Supporting Information

Median based absolute quantification of proteins using Fully Unlabelled Generic Internal Standard (**FUGIS**)

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Supplementary methods

GeLC-MS/MS

In-gel digestion workflow was adapted from the protocol by Shevchenko et al [1]. After electrophoresis the gel slab was stained with Coomassie Brilliant Blue R250 for 15 min at room temperature. After staining, gels were destained in 5:4:1 (v/v) of water: methanol: acetic acid. Slices corresponding to MW of interest were excised from the destained gel slab, cut into ca.1 mm size cubes and transferred to 1.5 ml LoBind Eppendorf tubes for further processing.

The gel pieces were destained completely by acetonitrile / water, and subsequently reduced by incubating the gels with 10 mM DTT at 56°C for 45 minutes. After reduction proteins were alkylated using 55 mM of iodoacetamide for 30 minutes in dark at room temperature. The reduced and alkylated samples were digested overnight with trypsin (10 ng/µl) in 10 mM ammonium bicarbonate. After digestion tryptic peptides were recovered from gel matrix using water / acetonitrile / formic acid, dried under vacuum and stored at -20°C for further analysis.

The dried extracts were reconstituted in 5% formic acid and 5 µl were injected into a Dionex Ultimate 3000 Nano-HPLC system equipped with two-column setup comprising of a trap column (5 mm × 300 µm i.d) and an analytical column (Acclaim PepMap100 C18 15 cm × 75 µm). Water with 0.1% (solvent A) and ACN with 0.1% (solvent B) were used as mobile phase. Samples were loaded into the trap column with a flow rate of 20 µl/min. Then the trap column was switched to the analytical column with a flow rate of 200 nL/min for peptides separation. The separation was carried out using Dionex Ultimate 3000 HPLC system (Thermo Scientific, Bremen,
Germany) running gradient elution program for 180 min and the output was hyphenated to Q-Exact HF (Thermo Fisher Scientific, Bremen, Germany) and mass spectra were acquired in data-dependent acquisition mode. The acquisition parameters are provided in Table S9.

Expression and metabolic labelling of chimeric protein standards

We adapted the same expression workflow as described in [2]. Synthetic genes produced by GenScript (Piscataway NJ) were sub-cloned into pET expression vector and transformed into an E.coli strain that was dual auxotroph for arginine and lysine (ΔArgΔLysBL21 (DE3) T1 pRARE). Successful transformants were then diluted and sub cultured in MDAG-135 media [3]. They were induced by 0.2mM isopropyl β-d-1-thiogalactopyranoside (IPTG). After 4 to 6 hr post induction cells were pelleted, re-suspended in 2x phosphate-buffered saline (PBS). The suspended cells were then aliquoted, snap frozen in liquid nitrogen and stored at -80°C until used for quantification.

Database searches and data processing

Peptide matching was carried out using Mascot v.2.2.04 software (Matrix Science, London, UK) against Homo sapiens (August 2020) proteome downloaded from Uniprot. A precursor mass tolerance of 5ppm and fragment mass tolerance of 0.03 Da was applied, fixed modification: carbamidomethyl (C); variable modifications: acetyl (protein N terminus), oxidation (M); labels: $^{13}$C(6) (K) and $^{13}$C(6)$^{15}$N(4) (R) (only
for MS Western the labelling was used); cleavage specificity: trypsin, with up to 2 missed cleavages allowed. Peptides having the ions score above 15 were accepted (significance threshold p < 0.05). The chromatographic alignment and feature detection were carried using Progenesis LC-MS v.4.1 (Nonlinear Dynamics, UK). The absolute quantification was performed by calculating the abundances for the labelled and the unlabelled peptide using an in-house software as previously published [4]. The statistical analysis were carried out in OriginLab (2017) (OriginLab Corp., Northampton, Massachusetts, USA).
**Figure S1.** MS1 peak area of CP01 and CP02 in 3 independent LC-MS/MS runs. Each point represents a peptide.

**Figure S2.** Retention times distribution of near median peptides; gradient elution profile is in grey.
Figure S 3. A) Full length sequence of FUGIS standard. B) Expressed FUGIS standard separated using 1D SDS page. C) Retention time distribution of peptides in the FUGIS standard; gradient elution profile in grey.
Figure S4. XIC peak areas of Top4 peptides of GAPDH (P04406) explains the rational behind the selection of BestN peptides. %CV is coefficient of variation of multiple selections.
Figure S5. Comparison of copy number per HEla cell proteins A) Nagaraj et al. (IBAQ)[5] vs. Raghuraman et al. (This paper), (843 proteins) B) Hein et al. (Proteomic Ruler)[6] vs. Raghuraman et al., (843 proteins), C) Nagaraj et al. (IBAQ)[5] vs. Hein et al. (Proteomic Ruler)[6], (843 proteins) D) Itzhak et al. (Proteomic Ruler)[7] vs. Hein et al. (Proteomic Ruler)[6] (82 proteins). R is Spearman correlation coefficient. All datasets were unified by Ensembl gene ID via gene symbol and/or major ID’s. Only proteins unequivocally matched between the two compared datasets were used.
**Table S1. MBAQ Quantification of UPS2 Standard**

| Uniprot ID | Protein name                          | MBAQ (fmol on column) | UPS2 (fmol on column) | Quantification error (%) |
|------------|---------------------------------------|-----------------------|-----------------------|--------------------------|
| P68871     | Haemoglobin beta chain                | 1960.62               | 2173.91               | -9.81                    |
| P02768     | Serum Albumin                         | 1883.46               | 2173.91               | -13.36                   |
| P41159     | Leptin                                | 2159.04               | 2173.91               | -0.68                    |
| P00915     | Carbonic anhydrase 1                  | 1891.46               | 2173.91               | -12.99                   |
| P00918     | Carbonic anhydrase 2                  | 2255.1                | 2173.91               | 3.73                     |
| P62988     | Ubiquitin                             | 1868.16               | 2173.91               | -14.06                   |
| P62937     | Peptidiclyl-prolyl cis-trans isomerase A | 238.38               | 217.39                | 9.65                     |
| Q06830     | Peroxiredoxin 1                       | 191.9                 | 217.39                | -11.73                   |
| P02144     | Myoglobin C                           | 182.91                | 217.39                | -15.86                   |
| P00167     | Cytochrome b5                          | 201.19                | 217.39                | -7.45                    |
| P04040     | Catalase                              | 138.13                | 217.39                | -36.46                   |
| P15559     | NAD(p)H dehydrogenase (quinone) 1 C   | 201.76                | 217.39                | -7.19                    |
| P63165     | Small ubiquitin related modifier (SUMO-1) | 197.075               | 217.39               | -9.35                    |
| P16083     | Ribosylidydrionicotinamide de dehydrogenase | 15.65                | 21.74               | -28.01                   |
| P06732     | Creatinine Kinase M-type              | 12.64                 | 21.74                 | -41.86                   |
| P61626     | Lysozyme C                            | 19.98                 | 21.74                 | -8.09                    |
| P12081     | Histidyl tRNA synthetase              | 19.24                 | 21.74                 | -11.50                   |

