid protein 2 OS=Homo sapiens OX=9606 GN=PLP2 PE=1 SV=1 |
| P62269 | 9 | 0.000379392 | 40S ribosomal protein S18 OS=Homo sapiens OX=9606 GN=RPS18 PE=1 SV=3 |
| P02647 | 9 | 0.003277086 | Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1 |
| Q9UD71-2 | 9 | 0.000442126 | Isoform 2 of Protein phosphatase 1 regulatory subunit 1B OS=Homo sapiens OX=9606 GN=PPP1R1B |
| J3KT77 | 9 | 0.00043437 | Protein phosphatase 1 regulatory subunit 1B OS=Homo sapiens OX=9606 GN=PPP1R1B PE=1 SV=1 |
| J3KSJ8 | 7 | 0.000137981 | Protein phosphatase 1 regulatory subunit 1B (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R1B PE=1 SV=8 |
| Q9UD71 | 9 | 0.000364104 | Protein phosphatase 1 regulatory subunit 1B OS=Homo sapiens OX=9606 GN=PPP1R1B PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: J3KT77, Q9UD71-2, J3KSJ8 |
| A5A3E0 | 9 | 0.004139304 | POTE ankyrin domain family member F OS=Homo sapiens OX=9606 GN=POTEF PE=1 SV=2 |
| P0CG39 | 9 | 0.002991812 | POTE ankyrin domain family member J OS=Homo sapiens OX=9606 GN=POTEJ PE=3 SV=1 |
| E7EVS6 | 9 | 0.030138589 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=8 |
| B8ZZJ2 | 8 | 0.031102743 | Actin, gamma-enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=1 |
| I3L1U9 | 9 | 0.027969311 | Actin, cytoplasmic 2 (Fragment) OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1 |
| C9JFL5 | 8 | 0.025702961 | Actin, gamma-enteric smooth muscle (Fragment) OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=8 |
| G5E9R0 | 9 | 0.036332202 | Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 |
| C9JUM1 | 9 | 0.04189388 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=2 |
| Q6S8J3 | 9 | 0.00416387 | POTE ankyrin domain family member E OS=Homo sapiens OX=9606 GN=POTEE PE=2 SV=3 |
| A6NL76 | 8 | 0.014925042 | Actin, alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=3 |
| P63267 | 9 | 0.012388647 | Actin, gamma-enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=1 |
| P68133 | 9 | 0.012370913 | Actin, alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1 |
| P63261 | 9 | 0.017846287 | Actin, cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1 |
| Q9BYX7 | 9 | 0.003786801 | Putative beta-actin-like protein 3 OS=Homo sapiens OX=9606 GN=POTEKP PE=5 SV=1 |
| P0CG38 | 9 | 0.003850314 | POTE ankyrin domain family member I OS=Homo sapiens OX=9606 GN=POTEI PE=3 SV=1 |
| A0A2R8Y793 | 9 | 0.02106813 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 |
| Q562R1 | 9 | 0.003151314 | Beta-actin-like protein 2 OS=Homo sapiens OX=9606 GN=ACTBL2 PE=1 SV=2 |
| K7EM38 | 9 | 0.034146806 | Actin, cytoplasmic 2 (Fragment) OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1 |
| A0A2R8YGF8 | 9 | 0.029773273 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 |
| C9JZR7 | 9 | 0.039429534 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=8 |
| A0A2R8YEA7 | 9 | 0.011343823 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 |
| P62736 | 9 | 0.012355786 | Actin, aortic smooth muscle OS=Homo sapiens OX=9606 GN=ACTA2 PE=1 SV=1 |
| P60709 | 9 | 0.017846287 | Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P63261, A0A2R8Y793, I3L4N8, I3L1U9, I3L3I0, Q6S8J3, P62736, P68133, P63267, A0A2R8YGF8, I3L3R2, E7EVS6, A5A3E0, J3KT65, K7EM38, G5E9R0, P0CG38, P63267-2, A6NL76, A0A2R8YEA7, F6UVQ4, F6QUT6, C9JFL5, B8ZZJ2, F8WB63, C9JZR7, C9JUM1, Q9BYX7, C9JTX5, P0CG39, F8WCH0, Q562R1 |
| P68032 | 9 | 0.012370913 | Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1 |
| I3L3I0 | 9 | 0.027969311 | Actin, cytoplasmic 2 (Fragment) OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1 |
| C9JTX5 | 8 | 0.045056839 | Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 |
| J3KT65 | 9 | 0.022936996 | Actin, cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1 |
| F6QUT6 | 8 | 0.024511433 | Actin, aortic smooth muscle (Fragment) OS=Homo sapiens OX=9606 GN=ACTA2 PE=1 SV=1 |
| F8WB63 | 8 | 0.035249775 | Actin, gamma-enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=1 |
| I3L4N8 | 9 | 0.024374274 | Actin, cytoplasmic 2 (Fragment) OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=8 |
| I3L3R2 | 9 | 0.029954817 | Actin, cytoplasmic 2 (Fragment) OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1 |
| F6UVQ4 | 8 | 0.024511433 | Actin, aortic smooth muscle (Fragment) OS=Homo sapiens OX=9606 GN=ACTA2 PE=1 SV=1 |
| P63267-2 | 9 | 0.012829881 | Isoform 2 of Actin, gamma-enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 |
| P61978-2 | 9 | 0.001799859 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK; Additional IDs concatenated into MaxParsimony group: P61978, P61978-3, Q5T6W2, S4R359, S4R457 |
| P61978-3 | 9 | 0.001898033 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK |
| S4R359 | 9 | 0.004728685 | Heterogeneous nuclear ribonucleoprotein K (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1 |
| P61978 | 9 | 0.001803746 | Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1 |
| Q5T6W2 | 9 | 0.001054888 | Heterogeneous nuclear ribonucleoprotein K (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1 |
| Q9H8Y8-2 | 9 | 0.002267998 | Isoform 2 of Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2 |
| Q9H8Y8-3 | 9 | 0.001876964 | Isoform 3 of Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2; Additional IDs concatenated into MaxParsimony group: Q9H8Y8, Q9H8Y8-2 |
| Q9H8Y8 | 9 | 0.001926795 | Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2 PE=1 SV=3 |
| G3V5R8 | 9 | 0.001167187 | Alpha-1-antitrypsin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1 |
| P01009 | 9 | 0.003946387 | Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P01009-2, A0A0G2JRN3, P01009-3, G3V544, A0A0B4J278, G3V387, G3V5R8, G3V2B9 |
| P01009-2 | 9 | 0.003390559 | Isoform 2 of Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 |
| A0A024R6I7 | 9 | 0.003969019 | Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1 |
| G3V2B9 | 9 | 0.002551568 | Alpha-1-antitrypsin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1 |
| A0A0B4J278 | 9 | 0.000745703 | Alpha-1-antitrypsin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1 |
| G3V544 | 9 | 0.001115911 | Alpha-1-antitrypsin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1 |
| P01009-3 | 9 | 0.002060913 | Isoform 3 of Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 |
| A0A0G2JRN3 | 9 | 0.00341691 | Alpha-1-antitrypsin OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1 |
| G3V387 | 9 | 0.000917788 | Alpha-1-antitrypsin (Fragment) OS=Homo sapiens OX=9606 GN=SERPINA1 PE=1 SV=1 |
| P31150 | 8 | 0.000138013 | Rab GDP dissociation inhibitor alpha OS=Homo sapiens OX=9606 GN=GDI1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P50395-2, Q5SX87, Q5SX91, Q5SX86 |
| P50395 | 8 | 8.61E-05 | Rab GDP dissociation inhibitor beta OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=2 |
| Q5SX86 | 8 | 0.000142622 | Rab GDP dissociation inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=1 |
| Q5SX87 | 8 | 8.89E-05 | Rab GDP dissociation inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=1 |
| P50395-2 | 8 | 9.58E-05 | Isoform 2 of Rab GDP dissociation inhibitor beta OS=Homo sapiens OX=9606 GN=GDI2 |
| Q5SX91 | 8 | 3.16E-05 | Rab GDP dissociation inhibitor (Fragment) OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=1 |
| P07602-3 | 9 | 0.027833998 | Isoform Sap-mu-9 of Prosaposin OS=Homo sapiens OX=9606 GN=PSAP; Additional IDs concatenated into MaxParsimony group: C9JIZ6, P07602-2, P07602, Q5BJH1, A0A0J9YXB8 |
| P07602 | 9 | 0.027993353 | Prosaposin OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=2 |
| P07602-2 | 9 | 0.027886915 | Isoform Sap-mu-6 of Prosaposin OS=Homo sapiens OX=9606 GN=PSAP |
| Q5BJH1 | 9 | 0.043015328 | PSAP protein OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=1 |
| C9JIZ6 | 9 | 0.027833998 | Prosaposin OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=2 |
| Q9H853 | 9 | 0.000321253 | Putative tubulin-like protein alpha-4B OS=Homo sapiens OX=9606 GN=TUBA4B PE=5 SV=2 |
| Q71U36 | 9 | 0.001797951 | Tubulin alpha-1A chain OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1 |
| F8VQQ4 | 9 | 0.002395887 | Tubulin alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1 |
| P68366-2 | 9 | 0.000888541 | Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens OX=9606 GN=TUBA4A |
| F8VVB9 | 9 | 0.002261446 | Tubulin alpha-1B chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=8 |
| C9JDS9 | 9 | 0.000848316 | Tubulin alpha-4A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA4A PE=1 SV=1 |
| P0DPH7-2 | 9 | 0.000711809 | Isoform 2 of Tubulin alpha-3C chain OS=Homo sapiens OX=9606 GN=TUBA3C |
| P0DPH8 | 9 | 0.000731617 | Tubulin alpha-3D chain OS=Homo sapiens OX=9606 GN=TUBA3D PE=1 SV=1 |
| P68363 | 9 | 0.001791208 | Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1 |
| Q9BQE3 | 9 | 0.001795814 | Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1 |
| F8VRK0 | 9 | 0.007371294 | Tubulin alpha-1B chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1 |
| F8VWV9 | 9 | 0.004727203 | Tubulin alpha-1B chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1 |
| A0A1W2PQM2 | 9 | 0.001531656 | Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1 |
| C9J2C0 | 9 | 0.000447664 | Tubulin alpha chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA8 PE=1 SV=1 |
| Q9NY65-2 | 9 | 0.000514323 | Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens OX=9606 GN=TUBA8 |
| Q9NY65 | 9 | 0.000465611 | Tubulin alpha-8 chain OS=Homo sapiens OX=9606 GN=TUBA8 PE=1 SV=1 |
| P0DPH7 | 9 | 0.000731617 | Tubulin alpha-3C chain OS=Homo sapiens OX=9606 GN=TUBA3C PE=1 SV=1 |
| F8VS66 | 9 | 0.003349289 | Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=4 SV=1 |
| F8VXZ7 | 9 | 0.003524557 | Tubulin alpha-1A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1 |
| F8W0F6 | 9 | 0.000406862 | Tubulin alpha-1A chain OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1 |
| F8VX09 | 9 | 0.005105379 | Tubulin alpha-1B chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1 |
| Q71U36-2 | 9 | 0.00194358 | Isoform 2 of Tubulin alpha-1A chain OS=Homo sapiens OX=9606 GN=TUBA1A |
| P68366 | 9 | 0.000858791 | Tubulin alpha-4A chain OS=Homo sapiens OX=9606 GN=TUBA4A PE=1 SV=1 |
| Q6PEY2 | 9 | 0.000663683 | Tubulin alpha-3E chain OS=Homo sapiens OX=9606 GN=TUBA3E PE=1 SV=2 |
| F8VRZ4 | 9 | 0.003866615 | Tubulin alpha-1A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1 |
| P68363-2 | 9 | 0.002119323 | Isoform 2 of Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B |
| F5H5D3 | 9 | 0.001553604 | Tubulin alpha chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P68363, Q9BQE3, Q71U36-2, P68363-2, F8VVB9, Q6PEY2, P0DPH8, P0DPH7, Q9NY65, P68366, P68366-2, F8VQQ4, P0DPH7-2, Q9NY65-2, A0A1W2PQM2, F8VS66, F8VRZ4, C9JDS9, F8VWV9, F8VX09, F8VRK0, V9GZ17, Q9H853, F8W0F6, F8VXZ7 |
| H0YH81 | 9 | 0.001232853 | ATP synthase subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=1 |
| F8W0P7 | 9 | 0.000483948 | ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=2 |
| F8W079 | 9 | 0.000937236 | ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=1 |
| P06576 | 9 | 0.000916207 | ATP synthase subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H0YH81, F8W079, F8W0P7 |
| P81605-2 | 9 | 0.00032309 | Isoform 2 of Dermcidin OS=Homo sapiens OX=9606 GN=DCD; Additional IDs concatenated into MaxParsimony group: P81605 |
| P81605 | 9 | 0.000355399 | Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2 |
| P15586-2 | 9 | 0.000902958 | Isoform 2 of N-acetylglucosamine-6-sulfatase OS=Homo sapiens OX=9606 GN=GNS |
| P15586 | 9 | 0.000878172 | N-acetylglucosamine-6-sulfatase OS=Homo sapiens OX=9606 GN=GNS PE=1 SV=3 |
| H7C3P4 | 9 | 0.000968496 | N-acetylglucosamine-6-sulfatase OS=Homo sapiens OX=9606 GN=GNS PE=1 SV=1 |
| F6S8M0 | 9 | 0.000822558 | N-acetylglucosamine-6-sulfatase OS=Homo sapiens OX=9606 GN=GNS PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P15586, P15586-2, H7C3P4, H0YFA9 |
| H0YFA9 | 9 | 0.001131043 | N-acetylglucosamine-6-sulfatase (Fragment) OS=Homo sapiens OX=9606 GN=GNS PE=1 SV=1 |
| Q13838 | 9 | 0.000231975 | Spliceosome RNA helicase DDX39B OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1 |
| A0A0G2JJZ9 | 9 | 0.000302699 | Spliceosome RNA helicase DDX39B (Fragment) OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1 |
| Q13838-2 | 9 | 0.000224121 | Isoform 2 of Spliceosome RNA helicase DDX39B OS=Homo sapiens OX=9606 GN=DDX39B; Additional IDs concatenated into MaxParsimony group: Q13838, A0A0G2JJZ9, O00148, H0Y400, Q5STU3, A0A140T9X3 |
| H0Y400 | 7 | 0.000371104 | Spliceosome RNA helicase DDX39B (Fragment) OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1 |
| O00148 | 7 | 0.000166056 | ATP-dependent RNA helicase DDX39A OS=Homo sapiens OX=9606 GN=DDX39A PE=1 SV=2 |
| J3QQ67 | 9 | 0.000325996 | 60S ribosomal protein L18 (Fragment) OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q07020, H0YHA7, G3V203, Q07020-2, F8VUA6, A0A075B7A0, F8VYV2 |
| Q07020 | 9 | 0.000329464 | 60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=2 |
| A0A075B7A0 | 9 | 0.000300478 | 60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=1 |
| F8VUA6 | 9 | 0.000460051 | 60S ribosomal protein L18 (Fragment) OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=1 |
| F8VYV2 | 9 | 0.000311774 | 60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=1 |
| H0YHA7 | 9 | 0.000370894 | 60S ribosomal protein L18 (Fragment) OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=1 |
| Q07020-2 | 9 | 0.000389555 | Isoform 2 of 60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 |
| G3V203 | 9 | 0.000377679 | 60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=1 |
| E5RGM4 | 8 | 0.000293969 | S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=1 |
| E5RJR5 | 8 | 0.000280029 | S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P63208, P63208-2, F8W8N3, E7ERH2, E5RGM3, E5RI56, E5RGM4, E5RHM3 |
| E5RHM3 | 8 | 0.000309044 | S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=1 |
| E7ERH2 | 8 | 0.000162055 | S-phase kinase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=1 |
| P63208-2 | 8 | 0.000143823 | Isoform 2 of S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 |
| F8W8N3 | 8 | 0.000145644 | S-phase kinase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=1 |
| E5RGM3 | 8 | 0.000225605 | S-phase kinase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=1 |
| E5RI56 | 8 | 0.000152852 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 |
| P63208 | 8 | 0.000280029 | S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=2 |
| H0YAB0 | 9 | 0.000480238 | Prelamin-A/C (Fragment) OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1 |
| P02545-5 | 9 | 0.000716536 | Isoform 5 of Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA |
| Q5TCI8 | 9 | 0.000679884 | Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1 |
| A0A0C4DGC5 | 9 | 0.000642096 | Prelamin-A/C (Fragment) OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1 |
| P02545-2 | 9 | 0.0013568 | Isoform C of Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA |
| P02545-6 | 9 | 0.00126399 | Isoform 6 of Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA |
| P02545-3 | 9 | 0.001168958 | Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA |
| P02545 | 9 | 0.001275767 | Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P02545-3, P02545-6, P02545-2, Q3BDU5, P02545-4, P02545-5, Q5TCI8, A0A0C4DGC5, H0YAB0 |
| Q3BDU5 | 9 | 0.001464902 | Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1 |
| P02545-4 | 9 | 0.000705301 | Isoform 4 of Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA |
| G3V4V8 | 8 | 0.00237288 | NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=1 |
| R4GMY2 | 8 | 0.001169729 | NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=1 |
| R4GNE6 | 9 | 0.001157252 | NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=1 |
| Q9UNZ2-5 | 9 | 0.00045194 | Isoform 3 of NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C; Additional IDs concatenated into MaxParsimony group: Q9UNZ2, Q9UNZ2-4, F2Z2K0, R4GNE6, R4GMY2, G3V4V8 |
| Q9UNZ2-4 | 9 | 0.000486659 | Isoform 2 of NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C |
| Q9UNZ2 | 9 | 0.000454382 | NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=2 |
| F2Z2K0 | 9 | 0.00049771 | NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=1 |
| P09455 | 9 | 0.011714485 | Retinol-binding protein 1 OS=Homo sapiens OX=9606 GN=RBP1 PE=1 SV=2 |
| H0YAK8 | 9 | 0.015499001 | Retinol-binding protein 1 OS=Homo sapiens OX=9606 GN=RBP1 PE=1 SV=2 |
| P09455-2 | 9 | 0.009927464 | Isoform 2 of Retinol-binding protein 1 OS=Homo sapiens OX=9606 GN=RBP1 |
| A0A0A0MQT0 | 9 | 0.008027693 | Retinol binding protein 1, cellular OS=Homo sapiens OX=9606 GN=RBP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P09455-3, P09455-2, P09455, H0YAK8, A0A0A0MTB9 |
| P09455-3 | 9 | 0.009674535 | Isoform 3 of Retinol-binding protein 1 OS=Homo sapiens OX=9606 GN=RBP1 |
| A0A0A0MTB9 | 9 | 0.016691231 | Retinol-binding protein 1 OS=Homo sapiens OX=9606 GN=RBP1 PE=1 SV=1 |
| A0A087X2D0 | 9 | 0.000814938 | Serine/arginine-rich-splicing factor 3 OS=Homo sapiens OX=9606 GN=SRSF3 PE=1 SV=1 |
| P84103 | 9 | 0.000545784 | Serine/arginine-rich splicing factor 3 OS=Homo sapiens OX=9606 GN=SRSF3 PE=1 SV=1 |
| Q16629-2 | 9 | 0.000712194 | Isoform 2 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 |