**Table S2. Peptide Sequence of GCP01**

```
LTANAADITVQDDTADK
YVIENEDLVANVVPSEQLAYAAAR
EASADVGDSEK
YDFFITDDNQVR
VETYAELGYEGLEK
VFDQNLADWVDNNVR
ELFELTQELFGVGSNPSTDK
AVLDEYSEGSPYR
QANEYADELISGYK
VIDQVTYILEPVGDPPIITVK
VLIEDDAPSPVPVQK
VYGIATEPIAEIEEGGAVK
AVFLSEAAAGAADEGAYK
```
| LFEAAQEEAQGGIEGILIIGK |
|------------------------|
| SGGEGYNEDGIAVWR       |
| EGQLIPK               |
| LFEDTEDAAYK           |
| EAAPASGGSSAGDDKFDK    |
| IQPFELAEVLTEFVSK      |
| GIIEQINEEQEIGTSPLK    |
| LAQAVQDDILK           |
| AFDDFSLGQVIK          |
| ELPTNVFHEDVSFAGDLLK   |
| NSYGFENDYWSVLR        |
| IEYASDVVK             |
| SFDQALSALEVK          |
| VELPGNWTDVLAR         |
| DLGFETNVLAAAK         |
| DQGAIQMPATGHVSEFVAAGK|
| ISEVANEISSSRR         |
| NTVTLDPPGVLQISTAGHFK  |
| TVTGHAEEAEVTR         |
| YVFALVQETVK           |
| NLDAGATFLLQK          |
| GFIVLDLLSNAGLR        |
| SGATALFNFVEK          |
| DLVLQSLVR             |
| SWAFISAIPTSTEQGR      |
| LYPYPSGQAILAK         |
| GYGGLALVTNR           |
| IYNLNAAAAR            |
| LVAYHGYPVVQGSR        |
| AVLASSVGLIANAGLNGK    |
| APLGVLAIVNPVR         |

**Table S3. Peptide sequence of GCP02**

| AAAYALQESPVVNAVLDENEIVYR |
|--------------------------|
| AAAYVLQETPVVNALVDENEIVYR |
| YVIENEDLVANVPSEQLAYAAAR  |
| ESDGVDIASEK              |
| SDGGEVIASEK              |
| SAIDVEEGDSK              |
| VVDSAYEIJK               |
| VIDTAYEIJK               |
| IEYASDVVK                |
| GIIGIGIEIQQAEEQAAEFLK   |
| GIIGIGEGINAEEQAAEFLK    |
Table S4. Peptide sequence of FUGIS

| Peptide sequence | Highest similarity found to a known sequence (%) | Sequence origin |
|------------------|-----------------------------------------------|-----------------|
| LGDYGFNNALIVR    | 84.62                                         | *Bos taurus*    |
| Sequence                  | Percentage | Species                  |
|--------------------------|------------|--------------------------|
| DAFIGTFLYEYSR            | 92.31      | Bos taurus               |
| AAAVLQETPVPNALVDENEIVYR  | 83.33      | Caenorhabditis elegans   |
| SDGEVESIASSDK            | 90         | Drosophila melanogaster  |
| VIDTAYEIJK               | 90         | Caenorhabditis elegans   |
| GIIIGEGIGNEAGAAFLFK      | 86.36      | Caenorhabditis elegans   |
| VQNDSSIVFFDYR            | 83.41      | Caenorhabditis elegans   |
| VLEATAQDSFK              | 90.91      | Caenorhabditis elegans   |
| LVTWYDFGTYTNR            | 92.86      | Caenorhabditis elegans   |
| YAGEDAAAGAELTVFAK        | 83.33      | Caenorhabditis elegans   |
| AEIEAVQIAETLK            | 85.71      | Drosophila melanogaster  |
| VVEFLEHILDLVAGFR         | 82.35      | Drosophila melanogaster  |
| IVQVNLDDVK              | 90.91      | Drosophila melanogaster  |
| VGDVTVEVEAAVFLASK        | 82.35      | Drosophila melanogaster  |
| AGLAEIGDIK              | 90         | Drosophila melanogaster  |
| ANEIISDIINTPFK           | 85.71      | Drosophila melanogaster  |
| GIAEDFAPTFVK            | 83.33      | Drosophila melanogaster  |
| IADLEGIYK               | 88.89      | Drosophila melanogaster  |
| ALQDFEYKE               | 88.91      | Drosophila melanogaster  |
| ALVFETWQPMEVR            | 85.71      | Caenorhabditis elegans   |
| WVAIDGEOYEGSSR           | 80         | Caenorhabditis elegans   |
| LIDDNVANLX              | 83.33      | Caenorhabditis elegans   |
| VVDDAVYAVVIGAGGLR        | 89.47      | Caenorhabditis elegans   |
| YLYVVAR                 | 95.23      | Bos taurus               |
| FHGATSNLVDLDVTNPK        | 85.71      | Caenorhabditis elegans   |
| GTVAHDGDYLIVAK           | 85.71      | Caenorhabditis elegans   |
| TVEADAAGHSVTR            | 92.31      | Caenorhabditis elegans   |
| TIEADAAGHSSVTR           | 84.62      | Caenorhabditis elegans   |
| VVELITYIATK             | 81.82      | Caenorhabditis elegans   |
| YAVFDTGSR               | 88.89      | Caenorhabditis elegans   |
| VTENVLAFIYK             | 81.82      | Caenorhabditis elegans   |
| QLLFSAGAELNK            | 83.33      | Caenorhabditis elegans   |
| LDLGTGSPSVGPK            | 92.86      | Caenorhabditis elegans   |
| LGANTLELVIFGR           | 85.71      | Caenorhabditis elegans   |
| AFGGGNTQDFGR            | 90         | Caenorhabditis elegans   |
| VFQFLEASAGSK            | 83.33      | Caenorhabditis elegans   |
| LNADTSLFLASK            | 84.62      | Caenorhabditis elegans   |
| GQETSTQPITIFAWSR         | 88.24      | Caenorhabditis elegans   |
| AGQSHLGLPIFSGAVEAK       | 77.78      | Caenorhabditis elegans   |
| GVEPSHAISGAR            | 83.33      | Caenorhabditis elegans   |
| ALIANGTGPYFYLPK         | 93.33      | Caenorhabditis elegans   |
| NTVIASGGYGR             | 90.91      | Caenorhabditis elegans   |
| AAAAQINYIR              | 90.41      | Caenorhabditis elegans   |
| SGNVPVHGAVLR            | 86.67      | Caenorhabditis elegans   |
| VALLGAGAGNPLGLLLK       | 84.21      | Caenorhabditis elegans   |
| VPQVIAGLGLPAR           | 69.23      | Caenorhabditis elegans   |
| HLVEEPCPLIK             | 90.91      | Bos taurus               |
**Table S5. MBAQ vs. MS Western vs. Hi-3 of 1 Million Cells in 500 µL**  
*(SEM= Standard Error of Means)*