| A0A0B4J1Z1 | 9 | 0.000701797 | Serine/arginine-rich-splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 PE=1 SV=1 |
| Q16629 | 9 | 0.000403975 | Serine/arginine-rich splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JAB2, Q16629-4, A0A0B4J1Z1, Q16629-2, Q16629-3, P84103, P84103-2, A0A087X2D0 |
| P84103-2 | 9 | 0.000721843 | Isoform 2 of Serine/arginine-rich splicing factor 3 OS=Homo sapiens OX=9606 GN=SRSF3 |
| Q16629-3 | 9 | 0.00072838 | Isoform 3 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 |
| Q16629-4 | 9 | 0.000425425 | Isoform 4 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 |
| C9JAB2 | 9 | 0.000409132 | Serine/arginine-rich-splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 PE=1 SV=1 |
| P0DP25 | 9 | 0.035140443 | Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1 |
| P0DP24 | 9 | 0.035140443 | Calmodulin-2 OS=Homo sapiens OX=9606 GN=CALM2 PE=1 SV=1 |
| M0QZ52 | 9 | 0.042508081 | Calmodulin 3 (Phosphorylase kinase, delta), isoform CRA\_d OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1 |
| Q96HY3 | 9 | 0.022004872 | CALM1 protein OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1 |
| E7ETZ0 | 9 | 0.034906173 | Calmodulin-1 OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1 |
| H0Y7A7 | 9 | 0.027999604 | Calmodulin-2 (Fragment) OS=Homo sapiens OX=9606 GN=CALM2 PE=1 SV=1 |
| P0DP23 | 9 | 0.035140443 | Calmodulin-1 OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1 |
| F8WBR5 | 9 | 0.042298084 | Calmodulin-2 OS=Homo sapiens OX=9606 GN=CALM2 PE=1 SV=1 |
| G3V479 | 9 | 0.033125006 | Calmodulin-1 OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1 |
| G3V361 | 9 | 0.017426074 | Calmodulin-1 (Fragment) OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1 |
| E7EMB3 | 9 | 0.026713908 | Calmodulin-2 OS=Homo sapiens OX=9606 GN=CALM2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0Y7A7, E7ETZ0, P0DP25, P0DP24, P0DP23, Q96HY3, G3V361, M0QZ52, G3V479, F8WBR5 |
| O00764-2 | 9 | 0.00069472 | Isoform 2 of Pyridoxal kinase OS=Homo sapiens OX=9606 GN=PDXK |
| O00764 | 9 | 0.000641324 | Pyridoxal kinase OS=Homo sapiens OX=9606 GN=PDXK PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O00764-2, F2Z2Y4 |
| F2Z2Y4 | 9 | 0.000711032 | Pyridoxal kinase OS=Homo sapiens OX=9606 GN=PDXK PE=1 SV=1 |
| D6R991 | 9 | 0.000157351 | Matrin-3 (Fragment) OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| A8MXP9 | 9 | 7.86E-05 | Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P43243, A0A0R4J2E8, D6REM6, D6R991 |
| P43243 | 9 | 8.30E-05 | Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=2 |
| A0A0R4J2E8 | 9 | 8.30E-05 | Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| D6REM6 | 9 | 8.58E-05 | Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| A0A2C9F2M7 | 9 | 0.000327077 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YFC8 | 9 | 0.000710261 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| O43175 | 9 | 0.000336921 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: A0A286YF22, A0A286YFA2, A0A2C9F2M7, A0A286YFL2, A0A286YFM8, A0A286YF78, A0A286YFB2, A0A286YFC8, A0A286YER3 |
| A0A286YF78 | 9 | 0.000235741 | D-3-phosphoglycerate dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YFM8 | 9 | 0.000637768 | D-3-phosphoglycerate dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YFB2 | 9 | 0.000529467 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YER3 | 9 | 0.00090064 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YFA2 | 9 | 0.000384526 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YF22 | 9 | 0.000341405 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A286YFL2 | 9 | 0.000361354 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| Q14697 | 8 | 0.0001148 | Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=3 |
| F5H6X6 | 8 | 0.000127947 | Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=1 |
| Q14697-2 | 8 | 0.000112186 | Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB; Additional IDs concatenated into MaxParsimony group: Q14697, F5H6X6 |
| H7BZL2 | 9 | 0.000155328 | 3-hydroxyisobutyrate dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HIBADH PE=1 SV=1 |
| P31937 | 9 | 0.000204158 | 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HIBADH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H7BZL2 |
| Q15102 | 8 | 9.74E-05 | Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens OX=9606 GN=PAFAH1B3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: M0R389 |
| M0R389 | 8 | 0.000137195 | Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens OX=9606 GN=PAFAH1B3 PE=1 SV=8 |
| Q13813 | 9 | 3.62E-05 | Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=3 |
| A0A0D9SFF6 | 9 | 0.000128959 | Spectrin alpha chain, non-erythrocytic 1 (Fragment) OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=1 |
| A0A1B0GTB7 | 9 | 0.000896854 | Spectrin alpha chain, non-erythrocytic 1 (Fragment) OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=1 |
| A0A0D9SF54 | 9 | 3.64E-05 | Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=1 |
| Q13813-2 | 9 | 3.61E-05 | Isoform 2 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 |
| A0A0D9SGF6 | 9 | 3.58E-05 | Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q13813-2, Q13813, A0A0D9SF54, Q13813-3, A0A0D9SFF6, A0A1B0GTB7 |
| Q13813-3 | 9 | 3.65E-05 | Isoform 3 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 |
| Q9H2U2-3 | 9 | 0.000144933 | Isoform 3 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 |
| Q9H2U2-2 | 9 | 0.000126661 | Isoform 2 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PPA2; Additional IDs concatenated into MaxParsimony group: Q9H2U2, Q9H2U2-3, Q9H2U2-6, Q9H2U2-4 |
| Q9H2U2-4 | 9 | 0.000245563 | Isoform 4 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 |
| Q9H2U2 | 9 | 0.000132349 | Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 PE=1 SV=2 |
| Q9H2U2-6 | 9 | 0.000190537 | Isoform 5 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 |
| Q12765 | 8 | 4.56E-05 | Secernin-1 OS=Homo sapiens OX=9606 GN=SCRN1 PE=1 SV=2 |
| Q12765-2 | 8 | 4.35E-05 | Isoform 2 of Secernin-1 OS=Homo sapiens OX=9606 GN=SCRN1; Additional IDs concatenated into MaxParsimony group: Q12765, Q12765-3, C9K052, C9J7U9, B8ZZP4 |
| Q12765-3 | 8 | 4.71E-05 | Isoform 3 of Secernin-1 OS=Homo sapiens OX=9606 GN=SCRN1 |
| J3KS22 | 9 | 0.000641115 | L-xylulose reductase (Fragment) OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=8 |
| Q7Z4W1 | 9 | 0.000585937 | L-xylulose reductase OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: J3QS36, J3KS22 |
| J3QS36 | 9 | 0.000635416 | L-xylulose reductase (Fragment) OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=1 |
| O60506 | 8 | 4.45E-05 | Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=2 |
| O60506-4 | 8 | 5.26E-05 | Isoform 4 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP |
| O60506-2 | 8 | 4.72E-05 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP |
| F6UXX1 | 8 | 0.000112809 | Heterogeneous nuclear ribonucleoprotein Q (Fragment) OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=1 |
| O43390 | 8 | 6.78E-05 | Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR PE=1 SV=1 |
| O60506-3 | 8 | 4.94E-05 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP |
| O43390-2 | 8 | 6.75E-05 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR; Additional IDs concatenated into MaxParsimony group: O43390, O60506, O60506-2, O60506-3, O43390-4, O60506-4, B7Z645, F6UXX1 |
| H0YA56 | 7 | 0.0001224 | Apoptosis regulator BAX (Fragment) OS=Homo sapiens OX=9606 GN=BAX PE=1 SV=1 |
| Q07812-2 | 8 | 0.000475686 | Isoform Beta of Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX; Additional IDs concatenated into MaxParsimony group: Q07812, Q07812-8, Q07812-7, Q07812-5, K4JQN1, Q07812-4, I6LPK7, H0YA56, Q07812-6 |
| Q07812 | 8 | 0.000540102 | Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX PE=1 SV=1 |
| Q07812-5 | 8 | 0.000632314 | Isoform Epsilon of Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX |
| I6LPK7 | 7 | 0.00011016 | Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX PE=1 SV=1 |
| Q07812-7 | 8 | 0.00015711 | Isoform Psi of Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX |
| Q07812-8 | 8 | 0.000579327 | Isoform Sigma of Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX |
| Q07812-4 | 8 | 0.000642951 | Isoform Delta of Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX |
| K4JQN1 | 7 | 0.000107837 | Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX PE=1 SV=1 |
| Q07812-6 | 7 | 0.000135285 | Isoform Zeta of Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX |
| J3KN67 | 8 | 0.00126887 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=1 |
| H0YKP3 | 8 | 0.001811285 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| H0YKX5 | 8 | 0.002255317 | Tropomyosin alpha-1 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| Q5TCU3 | 8 | 0.001302113 | Tropomyosin beta chain OS=Homo sapiens OX=9606 GN=TPM2 PE=1 SV=1 |
| H0YL80 | 8 | 0.004181938 | Tropomyosin alpha-1 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| P09493-2 | 8 | 0.001404628 | Isoform 2 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| A0A0S2Z4G6 | 8 | 0.001093175 | Tropomyosin 1 (Alpha), isoform CRA\_o (Fragment) OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| A0A2R8YEU4 | 8 | 0.002696688 | Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| P09493-3 | 8 | 0.001127659 | Isoform 3 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| H0YNC7 | 8 | 0.001392205 | Tropomyosin alpha-1 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| H0YKJ4 | 8 | 0.001271937 | Tropomyosin 1 (Alpha), isoform CRA\_b OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2 |
| P67936 | 8 | 0.002916566 | Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=3 |
| P09493-6 | 8 | 0.001093175 | Isoform 6 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| B7Z596 | 8 | 0.001182668 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| P07951 | 8 | 0.001302113 | Tropomyosin beta chain OS=Homo sapiens OX=9606 GN=TPM2 PE=1 SV=1 |
| P06753 | 8 | 0.00126887 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=2 |
| P09493-5 | 8 | 0.001287512 | Isoform 5 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| P67936-2 | 8 | 0.002309343 | Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 |
| P09493-8 | 8 | 0.001127659 | Isoform 8 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| K7ERG3 | 8 | 0.002510864 | Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| F5H7S3 | 8 | 0.001327484 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2 |
| P09493-4 | 8 | 0.001127659 | Isoform 4 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| K7EP68 | 8 | 0.002827516 | Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| P06753-6 | 8 | 0.001506194 | Isoform 6 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 |
| K7ENT6 | 8 | 0.002655277 | Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=2 |
| Q5TCU8 | 8 | 0.001148448 | Tropomyosin beta chain OS=Homo sapiens OX=9606 GN=TPM2 PE=1 SV=1 |
| P09493 | 8 | 0.001093175 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2 |
| P06753-2 | 8 | 0.001506194 | Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 |
| P07951-3 | 8 | 0.001479367 | Isoform 3 of Tropomyosin beta chain OS=Homo sapiens OX=9606 GN=TPM2 |
| A0A2R8YE05 | 8 | 0.002902006 | Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| H0YK48 | 8 | 0.001271937 | Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| P09493-7 | 8 | 0.001093175 | Isoform 7 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| A0A2R8Y5V9 | 8 | 0.00223829 | Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| A7XZE4 | 8 | 0.001291842 | Beta tropomyosin isoform OS=Homo sapiens OX=9606 GN=TPM2 PE=1 SV=1 |
| Q6ZN40 | 8 | 0.000952337 | Tropomyosin 1 (Alpha), isoform CRA\_f OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5TCU8, P06753, J3KN67, P09493-9, P09493-4, P09493-8, P67936-2, P09493-7, Q5TCU3, P09493, P07951, A7XZE4, P09493-10, P09493-3, A0A0S2Z4G6, P07951-2, P09493-6, B7Z596, P06753-5, H7BYY1, H0YK48, P07951-3, P06753-2, A0A2R8Y5V9, P06753-6, H0YKJ4, P67936, P06753-4, K7ENT6, P06753-3, P09493-5, F5H7S3, Q5HYB6, P09493-2, A0A087WWU8, A0A2R8YE05, H0YNC7, A0A2R8YH90, A0A2R8YGX3, A0A2R8YEU4, K7ERG3, H0YKP3, H0YKX5, K7EP68, D6R904, H0YL80 |
| D6R904 | 8 | 0.003144632 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=1 |
| H7BYY1 | 8 | 0.001311426 | Tropomyosin 1 (Alpha), isoform CRA\_m OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=1 |
| A0A087WWU8 | 8 | 0.001558433 | Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=1 |
| P07951-2 | 8 | 0.001291842 | Isoform 2 of Tropomyosin beta chain OS=Homo sapiens OX=9606 GN=TPM2 |
| A0A2R8YH90 | 8 | 0.002309111 | Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| A0A2R8YGX3 | 8 | 0.002917934 | Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=1 |
| Q5HYB6 | 8 | 0.001610069 | Epididymis luminal protein 189 OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=1 |
| P09493-9 | 8 | 0.001093175 | Isoform 9 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| P09493-10 | 8 | 0.001127659 | Isoform 10 of Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 |
| P06753-5 | 8 | 0.001506194 | Isoform 5 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 |
| P06753-4 | 8 | 0.001512291 | Isoform 4 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 |
| P06753-3 | 8 | 0.001512291 | Isoform 3 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 |
| P06748-2 | 8 | 0.000975744 | Isoform 2 of Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 |
| P06748-3 | 8 | 0.000983314 | Isoform 3 of Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 |
| P06748 | 8 | 0.000879497 | Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P06748-2, P06748-3 |
| A0A2R8Y7X9 | 8 | 0.026896644 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=3 SV=1 |
| P69891 | 8 | 0.030739022 | Hemoglobin subunit gamma-1 OS=Homo sapiens OX=9606 GN=HBG1 PE=1 SV=2 |
| F8W6P5 | 9 | 2.50E-01 | Hemoglobin subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=1 |
| P68871 | 9 | 1.90E-01 | Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A2R8Y7R2, F8W6P5, E9PFT6, E9PEW8, A0A2R8Y7X9, P69891, P02100, P69892, A8MUF7 |
| E9PEW8 | 8 | 6.27E-02 | Hemoglobin subunit delta (Fragment) OS=Homo sapiens OX=9606 GN=HBD PE=1 SV=1 |
| A8MUF7 | 8 | 5.12E-02 | Hemoglobin subunit epsilon (Fragment) OS=Homo sapiens OX=9606 GN=HBE1 PE=1 SV=1 |
| E9PFT6 | 9 | 5.80E-02 | Hemoglobin subunit delta OS=Homo sapiens OX=9606 GN=HBD PE=1 SV=1 |
| A0A2R8Y7R2 | 9 | 2.18E-01 | Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=1 |
| P02042 | 9 | 7.36E-02 | Hemoglobin subunit delta OS=Homo sapiens OX=9606 GN=HBD PE=1 SV=2 |
| P02100 | 8 | 3.04E-02 | Hemoglobin subunit epsilon OS=Homo sapiens OX=9606 GN=HBE1 PE=1 SV=2 |
| P69892 | 8 | 3.08E-02 | Hemoglobin subunit gamma-2 OS=Homo sapiens OX=9606 GN=HBG2 PE=1 SV=2 |
| Q15149 | 9 | 1.85E-05 | Plectin OS=Homo sapiens OX=9606 GN=PLEC PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q15149-2, Q15149-3, Q15149-6, Q15149-4, Q15149-5, Q15149-9, Q15149-8, Q15149-7 |
| Q15149-3 | 9 | 1.90E-05 | Isoform 3 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| Q15149-8 | 9 | 1.92E-05 | Isoform 8 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| Q15149-6 | 9 | 1.91E-05 | Isoform 6 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| Q15149-4 | 9 | 1.91E-05 | Isoform 4 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| Q15149-9 | 9 | 1.91E-05 | Isoform 9 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| Q15149-5 | 9 | 1.91E-05 | Isoform 5 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| Q15149-7 | 9 | 1.92E-05 | Isoform 7 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| Q15149-2 | 9 | 1.90E-05 | Isoform 2 of Plectin OS=Homo sapiens OX=9606 GN=PLEC |
| A0A087WV45 | 9 | 6.25E-03 | Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1 |
| P02766 | 9 | 6.70E-03 | Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087WT59, A0A087WV45 |
| A0A087WT59 | 9 | 5.13E-03 | Transthyretin OS=Homo sapiens OX=9606 GN=TTR PE=1 SV=1 |
| P22626 | 9 | 1.90E-03 | Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P22626-2, A0A087WUI2 |
| A0A087WUI2 | 9 | 7.17E-04 | Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 PE=1 SV=1 |
| P22626-2 | 9 | 1.94E-03 | Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 |
| P08195 | 9 | 2.23E-04 | 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P08195-4, J3KPF3, F5GZS6, P08195-3, P08195-2, H0YFS2, F5H0E2, F5H867 |
| F5H0E2 | 8 | 2.91E-04 | 4F2 cell-surface antigen heavy chain (Fragment) OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| H0YFS2 | 8 | 1.64E-04 | 4F2 cell-surface antigen heavy chain (Fragment) OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| F5H867 | 8 | 2.88E-04 | 4F2 cell-surface antigen heavy chain (Fragment) OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| P08195-3 | 9 | 2.47E-04 | Isoform 3 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 |
| P08195-2 | 9 | 2.66E-04 | Isoform 2 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 |
| J3KPF3 | 9 | 2.23E-04 | 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| P08195-4 | 9 | 2.13E-04 | Isoform 4 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 |
| F5GZS6 | 9 | 2.35E-04 | 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| A0A2R8Y5E5 | 9 | 1.23E-03 | Glutathione S-transferase P OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=1 |
| A8MX94 | 9 | 0.001037727 | Glutathione S-transferase P OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=1 |
| P09211 | 9 | 0.000927935 | Glutathione S-transferase P OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A8MX94, A0A2R8Y5E5 |
| U3KQK0 | 9 | 0.009864326 | Histone H2B OS=Homo sapiens OX=9606 GN=HIST1H2BN PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5QNW6-2, P33778, P06899, Q99879, P62807, P58876, Q16778, O60814, Q93079, Q99877, Q99880, Q5QNW6, P23527, P57053, Q8N257, Q96A08 |
| Q5QNW6-2 | 9 | 1.22E-02 | Isoform 2 of Histone H2B type 2-F OS=Homo sapiens OX=9606 GN=HIST2H2BF |
| Q5QNW6 | 9 | 1.30E-02 | Histone H2B type 2-F OS=Homo sapiens OX=9606 GN=HIST2H2BF PE=1 SV=3 |
| Q99880 | 9 | 1.30E-02 | Histone H2B type 1-L OS=Homo sapiens OX=9606 GN=HIST1H2BL PE=1 SV=3 |
| Q99877 | 9 | 1.30E-02 | Histone H2B type 1-N OS=Homo sapiens OX=9606 GN=HIST1H2BN PE=1 SV=3 |
| Q93079 | 9 | 1.30E-02 | Histone H2B type 1-H OS=Homo sapiens OX=9606 GN=HIST1H2BH PE=1 SV=3 |
| O60814 | 9 | 1.30E-02 | Histone H2B type 1-K OS=Homo sapiens OX=9606 GN=HIST1H2BK PE=1 SV=3 |
| Q16778 | 9 | 1.28E-02 | Histone H2B type 2-E OS=Homo sapiens OX=9606 GN=HIST2H2BE PE=1 SV=3 |
| P58876 | 9 | 1.30E-02 | Histone H2B type 1-D OS=Homo sapiens OX=9606 GN=HIST1H2BD PE=1 SV=2 |
| P62807 | 9 | 1.30E-02 | Histone H2B type 1-C/E/F/G/I OS=Homo sapiens OX=9606 GN=HIST1H2BC PE=1 SV=4 |
| Q8N257 | 9 | 8.40E-03 | Histone H2B type 3-B OS=Homo sapiens OX=9606 GN=HIST3H2BB PE=1 SV=3 |
| Q99879 | 9 | 1.30E-02 | Histone H2B type 1-M OS=Homo sapiens OX=9606 GN=HIST1H2BM PE=1 SV=3 |
| P06899 | 9 | 0.012773227 | Histone H2B type 1-J OS=Homo sapiens OX=9606 GN=HIST1H2BJ PE=1 SV=3 |
| P33778 | 9 | 1.28E-02 | Histone H2B type 1-B OS=Homo sapiens OX=9606 GN=HIST1H2BB PE=1 SV=2 |
| P23527 | 9 | 1.28E-02 | Histone H2B type 1-O OS=Homo sapiens OX=9606 GN=HIST1H2BO PE=1 SV=3 |
| P57053 | 9 | 1.30E-02 | Histone H2B type F-S OS=Homo sapiens OX=9606 GN=H2BFS PE=1 SV=2 |
| P55327-5 | 8 | 6.71E-05 | Isoform 5 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 |
| P55327-4 | 8 | 7.72E-05 | Isoform 4 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 |
| P55327 | 8 | 7.13E-05 | Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 PE=1 SV=2 |
| P55327-6 | 8 | 6.47E-05 | Isoform 6 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 |
| P55327-2 | 8 | 8.68E-05 | Isoform 2 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 |
| P55327-7 | 8 | 6.86E-05 | Isoform 7 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52 |
| P55327-3 | 8 | 6.44E-05 | Isoform 3 of Tumor protein D52 OS=Homo sapiens OX=9606 GN=TPD52; Additional IDs concatenated into MaxParsimony group: P55327-6, P55327-5, P55327-7, P55327, P55327-4, P55327-2, E5RK35 |
| P16278 | 8 | 5.69E-05 | Beta-galactosidase OS=Homo sapiens OX=9606 GN=GLB1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P16278-3, E7EQ29, P16278-2 |
| E7EQ29 | 8 | 7.02E-05 | Beta-galactosidase OS=Homo sapiens OX=9606 GN=GLB1 PE=1 SV=1 |
| P16278-3 | 8 | 5.95E-05 | Isoform 3 of Beta-galactosidase OS=Homo sapiens OX=9606 GN=GLB1 |
| P16278-2 | 8 | 7.05E-05 | Isoform 2 of Beta-galactosidase OS=Homo sapiens OX=9606 GN=GLB1 |
| P07919 | 8 | 1.67E-03 | Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRH PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A096LP55 |
| A0A096LP55 | 8 | 2.68E-04 | Cytochrome b-c1 complex subunit 6-like, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRHL PE=3 SV=1 |
| Q9Y6I3-3 | 9 | 3.04E-04 | Isoform 3 of Epsin-1 OS=Homo sapiens OX=9606 GN=EPN1 |
| Q9Y6I3 | 9 | 2.90E-04 | Epsin-1 OS=Homo sapiens OX=9606 GN=EPN1 PE=1 SV=2 |
| Q9Y6I3-1 | 9 | 2.53E-04 | Isoform 2 of Epsin-1 OS=Homo sapiens OX=9606 GN=EPN1; Additional IDs concatenated into MaxParsimony group: Q9Y6I3, Q9Y6I3-3 |
| P62829 | 8 | 3.40E-04 | 60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: J3KT29, B9ZVP7, C9JD32 |
| J3KT29 | 8 | 2.35E-04 | 60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1 |
| C9JD32 | 8 | 3.15E-04 | 60S ribosomal protein L23 (Fragment) OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1 |
| B9ZVP7 | 8 | 2.51E-04 | 60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1 |
| P11279-2 | 9 | 1.71E-03 | Isoform 2 of Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens OX=9606 GN=LAMP1 |
| P11279 | 9 | 3.86E-03 | Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens OX=9606 GN=LAMP1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P11279-2 |
| A0A1B0GUW4 | 9 | 6.42E-03 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GTM3 | 9 | 7.21E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GW68 | 9 | 7.25E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GVA3 | 8 | 1.06E-02 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GTP7 | 9 | 9.17E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GVE7 | 9 | 7.06E-03 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GV06 | 9 | 5.24E-03 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GUH5 | 9 | 6.90E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| Q13510 | 9 | 6.86E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: Q13510-2, A0A1B0GUH5, A0A1B0GTZ5, A0A1B0GTM3, A0A1B0GUA4, A0A1B0GW68, E7EMM4, A0A1B0GUW4, A0A1B0GUE3, Q13510-3, A0A1B0GUG1, A0A1B0GTP7, A0A1B0GV06, A0A1B0GVG2, A0A1B0GU62, A0A1B0GUJ3, A0A1B0GUB3, A0A1B0GU06, A0A1B0GVE7, A0A1B0GVJ1, A0A1B0GW48, A0A1B0GV95, A0A1B0GW66, A0A1B0GVA3 |
| A0A1B0GUA4 | 9 | 7.23E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GUE3 | 9 | 7.16E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| E7EMM4 | 9 | 7.33E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GUG1 | 9 | 4.06E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GU62 | 9 | 8.99E-03 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GW66 | 8 | 9.35E-03 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GU06 | 9 | 8.40E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GVJ1 | 9 | 9.19E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GUB3 | 9 | 6.59E-03 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GTZ5 | 9 | 7.02E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GW48 | 9 | 9.29E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| Q13510-2 | 9 | 6.59E-03 | Isoform 2 of Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 |
| A0A1B0GUJ3 | 8 | 8.09E-03 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| A0A1B0GV95 | 9 | 1.15E-02 | Acid ceramidase (Fragment) OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| Q13510-3 | 9 | 3.01E-03 | Isoform 3 of Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 |
| A0A1B0GVG2 | 9 | 4.91E-03 | Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=1 |
| C9J9K3 | 9 | 2.97E-04 | 40S ribosomal protein SA (Fragment) OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=8 |
| P08865 | 9 | 2.65E-04 | 40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=4 |
| A0A0C4DG17 | 9 | 2.60E-04 | 40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P08865, C9J9K3, F8WD59 |
| F8WD59 | 8 | 2.12E-04 | 40S ribosomal protein SA (Fragment) OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=2 |
| I3L2L4 | 9 | 9.95E-04 | N-sulphoglucosamine sulphohydrolase (Fragment) OS=Homo sapiens OX=9606 GN=SGSH PE=1 SV=8 |
| I3NI22 | 9 | 2.38E-03 | N-sulphoglucosamine sulphohydrolase (Fragment) OS=Homo sapiens OX=9606 GN=SGSH PE=1 SV=1 |
| P51688 | 9 | 1.78E-03 | N-sulphoglucosamine sulphohydrolase OS=Homo sapiens OX=9606 GN=SGSH PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: I3NI22, I3L2L4, I3L4B7, I3L2I6 |
| I3L4B7 | 9 | 1.70E-03 | N-sulphoglucosamine sulphohydrolase (Fragment) OS=Homo sapiens OX=9606 GN=SGSH PE=1 SV=1 |
| I3L2I6 | 9 | 1.76E-03 | N-sulphoglucosamine sulphohydrolase (Fragment) OS=Homo sapiens OX=9606 GN=SGSH PE=1 SV=1 |
| Q02539 | 9 | 8.65E-04 | Histone H1.1 OS=Homo sapiens OX=9606 GN=HIST1H1A PE=1 SV=3 |
| P16403 | 9 | 1.92E-03 | Histone H1.2 OS=Homo sapiens OX=9606 GN=HIST1H1C PE=1 SV=2 |
| P22492 | 9 | 8.43E-04 | Histone H1t OS=Homo sapiens OX=9606 GN=HIST1H1T PE=2 SV=4 |
| P10412 | 9 | 1.86E-03 | Histone H1.4 OS=Homo sapiens OX=9606 GN=HIST1H1E PE=1 SV=2 |
| P16402 | 9 | 1.89E-03 | Histone H1.3 OS=Homo sapiens OX=9606 GN=HIST1H1D PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P10412, P16403, Q02539, P22492 |
| C9J1Z8 | 9 | 1.74E-04 | ADP-ribosylation factor 5 (Fragment) OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=1 |
| P61204 | 9 | 1.44E-03 | ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=2 |
| P84077 | 9 | 1.44E-03 | ADP-ribosylation factor 1 OS=Homo sapiens OX=9606 GN=ARF1 PE=1 SV=2 |
| P61204-2 | 9 | 1.81E-03 | Isoform 2 of ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 |
| P84085 | 9 | 1.45E-04 | ADP-ribosylation factor 5 OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=2 |
| F5H423 | 9 | 1.23E-03 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=3 SV=1; Additional IDs concatenated into MaxParsimony group: P61204, P84077, P61204-2, P84085, C9J1Z8 |
| P05023 | 9 | 1.86E-04 | Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P05023-4, P05023-3, P05023-2 |
| P05023-4 | 9 | 1.86E-04 | Isoform 4 of Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 |
| P05023-3 | 9 | 1.91E-04 | Isoform 3 of Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 |
| P05023-2 | 9 | 2.39E-04 | Isoform 2 of Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 |
| E7EMC6 | 9 | 2.38E-03 | Annexin OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=1 |
| E5RIU8 | 7 | 6.32E-04 | Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=2 |
| E5RFF0 | 9 | 1.39E-03 | Annexin A6 (Fragment) OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=1 |
| E5RJF5 | 9 | 1.41E-03 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=8 |
| E5RJR0 | 7 | 5.46E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=1 |
| E5RI05 | 9 | 1.08E-03 | Annexin OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=1 |
| P08133 | 9 | 0.001823913 | Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P08133-2, E7EMC6, E5RK69, E5RK63, E5RJF5, E5RI05, E5RFF0, E5RJR0, E5RIU8 |
| E5RK69 | 9 | 1.67E-03 | Annexin OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=1 |
| P08133-2 | 9 | 1.91E-03 | Isoform 2 of Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 |
| E5RK63 | 9 | 1.63E-03 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=1 |
| M0QZL1 | 8 | 1.90E-04 | Flavin reductase (NADPH) OS=Homo sapiens OX=9606 GN=BLVRB PE=1 SV=1 |
| M0R192 | 8 | 2.07E-04 | Flavin reductase (NADPH) OS=Homo sapiens OX=9606 GN=BLVRB PE=1 SV=1 |
| A0A2R8YEP4 | 8 | 1.34E-04 | Flavin reductase (NADPH) OS=Homo sapiens OX=9606 GN=BLVRB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P30043, M0R192, M0QZL1, A0A2R8Y7Y9 |
| P30043 | 8 | 2.22E-04 | Flavin reductase (NADPH) OS=Homo sapiens OX=9606 GN=BLVRB PE=1 SV=3 |
| A0A2R8Y7Y9 | 8 | 2.42E-04 | Flavin reductase (NADPH) OS=Homo sapiens OX=9606 GN=BLVRB PE=1 SV=1 |
| A0A2U3TZH3 | 9 | 8.80E-04 | Elongation factor 1-alpha 2 OS=Homo sapiens OX=9606 GN=EEF1A2 PE=4 SV=1; Additional IDs concatenated into MaxParsimony group: Q05639, P68104, Q5VTE0, P68104-2, A0A087WVQ9 |
| P68104 | 9 | 1.16E-03 | Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1 |
| P68104-2 | 9 | 1.21E-03 | Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 |
| Q05639 | 9 | 9.43E-04 | Elongation factor 1-alpha 2 OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1 |
| A0A087WVQ9 | 9 | 1.21E-03 | Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1 |
| Q5VTE0 | 9 | 1.16E-03 | Putative elongation factor 1-alpha-like 3 OS=Homo sapiens OX=9606 GN=EEF1A1P5 PE=5 SV=1 |
| O14950 | 9 | 1.06E-03 | Myosin regulatory light chain 12B OS=Homo sapiens OX=9606 GN=MYL12B PE=1 SV=2 |
| P19105 | 9 | 1.07E-03 | Myosin regulatory light chain 12A OS=Homo sapiens OX=9606 GN=MYL12A PE=1 SV=2 |
| J3QRS3 | 9 | 1.03E-03 | Myosin regulatory light chain 12A OS=Homo sapiens OX=9606 GN=MYL12A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O14950, P19105 |
| Q9UL46 | 9 | 7.35E-04 | Proteasome activator complex subunit 2 OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=4 |
| H0YM70 | 9 | 7.46E-04 | Proteasome activator complex subunit 2 OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=1 |
| A0A087X1Z3 | 9 | 6.91E-04 | Proteasome activator complex subunit 2 OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UL46, H0YM70 |
| P18827 | 9 | 9.79E-04 | Syndecan-1 OS=Homo sapiens OX=9606 GN=SDC1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: H7C1K4, E9PHH3 |
| E9PHH3 | 9 | 1.80E-03 | Syndecan-1 OS=Homo sapiens OX=9606 GN=SDC1 PE=1 SV=1 |
| H7C1K4 | 9 | 1.41E-03 | Syndecan-1 (Fragment) OS=Homo sapiens OX=9606 GN=SDC1 PE=1 SV=1 |
| J3KTL2 | 9 | 4.70E-04 | Serine/arginine-rich-splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=1 |
| Q07955-2 | 9 | 3.40E-04 | Isoform ASF-2 of Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1; Additional IDs concatenated into MaxParsimony group: J3KTL2, Q07955, Q07955-3 |
| Q07955 | 9 | 4.80E-04 | Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2 |
| Q07955-3 | 9 | 4.94E-04 | Isoform ASF-3 of Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 |
| H0YN28 | 9 | 4.56E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YM50 | 9 | 2.56E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YMD0 | 9 | 4.46E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YNA0 | 9 | 8.02E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YNP5 | 9 | 3.62E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YN52 | 9 | 1.00E-03 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YMU9 | 9 | 4.40E-04 | Annexin OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YN42 | 9 | 3.95E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| A6NMY6 | 9 | 2.69E-04 | Putative annexin A2-like protein OS=Homo sapiens OX=9606 GN=ANXA2P2 PE=5 SV=2 |
| P07355-2 | 9 | 2.91E-04 | Isoform 2 of Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2; Additional IDs concatenated into MaxParsimony group: A6NMY6, P07355, H0YN42, H0YM50, H0YMU9, H0YMD0, H0YKS4, H0YNP5, H0YL33, H0YN28, H0YNA0, H0YN52 |
| P07355 | 9 | 3.06E-04 | Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2 |
| H0YL33 | 9 | 4.46E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| H0YKS4 | 9 | 5.50E-04 | Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1 |
| P62899 | 8 | 1.57E-03 | 60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1 |
| P62899-2 | 8 | 1.53E-03 | Isoform 2 of 60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 |
| C9JU56 | 8 | 1.71E-03 | 60S ribosomal protein L31 (Fragment) OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1 |
| B7Z4C8 | 8 | 1.51E-03 | cDNA FLJ57527, highly similar to 60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P62899-2, P62899, P62899-3, B7Z4E3, C9JU56, H7C2W9, B8ZZK4 |
| H7C2W9 | 8 | 1.82E-03 | 60S ribosomal protein L31 (Fragment) OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1 |
| P62899-3 | 8 | 1.62E-03 | Isoform 3 of 60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 |
| B7Z4E3 | 8 | 1.64E-03 | cDNA FLJ58908, highly similar to 60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1 |
| B8ZZK4 | 8 | 2.21E-03 | 60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1 |
| Q5JYR4 | 7 | 2.53E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=8 |
| P04844 | 8 | 7.55E-06 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P04844-2, Q5JYR7, Q5JYR4, F2Z3K5 |
| F2Z3K5 | 7 | 2.59E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=1 |
| Q5JYR7 | 7 | 1.22E-05 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=8 |
| P04844-2 | 8 | 7.75E-06 | Isoform 2 of Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 |
| H7BZB9 | 9 | 1.05E-03 | Microtubule-associated protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=MAP2 PE=1 SV=1 |
| P11137-4 | 9 | 8.26E-04 | Isoform 4 of Microtubule-associated protein 2 OS=Homo sapiens OX=9606 GN=MAP2 |
| P11137 | 9 | 2.53E-04 | Microtubule-associated protein 2 OS=Homo sapiens OX=9606 GN=MAP2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P11137-3, E7EV03, P11137-4, P11137-2, H7BZB9, A8MZ31 |
| P11137-2 | 9 | 9.80E-04 | Isoform 2 of Microtubule-associated protein 2 OS=Homo sapiens OX=9606 GN=MAP2 |
| E7EV03 | 9 | 7.85E-04 | Microtubule-associated protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=MAP2 PE=1 SV=1 |
| P11137-3 | 9 | 0.000253946 | Isoform 3 of Microtubule-associated protein 2 OS=Homo sapiens OX=9606 GN=MAP2 |
| A8MZ31 | 9 | 3.57E-03 | Microtubule-associated protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=MAP2 PE=1 SV=1 |
| H3BLU2 | 9 | 3.13E-03 | Limbic system-associated membrane protein (Fragment) OS=Homo sapiens OX=9606 GN=LSAMP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q13449, F5H5G1 |
| Q13449 | 9 | 3.19E-03 | Limbic system-associated membrane protein OS=Homo sapiens OX=9606 GN=LSAMP PE=1 SV=2 |
| F5H5G1 | 9 | 2.53E-03 | Limbic system-associated membrane protein OS=Homo sapiens OX=9606 GN=LSAMP PE=1 SV=2 |
| P13639 | 8 | 6.20E-05 | Elongation factor 2 OS=Homo sapiens OX=9606 GN=EEF2 PE=1 SV=4 |
| B8ZZ54 | 9 | 5.15E-03 | 10 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPE1 PE=1 SV=1 |
| B8ZZL8 | 9 | 4.98E-03 | 10 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPE1 PE=1 SV=1 |
| P61604 | 9 | 5.08E-03 | 10 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPE1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: B8ZZL8, B8ZZ54 |