| Protein name | MBAQ (fmol) | SEM | MS Western (fmol) | SEM | Hi-3 quantification (fmol) | SEM | % Error (MBAQ vs MS Western) | % Error (Hi-3 vs MS Western) |
|--------------|-------------|-----|-------------------|-----|---------------------------|-----|-----------------------------|-------------------------------|
| PLK-1        | 1.6         | 0.04| 1.95              | 0.03| 1.62                      | 0.06| 17.95                       | 16.92                         |
| CAT          | 32.75       | 1.45| 42.97             | 1.04| 27.81                     | 1.08| 23.78                       | 35.28                         |
| TBA1A        | 2356.83     | 72.62| 2357.92          | 60.11| 2153.74                   | 70.32| 0.05                        | 8.66                          |
| GAPDH        | 4242.35     | 110.21| 4488.92         | 89.04| 3552.61                   | 74.32| 5.49                        | 20.86                         |

**Table S6. MBAQ vs. MS Western vs. Hi-3 of 1 Million Cells in 1000 µL**  
*(SEM= Standard Error of Means)*

| Protein name | MBAQ (fmol) | SEM | MS Western (fmol) | SEM | Hi-3 quantification (fmol) | SEM | % Error (MBAQ vs MS Western) | % Error (Hi-3 vs MS Western) |
|--------------|-------------|-----|-------------------|-----|---------------------------|-----|-----------------------------|-------------------------------|
| PLK-1        | 0.751       | 0.002| 0.852             | 0.005| 0.715                     | 0.009| 11.85                       | 16.08                         |
| CAT          | 17.65       | 1.82| 19.61             | 1.21| 15.75                     | 1.32| 9.99                        | 19.68                         |
| TBA1A        | 1243.14     | 85.42| 1226.09          | 70.21| 1037.04                   | 60.51| 1.39                        | 15.42                         |
| GAPDH        | 2266.94     | 63.25| 2364.12          | 59.12| 2066.41                   | 48.32| 4.11                        | 12.59                         |