| H0YA55 | 9 | 3.60E-02 | Serum albumin (Fragment) OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=1 |
| H7C013 | 9 | 5.18E-02 | Serum albumin (Fragment) OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=1 |
| contaminant\_INT-STD1 | 9 | 6.33E-03 | BSA |
| P02768-2 | 9 | 3.37E-02 | Isoform 2 of Serum albumin OS=Homo sapiens OX=9606 GN=ALB |
| B7WNR0 | 9 | 3.38E-02 | Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=1 |
| P02768 | 9 | 4.13E-02 | Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A0C4DGB6, B7WNR0, D6RHD5, H0YA55, A0A087WWT3, P02768-2, C9JKR2, P02768-3, H7C013, contaminant\_INT-STD1 |
| A0A087WWT3 | 9 | 4.23E-02 | Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=1 |
| P02768-3 | 9 | 4.07E-02 | Isoform 3 of Serum albumin OS=Homo sapiens OX=9606 GN=ALB |
| D6RHD5 | 9 | 3.56E-02 | Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=1 |
| A0A0C4DGB6 | 9 | 3.95E-02 | Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=1 |
| C9JKR2 | 9 | 3.37E-02 | Albumin, isoform CRA\_k OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=1 |
| P16989 | 9 | 2.00E-04 | Y-box-binding protein 3 OS=Homo sapiens OX=9606 GN=YBX3 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P16989-3, P16989-2 |
| P16989-3 | 9 | 2.17E-04 | Isoform 3 of Y-box-binding protein 3 OS=Homo sapiens OX=9606 GN=YBX3 |
| P16989-2 | 9 | 2.45E-04 | Isoform 2 of Y-box-binding protein 3 OS=Homo sapiens OX=9606 GN=YBX3 |
| A0A2R8Y7U1 | 9 | 0.00366873 | Tripeptidyl-peptidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=1 |
| A0A2R8YD72 | 9 | 0.004638529 | Tripeptidyl-peptidase 1 (Fragment) OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=1 |
| A0A2R8YD45 | 9 | 0.00252145 | Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=1 |
| A0A2R8Y7I4 | 9 | 4.03E-03 | Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=1 |
| A0A2R8YGD1 | 9 | 3.60E-03 | Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=1 |
| O14773-2 | 9 | 5.28E-03 | Isoform 2 of Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 |
| O14773 | 9 | 3.00E-03 | Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A2R8YGD1, A0A2R8Y7U1, O14773-2, A0A2R8YD45, A0A2R8Y7I4, A0A2R8YD72 |
| Q5T0I0 | 9 | 1.14E-03 | Gelsolin (Fragment) OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1 |
| P06396-4 | 9 | 2.58E-03 | Isoform 4 of Gelsolin OS=Homo sapiens OX=9606 GN=GSN |
| A0A0U1RQL8 | 9 | 6.75E-04 | Gelsolin (Fragment) OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1 |
| P06396-2 | 9 | 2.61E-03 | Isoform 2 of Gelsolin OS=Homo sapiens OX=9606 GN=GSN |
| P06396-3 | 9 | 2.57E-03 | Isoform 3 of Gelsolin OS=Homo sapiens OX=9606 GN=GSN |
| P06396 | 9 | 2.44E-03 | Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0A0MT01, A0A0A0MS51, P06396-3, P06396-4, P06396-2, Q5T0I0, A0A0U1RQL8 |
| A0A0A0MS51 | 9 | 2.55E-03 | Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1 |
| A0A0A0MT01 | 9 | 2.48E-03 | Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1 |
| G3V576 | 8 | 5.57E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V4C1 | 8 | 5.44E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| B2R5W2 | 8 | 4.75E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V555 | 8 | 0.000664758 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V575 | 8 | 6.22E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V2Q1 | 8 | 5.10E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| P07910-4 | 8 | 6.26E-04 | Isoform 4 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC |
| B4DY08 | 8 | 4.71E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V4W0 | 8 | 5.17E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V3K6 | 8 | 4.64E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V5X6 | 8 | 4.80E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| P07910 | 8 | 5.09E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: G3V2Q1, P07910-2, G3V4C1, P07910-4, B2R5W2, B4DY08, G3V4W0, G3V576, G3V575, G3V555, P07910-3, B4DSU6, G3V251, G3V3K6, G3V5X6, G3V4M8, A0A0G2JNQ3, B7ZW38, A0A0G2JPF8, O60812, P0DMR1, B2RXH8, G3V2H6 |
| P07910-2 | 8 | 5.42E-04 | Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC |
| B4DSU6 | 8 | 3.60E-04 | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| G3V251 | 8 | 0.000446005 | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=1 |
| O43852-10 | 9 | 2.04E-03 | Isoform 10 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| H0Y875 | 9 | 1.29E-03 | Calumenin (Fragment) OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=1 |
| O43852-14 | 9 | 2.00E-03 | Isoform 14 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-15 | 9 | 1.48E-03 | Isoform 15 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-6 | 9 | 0.001888095 | Isoform 6 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-3 | 9 | 1.66E-03 | Isoform 3 of Calumenin OS=Homo sapiens OX=9606 GN=CALU; Additional IDs concatenated into MaxParsimony group: O43852-4, O43852, O43852-2, O43852-6, O43852-5, O43852-8, O43852-15, O43852-9, H0Y875, O43852-10, O43852-11, O43852-7, O43852-14, O43852-13, O43852-12 |
| O43852-12 | 9 | 0.003305795 | Isoform 12 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-9 | 9 | 0.002348006 | Isoform 9 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852 | 9 | 0.001704183 | Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2 |
| O43852-5 | 9 | 0.001610672 | Isoform 5 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-11 | 9 | 1.73E-03 | Isoform 11 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-8 | 9 | 1.82E-03 | Isoform 8 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-2 | 9 | 1.63E-03 | Isoform 2 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-7 | 9 | 1.67E-03 | Isoform 7 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-13 | 9 | 2.11E-03 | Isoform 13 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| O43852-4 | 9 | 1.59E-03 | Isoform 4 of Calumenin OS=Homo sapiens OX=9606 GN=CALU |
| P09651-3 | 9 | 1.67E-04 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 |
| F8W646 | 9 | 1.44E-04 | Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=1 |
| P09651-2 | 9 | 1.39E-04 | Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 |
| F8VTQ5 | 9 | 2.45E-04 | Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=1 |
| Q32P51 | 9 | 1.12E-04 | Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens OX=9606 GN=HNRNPA1L2 PE=2 SV=2 |
| F8VZ49 | 9 | 1.56E-04 | Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=1 |
| P09651 | 9 | 1.20E-04 | Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=5; Additional IDs concatenated into MaxParsimony group: P09651-2, Q32P51, F8W6I7, P09651-3, F8VZ49, F8VTQ5, F8W646 |
| F8W6I7 | 9 | 1.45E-04 | Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=2 |
| Q8NHP8-2 | 9 | 1.59E-04 | Isoform 2 of Putative phospholipase B-like 2 OS=Homo sapiens OX=9606 GN=PLBD2 |
| Q8NHP8 | 9 | 1.98E-04 | Putative phospholipase B-like 2 OS=Homo sapiens OX=9606 GN=PLBD2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q8NHP8-2, H0YIX0 |
| H0YIX0 | 9 | 6.33E-04 | Putative phospholipase B-like 2 (Fragment) OS=Homo sapiens OX=9606 GN=PLBD2 PE=1 SV=1 |
| A0A087WTP3 | 9 | 4.05E-04 | Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q92945 |
| Q92945 | 9 | 4.05E-04 | Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=4 |
| Q07157 | 7 | 2.83E-05 | Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=3 |
| H0YKB1 | 7 | 6.96E-05 | Tight junction protein 1 (Zona occludens 1), isoform CRA\_d OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=1 |
| H0YLT6 | 7 | 1.10E-04 | Tight junction protein ZO-1 (Fragment) OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=1 |
| G5E9E7 | 7 | 2.92E-05 | Tight junction protein 1 (Zona occludens 1), isoform CRA\_e OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=1 |
| A0A087X0K9 | 7 | 2.95E-05 | Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=1 |
| Q07157-2 | 7 | 2.96E-05 | Isoform Short of Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 |
| G3V1L9 | 7 | 2.80E-05 | Tight junction protein 1 (Zona occludens 1), isoform CRA\_a OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q07157, G5E9E7, A0A087X0K9, Q07157-2, H0YKB1, H0YLT6 |
| E9PL09 | 8 | 3.08E-04 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| P23396-2 | 8 | 2.75E-04 | Isoform 2 of 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3; Additional IDs concatenated into MaxParsimony group: P23396, E9PL09, H0YEU2, E9PPU1, H0YCJ7, E9PK82, H0YF32, F2Z2S8, E9PJH4, E9PQ96 |
| P23396 | 8 | 2.97E-04 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=2 |
| E9PPU1 | 8 | 4.57E-04 | 40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| H0YEU2 | 8 | 0.000416714 | 40S ribosomal protein S3 (Fragment) OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1 |
| F5GZQ4 | 8 | 0.000176597 | L-lactate dehydrogenase A chain (Fragment) OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=1 |
| F5GXH2 | 9 | 5.69E-04 | L-lactate dehydrogenase A chain (Fragment) OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=1 |
| A0A087WUM2 | 9 | 2.63E-04 | L-lactate dehydrogenase OS=Homo sapiens OX=9606 GN=LDHAL6A PE=1 SV=1 |
| F5H5J4 | 9 | 0.000193461 | L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=1 |
| P00338 | 9 | 6.54E-04 | L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=2 |
| F5GXY2 | 9 | 0.000415978 | L-lactate dehydrogenase A chain (Fragment) OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=8 |
| P00338-4 | 9 | 0.000618286 | Isoform 4 of L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA |
| F5H6W8 | 9 | 1.83E-04 | L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=1 |
| Q6ZMR3 | 9 | 0.00018461 | L-lactate dehydrogenase A-like 6A OS=Homo sapiens OX=9606 GN=LDHAL6A PE=2 SV=1 |
| Q9BYZ2 | 9 | 1.25E-04 | L-lactate dehydrogenase A-like 6B OS=Homo sapiens OX=9606 GN=LDHAL6B PE=1 SV=3 |
| P00338-5 | 9 | 3.50E-04 | Isoform 5 of L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA |
| F5GYU2 | 9 | 4.51E-04 | L-lactate dehydrogenase A chain (Fragment) OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=1 |
| P00338-2 | 9 | 3.08E-04 | Isoform 2 of L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA |
| P00338-3 | 9 | 6.01E-04 | Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA; Additional IDs concatenated into MaxParsimony group: P00338, P00338-4, P00338-2, P00338-5, F5GXY2, F5GYU2, F5GXH2, Q9BYZ2, Q6ZMR3, A0A087WUM2, F5H6W8, F5H5J4, F5GZQ4 |
| K7ERS8 | 9 | 1.90E-03 | Alpha-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=9 |
| A0A2R8Y798 | 9 | 2.02E-03 | Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1 |
| K7EM90 | 9 | 1.29E-03 | Alpha-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1 |
| P06733-2 | 9 | 5.48E-04 | Isoform MBP-1 of Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 |
| P06733 | 9 | 9.23E-04 | Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A2R8Y6G6, P09104-2, F5H0C8, K7EM90, P06733-2, A0A2R8YEM5, A0A2R8Y879, A0A2R8YEG5, K7ERS8, A0A2R8Y798, U3KQP4 |
| A0A2R8YEM5 | 9 | 1.25E-03 | Alpha-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1 |
| P09104 | 9 | 1.14E-03 | Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=3 |
| A0A2R8YEG5 | 9 | 1.40E-03 | Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1 |
| A0A2R8Y6G6 | 9 | 8.86E-04 | Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1 |
| A0A2R8Y879 | 9 | 0.001710213 | Alpha-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1 |
| U3KQP4 | 8 | 0.000617567 | Gamma-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=1 |
| F5H0C8 | 9 | 0.001374089 | Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=1 |
| P09104-2 | 9 | 0.00118808 | Isoform 2 of Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 |
| P22314-2 | 9 | 1.14E-04 | Isoform 2 of Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 |
| P22314 | 9 | 1.10E-04 | Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: contaminant\_UBIQUITIN02, P22314-2, Q5JRR6 |
| contaminant\_UBIQUITIN02 | 9 | 1.10E-04 |  |
| Q5JRR6 | 8 | 9.55E-05 | Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=1 |
| P31942-5 | 8 | 2.64E-04 | Isoform 5 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 |
| P31942-3 | 8 | 1.60E-04 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 |
| P31942 | 8 | 1.37E-04 | Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P31942-2, P31942-3, P31942-4, P31942-5, P31942-6 |
| P31942-6 | 8 | 2.76E-04 | Isoform 6 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 |
| P31942-2 | 8 | 1.43E-04 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 |
| P31942-4 | 8 | 2.21E-04 | Isoform 4 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 |
| P51149 | 8 | 1.67E-04 | Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9J592 |
| C9J592 | 8 | 1.75E-04 | Ras-related protein Rab-7a (Fragment) OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 |
| J3KTA4 | 7 | 7.95E-05 | Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1 |
| A0A1X7SBZ2 | 7 | 5.57E-05 | Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=1 |
| Q92841-1 | 7 | 4.66E-05 | Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 |
| Q92841-2 | 7 | 4.64E-05 | Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 |
| A0A1W2PQ51 | 7 | 5.56E-05 | Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A1X7SBZ2, Q92841, Q92841-2, Q92841-3, Q92841-1, J3KTA4, P17844, P17844-2 |
| P17844 | 7 | 7.95E-05 | Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1 |
| P17844-2 | 7 | 9.12E-05 | Isoform 2 of Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 |
| Q92841 | 7 | 5.57E-05 | Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=2 |
| Q92841-3 | 7 | 4.64E-05 | Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 |
| Q96B54 | 9 | 2.01E-04 | Zinc finger protein 428 OS=Homo sapiens OX=9606 GN=ZNF428 PE=1 SV=2 |
| M0QXZ5 | 9 | 1.73E-04 | Zinc finger protein 428 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF428 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q96B54 |
| P02751-13 | 9 | 9.32E-05 | Isoform 13 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-4 | 9 | 6.62E-05 | Isoform 4 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-8 | 9 | 9.20E-05 | Isoform 8 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| H0Y7Z1 | 9 | 1.22E-04 | Fibronectin (Fragment) OS=Homo sapiens OX=9606 GN=FN1 PE=1 SV=1 |
| P02751 | 9 | 8.99E-05 | Fibronectin OS=Homo sapiens OX=9606 GN=FN1 PE=1 SV=4 |
| P02751-6 | 9 | 6.15E-05 | Isoform 6 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-15 | 9 | 8.66E-05 | Isoform 15 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1; Additional IDs concatenated into MaxParsimony group: P02751-7, P02751, P02751-3, P02751-17, P02751-8, P02751-13, P02751-14, P02751-9, P02751-5, P02751-10, H0Y7Z1, P02751-11, P02751-6, P02751-4 |
| P02751-5 | 9 | 9.70E-05 | Isoform 5 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-17 | 9 | 9.20E-05 | Isoform 17 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-11 | 9 | 8.08E-05 | Isoform 11 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-3 | 9 | 9.11E-05 | Isoform 3 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-7 | 9 | 8.77E-05 | Isoform 7 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-14 | 9 | 9.33E-05 | Isoform 14 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-9 | 9 | 9.43E-05 | Isoform 9 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P02751-10 | 9 | 9.71E-05 | Isoform 10 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| E9PPR1 | 8 | 1.95E-04 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| E9PQ49 | 8 | 1.63E-04 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=8 |
| E9PI39 | 8 | 0.000158656 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| P29692-3 | 8 | 1.28E-04 | Isoform 3 of Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D |
| A0A087X1X7 | 8 | 5.13E-05 | Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| P29692-2 | 8 | 5.74E-05 | Isoform 2 of Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D |
| E9PRY8 | 8 | 5.33E-05 | Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P29692-2, A0A087X1X7, P29692, E9PK01, P29692-3, H0YCK7, E9PI39, E9PQ49, E9PL71, E9PL12, E9PPR1, E9PIZ1, E9PMW7, E9PN91 |
| E9PIZ1 | 8 | 2.36E-04 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| E9PN91 | 8 | 2.66E-04 | Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| E9PMW7 | 8 | 2.49E-04 | Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| E9PL12 | 8 | 1.93E-04 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| H0YCK7 | 8 | 1.54E-04 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| E9PL71 | 8 | 1.51E-04 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| E9PK01 | 8 | 1.24E-04 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| P29692 | 8 | 1.32E-04 | Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=5 |
| P14314 | 9 | 2.44E-04 | Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=2 |
| P14314-2 | 9 | 2.45E-04 | Isoform 2 of Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH |
| K7ELL7 | 9 | 2.41E-04 | Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P14314, P14314-2 |
| A8MU27 | 8 | 6.21E-04 | Small ubiquitin-related modifier 3 OS=Homo sapiens OX=9606 GN=SUMO3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P55854-2, A8MUA9, P55854, Q6EEV6, P61956, P61956-2 |
| Q6EEV6 | 8 | 8.35E-04 | Small ubiquitin-related modifier 4 OS=Homo sapiens OX=9606 GN=SUMO4 PE=1 SV=2 |
| P55854-2 | 8 | 6.14E-04 | Isoform 2 of Small ubiquitin-related modifier 3 OS=Homo sapiens OX=9606 GN=SUMO3 |