**Table S7. Best N Peptides of 4 HeLa Proteins**

| Protein name | Best N peptides used                                                                 | %CV |
|--------------|-------------------------------------------------------------------------------------|-----|
| PLK-1*       | HINPVAASLIQK, FSIAPSSLDPSNR                                                         | 12.2|
| CAT          | FNTANDDNVTQVR, AFYVNVLNEEQR                                                         | 6.2 |
| TBA1A        | AVFVDLEPTVIDEVR, TIGGDDSFNFFSETGAGK,NLDIERPTYTNLNR                                 | 4.8 |
| GAPDH        | VPTANVSVDLTCR, LISYWYDNEFGYSNR, GILGYTEHQVVSSDFNDSSTHSSTFDAGAGIALNDHFVK             | 7.1 |
| Proteins | 1 million HeLa cells in 1000 µl (fmol) | 1 million HeLa cells in 500 µl (fmol) | Fold Change | Log2FC |
|----------|--------------------------------------|--------------------------------------|-------------|--------|
| sp|P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 | 4088.96 | 7353.35 | 1.80 | 0.85 |
| sp|P63261|ACTG_HUMAN Actin, cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1 | 3740.36 | 7013.21 | 1.88 | 0.91 |
| sp|Q6S8J3|POTEE_HUMAN POTE ankyrin domain family member E OS=Homo sapiens OX=9606 GN=POTEE PE=2 SV=3 | 2330.73 | 2402.03 | 1.03 | 0.04 |
| sp|P0CG39|POTEJ_HUMAN POTE ankyrin domain family member J OS=Homo sapiens OX=9606 GN=POTEJ PE=3 SV=1 | 2330.73 | 1622.79 | 0.70 | -0.52 |
| sp|P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3 | 2226.29 | 4307.67 | 1.93 | 0.95 |
| sp|P68032|ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1 | 1395.87 | 2340.83 | 1.68 | 0.75 |
| sp|P68104|EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1 | 1315.90 | 2412.97 | 1.83 | 0.87 |
| sp|P68363|TBA1B_HUMAN Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1 | 1253.39 | 2447.40 | 1.95 | 0.97 |
| sp|Q71U36|TBA1A_HUMAN Tubulin alpha-1A chain OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1 | 1243.14 | 2356.83 | 1.90 | 0.92 |
| sp|Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1 | 1175.81 | 2370.49 | 2.02 | 1.01 |
| sp|P68366|TBA4A_HUMAN Tubulin alpha-4A chain OS=Homo sapiens OX=9606 GN=TUBA4A | 1134.91 | 2257.92 | 1.99 | 0.99 |
| sp|P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2 | 926.28 | 1832.44 | 1.98 | 0.98 |
| Accession | Description | Symbol | OS | OX | GN | PE | SV | p | m/z | DPM | DPM/m/z |
|-----------|-------------|--------|----|----|----|----|----|---|---|-----|-------|----------|
| sp|P06733|ENOA_HUMAN Alpha-enolase| Homo sapiens | 9606 | ENO1 | 1 | 2 | 904.37 | 1521.40 | 1.68 | 0.75 | 0.67 |
| tr|K7EPT8|K7EPT8_HUMAN Glial fibrillary acidic protein (Fragment)| Homo sapiens | 9606 | GFAP | 1 | 2 | 718.96 | 482.84 | 0.67 | -0.57 | 0.67 |
| tr|A0A0A0MRX1|A0A0A0MRX1_HUMAN ELAV-like protein| Homo sapiens | 9606 | ELAVL2 | 1 | 1 | 689.90 | 762.32 | 1.10 | 0.14 | 0.67 |
| sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha| Homo sapiens | 9606 | HSP90AA1 | 1 | 5 | 645.76 | 1315.99 | 2.04 | 1.03 | 1.03 |
| sp|P62805|H4_HUMAN Histone H4| Homo sapiens | 9606 | HIST1H4A | 1 | 1 | 611.41 | 303.90 | 0.50 | -1.01 | -1.01 |
| sp|P68371|TBB4B_HUMAN Tubulin beta-4B chain| Homo sapiens | 9606 | TUBB4B | 1 | 1 | 594.16 | 1403.17 | 2.36 | 1.24 | 1.24 |
| sp|P11021|BIP_HUMAN Endoplasmic reticulum chaperone BIP| Homo sapiens | 9606 | HSPA5 | 1 | 2 | 581.80 | 1395.68 | 2.40 | 1.26 | 1.26 |
| sp|P07195|LDHB_HUMAN L-lactate dehydrogenase B chain| Homo sapiens | 9606 | LDHB | 1 | 2 | 579.65 | 1117.72 | 1.93 | 0.95 | 0.95 |
| sp|P04350|TBB4A_HUMAN Tubulin beta-4A chain| Homo sapiens | 9606 | TUBB4A | 1 | 2 | 575.87 | 1277.06 | 2.22 | 1.15 | 1.15 |
| sp|Q9BV01|TBB2B_HUMAN Tubulin beta-2B chain| Homo sapiens | 9606 | TUBB2B | 1 | 1 | 575.87 | 1277.06 | 2.22 | 1.15 | 1.15 |
| sp|Q13509|TBB3_HUMAN Tubulin beta-3 chain| Homo sapiens | 9606 | TUBB3 | 1 | 2 | 575.87 | 1277.06 | 2.22 | 1.15 | 1.15 |
| sp|Q9BUF5|TBB6_HUMAN Tubulin beta-6 chain| Homo sapiens | 9606 | TUBB6 | 1 | 1 | 575.87 | 1277.06 | 2.22 | 1.15 | 1.15 |
| sp|P00338|LDHA_HUMAN L-lactate dehydrogenase A chain| Homo sapiens | 9606 | LDHA | 1 | 2 | 549.56 | 980.09 | 1.78 | 0.83 | 0.83 |
| tr|H3BTA2|H3BTA2_HUMAN Serine/threonine-protein phosphatase (Fragment)| Homo sapiens | 9606 | PPP4C | 1 | 1 | 538.08 | 36.09 | 0.07 | -3.90 | -3.90 |
| Accession       | Description                                    | Homo sapiens   | OS      | OX      | GN     | PE | SV | 526.62 | 1182.21 | 2.24 | 1.17  |
|-----------------|-----------------------------------------------|----------------|---------|---------|--------|----|----|--------|---------|------|-------|
| sp|P0DMV8|HS71A_HUMAN Heat shock 70 kDa protein 1A | Homo sapiens   | OS=Homo sapiens   | OX=9606 | GN=HSPA1A | PE=1 | SV=1 | 526.62 | 1182.21 | 2.24 | 1.17  |
| sp|Q06830|PRDX1_HUMAN Peroxiredoxin-1 | Homo sapiens   | OX=9606 | GN=PRDX1 | PE=1 | SV=1 | 525.66 | 1453.85 | 2.77 | 1.47  |
| sp|P60174-1|TPIS_HUMAN Isoform 2 of Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TP1 | Homo sapiens   | OX=9606 | GN=TP1 | PE=1 | SV=1 | 518.29 | 412.50 | 0.80 | -0.33 |