| P55854 | 8 | 8.86E-04 | Small ubiquitin-related modifier 3 OS=Homo sapiens OX=9606 GN=SUMO3 PE=1 SV=2 |
| P61956 | 8 | 1.04E-03 | Small ubiquitin-related modifier 2 OS=Homo sapiens OX=9606 GN=SUMO2 PE=1 SV=3 |
| A8MUA9 | 8 | 6.76E-04 | SMT3 suppressor of mif two 3 homolog 3 (Yeast), isoform CRA\_d OS=Homo sapiens OX=9606 GN=SUMO3 PE=1 SV=1 |
| P61956-2 | 8 | 1.33E-03 | Isoform 2 of Small ubiquitin-related modifier 2 OS=Homo sapiens OX=9606 GN=SUMO2 |
| A0A0B4J269 | 9 | 1.00E-03 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=1 SV=1 |
| A6NNZ2 | 9 | 6.49E-04 | Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens OX=9606 PE=1 SV=1 |
| G3V2N6 | 9 | 2.61E-03 | HCG1983504, isoform CRA\_d OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=1 |
| M0QZL7 | 8 | 2.66E-04 | Tubulin beta-4A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=8 |
| M0QY85 | 8 | 3.91E-04 | Tubulin beta-4A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| Q13885 | 9 | 1.94E-03 | Tubulin beta-2A chain OS=Homo sapiens OX=9606 GN=TUBB2A PE=1 SV=1 |
| Q9BUF5 | 9 | 5.96E-04 | Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| Q5SQY0 | 9 | 6.21E-04 | Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB8 PE=1 SV=1 |
| P07437 | 9 | 0.002617847 | Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q5JP53, Q13885, P04350, Q5ST81, A0A0B4J269, Q13509, Q9BUF5, A6NNZ2, Q3ZCM7, K7ESM5, Q5SQY0, A0A075B736, Q13509-2, M0QYM7, M0R2D3, M0R278, G3V2N6, M0QZL7, G3V3R4, M0R042, G3V2R8, M0QX14, M0QY37, M0QY85, M0R0X0, G3V5W4, Q9H4B7, A0A075B724 |
| A0A075B736 | 9 | 6.25E-04 | Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB8 PE=1 SV=1 |
| M0R2D3 | 8 | 1.22E-03 | Tubulin beta-4A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| P68371 | 9 | 1.40E-03 | Tubulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1 |
| P04350 | 9 | 1.28E-03 | Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=2 |
| Q5ST81 | 9 | 1.67E-03 | Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=1 |
| K7ESM5 | 9 | 7.85E-04 | Tubulin beta chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 |
| Q13509 | 9 | 1.77E-03 | Tubulin beta-3 chain OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=2 |
| Q9BVA1 | 9 | 1.95E-03 | Tubulin beta-2B chain OS=Homo sapiens OX=9606 GN=TUBB2B PE=1 SV=1 |
| M0QY37 | 8 | 3.42E-04 | Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| Q5JP53 | 9 | 2.73E-03 | Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=1 |
| G3V2R8 | 9 | 3.62E-03 | HCG1983504, isoform CRA\_e OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=1 |
| Q3ZCM7 | 9 | 6.63E-04 | Tubulin beta-8 chain OS=Homo sapiens OX=9606 GN=TUBB8 PE=1 SV=2 |
| G3V5W4 | 9 | 4.41E-03 | Tubulin beta-3 chain OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=1 |
| Q13509-2 | 9 | 9.77E-04 | Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens OX=9606 GN=TUBB3 |
| Q9H4B7 | 9 | 3.81E-04 | Tubulin beta-1 chain OS=Homo sapiens OX=9606 GN=TUBB1 PE=1 SV=1 |
| M0QX14 | 8 | 3.39E-04 | Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| M0R0X0 | 8 | 3.62E-04 | Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| A0A075B724 | 8 | 2.80E-04 | Tubulin beta-8 chain OS=Homo sapiens OX=9606 GN=TUBB8 PE=1 SV=1 |
| M0R042 | 8 | 8.13E-04 | Tubulin beta chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| M0QYM7 | 8 | 7.56E-04 | Tubulin beta-4A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=8 |
| G3V3R4 | 9 | 2.89E-03 | HCG1983504, isoform CRA\_c OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=1 |
| M0R278 | 8 | 2.50E-04 | Tubulin beta-4A chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=1 |
| E9PEX6 | 8 | 1.57E-04 | Dihydrolipoyl dehydrogenase OS=Homo sapiens OX=9606 GN=DLD PE=1 SV=1 |
| P09622-3 | 8 | 1.65E-04 | Isoform 3 of Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=DLD |
| P09622 | 8 | 1.50E-04 | Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=DLD PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PEX6, P09622-3, P09622-2 |
| P09622-2 | 8 | 1.86E-04 | Isoform 2 of Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=DLD |
| P62258 | 9 | 3.53E-03 | 14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P63104, P62258-2, P63104-2, B0AZS6, H0YB80, B7Z2E6, K7EM20, P31946-2, I3L3T1, B4DJF2, P31947, Q04917, P31947-2, E9PG15, E7ESK7, K7EIT4, E7EVZ2, E9PD24, E5RIR4, E5RGE1 |
| K7EM20 | 9 | 4.56E-03 | 14-3-3 protein epsilon (Fragment) OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1 |
| B0AZS6 | 9 | 3.11E-03 | cDNA, FLJ79516, highly similar to 14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| E7EX29 | 9 | 2.88E-03 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| E9PD24 | 9 | 2.02E-03 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| P31946 | 9 | 1.72E-03 | 14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=3 |
| B4DJF2 | 9 | 3.51E-03 | cDNA FLJ51975, moderately similar to 14-3-3 protein epsilon (14-3-3E) OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1 |
| P31947 | 9 | 1.23E-03 | 14-3-3 protein sigma OS=Homo sapiens OX=9606 GN=SFN PE=1 SV=1 |
| E9PG15 | 9 | 5.80E-04 | 14-3-3 protein theta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1 |
| K7EIT4 | 9 | 2.08E-03 | 14-3-3 protein epsilon (Fragment) OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1 |
| Q04917 | 9 | 1.27E-03 | 14-3-3 protein eta OS=Homo sapiens OX=9606 GN=YWHAH PE=1 SV=4 |
| I3L3T1 | 9 | 3.09E-03 | 14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1 |
| P63104 | 9 | 2.89E-03 | 14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| E5RIR4 | 9 | 2.48E-03 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| P31947-2 | 9 | 1.41E-03 | Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens OX=9606 GN=SFN |
| P61981 | 9 | 1.45E-03 | 14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2 |
| P27348 | 9 | 1.74E-03 | 14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1 |
| P63104-2 | 9 | 3.06E-03 | Isoform 2 of 14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ |
| P31946-2 | 9 | 1.73E-03 | Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB |
| B7Z2E6 | 9 | 4.09E-03 | cDNA FLJ50142, highly similar to 14-3-3 protein zeta/delta (Protein kinase Cinhibitor protein 1) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| P62258-2 | 9 | 3.38E-03 | Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE |
| E7EVZ2 | 9 | 1.90E-03 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| E7ESK7 | 9 | 1.44E-03 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| H0YB80 | 9 | 3.93E-03 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 |
| E5RGE1 | 9 | 2.80E-03 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=8 |
| I3L0S5 | 8 | 1.52E-03 | Lysosomal alpha-glucosidase (Fragment) OS=Homo sapiens OX=9606 GN=GAA PE=1 SV=1 |
| P10253 | 9 | 7.55E-04 | Lysosomal alpha-glucosidase OS=Homo sapiens OX=9606 GN=GAA PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: I3L3L3, I3L0S5 |
| I3L3L3 | 8 | 1.12E-03 | Lysosomal alpha-glucosidase (Fragment) OS=Homo sapiens OX=9606 GN=GAA PE=1 SV=8 |
| O43707-2 | 9 | 3.33E-04 | Isoform ACTN4ISO of Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 |
| P12814-2 | 9 | 1.30E-04 | Isoform 2 of Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 |
| H7C5W8 | 9 | 2.69E-04 | Alpha-actinin-1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1 |
| H0YJ11 | 9 | 3.86E-04 | Alpha-actinin-1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1 |
| P12814-4 | 9 | 1.24E-04 | Isoform 4 of Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 |
| P12814 | 9 | 1.29E-04 | Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=2 |
| F5GXS2 | 9 | 4.33E-04 | Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2 |
| H0YJW3 | 9 | 3.63E-04 | Alpha-actinin-1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1 |
| H7C144 | 9 | 5.55E-04 | Alpha-actinin-4 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=1 |
| P12814-3 | 9 | 1.26E-04 | Isoform 3 of Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 |
| O43707 | 9 | 2.54E-04 | Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: O43707-2, F5GXS2, O43707-3, H7C144, P12814-4, P12814-3, P12814, P12814-2, H9KV75, H7C5W8, H0YJW3, H0YJ11 |
| O43707-3 | 9 | 4.33E-04 | Isoform 3 of Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 |
| H9KV75 | 9 | 1.13E-04 | Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1 |
| B1AHC9 | 9 | 8.13E-05 | X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=1 |
| P12956 | 9 | 7.69E-05 | X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P12956-2, B1AHC9 |
| P12956-2 | 9 | 8.09E-05 | Isoform 2 of X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 |
| P30048-2 | 9 | 3.00E-04 | Isoform 2 of Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens OX=9606 GN=PRDX3 |
| P30048 | 9 | 2.79E-04 | Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens OX=9606 GN=PRDX3 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P30048-2 |
| B4E1S2 | 9 | 1.65E-03 | Annexin OS=Homo sapiens OX=9606 GN=ANXA4 PE=1 SV=1 |
| Q6P452 | 9 | 1.94E-03 | Annexin OS=Homo sapiens OX=9606 GN=ANXA4 PE=1 SV=1 |
| P09525 | 9 | 1.82E-03 | Annexin A4 OS=Homo sapiens OX=9606 GN=ANXA4 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: Q6P452, P09525-2, B4E1S2 |
| P09525-2 | 9 | 2.29E-03 | Isoform 2 of Annexin A4 OS=Homo sapiens OX=9606 GN=ANXA4 |
| P01011 | 9 | 0.00024896 | Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: G3V3A0 |
| G3V3A0 | 9 | 4.09E-04 | Alpha-1-antichymotrypsin OS=Homo sapiens OX=9606 GN=SERPINA3 PE=1 SV=1 |
| D6RGZ6 | 8 | 2.21E-04 | Versican core protein (Fragment) OS=Homo sapiens OX=9606 GN=VCAN PE=1 SV=1 |
| P13611-2 | 8 | 1.33E-04 | Isoform V1 of Versican core protein OS=Homo sapiens OX=9606 GN=VCAN |
| P13611 | 8 | 1.12E-04 | Versican core protein OS=Homo sapiens OX=9606 GN=VCAN PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P13611-5, P13611-2, D6RGZ6 |
| P13611-5 | 8 | 1.13E-04 | Isoform Vint of Versican core protein OS=Homo sapiens OX=9606 GN=VCAN |
| F5GXK7 | 9 | 2.67E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=2 |
| F5GYU3 | 9 | 3.36E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1 |
| B4DV12 | 9 | 2.94E-02 | Polyubiquitin-B OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1 |
| contaminant\_UBIQUITIN08 | 9 | 5.93E-02 |  |
| F5H388 | 9 | 2.91E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1 |
| P0CG47 | 9 | 1.97E-02 | Polyubiquitin-B OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1 |
| M0R1V7 | 9 | 5.99E-02 | Ubiquitin-60S ribosomal protein L40 (Fragment) OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=1 |
| M0R1M6 | 8 | 2.87E-02 | Ubiquitin-60S ribosomal protein L40 (Fragment) OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=1 |
| Q49A90 | 9 | 3.97E-02 | RPS27A protein OS=Homo sapiens OX=9606 GN=RPS27A PE=2 SV=1 |
| F5H2Z3 | 9 | 3.31E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1 |
| J3QSA3 | 9 | 5.95E-02 | Polyubiquitin-B (Fragment) OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1 |
| F5H6Q2 | 9 | 3.69E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=8 |
| P62979 | 9 | 2.89E-02 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens OX=9606 GN=RPS27A PE=1 SV=2 |
| Q96C32 | 9 | 1.48E-02 | Polyubiquitin-C OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1 |
| F5H747 | 9 | 2.82E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=8 |
| J3QTR3 | 9 | 4.25E-02 | Ubiquitin-40S ribosomal protein S27a (Fragment) OS=Homo sapiens OX=9606 GN=RPS27A PE=1 SV=1 |
| P0CG48 | 9 | 6.58E-03 | Polyubiquitin-C OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q96C32, Q5PY61, P0CG47, J3QKN0, F5GXK7, F5H747, P62979, F5H388, B4DV12, F5H265, F5H2Z3, F5GYU3, P62987, F5H6Q2, J3QTR3, Q49A90, J3QS39, contaminant\_UBIQUITIN08, M0R1V7, A0A2R8Y422, M0R2S1, M0R1M6, F5GZ39, J3QSA3 |
| F5GZ39 | 9 | 4.27E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1 |
| Q5PY61 | 9 | 1.97E-02 | Polyubiquitin-C OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1 |
| J3QKN0 | 9 | 2.19E-02 | Polyubiquitin-B (Fragment) OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1 |
| P62987 | 9 | 3.52E-02 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=2 |
| F5H265 | 9 | 3.02E-02 | Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1 |
| A0A2R8Y422 | 8 | 2.10E-02 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |
| J3QS39 | 9 | 4.84E-02 | Polyubiquitin-B (Fragment) OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1 |
| M0R2S1 | 8 | 2.37E-02 | Ubiquitin-60S ribosomal protein L40 (Fragment) OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=1 |
| Q9BTM1 | 9 | 1.85E-02 | Histone H2A.J OS=Homo sapiens OX=9606 GN=H2AFJ PE=1 SV=1 |
| H0YFX9 | 9 | 1.18E-02 | Histone H2A (Fragment) OS=Homo sapiens OX=9606 GN=H2AFJ PE=1 SV=1 |
| Q96KK5 | 9 | 1.86E-02 | Histone H2A type 1-H OS=Homo sapiens OX=9606 GN=HIST1H2AH PE=1 SV=3 |
| A0A0U1RRH7 | 9 | 1.40E-02 | Histone H2A OS=Homo sapiens OX=9606 PE=3 SV=1 |
| Q7L7L0 | 9 | 1.83E-02 | Histone H2A type 3 OS=Homo sapiens OX=9606 GN=HIST3H2A PE=1 SV=3 |
| P0C0S5 | 9 | 1.66E-02 | Histone H2A.Z OS=Homo sapiens OX=9606 GN=H2AFZ PE=1 SV=2 |
| C9J386 | 8 | 7.99E-03 | Histone H2A OS=Homo sapiens OX=9606 GN=H2AFV PE=3 SV=1 |
| Q96QV6 | 9 | 1.83E-02 | Histone H2A type 1-A OS=Homo sapiens OX=9606 GN=HIST1H2AA PE=1 SV=3 |
| P0C0S8 | 9 | 1.84E-02 | Histone H2A type 1 OS=Homo sapiens OX=9606 GN=HIST1H2AG PE=1 SV=2 |
| Q71UI9-2 | 9 | 1.86E-02 | Isoform 2 of Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AFV |
| P20671 | 9 | 1.83E-02 | Histone H2A type 1-D OS=Homo sapiens OX=9606 GN=HIST1H2AD PE=1 SV=2 |
| Q8IUE6 | 8 | 1.19E-02 | Histone H2A type 2-B OS=Homo sapiens OX=9606 GN=HIST2H2AB PE=1 SV=3 |
| Q16777 | 9 | 1.85E-02 | Histone H2A type 2-C OS=Homo sapiens OX=9606 GN=HIST2H2AC PE=1 SV=4 |
| Q9BTM1-2 | 9 | 1.41E-02 | Isoform 2 of Histone H2A.J OS=Homo sapiens OX=9606 GN=H2AFJ |
| C9J0D1 | 9 | 1.74E-02 | Histone H2A OS=Homo sapiens OX=9606 GN=H2AFV PE=1 SV=1 |
| Q71UI9 | 9 | 0.016623481 | Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AFV PE=1 SV=3 |
| Q71UI9-4 | 8 | 6.01E-03 | Isoform 4 of Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AFV |
| A0A0U1RR32 | 9 | 1.41E-02 | Histone H2A OS=Homo sapiens OX=9606 GN=hCG\_2039566 PE=3 SV=1 |
| Q93077 | 9 | 1.83E-02 | Histone H2A type 1-C OS=Homo sapiens OX=9606 GN=HIST1H2AC PE=1 SV=3 |
| P04908 | 9 | 1.83E-02 | Histone H2A type 1-B/E OS=Homo sapiens OX=9606 GN=HIST1H2AB PE=1 SV=2 |
| Q71UI9-3 | 8 | 6.81E-03 | Isoform 3 of Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AFV |
| P16104 | 9 | 1.67E-02 | Histone H2AX OS=Homo sapiens OX=9606 GN=H2AFX PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q96QV6, A0A0U1RRH7, A0A0U1RR32, P04908, Q93077, P20671, Q6FI13, P0C0S8, Q7L7L0, Q16777, Q9BTM1, Q99878, Q96KK5, P0C0S5, C9J0D1, Q71UI9-2, H0YFX9, Q9BTM1-2, Q71UI9-4, Q71UI9-3, C9J386 |
| Q99878 | 9 | 1.86E-02 | Histone H2A type 1-J OS=Homo sapiens OX=9606 GN=HIST1H2AJ PE=1 SV=3 |
| Q6FI13 | 9 | 1.84E-02 | Histone H2A type 2-A OS=Homo sapiens OX=9606 GN=HIST2H2AA3 PE=1 SV=3 |
| Q13228-2 | 9 | 6.17E-03 | Isoform 2 of Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 |
| C9JVL0 | 9 | 5.64E-03 | Methanethiol oxidase (Fragment) OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=8 |
| F2Z2W8 | 9 | 7.94E-03 | Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=1 |
| F8WCR4 | 9 | 5.92E-03 | Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=1 |
| H0Y532 | 9 | 3.82E-03 | Methanethiol oxidase (Fragment) OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=8 |
| Q13228 | 9 | 6.29E-03 | Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=2 |
| A6PVX1 | 9 | 5.69E-03 | Methanethiol oxidase (Fragment) OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=1 |
| Q13228-4 | 9 | 5.77E-03 | Isoform 4 of Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1; Additional IDs concatenated into MaxParsimony group: Q13228, Q13228-2, Q13228-3, A6PVX1, H0Y532, F8WCR4, F2Z2W8, C9JVL0 |
| Q13228-3 | 9 | 5.28E-03 | Isoform 3 of Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 |
| Q08380 | 9 | 5.45E-03 | Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: K7EP36, K7EKQ5, K7ESM3, K7EJY8 |
| K7EKQ5 | 9 | 6.37E-03 | Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| K7ESM3 | 9 | 6.40E-03 | Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| K7EJY8 | 9 | 0.008525838 | Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| K7EP36 | 9 | 6.33E-03 | Galectin-3-binding protein (Fragment) OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1 |
| A0A087WZ51 | 9 | 1.35E-03 | Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 PE=1 SV=1 |
| O43399-4 | 9 | 1.07E-03 | Isoform 4 of Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 |
| O43399-2 | 9 | 1.15E-03 | Isoform 2 of Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 |
| O43399-7 | 9 | 9.35E-04 | Isoform 7 of Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2; Additional IDs concatenated into MaxParsimony group: A0A087WYR3, O43399-5, O43399-3, O43399, O43399-4, O43399-2, A0A087WZ51, O43399-6 |
| O43399-6 | 9 | 9.26E-04 | Isoform 6 of Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 |
| O43399-5 | 9 | 9.74E-04 | Isoform 5 of Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 |
| O43399 | 9 | 1.04E-03 | Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 PE=1 SV=2 |
| O43399-3 | 9 | 1.02E-03 | Isoform 3 of Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 |