| sp|P08670|VIME_HUMAN Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4 | Homo sapiens   | OX=9606 | GN=VIM | PE=1 | SV=4 | 506.97 | 687.10 | 1.36 | 0.44  |
| sp|P62937|PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=2 | Homo sapiens   | OX=9606 | GN=PPIA | PE=1 | SV=2 | 495.49 | 1836.04 | 3.71 | 1.89  |
| sp|P54652|HSP72_HUMAN Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1 | Homo sapiens   | OX=9606 | GN=HSPA2 | PE=1 | SV=1 | 469.04 | 1179.88 | 2.52 | 1.33  |
| tr|A0A2R8YFE2|A0A2R8YFE2_HUMAN Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 | Homo sapiens   | OX=9606 | GN=ACTB | PE=1 | SV=1 | 469.00 | 2336.02 | 4.98 | 2.32  |
| sp|P14618|KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4 | Homo sapiens   | OX=9606 | GN=PKM | PE=1 | SV=4 | 457.44 | 859.72 | 1.88 | 0.91  |
| sp|P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=2 | Homo sapiens   | OX=9606 | GN=HSPD1 | PE=1 | SV=2 | 417.31 | 747.53 | 1.79 | 0.84  |
| sp|P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=3 | Homo sapiens   | OX=9606 | GN=CFL1 | PE=1 | SV=3 | 412.68 | 1415.25 | 3.43 | 1.78  |
| sp|P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=2 | Homo sapiens   | OX=9606 | GN=ALDOA | PE=1 | SV=2 | 411.37 | 1026.12 | 2.49 | 1.32  |
| sp|Q8WXI7|MUC16_HUMAN Mucin-16 OS=Homo sapiens OX=9606 GN=MUC16 PE=1 SV=3 | Homo sapiens   | OX=9606 | GN=MUC16 | PE=1 | SV=3 | 406.82 | 724.08 | 1.78 | 0.83  |
| tr|A0A0J9YYC8|A0A0J9YYC8_HUMAN Trypsin-2 OS=Homo sapiens OX=9606 GN=PRSS2 PE=1 SV=1 | Homo sapiens   | OX=9606 | GN=PRSS2 | PE=1 | SV=1 | 402.25 | 7.90 | 0.02 | -5.67 |
| sp|Q58FF6|H90B4_HUMAN Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens OX=9606 GN=HSP90AB4 PE=5 | Homo sapiens   | OX=9606 | GN=HSP90AB4 | PE=5 | SV=5 | 388.15 | 594.44 | 1.53 | 0.61  |
| sp|P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 | Homo sapiens   | OX=9606 | GN=YWHAZ | PE=1 | SV=1 | 382.56 | 1140.22 | 2.98 | 1.58  |
| tr|Q53FA3|Q53FA3_HUMAN HSPA1L (Fragment) OS=Homo sapiens OX=9606 GN=HSPA1L PE=1 SV=1 | Homo sapiens   | OX=9606 | GN=HSPA1L | PE=1 | SV=1 | 380.88 | 1456.68 | 3.82 | 1.94  |
| sp|P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 PE=1 SV=3 | Homo sapiens   | OX=9606 | GN=PGK1 | PE=1 | SV=3 | 375.13 | 751.94 | 2.00 | 1.00  |
| tr|H0YA27|H0YA27_HUMAN Cyclin-I (Fragment) OS=Homo sapiens OX=9606 GN=CCNI PE=1 SV=1 | Homo sapiens   | OX=9606 | GN=CCNI | PE=1 | SV=1 | 365.10 | 653.46 | 1.79 | 0.84  |
| Gene ID | Description                                      | Organism   | Protein ID | Molecular Weight | pI | Fold Change |
|--------|--------------------------------------------------|------------|------------|-------------------|----|-------------|
| tr|M0R0M7|M0R0M7_HUMAN Syntaxin-binding protein 2 OS=Homo sapiens OX=9606 GN=STXBP2 PE=1 SV=1 | | 365.10 | 19.65 | 0.05 | -4.22 |
| sp|P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2 | | 364.39 | 822.60 | 2.26 | 1.17 |
| sp|P13639|EF2_HUMAN Elongation factor 2 OS=Homo sapiens OX=9606 GN=EF2 PE=1 SV=4 | | 364.14 | 100.17 | 0.28 | -1.86 |
| sp|P27797|CALR_HUMAN Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1 | | 362.86 | 1104.58 | 3.04 | 1.61 |
| tr|A0A0C4DG17|A0A0C4DG17_HUMAN 40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=1 | | 356.14 | 848.46 | 2.38 | 1.25 |
| sp|P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2 | | 351.94 | 226.27 | 0.64 | -0.64 |
| sp|P60842|IF4A1_HUMAN Eukaryotic initiation factor 4A-1 OS=Homo sapiens OX=9606 GN=EIF4A1 PE=1 SV=1 | | 345.54 | 592.08 | 1.71 | 0.78 |
| sp|P05388|RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 | | 327.34 | 699.40 | 2.14 | 1.10 |
| sp|P29401|TKT_HUMAN Isoform 2 of Transketolase OS=Homo sapiens OX=9606 GN=TKT | | 319.78 | 661.59 | 2.07 | 1.05 |
| sp|P61978|HNRPK_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK | | 319.39 | 382.18 | 1.20 | 0.26 |
| tr|A0A0U1RRM8|A0A0U1RRM8_HUMAN Fermitin family homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1 | | 313.63 | 6.24 | 0.02 | -5.65 |
| sp|P68431|H31_HUMAN Histone H3.1 OS=Homo sapiens OX=9606 GN=HIST1H3A PE=1 SV=2 | | 308.81 | 99.58 | 0.32 | -1.63 |
| tr|K7EK07|K7EK07_HUMAN Histone H3 (Fragment) OS=Homo sapiens OX=9606 GN=H3F3B PE=1 SV=1 | | 308.81 | 99.58 | 0.32 | -1.63 |
| sp|Q71DI3|H32_HUMAN Histone H3.2 OS=Homo sapiens OX=9606 GN=HIST2H3A PE=1 SV=3 | | 308.81 | 99.58 | 0.32 | -1.63 |
| sp|P05386|RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens OX=9606 GN=RPLP1 PE=1 SV=1 | | 305.50 | 1155.85 | 3.78 | 1.92 |
| tr|G8JLB6|G8JLB6_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1 | | 298.44 | 450.57 | 1.51 | 0.59 |
| tr|B5MDF5|B5MDF5_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=1 | | 296.10 | 578.25 | 1.95 | 0.97 |
| Accession     | Description                                                                 | Species          | Value   | Std. Dev. | Ratio | Fold Change |
|---------------|-----------------------------------------------------------------------------|------------------|---------|-----------|-------|-------------|