| A0A087WYR3 | 9 | 9.65E-04 | Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 PE=1 SV=1 |
| P25705 | 9 | 2.04E-03 | ATP synthase subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P25705-2, K7ERX7, P25705-3, K7EK77, K7EJP1, K7EQH4, K7ENJ4, K7ESA0 |
| K7EJP1 | 9 | 5.76E-03 | ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=8 |
| K7ESA0 | 9 | 7.40E-03 | ATP synthase subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1 |
| K7EQH4 | 9 | 7.47E-03 | ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1 |
| P25705-3 | 9 | 1.82E-03 | Isoform 3 of ATP synthase subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A |
| K7ENJ4 | 9 | 4.78E-04 | ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1 |
| K7ERX7 | 9 | 5.34E-03 | ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1 |
| K7EK77 | 9 | 4.21E-03 | ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1 |
| P25705-2 | 9 | 1.79E-03 | Isoform 2 of ATP synthase subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A |
| P20962 | 9 | 7.61E-02 | Parathymosin OS=Homo sapiens OX=9606 GN=PTMS PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F5GXR3, F5H7R9 |
| F5H7R9 | 9 | 5.66E-02 | Parathymosin (Fragment) OS=Homo sapiens OX=9606 GN=PTMS PE=1 SV=1 |
| F5GXR3 | 9 | 3.10E-02 | Parathymosin OS=Homo sapiens OX=9606 GN=PTMS PE=1 SV=1 |
| Q14257 | 9 | 2.80E-04 | Reticulocalbin-2 OS=Homo sapiens OX=9606 GN=RCN2 PE=1 SV=1 |
| A8MXP8 | 9 | 2.79E-04 | Reticulocalbin-2 OS=Homo sapiens OX=9606 GN=RCN2 PE=1 SV=1 |
| Q14257-2 | 9 | 2.65E-04 | Isoform 2 of Reticulocalbin-2 OS=Homo sapiens OX=9606 GN=RCN2; Additional IDs concatenated into MaxParsimony group: Q14257, A8MXP8 |
| H3BUK7 | 9 | 1.03E-03 | Major vault protein (Fragment) OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=1 |
| H3BNF6 | 9 | 7.62E-04 | Major vault protein (Fragment) OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=1 |
| H3BRL2 | 9 | 7.54E-04 | Major vault protein (Fragment) OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=8 |
| Q14764 | 9 | 4.05E-04 | Major vault protein OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: H3BQK6, H3BRL2, H3BNF6, H3BUK7, H3BP76 |
| H3BQK6 | 9 | 5.13E-04 | Major vault protein (Fragment) OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=1 |
| P52272 | 9 | 3.75E-04 | Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A0A087X0X3, P52272-2, M0QZM1, M0R2I7, M0QY96 |
| P52272-2 | 9 | 3.96E-04 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM |
| M0QZM1 | 9 | 6.41E-04 | Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1 |
| A0A087X0X3 | 9 | 3.75E-04 | Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1 |
| M0R2I7 | 9 | 8.22E-04 | Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1 |
| M0QY96 | 8 | 6.41E-04 | Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1 |
| P02671-2 | 8 | 3.59E-04 | Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA |
| P02671 | 8 | 2.67E-04 | Fibrinogen alpha chain OS=Homo sapiens OX=9606 GN=FGA PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P02671-2 |
| A0A2R8Y5C3 | 9 | 8.20E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| A0A2R8Y7Z0 | 9 | 5.52E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| A0A2R8Y5A3 | 9 | 8.04E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P35222, A0A2R8YCH5, B4DGU4, A0A2R8Y5Z1, A0A2R8Y750, A0A2R8Y5C3, A0A2R8Y543, A0A2R8Y804, A0A2R8Y7Z0 |
| A0A2R8YCH5 | 9 | 8.08E-05 | Catenin beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| A0A2R8Y5Z1 | 9 | 8.17E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| P35222 | 9 | 8.06E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| A0A2R8Y543 | 9 | 8.80E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| B4DGU4 | 9 | 8.13E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| A0A2R8Y804 | 9 | 8.96E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| A0A2R8Y750 | 9 | 8.13E-05 | Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1 |
| Q7Z3Y7 | 9 | 8.97E-04 | Keratin, type I cytoskeletal 28 OS=Homo sapiens OX=9606 GN=KRT28 PE=1 SV=2 |
| P02533 | 9 | 7.63E-04 | Keratin, type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4 |
| contaminant\_KERATIN03 | 9 | 2.27E-03 | ; Additional IDs concatenated into MaxParsimony group: P13645, contaminant\_KERATIN07, P02533, contaminant\_KERATIN05, contaminant\_KERATIN08, P13646, contaminant\_KERATIN06, P19012, P13646-3, K7ERE3, P13646-2, K7EMD9, Q2M2I5, Q7Z3Y7, Q7Z3Y8, contaminant\_KERATIN04, Q04695, contaminant\_KERATIN12, P08727, contaminant\_KERATIN10, F5GWP8, K7EPJ9, C9JM50, Q7Z3Z0 |
| Q7Z3Y8 | 8 | 5.14E-04 | Keratin, type I cytoskeletal 27 OS=Homo sapiens OX=9606 GN=KRT27 PE=1 SV=2 |
| contaminant\_KERATIN08 | 9 | 7.68E-04 |  |
| P08779 | 9 | 7.61E-04 | Keratin, type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4 |
| P13645 | 9 | 2.30E-03 | Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6 |
| contaminant\_KERATIN05 | 9 | 7.64E-04 |  |
| Q7Z3Z0 | 8 | 4.04E-04 | Keratin, type I cytoskeletal 25 OS=Homo sapiens OX=9606 GN=KRT25 PE=1 SV=1 |
| P04062 | 8 | 4.12E-04 | Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A0A0G2JLB3, P04062-2, P04062-5, A0A0G2JNZ0, P04062-4, A0A0G2JNZ5 |
| P04062-5 | 8 | 4.39E-04 | Isoform 5 of Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA |
| A0A0G2JNZ0 | 8 | 4.39E-04 | Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA PE=1 SV=1 |
| A0A0G2JLB3 | 8 | 4.12E-04 | Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA PE=1 SV=1 |
| P04062-4 | 8 | 4.90E-04 | Isoform 4 of Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA |
| A0A0G2JNZ5 | 8 | 4.90E-04 | Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA PE=1 SV=1 |
| P04062-2 | 8 | 4.28E-04 | Isoform Short of Glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA |
| P51858-3 | 8 | 1.31E-03 | Isoform 3 of Hepatoma-derived growth factor OS=Homo sapiens OX=9606 GN=HDGF; Additional IDs concatenated into MaxParsimony group: P51858, P51858-2 |
| P51858-2 | 8 | 1.44E-03 | Isoform 2 of Hepatoma-derived growth factor OS=Homo sapiens OX=9606 GN=HDGF |
| P51858 | 8 | 1.40E-03 | Hepatoma-derived growth factor OS=Homo sapiens OX=9606 GN=HDGF PE=1 SV=1 |
| H0YIN9 | 8 | 2.68E-04 | Keratin, type II cytoskeletal 5 (Fragment) OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=1 |
| P02538 | 9 | 2.92E-04 | Keratin, type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3 |
| contaminant\_KERATIN22 | 9 | 1.55E-03 |  |
| Q5XKE5 | 9 | 2.57E-04 | Keratin, type II cytoskeletal 79 OS=Homo sapiens OX=9606 GN=KRT79 PE=1 SV=2 |
| P48668 | 9 | 2.92E-04 | Keratin, type II cytoskeletal 6C OS=Homo sapiens OX=9606 GN=KRT6C PE=1 SV=3 |
| H0YI76 | 9 | 5.36E-04 | Keratin, type II cytoskeletal 5 (Fragment) OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=1 |
| Q7Z794 | 9 | 2.90E-04 | Keratin, type II cytoskeletal 1b OS=Homo sapiens OX=9606 GN=KRT77 PE=2 SV=3 |
| P13647 | 9 | 2.53E-04 | Keratin, type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3 |
| contaminant\_KERATIN17 | 9 | 2.53E-04 |  |
| contaminant\_KERATIN21 | 9 | 4.61E-04 |  |
| P04264 | 9 | 2.79E-03 | Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6; Additional IDs concatenated into MaxParsimony group: P35908, contaminant\_KERATIN22, contaminant\_KERATIN13, P04259, Q01546, P48668, P02538, contaminant\_KERATIN18, Q5XKE5, contaminant\_KERATIN21, contaminant\_KERATIN14, contaminant\_KERATIN15, P12035, P13647, contaminant\_KERATIN17, O95678, H0YI76, H0YID6, Q7Z794, H0YIN9 |
| P35908 | 9 | 1.61E-03 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2 |
| O95678 | 9 | 1.95E-04 | Keratin, type II cytoskeletal 75 OS=Homo sapiens OX=9606 GN=KRT75 PE=1 SV=2 |
| P04259 | 9 | 5.59E-04 | Keratin, type II cytoskeletal 6B OS=Homo sapiens OX=9606 GN=KRT6B PE=1 SV=5 |
| contaminant\_KERATIN18 | 9 | 2.29E-04 |  |
| contaminant\_KERATIN13 | 9 | 2.26E-03 |  |
| B8ZZA1 | 9 | 5.77E-02 | Prothymosin alpha OS=Homo sapiens OX=9606 GN=PTMA PE=1 SV=1 |
| B8ZZQ6 | 9 | 7.05E-02 | Prothymosin alpha OS=Homo sapiens OX=9606 GN=PTMA PE=1 SV=1 |
| P06454 | 9 | 6.81E-02 | Prothymosin alpha OS=Homo sapiens OX=9606 GN=PTMA PE=1 SV=2 |
| P06454-2 | 9 | 6.88E-02 | Isoform 2 of Prothymosin alpha OS=Homo sapiens OX=9606 GN=PTMA |
| B8ZZW7 | 9 | 5.55E-02 | Prothymosin alpha OS=Homo sapiens OX=9606 GN=PTMA PE=1 SV=1 |
| H7C2N1 | 9 | 5.10E-02 | Prothymosin alpha (Fragment) OS=Homo sapiens OX=9606 GN=PTMA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: B8ZZW7, B8ZZA1, P06454, P06454-2, B8ZZQ6 |
| Q9UHD9 | 9 | 1.58E-04 | Ubiquilin-2 OS=Homo sapiens OX=9606 GN=UBQLN2 PE=1 SV=2 |
| Q9UMX0-3 | 9 | 2.83E-04 | Isoform 3 of Ubiquilin-1 OS=Homo sapiens OX=9606 GN=UBQLN1 |
| Q9UMX0 | 9 | 2.02E-04 | Ubiquilin-1 OS=Homo sapiens OX=9606 GN=UBQLN1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UMX0-2, Q9UMX0-3, Q9UHD9, Q9NRR5 |
| Q9NRR5 | 9 | 1.54E-04 | Ubiquilin-4 OS=Homo sapiens OX=9606 GN=UBQLN4 PE=1 SV=2 |
| Q9UMX0-2 | 9 | 2.12E-04 | Isoform 2 of Ubiquilin-1 OS=Homo sapiens OX=9606 GN=UBQLN1 |
| A0A0U1RRM4 | 9 | 3.25E-05 | Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P26599-3, P26599-2, P26599, A6NLN1, K7EK45 |
| P26599-2 | 9 | 3.47E-05 | Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 |
| A6NLN1 | 9 | 3.62E-05 | Polypyrimidine tract binding protein 1, isoform CRA\_b OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=4 |
| P26599-3 | 9 | 3.43E-05 | Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 |
| K7EK45 | 9 | 6.52E-05 | Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1 |
| P26599 | 9 | 3.60E-05 | Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1 |
| H7C1J8 | 9 | 2.59E-04 | Heterogeneous nuclear ribonucleoprotein A3 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA3 PE=1 SV=1 |
| P51991-2 | 9 | 1.45E-04 | Isoform 2 of Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3 |
| P51991 | 9 | 1.36E-04 | Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: P51991-2, H7C1J8 |
| P06744-2 | 9 | 2.56E-04 | Isoform 2 of Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI |
| A0A2U3TZU2 | 9 | 2.44E-04 | Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=4 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0A0MTS2, P06744-2, P06744 |
| A0A0A0MTS2 | 9 | 2.55E-04 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| P06744 | 9 | 2.62E-04 | Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4 |
| K7ERZ3 | 9 | 4.11E-04 | Perilipin-3 (Fragment) OS=Homo sapiens OX=9606 GN=PLIN3 PE=1 SV=1 |
| K7EL96 | 8 | 5.91E-04 | Perilipin-3 (Fragment) OS=Homo sapiens OX=9606 GN=PLIN3 PE=1 SV=8 |
| O60664-3 | 9 | 3.04E-04 | Isoform 3 of Perilipin-3 OS=Homo sapiens OX=9606 GN=PLIN3 |
| O60664-4 | 9 | 3.12E-04 | Isoform 4 of Perilipin-3 OS=Homo sapiens OX=9606 GN=PLIN3 |
| O60664 | 9 | 3.03E-04 | Perilipin-3 OS=Homo sapiens OX=9606 GN=PLIN3 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O60664-3, O60664-4, K7ERZ3, K7EL96 |
| P35527 | 9 | 5.13E-04 | Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: contaminant\_KERATIN02, K7EQQ3 |
| contaminant\_KERATIN02 | 9 | 5.14E-04 |  |
| K7EQQ3 | 8 | 3.32E-04 | Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=1 |
| P04406-2 | 9 | 4.91E-03 | Isoform 2 of Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH |
| E7EUT5 | 9 | 5.29E-03 | Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=1 |
| P04406 | 9 | 4.68E-03 | Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P04406-2, E7EUT5 |
| P07900 | 9 | 4.43E-04 | Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5 |
| P07900-2 | 9 | 3.80E-04 | Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1; Additional IDs concatenated into MaxParsimony group: P07900, Q58FG1 |
| E9PK25 | 9 | 5.76E-04 | Cofilin-1 OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P23528, G3V1A4 |
| G3V1A4 | 9 | 7.89E-04 | Cofilin 1 (Non-muscle), isoform CRA\_a OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=1 |
| P23528 | 9 | 7.08E-04 | Cofilin-1 OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=3 |
| E7ESE2 | 8 | 2.29E-04 | Prohibitin (Fragment) OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=2 |
| C9JW96 | 8 | 3.22E-04 | Prohibitin (Fragment) OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=2 |
| E9PCW0 | 8 | 2.14E-04 | Prohibitin (Fragment) OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=2 |
| P35232 | 9 | 4.12E-04 | Prohibitin OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: C9JW96, E9PCW0, E7ESE2, C9JZ20, P35232-2, D6RBK0 |
| P35232-2 | 7 | 1.92E-04 | Isoform 2 of Prohibitin OS=Homo sapiens OX=9606 GN=PHB |
| D6RBK0 | 7 | 1.91E-04 | Prohibitin (Fragment) OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=1 |
| C9JZ20 | 8 | 2.30E-04 | Prohibitin (Fragment) OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=1 |
| P62917 | 9 | 4.11E-04 | 60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: E9PKU4, E9PKZ0, E9PP36 |
| E9PKZ0 | 9 | 4.11E-04 | 60S ribosomal protein L8 (Fragment) OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=1 |
| E9PKU4 | 9 | 4.49E-04 | 60S ribosomal protein L8 (Fragment) OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=1 |
| E9PP36 | 9 | 5.71E-04 | 60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=1 |
| Q5T123 | 9 | 6.00E-03 | SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens OX=9606 GN=SH3BGRL3 PE=1 SV=1 |
| Q9H299 | 9 | 5.68E-03 | SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens OX=9606 GN=SH3BGRL3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5T123 |
| P61088 | 9 | 1.85E-03 | Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens OX=9606 GN=UBE2N PE=1 SV=1 |
| Q5JXB2 | 9 | 1.76E-03 | Putative ubiquitin-conjugating enzyme E2 N-like OS=Homo sapiens OX=9606 GN=UBE2NL PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P61088, F8VQQ8 |
| F8VQQ8 | 9 | 1.81E-03 | Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens OX=9606 GN=UBE2N PE=1 SV=1 |
| E9PHY3 | 8 | 4.20E-04 | Dickkopf-related protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=DKK3 PE=1 SV=1 |
| E9PKK9 | 8 | 5.77E-04 | Dickkopf-related protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=DKK3 PE=1 SV=1 |
| E9PKW6 | 8 | 3.28E-04 | Dickkopf-related protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=DKK3 PE=1 SV=8 |
| F6SYF8 | 9 | 5.13E-04 | Dickkopf-related protein 3 OS=Homo sapiens OX=9606 GN=DKK3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9UBP4, E9PKW6, E9PHY3, E9PKK9 |
| Q9UBP4 | 9 | 5.34E-04 | Dickkopf-related protein 3 OS=Homo sapiens OX=9606 GN=DKK3 PE=1 SV=2 |
| Q15758 | 9 | 6.33E-04 | Neutral amino acid transporter B(0) OS=Homo sapiens OX=9606 GN=SLC1A5 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0QXM4, Q15758-2, Q15758-3 |
| Q15758-2 | 9 | 8.55E-04 | Isoform 2 of Neutral amino acid transporter B(0) OS=Homo sapiens OX=9606 GN=SLC1A5 |
| Q15758-3 | 9 | 9.26E-04 | Isoform 3 of Neutral amino acid transporter B(0) OS=Homo sapiens OX=9606 GN=SLC1A5 |
| M0QXM4 | 9 | 8.55E-04 | Amino acid transporter OS=Homo sapiens OX=9606 GN=SLC1A5 PE=1 SV=1 |
| P55011-3 | 8 | 1.97E-05 | Isoform 2 of Solute carrier family 12 member 2 OS=Homo sapiens OX=9606 GN=SLC12A2 |
| G3XAL9 | 8 | 2.05E-05 | Solute carrier family 12 (Sodium/potassium/chloride transporters), member 2, isoform CRA\_a OS=Homo sapiens OX=9606 GN=SLC12A2 PE=1 SV=1 |
| P55011 | 8 | 1.95E-05 | Solute carrier family 12 member 2 OS=Homo sapiens OX=9606 GN=SLC12A2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P55011-3, G3XAL9 |
| A0A0A0MSI0 | 9 | 2.63E-03 | Peroxiredoxin-1 (Fragment) OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1 |
| P32119 | 9 | 3.10E-03 | Peroxiredoxin-2 OS=Homo sapiens OX=9606 GN=PRDX2 PE=1 SV=5 |
| Q06830 | 9 | 2.26E-03 | Peroxiredoxin-1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0A0MSI0, A0A0A0MRQ5, A6NIW5 |
| A6NIW5 | 8 | 9.40E-04 | Peroxiredoxin 2, isoform CRA\_a OS=Homo sapiens OX=9606 GN=PRDX2 PE=1 SV=2 |
| A0A0A0MRQ5 | 9 | 4.14E-03 | Peroxiredoxin-1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1 |
| K7ENE5 | 9 | 3.17E-04 | Deoxyribonuclease-2-alpha (Fragment) OS=Homo sapiens OX=9606 GN=DNASE2 PE=1 SV=1 |
| O00115-2 | 9 | 2.27E-04 | Isoform 2 of Deoxyribonuclease-2-alpha OS=Homo sapiens OX=9606 GN=DNASE2 |
| O00115 | 9 | 1.92E-04 | Deoxyribonuclease-2-alpha OS=Homo sapiens OX=9606 GN=DNASE2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: O00115-2, K7ENE5 |
| Q92542 | 8 | 8.43E-05 | Nicastrin OS=Homo sapiens OX=9606 GN=NCSTN PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q92542-2, H0Y6T7 |
| H0Y6T7 | 8 | 2.14E-04 | Nicastrin (Fragment) OS=Homo sapiens OX=9606 GN=NCSTN PE=1 SV=1 |
| Q92542-2 | 8 | 8.68E-05 | Isoform 2 of Nicastrin OS=Homo sapiens OX=9606 GN=NCSTN |
| P41227 | 8 | 1.07E-04 | N-alpha-acetyltransferase 10 OS=Homo sapiens OX=9606 GN=NAA10 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P41227-2 |
| P41227-2 | 8 | 1.14E-04 | Isoform 2 of N-alpha-acetyltransferase 10 OS=Homo sapiens OX=9606 GN=NAA10 |
| E5RJA8 | 9 | 7.91E-04 | Carboxypeptidase Q (Fragment) OS=Homo sapiens OX=9606 GN=CPQ PE=1 SV=1 |
| E5RH35 | 9 | 1.13E-03 | Carboxypeptidase Q (Fragment) OS=Homo sapiens OX=9606 GN=CPQ PE=1 SV=1 |
| E5RJP8 | 9 | 1.07E-03 | Carboxypeptidase Q (Fragment) OS=Homo sapiens OX=9606 GN=CPQ PE=1 SV=1 |
| Q9Y646 | 9 | 3.73E-04 | Carboxypeptidase Q OS=Homo sapiens OX=9606 GN=CPQ PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: E5RJA8, E5RJP8, E5RJZ7, E5RH35 |
| E5RJZ7 | 9 | 1.12E-03 | Carboxypeptidase Q (Fragment) OS=Homo sapiens OX=9606 GN=CPQ PE=1 SV=1 |