| sp|P27824-2|CALX_HUMAN Isoform 2 of Calnexin | Homo sapiens | 275.16  | 14.68  | 0.05 | -4.23 |
| tr|A0A0A0MTS2|Glucose-6-phosphate isomerase (Fragment) | Homo sapiens | 267.44  | 495.07  | 1.85 | 0.89 |
| sp|P07237|Protein disulfide-isomerase | Homo sapiens | 265.91  | 263.99  | 0.99 | -0.01 |
| tr|D6RB85|Calnexin (Fragment) | Homo sapiens | 265.71  | 56.42  | 0.21 | -2.24 |
| sp|P16403|Histone H1.2 | Homo sapiens | 244.74  | 408.21  | 1.67 | 0.74 |
| sp|P22626|Heterogeneous nuclear ribonucleoproteins A2/B1 | Homo sapiens | 244.49  | 835.24  | 3.42 | 1.77 |
| tr|A0A2R8Y811|40S ribosomal protein S14 (Fragment) | Homo sapiens | 241.53  | 78.53  | 0.33 | -1.62 |
| sp|O14556|Glyceraldehyde-3-phosphate dehydrogenase, testis-specific | Homo sapiens | 240.92  | 589.38  | 2.45 | 1.29 |
| sp|P38646|Stress-70 protein, mitochondrial | Homo sapiens | 229.03  | 412.85  | 1.80 | 0.85 |
| sp|Q96AY3|Peptidyl-prolyl cis-trans isomerase FKBP10 | Homo sapiens | 227.76  | 26.17  | 0.11 | -3.12 |
| tr|E7EQG2|Eukaryotic initiation factor 4A-II | Homo sapiens | 226.98  | 549.45  | 2.42 | 1.28 |
| sp|P37802-2|Transgelin-2 | Homo sapiens | 222.46  | 318.62  | 1.43 | 0.52 |
| sp|P30101|Protein disulfide-isomerase A3 | Homo sapiens | 219.71  | 258.77  | 1.18 | 0.24 |
| sp|P14625|Endoplasmic | Homo sapiens | 218.68  | 215.11  | 0.98 | -0.02 |
| sp|P62241|40S ribosomal protein S8 | Homo sapiens | 214.13  | 579.57  | 2.71 | 1.44 |
| sp|P62269|40S ribosomal protein S18 | Homo sapiens | 208.55  | 523.90  | 2.51 | 1.33 |
| tr|Q32Q12|Nucleoside diphosphate kinase | Homo sapiens | 204.47  | 724.04  | 3.54 | 1.82 |
| Accession | Description | Mass (Da) | Charge | pI | Similarity |
|-----------|-------------|-----------|--------|----|------------|
| sp|P15531-2|NDKA_HUMAN Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 | 204.47 | 724.04 | 3.54 | 1.82 |
| tr|H0YHX9|H0YHX9_HUMAN Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1 | 200.98 | 453.20 | 2.25 | 1.17 |
| sp|P15880|RS2_HUMAN 40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2 | 187.89 | 342.19 | 1.82 | 0.86 |
| sp|P62249|RS16_HUMAN 40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=2 | 186.77 | 479.64 | 2.57 | 1.36 |
| sp|P06748-2|NPM_HUMAN Isoform 2 of Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 | 185.67 | 276.56 | 1.49 | 0.57 |
| sp|P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2 | 185.66 | 570.82 | 3.07 | 1.62 |
| sp|P62081|RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1 | 185.12 | 174.80 | 0.94 | -0.08 |
| sp|P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens OX=9606 GN=PPIB PE=1 SV=2 | 182.40 | 439.20 | 2.41 | 1.27 |
| sp|P18669|PGAM1_HUMAN Phosphoglycerate mutase 1 OS=Homo sapiens OX=9606 GN=PGAM1 PE=1 SV=2 | 181.28 | 170.43 | 0.94 | -0.09 |
| sp|P63244|RACK1_HUMAN Receptor of activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=3 | 180.24 | 444.13 | 2.46 | 1.30 |
| sp|P26641-2|EF1G_HUMAN Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EF1G | 175.09 | 335.79 | 1.92 | 0.94 |
| sp|P50990|TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens OX=9606 GN=CCT8 PE=1 SV=4 | 173.24 | 334.00 | 1.93 | 0.95 |
| tr|E5RI99|E5RI99_HUMAN 60S ribosomal protein L30 (Fragment) OS=Homo sapiens OX=9606 GN=RPL30 PE=1 SV=1 | 172.03 | 370.97 | 2.16 | 1.11 |
| sp|P63241|IF5A1_HUMAN Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=2 | 171.93 | 387.53 | 2.25 | 1.17 |
| sp|Q58FG1|HS904_HUMAN Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens OX=9606 GN=HSP90AA4P PE=5 SV=1 | 167.90 | 385.20 | 2.29 | 1.20 |
| tr|A0A2R8Y4W8|A0A2R8Y4W8_HUMAN Girdin OS=Homo sapiens OX=9606 GN=CCDC88A PE=1 SV=1 | 166.46 | 98.08 | 0.59 | -0.76 |
| sp|P62851|RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens OX=9606 GN=RPS25 PE=1 SV=1 | 163.34 | 357.86 | 2.19 | 1.13 |
| Accession  | Description                                      | OS      | OX     | GN     | PE | SV | 162  | 122  | 0.75 | 0.41 |
|------------|--------------------------------------------------|---------|--------|--------|----|----|-------|------|------|------|
| sp|P48643|TCPE_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1 | Homo sapiens | 9606 | CCT5 | 1 | 1 | 162.72 | 122.27 | 0.75 | -0.41 |
| sp|P30050|RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens OX=9606 GN=RPL12 PE=1 SV=1 | Homo sapiens | 9606 | RPL12 | 1 | 1 | 162.42 | 312.89 | 1.93 | 0.95 |
| sp|P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2 | Homo sapiens | 9606 | ANXA1 | 1 | 2 | 162.08 | 330.58 | 2.04 | 1.03 |
| tr|G3V203|G3V203_HUMAN 60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=1 | Homo sapiens | 9606 | RPL18 | 1 | 1 | 158.78 | 510.99 | 3.22 | 1.69 |
| sp|Q9BR22|TRI56_HUMAN E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens OX=9606 GN=TRIM56 PE=1 SV=3 | Homo sapiens | 9606 | TRIM56 | 1 | 3 | 154.97 | 11.88 | 0.08 | -3.71 |
| tr|F5H157|F5H157_HUMAN Ras-related protein Rab-35 (Fragment) OS=Homo sapiens OX=9606 GN=RAB35 PE=1 SV=1 | Homo sapiens | 9606 | RAB35 | 1 | 1 | 154.46 | 313.69 | 2.03 | 1.02 |
| sp|P61026|RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens OX=9606 GN=RAB10 PE=1 SV=1 | Homo sapiens | 9606 | RAB10 | 1 | 1 | 154.46 | 313.69 | 2.03 | 1.02 |
| sp|P61006|RAB8A_HUMAN Ras-related protein Rab-8A OS=Homo sapiens OX=9606 GN=RAB8A PE=1 SV=1 | Homo sapiens | 9606 | RAB8A | 1 | 1 | 154.46 | 313.69 | 2.03 | 1.02 |
| sp|P14174|MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens OX=9606 GN=MIF PE=1 SV=4 | Homo sapiens | 9606 | MIF | 1 | 4 | 154.30 | 575.93 | 3.73 | 1.90 |
| tr|A0A1B0GTU8|A0A1B0GTU8_HUMAN Renin receptor OS=Homo sapiens OX=9606 GN=ATP6AP2 PE=1 SV=1 | Homo sapiens | 9606 | ATP6AP2 | 1 | 1 | 152.73 | 13.44 | 0.09 | -3.51 |
| sp|P54727|RD23B_HUMAN UV excision repair protein RAD23 homolog B OS=Homo sapiens OX=9606 GN=RAD23B PE=1 SV=1 | Homo sapiens | 9606 | RAD23B | 1 | 1 | 152.13 | 28.62 | 0.19 | -2.41 |
| tr|H7BZ3|H7BZ3_HUMAN Protein disulfide-isomerase A3 (Fragment) OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=1 | Homo sapiens | 9606 | PDIA3 | 1 | 1 | 149.29 | 253.79 | 1.70 | 0.77 |
| sp|P62854|RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens OX=9606 GN=RPS26 PE=1 SV=3 | Homo sapiens | 9606 | RPS26 | 1 | 3 | 149.15 | 53.14 | 0.36 | -1.49 |
| sp|P61247|RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=2 | Homo sapiens | 9606 | RPS3A | 1 | 2 | 149.15 | 205.93 | 1.38 | 0.47 |
| sp|P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=3 | Homo sapiens | 9606 | ATP5F1B | 1 | 3 | 148.57 | 271.61 | 1.83 | 0.87 |
| sp|P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=2 | Homo sapiens | 9606 | SERPINH1 | 1 | 2 | 148.28 | 277.94 | 1.87 | 0.91 |
| sp|P81605|DCD_HUMAN Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2 | Homo sapiens | 9606 | DCD | 1 | 2 | 147.65 | 67.80 | 0.46 | -1.12 |
| tr|M0R0F0|M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=1 | Homo sapiens | 9606 | RPS5 | 1 | 1 | 147.58 | 575.63 | 3.90 | 1.96 |
| Accession | Description | OS       | OX     | GN     | PE | SV | Mw   | Mr   | pI   |
|-----------|-------------|----------|--------|--------|----|----|------|------|------|
| tr|A0A0U1RRM4|A0A0U1RRM4_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1 | 146.10 | 42.68 | 0.29 | -1.78 |
| sp|P46783|RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens OX=9606 GN=RPS10 PE=1 SV=1 | 145.43 | 408.47 | 2.81 | 1.49 |
| sp|P30041|PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens OX=9606 GN=PRDX6 PE=1 SV=3 | 144.63 | 283.14 | 1.96 | 0.97 |
| tr|V9GZ17|V9GZ17_HUMAN Tubulin alpha-8 chain (Fragment) OS=Homo sapiens OX=9606 GN=TUBA8 PE=1 SV=1 | 144.62 | 328.83 | 2.27 | 1.19 |
| sp|P62277|RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens OX=9606 GN=RPS13 PE=1 SV=2 | 142.19 | 340.74 | 2.40 | 1.26 |
| sp|P36578|RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5 | 141.39 | 252.19 | 1.78 | 0.83 |
| sp|Q01650|LAT1_HUMAN Large neutral amino acids transporter small subunit 1 OS=Homo sapiens OX=9606 GN=SLC7A5 PE=1 SV=2 | 139.63 | 81.21 | 0.58 | -0.78 |
| sp|Q02878|RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3 | 138.94 | 388.74 | 2.80 | 1.48 |
| sp|P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens OX=9606 GN=TUFM PE=1 SV=2 | 138.46 | 254.76 | 1.84 | 0.88 |
| sp|Q15084|PDIA6_HUMAN Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 | 138.19 | 147.72 | 1.07 | 0.10 |
| sp|P62244|RS15A_HUMAN 40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 SV=2 | 136.16 | 371.64 | 2.73 | 1.45 |
| sp|Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2 | 134.37 | 206.86 | 1.54 | 0.62 |
| sp|P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1 | 134.09 | 301.54 | 2.25 | 1.17 |
| sp|P00966|ASSY_HUMAN Argininosuccinate synthase OS=Homo sapiens OX=9606 GN=ASS1 PE=1 SV=2 | 132.36 | 259.68 | 1.96 | 0.97 |
| sp|P62701|RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens OX=9606 GN=RPS4X PE=1 SV=2 | 129.69 | 256.55 | 1.98 | 0.98 |
| sp|O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens OX=9606 GN=CLIC1 PE=1 SV=4 | 129.48 | 115.21 | 0.89 | -0.17 |
| tr|J3KPF3|J3KPF3_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 | 129.04 | 264.47 | 2.05 | 1.04 |
| Accession  | Description                                      | OS       | OX      | GN      | PE  | SV  | IUPM   | pG   | pI   |
|------------|--------------------------------------------------|----------|---------|---------|-----|-----|--------|------|------|
| sp|P18124|RL7_HUMAN 60S ribosomal protein L7 | Homo sapiens | 9606 | RPL7 | 1 | 1 | 127.52 | 206.78 | 1.62 | 0.70 |
| sp|P23396|RS3_HUMAN 40S ribosomal protein S3 | Homo sapiens | 9606 | RPS3 | 1 | 2 | 123.54 | 431.74 | 3.49 | 1.81 |
| sp|P47914|RL29_HUMAN 60S ribosomal protein L29 | Homo sapiens | 9606 | RPL29 | 1 | 2 | 123.54 | 181.95 | 1.47 | 0.56 |
| sp|Q5VT79|AXA81_HUMAN Annexin A8-like protein 1 | Homo sapiens | 9606 | ANXA8L1 | 2 | 2 | 123.37 | 369.55 | 3.00 | 1.58 |
| sp|P38919|LS3_HUMAN 40S ribosomal protein S3 | Homo sapiens | 9606 | RPS3 | 1 | 4 | 123.19 | 228.49 | 1.85 | 0.89 |