| F8VWS0 | 9 | 1.18E-04 | 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| P05388-2 | 9 | 1.30E-04 | Isoform 2 of 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 |
| P05388 | 9 | 1.11E-04 | 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: F8VWS0, P05388-2, F8W1K8 |
| F8W1K8 | 9 | 2.11E-04 | 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 |
| H3BRM5 | 9 | 5.11E-03 | Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens OX=9606 GN=COX5A PE=1 SV=1 |
| H3BV69 | 9 | 3.62E-03 | Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens OX=9606 GN=COX5A PE=1 SV=1 |
| P20674 | 9 | 2.87E-03 | Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens OX=9606 GN=COX5A PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: H3BV69, H3BRM5 |
| Q9BXK5 | 9 | 1.47E-03 | Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1 |
| Q9BXK5-4 | 9 | 2.20E-03 | Isoform 3 of Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 |
| A0A087WX97 | 9 | 1.40E-03 | Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9BXK5, A0A087WTL4, Q9BXK5-4 |
| A0A087WTL4 | 9 | 1.55E-03 | Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1 |
| A0A087WTA2 | 9 | 6.57E-04 | SYNJ2BP-COX16 readthrough OS=Homo sapiens OX=9606 GN=SYNJ2BP-COX16 PE=4 SV=1 |
| A0A087WUM0 | 9 | 1.45E-04 | SYNJ2BP-COX16 readthrough (Fragment) OS=Homo sapiens OX=9606 GN=SYNJ2BP-COX16 PE=4 SV=1; Additional IDs concatenated into MaxParsimony group: A0A087WYV9, A0A087X1F5, P57105, A0A087WTA2 |
| A0A087WYV9 | 9 | 1.48E-04 | SYNJ2BP-COX16 readthrough OS=Homo sapiens OX=9606 GN=SYNJ2BP-COX16 PE=4 SV=1 |
| P57105 | 9 | 1.86E-04 | Synaptojanin-2-binding protein OS=Homo sapiens OX=9606 GN=SYNJ2BP PE=1 SV=2 |
| A0A087X1F5 | 9 | 1.77E-04 | SYNJ2BP-COX16 readthrough (Fragment) OS=Homo sapiens OX=9606 GN=SYNJ2BP-COX16 PE=4 SV=6 |
| H0YIH9 | 9 | 1.49E-03 | Protein canopy homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=CNPY2 PE=4 SV=1 |
| F8VXJ7 | 9 | 1.93E-03 | Protein canopy homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=CNPY2 PE=1 SV=1 |
| Q9Y2B0-2 | 9 | 7.29E-04 | Isoform 2 of Protein canopy homolog 2 OS=Homo sapiens OX=9606 GN=CNPY2 |
| F8VP03 | 9 | 6.00E-04 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1 |
| H0YI18 | 9 | 2.32E-03 | Protein canopy homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=CNPY2 PE=1 SV=1 |
| F8W031 | 9 | 1.24E-03 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q9Y2B0, F8VXJ7, F8W1K5, F8VP03, H0YI18, Q9Y2B0-2, F8W1U5, H0YIH9 |
| F8W1U5 | 9 | 7.46E-04 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=8 |
| F8W1K5 | 9 | 2.58E-03 | Protein canopy homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=CNPY2 PE=1 SV=1 |
| Q9Y2B0 | 9 | 1.80E-03 | Protein canopy homolog 2 OS=Homo sapiens OX=9606 GN=CNPY2 PE=1 SV=1 |
| H3BQN4 | 9 | 5.49E-04 | Fructose-bisphosphate aldolase OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1 |
| P04075-2 | 9 | 4.86E-04 | Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens OX=9606 GN=ALDOA; Additional IDs concatenated into MaxParsimony group: J3KPS3, P04075, H3BQN4, H3BPS8, H3BUH7, H3BR68 |
| H3BUH7 | 9 | 9.92E-04 | Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1 |
| J3KPS3 | 9 | 5.52E-04 | Fructose-bisphosphate aldolase OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1 |
| P04075 | 9 | 5.58E-04 | Fructose-bisphosphate aldolase A OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=2 |
| H3BPS8 | 9 | 5.71E-04 | Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1 |
| Q96AE4-2 | 7 | 2.44E-04 | Isoform 2 of Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 |
| E9PEB5 | 7 | 2.44E-04 | Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=1 |
| Q96AE4 | 7 | 2.48E-04 | Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: E9PEB5, Q96AE4-2 |
| C9JF79 | 9 | 9.95E-05 | Malate dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=MDH1 PE=1 SV=1 |
| P40925 | 9 | 1.61E-04 | Malate dehydrogenase, cytoplasmic OS=Homo sapiens OX=9606 GN=MDH1 PE=1 SV=4 |
| C9JLV6 | 9 | 1.76E-04 | Malate dehydrogenase, cytoplasmic (Fragment) OS=Homo sapiens OX=9606 GN=MDH1 PE=1 SV=1 |
| C9JRL4 | 9 | 1.68E-04 | Malate dehydrogenase, cytoplasmic (Fragment) OS=Homo sapiens OX=9606 GN=MDH1 PE=1 SV=8 |
| P40925-3 | 9 | 1.52E-04 | Isoform 3 of Malate dehydrogenase, cytoplasmic OS=Homo sapiens OX=9606 GN=MDH1; Additional IDs concatenated into MaxParsimony group: P40925, C9JF79, C9JRL4, C9JLV6 |
| P30044-3 | 8 | 8.42E-04 | Isoform 3 of Peroxiredoxin-5, mitochondrial OS=Homo sapiens OX=9606 GN=PRDX5 |
| P30044-2 | 8 | 8.91E-04 | Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial OS=Homo sapiens OX=9606 GN=PRDX5 |
| P30044 | 8 | 6.74E-04 | Peroxiredoxin-5, mitochondrial OS=Homo sapiens OX=9606 GN=PRDX5 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P30044-3, P30044-2, P30044-4 |
| Q9Y5Z4 | 8 | 3.14E-04 | Heme-binding protein 2 OS=Homo sapiens OX=9606 GN=HEBP2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5THN1 |
| Q5THN1 | 8 | 0.000304136 | Heme-binding protein 2 OS=Homo sapiens OX=9606 GN=HEBP2 PE=1 SV=1 |
| A0A2R8Y430 | 9 | 2.92E-04 | Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 |
| P48637-2 | 9 | 3.62E-04 | Isoform 2 of Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS |
| P48637 | 9 | 2.79E-04 | Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A2R8Y430, P48637-2, A0A2R8YF34, A0A0S2Z4J7, A0A2R8Y446, A0A2R8Y790, A0A2R8Y4V9, A0A2R8Y6Y6, A0A2R8Y2X9 |
| P21796 | 8 | 3.35E-04 | Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens OX=9606 GN=VDAC1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9JI87 |
| C9JI87 | 8 | 3.79E-04 | Voltage-dependent anion-selective channel protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=VDAC1 PE=1 SV=6 |
| P02763 | 9 | 3.71E-03 | Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1 |
| P19652 | 9 | 0.00288438 | Alpha-1-acid glycoprotein 2 OS=Homo sapiens OX=9606 GN=ORM2 PE=1 SV=2 |
| D6RCN3 | 9 | 4.33E-03 | Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=1 |
| E9PHT9 | 9 | 0.00246892 | Annexin OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=1 |
| D6RBE9 | 9 | 1.16E-03 | Annexin OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=1 |
| P08758 | 9 | 1.58E-03 | Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: D6RBL5, D6RBE9, E9PHT9, D6RCN3 |
| J3KP15 | 9 | 7.23E-03 | Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF2 PE=1 SV=8 |
| Q01130-2 | 9 | 4.60E-03 | Isoform 2 of Serine/arginine-rich splicing factor 2 OS=Homo sapiens OX=9606 GN=SRSF2 |
| J3QL05 | 9 | 7.39E-03 | Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF2 PE=1 SV=1 |
| Q01130 | 9 | 0.004348316 | Serine/arginine-rich splicing factor 2 OS=Homo sapiens OX=9606 GN=SRSF2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: Q01130-2, J3KP15, J3QL05 |
| P05387 | 9 | 0.009314343 | 60S acidic ribosomal protein P2 OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H0YDD8, P05386-2 |
| P05386-2 | 8 | 0.004376891 | Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens OX=9606 GN=RPLP1 |
| H0YDD8 | 9 | 0.009713608 | 60S acidic ribosomal protein P2 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1 |
| P05386 | 9 | 0.004891954 | 60S acidic ribosomal protein P1 OS=Homo sapiens OX=9606 GN=RPLP1 PE=1 SV=1 |
| O00754-2 | 9 | 3.89E-04 | Isoform 2 of Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 |
| O00754 | 9 | 3.88E-04 | Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: O00754-2, M0QZ24 |
| M0QZ24 | 9 | 1.44E-03 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1 |
| Q5VV89 | 7 | 4.20E-05 | Microsomal glutathione S-transferase 3 OS=Homo sapiens OX=9606 GN=MGST3 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O14880, Q5VV87 |
| O14880 | 7 | 4.58E-05 | Microsomal glutathione S-transferase 3 OS=Homo sapiens OX=9606 GN=MGST3 PE=1 SV=1 |
| Q5VV87 | 7 | 5.40E-05 | Microsomal glutathione S-transferase 3 OS=Homo sapiens OX=9606 GN=MGST3 PE=1 SV=1 |
| Q9UBS4 | 8 | 7.47E-05 | DnaJ homolog subfamily B member 11 OS=Homo sapiens OX=9606 GN=DNAJB11 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: H7C2Y5 |
| H7C2Y5 | 8 | 1.60E-04 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=8 |
| P00505 | 9 | 1.27E-04 | Aspartate aminotransferase, mitochondrial OS=Homo sapiens OX=9606 GN=GOT2 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P00505-2 |
| P00505-2 | 9 | 1.41E-04 | Isoform 2 of Aspartate aminotransferase, mitochondrial OS=Homo sapiens OX=9606 GN=GOT2 |
| Q8NFU3-4 | 9 | 6.31E-04 | Isoform 4 of Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1; Additional IDs concatenated into MaxParsimony group: Q8NFU3, Q8NFU3-3, Q8NFU3-2, R4GNF9 |
| Q8NFU3-3 | 9 | 4.65E-04 | Isoform 3 of Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 |
| Q8NFU3-2 | 9 | 1.03E-03 | Isoform 2 of Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 |
| Q8NFU3 | 9 | 6.70E-04 | Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 PE=1 SV=3 |
| R4GNF9 | 9 | 1.22E-03 | Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 PE=1 SV=1 |
| B1AR62 | 8 | 1.21E-04 | Phosphotransferase (Fragment) OS=Homo sapiens OX=9606 GN=HK1 PE=1 SV=1 |
| P19367-3 | 9 | 1.55E-04 | Isoform 3 of Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1; Additional IDs concatenated into MaxParsimony group: P19367, P19367-2, P19367-4, B1AR63, P52789, E9PB90, B1AR62 |
| P19367 | 9 | 1.56E-04 | Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1 PE=1 SV=3 |
| P19367-4 | 9 | 1.58E-04 | Isoform 4 of Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1 |
| P19367-2 | 9 | 1.56E-04 | Isoform 2 of Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1 |
| B1AR63 | 8 | 1.76E-04 | Phosphotransferase (Fragment) OS=Homo sapiens OX=9606 GN=HK1 PE=1 SV=8 |
| P69905 | 9 | 7.27E-02 | Hemoglobin subunit alpha OS=Homo sapiens OX=9606 GN=HBA1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A2R8Y7C0, G3V1N2 |
| A0A2R8Y7C0 | 9 | 7.48E-02 | Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1 |
| G3V1N2 | 9 | 5.44E-02 | HCG1745306, isoform CRA\_a OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1 |
| P00558-2 | 9 | 2.60E-03 | Isoform 2 of Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 |
| P00558 | 9 | 2.60E-03 | Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P00558-2, P07205 |
| P07205 | 9 | 1.48E-03 | Phosphoglycerate kinase 2 OS=Homo sapiens OX=9606 GN=PGK2 PE=1 SV=3 |
| P62263 | 8 | 2.31E-04 | 40S ribosomal protein S14 OS=Homo sapiens OX=9606 GN=RPS14 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: A0A2R8Y811 |
| A0A2R8Y811 | 8 | 2.32E-04 | 40S ribosomal protein S14 (Fragment) OS=Homo sapiens OX=9606 GN=RPS14 PE=1 SV=1 |
| A0A2R8Y614 | 7 | 2.17E-05 | Rho guanine nucleotide exchange factor 35 OS=Homo sapiens OX=9606 GN=ARHGEF35 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A5YM69 |
| A5YM69 | 7 | 2.17E-05 | Rho guanine nucleotide exchange factor 35 OS=Homo sapiens OX=9606 GN=ARHGEF35 PE=1 SV=1 |
| P58546 | 9 | 2.13E-03 | Myotrophin OS=Homo sapiens OX=9606 GN=MTPN PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: C9JL85 |
| C9JL85 | 9 | 4.11E-03 | Myotrophin OS=Homo sapiens OX=9606 GN=MTPN PE=1 SV=1 |
| Q07021 | 9 | 9.47E-04 | Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=C1QBP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: I3L3B0, I3L3Q7 |
| I3L3Q7 | 9 | 1.32E-03 | Complement component 1 Q subcomponent-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=C1QBP PE=1 SV=1 |
| I3L3B0 | 9 | 1.31E-03 | Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=C1QBP PE=1 SV=1 |
| S4R3Y4 | 8 | 1.20E-04 | Protein AMBP OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1 |
| P02760 | 8 | 8.78E-05 | Protein AMBP OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: S4R3Y4, S4R471 |
| S4R471 | 8 | 1.48E-04 | Protein AMBP (Fragment) OS=Homo sapiens OX=9606 GN=AMBP PE=1 SV=1 |
| E9PCD7 | 9 | 4.06E-05 | Alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B2 PE=1 SV=1 |
| H0YA68 | 9 | 4.08E-05 | Alpha-mannosidase (Fragment) OS=Homo sapiens OX=9606 GN=MAN2B2 PE=1 SV=1 |
| Q9Y2E5-2 | 9 | 4.07E-05 | Isoform 2 of Epididymis-specific alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B2 |
| Q9Y2E5 | 9 | 3.85E-05 | Epididymis-specific alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B2 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: E9PCD7, Q9Y2E5-2, H0YA68 |
| P13473-3 | 9 | 1.88E-03 | Isoform LAMP-2C of Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens OX=9606 GN=LAMP2; Additional IDs concatenated into MaxParsimony group: P13473-2, P13473 |
| P13473-2 | 9 | 1.89E-03 | Isoform LAMP-2B of Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens OX=9606 GN=LAMP2 |
| P13473 | 9 | 1.89E-03 | Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens OX=9606 GN=LAMP2 PE=1 SV=2 |
| A0A140T971 | 9 | 2.07E-03 | N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=1 |
| H0Y7N1 | 8 | 1.87E-03 | N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=1 |
| Q5SRR8 | 9 | 1.97E-03 | N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=2 |
| Q5SSV3 | 9 | 2.06E-03 | N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=1 |
| O95865 | 9 | 1.94E-03 | N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q5SRR8, Q5SSV3, A0A140T971, H0Y7N1 |
| P02786 | 8 | 4.67E-05 | Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: F8WBE5 |
| F8WBE5 | 8 | 3.94E-04 | Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=1 |
| H3BUX2 | 9 | 7.56E-04 | Cytochrome b5 type B OS=Homo sapiens OX=9606 GN=CYB5B PE=1 SV=1 |
| D6RFH4 | 9 | 8.08E-04 | Cytochrome b5 type B OS=Homo sapiens OX=9606 GN=CYB5B PE=1 SV=1 |
| J3KNF8 | 9 | 7.06E-04 | Cytochrome b5 type B (Outer mitochondrial membrane), isoform CRA\_a OS=Homo sapiens OX=9606 GN=CYB5B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: O43169, H3BUX2, D6RFH4 |
| O43169 | 9 | 7.25E-04 | Cytochrome b5 type B OS=Homo sapiens OX=9606 GN=CYB5B PE=1 SV=2 |
| Q9NQC3-2 | 9 | 1.53E-03 | Isoform 2 of Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 |
| Q9NQC3 | 9 | 4.78E-04 | Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9NQC3-5, Q9NQC3-2, F8W914, Q9NQC3-4 |
| F8W914 | 9 | 1.65E-03 | Reticulon OS=Homo sapiens OX=9606 GN=RTN4 PE=1 SV=1 |
| Q9NQC3-5 | 9 | 1.45E-03 | Isoform 5 of Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 |
| A0A1W2PS70 | 8 | 2.72E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| A0A1W2PS43 | 9 | 1.29E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| A0A1W2PQR6 | 9 | 1.36E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| Q14108-2 | 9 | 1.48E-03 | Isoform 2 of Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 |
| A0A1W2PRS1 | 9 | 1.18E-03 | Lysosome membrane protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: Q14108, A0A1W2PS43, A0A1W2PQB7, A0A1W2PQR6, A0A1W2PPX5, A0A1W2PPU6, Q14108-2, A0A1W2PRF6, A0A1W2PSE4, A0A1W2PNX7, A0A1W2PS70, D6RDG0 |
| Q14108 | 9 | 1.28E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=2 |
| A0A1W2PSE4 | 8 | 1.86E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| A0A1W2PPU6 | 9 | 1.33E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| D6RDG0 | 8 | 2.74E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| A0A1W2PNX7 | 8 | 2.65E-03 | Lysosome membrane protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| A0A1W2PRF6 | 9 | 5.04E-04 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| A0A1W2PQB7 | 9 | 1.30E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| A0A1W2PPX5 | 9 | 1.41E-03 | Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=1 |
| Q99536-3 | 8 | 1.05E-03 | Isoform 3 of Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens OX=9606 GN=VAT1 |
| K7ERT7 | 9 | 2.71E-03 | Synaptic vesicle membrane protein VAT-1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=1 |
| Q99536 | 9 | 1.18E-03 | Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q99536-3, K7ERT7 |
| K7EJ44 | 9 | 0.001317073 | Profilin OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=1 |
| P07737 | 9 | 0.002155406 | Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: I3L3D5, K7EJ44 |
| I3L3D5 | 8 | 0.001049986 | Profilin (Fragment) OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=1 |
| C9JVG0 | 8 | 1.06E-03 | Serotransferrin (Fragment) OS=Homo sapiens OX=9606 GN=TF PE=1 SV=1 |
| P02787 | 9 | 1.10E-03 | Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: C9JVG0 |
| B0YJC5 | 9 | 1.36E-02 | Vimentin variant 4 OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=1 |
| B0YJC4 | 9 | 1.39E-02 | Vimentin variant 3 OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=1 |
| P41219 | 9 | 4.39E-04 | Peripherin OS=Homo sapiens OX=9606 GN=PRPH PE=1 SV=2 |
| A0A1B0GVG8 | 9 | 1.22E-02 | Vimentin (Fragment) OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=1 |
| P17661 | 9 | 1.18E-03 | Desmin OS=Homo sapiens OX=9606 GN=DES PE=1 SV=3 |
| F8W835 | 9 | 2.96E-04 | Peripherin (Fragment) OS=Homo sapiens OX=9606 GN=PRPH PE=1 SV=2 |
| P41219-2 | 9 | 4.38E-04 | Isoform 2 of Peripherin OS=Homo sapiens OX=9606 GN=PRPH |
| A0A1B0GTT5 | 9 | 1.32E-02 | Vimentin (Fragment) OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=1 |
| P08670 | 9 | 1.63E-02 | Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: B0YJC4, B0YJC5, A0A1B0GTT5, A0A1B0GVG8, P41219-2, P41219, P17661, H7C5W5, F8W835 |
| H7C5W5 | 9 | 1.03E-03 | Peripherin (Fragment) OS=Homo sapiens OX=9606 GN=PRPH PE=1 SV=1 |
| P15289 | 9 | 9.37E-04 | Arylsulfatase A OS=Homo sapiens OX=9606 GN=ARSA PE=1 SV=3 |
| P15289-2 | 9 | 9.27E-04 | Isoform 2 of Arylsulfatase A OS=Homo sapiens OX=9606 GN=ARSA |
| A0A0C4DFZ2 | 9 | 9.34E-04 | Arylsulfatase A OS=Homo sapiens OX=9606 GN=ARSA PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P15289, P15289-2 |
| Q99714-2 | 9 | 4.94E-04 | Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 |
| Q99714 | 9 | 5.53E-04 | 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: Q99714-2, Q5H928 |
| Q5H928 | 9 | 1.86E-04 | 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=1 |
| P10599 | 9 | 2.55E-03 | Thioredoxin OS=Homo sapiens OX=9606 GN=TXN PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: P10599-2 |
| P10599-2 | 9 | 3.15E-03 | Isoform 2 of Thioredoxin OS=Homo sapiens OX=9606 GN=TXN |
| A0A1W2PRR1 | 9 | 5.94E-04 | Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1 |
| P14625 | 9 | 3.44E-04 | Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A1W2PRR1, Q96GW1 |
| Q96GW1 | 9 | 5.94E-04 | Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1 |
| P14618 | 9 | 4.86E-03 | Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: P14618-3, B4DNK4, P14618-2, H3BTN5, H3BR70, H3BQ34, H3BTJ2, H3BUW1, H3BT25, H3BU13, H3BQZ3, H3BN34 |
| H3BTJ2 | 9 | 5.36E-03 | Pyruvate kinase PKM (Fragment) OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| H3BU13 | 9 | 7.84E-03 | Pyruvate kinase PKM (Fragment) OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| H3BTN5 | 9 | 4.96E-03 | Pyruvate kinase (Fragment) OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| H3BUW1 | 9 | 5.56E-03 | Pyruvate kinase PKM (Fragment) OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| H3BN34 | 9 | 1.19E-02 | Pyruvate kinase PKM (Fragment) OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=8 |
| P14618-3 | 9 | 3.76E-03 | Isoform 3 of Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM |
| H3BR70 | 9 | 4.16E-03 | Pyruvate kinase OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| H3BQZ3 | 9 | 8.83E-03 | Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| B4DNK4 | 9 | 5.18E-03 | Pyruvate kinase OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| H3BQ34 | 9 | 4.34E-03 | Pyruvate kinase OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| P14618-2 | 9 | 4.68E-03 | Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM |
| H3BT25 | 9 | 5.96E-03 | Pyruvate kinase PKM (Fragment) OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| P15311 | 8 | 1.76E-04 | Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: E7EQR4 |
| E7EQR4 | 8 | 1.76E-04 | Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=3 |
| R4GN05 | 8 | 9.77E-04 | Dipeptidyl peptidase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DPP7 PE=1 SV=1 |
| R4GMR2 | 8 | 9.22E-04 | Dipeptidyl peptidase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DPP7 PE=1 SV=1 |
| R4GNE8 | 8 | 0.00183929 | Dipeptidyl peptidase 2 (Fragment) OS=Homo sapiens OX=9606 GN=DPP7 PE=1 SV=1 |
| Q9UHL4 | 9 | 0.002054385 | Dipeptidyl peptidase 2 OS=Homo sapiens OX=9606 GN=DPP7 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: R4GNE8, R4GMR2, R4GN05 |
| E9PQM1 | 9 | 1.03E-01 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| E9PJ67 | 9 | 1.63E-01 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| P07858 | 9 | 5.58E-02 | Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: E9PQM1, E9PSG5, E9PLY3, E9PHZ5, E9PNL5, E9PKQ7, E9PCB3, E9PJ67, E9PR54, E9PS78, R4GMQ5 |
| E9PKQ7 | 9 | 1.33E-01 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| E9PR54 | 9 | 1.68E-01 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| E9PNL5 | 9 | 1.26E-01 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| E9PCB3 | 9 | 1.50E-01 | Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=2 |
| E9PLY3 | 9 | 1.09E-01 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| E9PHZ5 | 9 | 0.121816708 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=8 |
| E9PSG5 | 9 | 1.06E-01 | Cathepsin B (Fragment) OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=1 |
| A0A1B0GVP3 | 9 | 3.71E-03 | Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| C9JH19 | 9 | 1.83E-03 | Cathepsin D (Fragment) OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| A0A1B0GU03 | 9 | 1.10E-03 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=1 SV=1 |
| H7C469 | 9 | 1.39E-03 | Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=7 |
| A0A1B0GWE8 | 9 | 3.68E-03 | Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| F8WD96 | 9 | 1.92E-03 | Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| A0A1B0GW44 | 9 | 3.58E-03 | Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| A0A1B0GU92 | 9 | 1.15E-03 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=1 SV=1 |
| A0A1B0GVD5 | 9 | 3.69E-03 | Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| F8W787 | 8 | 1.67E-03 | Cathepsin D (Fragment) OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| H7C1V0 | 8 | 4.29E-03 | Cathepsin D (Fragment) OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| P07339 | 9 | 3.66E-03 | Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A1B0GWE8, A0A1B0GVD5, A0A1B0GV23, A0A1B0GVP3, A0A1B0GW44, A0A1B0GU03, A0A1B0GU92, H7C469, C9JH19, F8WD96, F8W787, H7C1V0 |
| A0A1B0GV23 | 9 | 3.72E-03 | Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 |
| A0A0G2JIW1 | 9 | 8.92E-04 | Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P0DMV9, P0DMV8, P0DMV8-2, E9PKE3, P11142-2, P34931, Q53FA3, P54652, contaminant\_GR78\_MESAU, contaminant\_GR78\_RAT, P11021, contaminant\_GR78\_HUMAN, E9PNE6, V9GZ37, E9PN89, A8K7Q2, E9PLF4, E9PI65, contaminant\_GR78\_LYCES, contaminant\_GR78\_MAIZE |
| contaminant\_GR78\_MOUSE | 9 | 2.17E-04 | 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN... |
| contaminant\_GR78\_LYCES | 9 | 4.96E-05 | 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN... |
| contaminant\_GR78\_HUMAN | 9 | 2.33E-04 | 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN... |
| P0DMV8-2 | 9 | 9.76E-04 | Isoform 2 of Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A |
| E9PN89 | 9 | 1.02E-03 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| P11142-2 | 9 | 1.26E-03 | Isoform 2 of Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 |
| E9PKE3 | 9 | 1.02E-03 | Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| P0DMV8 | 9 | 8.94E-04 | Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1 |
| P11021 | 9 | 2.33E-04 | Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2 |
| A8K7Q2 | 9 | 5.91E-04 | Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| P11142 | 9 | 9.97E-04 | Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| E9PLF4 | 9 | 1.90E-03 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| contaminant\_GR78\_RAT | 9 | 2.17E-04 | 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN... |
| contaminant\_GR78\_MAIZE | 9 | 7.08E-05 | IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG B70 (HEAT SHOCK PROTEIN... |
| P0DMV9 | 9 | 8.94E-04 | Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1 |
| contaminant\_GR78\_MESAU | 9 | 2.17E-04 | 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN... |
| E9PNE6 | 9 | 1.05E-03 | Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| P54652 | 9 | 6.83E-04 | Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1 |
| P34931 | 9 | 6.71E-04 | Heat shock 70 kDa protein 1-like OS=Homo sapiens OX=9606 GN=HSPA1L PE=1 SV=2 |
| P17066 | 9 | 5.76E-04 | Heat shock 70 kDa protein 6 OS=Homo sapiens OX=9606 GN=HSPA6 PE=1 SV=2 |
| E9PI65 | 9 | 1.81E-03 | Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 |
| Q53FA3 | 9 | 6.71E-04 | HSPA1L (Fragment) OS=Homo sapiens OX=9606 GN=HSPA1L PE=1 SV=1 |
| P27824 | 9 | 2.69E-04 | Calnexin OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=2 |
| P27824-3 | 9 | 2.76E-04 | Isoform 3 of Calnexin OS=Homo sapiens OX=9606 GN=CANX |
| P27824-2 | 9 | 2.54E-04 | Isoform 2 of Calnexin OS=Homo sapiens OX=9606 GN=CANX; Additional IDs concatenated into MaxParsimony group: P27824, P27824-3, H0Y9Q7, D6RDP7, D6RB85, D6RAU8, D6RAQ8, D6RD16, D6RHJ3 |
| P01834 | 8 | 3.46E-03 | Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2 |
| Q07065 | 8 | 1.62E-04 | Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2 |
| Q9H3Z4 | 6 | 3.46E-04 | DnaJ homolog subfamily C member 5 OS=Homo sapiens OX=9606 GN=DNAJC5 PE=1 SV=1 |
| Q12962 | 8 | 8.21E-05 | Transcription initiation factor TFIID subunit 10 OS=Homo sapiens OX=9606 GN=TAF10 PE=1 SV=1 |
| P12236 | 8 | 3.24E-04 | ADP/ATP translocase 3 OS=Homo sapiens OX=9606 GN=SLC25A6 PE=1 SV=4 |
| P02751-12 | 8 | 7.59E-05 | Isoform 12 of Fibronectin OS=Homo sapiens OX=9606 GN=FN1 |
| P62249 | 8 | 3.83E-04 | 40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: M0R210, Q6IPX4, M0R3H0 |
| M0R210 | 8 | 4.34E-04 | 40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=1 |
| M0R3H0 | 7 | 2.28E-04 | 40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=1 |
| Q6IPX4 | 7 | 1.50E-04 | 40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=1 |
| Q5JRS0 | 7 | 1.08E-04 | Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=1 |
| Q5JRR9 | 7 | 1.13E-04 | Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=8 |
| Q02952-2 | 8 | 2.40E-04 | Isoform 2 of A-kinase anchor protein 12 OS=Homo sapiens OX=9606 GN=AKAP12 |
| Q02952 | 8 | 2.29E-04 | A-kinase anchor protein 12 OS=Homo sapiens OX=9606 GN=AKAP12 PE=1 SV=4; Additional IDs concatenated into MaxParsimony group: Q02952-2, Q02952-3 |
| Q02952-3 | 8 | 2.41E-04 | Isoform 3 of A-kinase anchor protein 12 OS=Homo sapiens OX=9606 GN=AKAP12 |
| Q99733-2 | 8 | 1.31E-04 | Isoform 2 of Nucleosome assembly protein 1-like 4 OS=Homo sapiens OX=9606 GN=NAP1L4; Additional IDs concatenated into MaxParsimony group: Q99733, C9JZI7, C9J6D1, E9PKT8, A8MXH2, E9PP22, E9PNJ7, E9PS34, E9PJJ2, E9PNW0, C9J1B1, E9PKI2 |
| C9JZI7 | 8 | 1.81E-04 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| E9PNJ7 | 8 | 3.40E-04 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| Q99733 | 8 | 0.000134779 | Nucleosome assembly protein 1-like 4 OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| A8MXH2 | 8 | 2.57E-04 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=2 |
| E9PNW0 | 8 | 4.46E-04 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| E9PKI2 | 8 | 6.11E-04 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| E9PS34 | 8 | 0.00035842 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| E9PKT8 | 8 | 0.000298194 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| E9PP22 | 8 | 0.000309545 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=2 |
| E9PJJ2 | 8 | 3.72E-04 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| C9J1B1 | 8 | 4.72E-04 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=2 |
| C9J6D1 | 8 | 0.000283117 | Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1 |
| F1T0E5 | 8 | 0.000142404 | Calcium-dependent secretion activator 1 OS=Homo sapiens OX=9606 GN=CADPS PE=1 SV=1 |
| Q9ULU8-3 | 8 | 0.000145655 | Isoform 3 of Calcium-dependent secretion activator 1 OS=Homo sapiens OX=9606 GN=CADPS |
| Q9ULU8-2 | 8 | 1.50E-04 | Isoform 2 of Calcium-dependent secretion activator 1 OS=Homo sapiens OX=9606 GN=CADPS |
| Q9ULU8 | 8 | 1.42E-04 | Calcium-dependent secretion activator 1 OS=Homo sapiens OX=9606 GN=CADPS PE=1 SV=3 |
| Q9ULU8-4 | 8 | 1.41E-04 | Isoform 4 of Calcium-dependent secretion activator 1 OS=Homo sapiens OX=9606 GN=CADPS; Additional IDs concatenated into MaxParsimony group: Q9ULU8, F1T0E5, Q9ULU8-3, Q9ULU8-2, Q9ULU8-5 |
| E7EXB4 | 8 | 3.60E-04 | 60 kDa heat shock protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=1 |
| E7ESH4 | 8 | 3.42E-04 | 60 kDa heat shock protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=1 |
| P13929-3 | 8 | 2.55E-04 | Isoform 3 of Beta-enolase OS=Homo sapiens OX=9606 GN=ENO3 |
| E5RGZ4 | 8 | 3.52E-04 | Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1 |
| E5RI09 | 8 | 5.17E-04 | Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1 |
| F5H1C3 | 8 | 1.17E-03 | Gamma-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=1 |
| P13929-2 | 8 | 2.46E-04 | Isoform 2 of Beta-enolase OS=Homo sapiens OX=9606 GN=ENO3 |
| K7EPM1 | 8 | 3.90E-04 | Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1 |
| K7EKN2 | 8 | 3.61E-04 | Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1 |
| P13929 | 8 | 2.30E-04 | Beta-enolase OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=5 |
| E5RG95 | 8 | 4.97E-04 | Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1 |
| P35749 | 8 | 3.17E-05 | Myosin-11 OS=Homo sapiens OX=9606 GN=MYH11 PE=1 SV=3 |
| P35579-2 | 8 | 9.26E-05 | Isoform 2 of Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 |
| P35580-5 | 7 | 1.94E-05 | Isoform 5 of Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 |
| P35749-4 | 8 | 3.23E-05 | Isoform 4 of Myosin-11 OS=Homo sapiens OX=9606 GN=MYH11 |
| P35580-2 | 7 | 1.93E-05 | Isoform 2 of Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 |
| P35580-3 | 7 | 1.93E-05 | Isoform 3 of Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 |
| P35580-4 | 7 | 1.92E-05 | Isoform 4 of Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 |
| P35749-2 | 8 | 3.16E-05 | Isoform 2 of Myosin-11 OS=Homo sapiens OX=9606 GN=MYH11 |
| P35749-3 | 8 | 3.22E-05 | Isoform 3 of Myosin-11 OS=Homo sapiens OX=9606 GN=MYH11 |
| P35580 | 7 | 1.95E-05 | Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3 |
| Q15121 | 8 | 3.95E-04 | Astrocytic phosphoprotein PEA-15 OS=Homo sapiens OX=9606 GN=PEA15 PE=1 SV=2 |
| Q15121-2 | 8 | 3.40E-04 | Isoform 2 of Astrocytic phosphoprotein PEA-15 OS=Homo sapiens OX=9606 GN=PEA15; Additional IDs concatenated into MaxParsimony group: Q15121, B1AKZ5 |
| B1AKZ5 | 8 | 4.51E-04 | Astrocytic phosphoprotein PEA-15 OS=Homo sapiens OX=9606 GN=PEA15 PE=1 SV=1 |
| Q15084-2 | 8 | 4.05E-05 | Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6; Additional IDs concatenated into MaxParsimony group: Q15084-5, Q15084-4, Q15084, Q15084-3 |
| Q15084-4 | 8 | 4.48E-05 | Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 |
| Q15084-5 | 8 | 4.08E-05 | Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 |
| Q15084-3 | 8 | 4.56E-05 | Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 |
| Q15084 | 8 | 4.53E-05 | Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 PE=1 SV=1 |
| Q9UN36-4 | 8 | 9.93E-05 | Isoform 4 of Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 |
| Q9UN36-2 | 8 | 9.12E-05 | Isoform 2 of Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 |
| Q9UN36-5 | 8 | 9.55E-05 | Isoform 5 of Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 |
| G3V578 | 8 | 1.15E-04 | Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 PE=1 SV=1 |
| Q9UN36 | 8 | 8.78E-05 | Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: Q9UN36-6, Q9UN36-3, Q9UN36-2, A0A0A0MS87, Q9UN36-5, Q9UN36-4, H0YJT9, G3V578 |
| A0A0A0MS87 | 8 | 9.65E-05 | Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 PE=1 SV=1 |
| Q9UN36-3 | 8 | 9.04E-05 | Isoform 3 of Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 |
| Q9UN36-6 | 8 | 8.87E-05 | Isoform 6 of Protein NDRG2 OS=Homo sapiens OX=9606 GN=NDRG2 |
| H0YJT9 | 8 | 1.13E-04 | Protein NDRG2 (Fragment) OS=Homo sapiens OX=9606 GN=NDRG2 PE=1 SV=1 |
| Q15717 | 7 | 7.63E-05 | ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=2 |
| Q15717-2 | 7 | 7.05E-05 | Isoform 2 of ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1; Additional IDs concatenated into MaxParsimony group: Q15717 |
| A8MW50 | 8 | 2.24E-04 | L-lactate dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=1 |
| F5H793 | 8 | 3.65E-04 | L-lactate dehydrogenase B chain (Fragment) OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=1 |
| C9J7H8 | 8 | 2.82E-04 | L-lactate dehydrogenase B chain (Fragment) OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=8 |
| P07195 | 8 | 2.78E-04 | L-lactate dehydrogenase B chain OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A8MW50, C9J7H8, F5H793 |
| Q15233-2 | 8 | 3.18E-04 | Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NONO |
| Q15233 | 8 | 2.62E-04 | Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NONO PE=1 SV=4 |
| P27816-6 | 8 | 1.77E-04 | Isoform 6 of Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 |
| E7EVA0 | 8 | 8.75E-05 | Microtubule-associated protein OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: P27816, P27816-6, P27816-2 |
| P27816-2 | 8 | 1.82E-04 | Isoform 2 of Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 |
| P27816 | 8 | 1.75E-04 | Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=3 |
| G3V2A3 | 8 | 8.87E-04 | Tubulin beta chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=1 |
| Q16186 | 8 | 3.12E-04 | Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens OX=9606 GN=ADRM1 PE=1 SV=2; Additional IDs concatenated into MaxParsimony group: A0A087WX59 |
| A0A087WX59 | 8 | 3.45E-04 | Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens OX=9606 GN=ADRM1 PE=1 SV=1 |
| O95777 | 8 | 1.08E-03 | U6 snRNA-associated Sm-like protein LSm8 OS=Homo sapiens OX=9606 GN=LSM8 PE=1 SV=3; Additional IDs concatenated into MaxParsimony group: C9JNV3, C9JIZ0, F2Z2Y6 |
| C9JNV3 | 8 | 1.23E-03 | U6 snRNA-associated Sm-like protein LSm8 (Fragment) OS=Homo sapiens OX=9606 GN=LSM8 PE=1 SV=8 |
| F2Z2Y6 | 8 | 1.42E-03 | U6 snRNA-associated Sm-like protein LSm8 OS=Homo sapiens OX=9606 GN=LSM8 PE=1 SV=1 |
| A0A0J9YXZ5 | 8 | 3.67E-05 | Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1 |
| P46940 | 8 | 3.07E-05 | Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1; Additional IDs concatenated into MaxParsimony group: A0A0J9YXZ5 |