| sp|P62424|RL7A_HUMAN 60S ribosomal protein L7a | Homo sapiens | 9606 | RPL7A | 1 | 2 | 123.11 | 335.43 | 2.72 | 1.45 |
| sp|Q9UQ80|PA2G4_HUMAN Proliferation-associated protein 2G4 | Homo sapiens | 9606 | PA2G4 | 1 | 3 | 121.35 | 216.66 | 1.79 | 0.84 |
| sp|P05141|ADT2_HUMAN ADP/ATP translocase 2 | Homo sapiens | 9606 | SLC25A5 | 1 | 7 | 121.15 | 205.42 | 1.70 | 0.76 |
| tr|A0A024R4M0|A0A024R4M0_HUMAN 40S ribosomal protein S9 | Homo sapiens | 9606 | RPS9 | 1 | 2 | 120.94 | 375.10 | 3.10 | 1.63 |
| sp|P78371|TCPB_HUMAN T-complex protein 1 subunit beta | Homo sapiens | 9606 | CCT2 | 1 | 4 | 120.75 | 546.76 | 4.53 | 2.18 |
| tr|J3KTE4|J3KTE4_HUMAN Ribosomal protein L19 | Homo sapiens | 9606 | RPL19 | 1 | 1 | 120.50 | 59.85 | 0.50 | -1.01 |
| tr|E7EQR4|E7EQR4_HUMAN Ezrin | Homo sapiens | 9606 | EZR | 1 | 3 | 120.21 | 179.43 | 1.49 | 0.58 |
| tr|A0A004MR02|A0A004MR02_HUMAN Voltage-dependent anion-selective channel protein 2 (Fragment) | Homo sapiens | 9606 | VDAC2 | 1 | 1 | 118.53 | 239.80 | 2.02 | 1.02 |
| sp|P35232|PHB_HUMAN Prohibitin | Homo sapiens | 9606 | PHB | 1 | 1 | 116.63 | 260.65 | 2.23 | 1.16 |
| sp|P26038|MOES_HUMAN Moesin | Homo sapiens | 9606 | MSN | 1 | 3 | 116.61 | 262.88 | 2.25 | 1.17 |
| tr|F8W6I7|F8W6I7_HUMAN Heterogeneous nuclear ribonucleoprotein A1 | Homo sapiens | 9606 | HNRNPA1 | 1 | 2 | 115.87 | 252.96 | 2.18 | 1.13 |
| tr|H0YIV4|H0YIV4_HUMAN Nucleosome assembly protein 1-like 1 (Fragment) | Homo sapiens | 9606 | NAP1L1 | 1 | 1 | 115.41 | 145.08 | 1.26 | 0.33 |
| sp|P52272-2|HNRPM_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein M | Homo sapiens | 9606 | HNRNPM | 1 | 1 | 115.18 | 221.93 | 1.93 | 0.95 |
| Accession | Description | OS | OX | GN | PE | SV | Fold Change | Difference |
|-----------|-------------|----|----|----|----|----|-------------|-------------|
| sp|Q16658|FSCN1 HUMAN Fascin | Homo sapiens | 9606 | FSCN1 | 1 | 3 | 114.88 | 152.33 | 1.33 | 0.41 |
| tr|A0A2R8Y5SS7|A0A2R8Y5SS7 HUMAN Radixin | Homo sapiens | 9606 | RDX | 1 | 1 | 114.62 | 262.88 | 2.29 | 1.20 |
| sp|P02545|LMNA HUMAN Prelamin-A/C | Homo sapiens | 9606 | LMNA | 1 | 1 | 114.47 | 113.18 | 0.99 | -0.02 |
| sp|P62906|RL10A HUMAN 60S ribosomal protein L10a | Homo sapiens | 9606 | RPL10A | 1 | 2 | 113.80 | 121.60 | 1.07 | 0.10 |
| sp|Q8WZ42-11|TITIN_HUMAN Isoform 11 of Titin | Homo sapiens | 9606 | TTN | 1 | 1 | 113.18 | 5.19 | 0.05 | -4.45 |
| tr|B2R5W2|B2R5W2 HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 | Homo sapiens | 9606 | HNRNPC | 1 | 1 | 113.14 | 106.94 | 0.95 | -0.08 |
| sp|P12277|KCRB_HUMAN Creatine kinase B-type | Homo sapiens | 9606 | CKB | 1 | 1 | 112.82 | 219.66 | 1.95 | 0.96 |
| sp|P50502|F10A1_HUMAN ADP/ATP translocase 3 | Homo sapiens | 9606 | ST13 | 1 | 4 | 107.65 | 130.86 | 1.22 | 0.28 |
| sp|P61353|RL27 HUMAN 60S ribosomal protein L27 | Homo sapiens | 9606 | RPL27 | 1 | 2 | 110.28 | 241.83 | 2.19 | 1.13 |
| sp|P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 | Homo sapiens | 9606 | VDAC1 | 1 | 2 | 110.19 | 276.11 | 2.51 | 1.33 |
| sp|P40227|TCPZ_HUMAN T-complex protein 1 subunit zeta | Homo sapiens | 9606 | CCT6A | 1 | 3 | 109.07 | 218.48 | 2.00 | 1.00 |
| tr|A0A286YF22|A0A286YF22 HUMAN D-3-phosphoglycerate dehydrogenase | Homo sapiens | 9606 | PHGDH | 1 | 1 | 107.97 | 198.44 | 1.84 | 0.88 |
| sp|P12236|ADT3_HUMAN ADP/ATP translocase 3 | Homo sapiens | 9606 | SLC25A6 | 1 | 4 | 107.65 | 130.86 | 1.22 | 0.28 |
| tr|A0A087WXM6|A0A087WXM6 HUMAN 60S ribosomal protein L17 (Fragment) | Homo sapiens | 9606 | RPL17 | 1 | 3 | 105.49 | 113.12 | 1.07 | 0.10 |
| tr|E7EPB3|E7EPB3 HUMAN 60S ribosomal protein L14 | Homo sapiens | 9606 | RPL14 | 1 | 1 | 105.49 | 113.12 | 1.07 | 0.10 |
| sp|P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial | Homo sapiens | 9606 | HSPE1 | 1 | 2 | 105.06 | 159.60 | 1.52 | 0.60 |
| sp|P31946-2|1433B_HUMAN Isoform Short of 14-3-3 protein beta/alpha | Homo sapiens | 9606 | YWHAB | 1 | 1 | 104.27 | 246.52 | 2.36 | 1.24 |
| tr|A0A0B4J1R4|A0A0B4J1R4_HUMAN 4-hydroxyphenylpyruvate dioxygenase | Homo sapiens | 9606 | HPD | 1 | 1 | 101.52 | 135.67 | 1.34 | 0.42 |
| Accession Number | Description | Species | Organism | Gene Name | Protein Level | Fold Change | p-Value |
|------------------|-------------|---------|----------|-----------|--------------|-------------|---------|
| sp|P09382|LEG1_HUMAN Galectin-1 | Homo sapiens | OX=9606 | GN=LGALS1 | PE=1 | SV=2 | 101.49 | 64.93 | 0.64 | -0.64 |
| sp|P30048-2|PRDX3_HUMAN Isoform 2 of Thioredoxin-dependent peroxide reductase, mitochondrial | Homo sapiens | OX=9606 | GN=PRDX3 | PE=1 | SV=2 | 100.77 | 258.29 | 2.56 | 1.36 |
| sp|Q99832|TCPH_HUMAN T-complex protein 1 subunit eta | Homo sapiens | OX=9606 | GN=CCT7 | PE=1 | SV=2 | 100.40 | 151.21 | 1.51 | 0.59 |
| sp|P62258|1433E_HUMAN 14-3-3 protein epsilon | Homo sapiens | OX=9606 | GN=YWHAE | PE=1 | SV=1 | 99.86 | 249.66 | 2.50 | 1.32 |
| sp|P23526|SAHH_HUMAN Adenosylhomocysteinase | Homo sapiens | OX=9606 | GN=AHCY | PE=1 | SV=2 | 99.51 | 214.37 | 2.15 | 1.11 |
| sp|P39019|RS19_HUMAN 40S ribosomal protein S19 | Homo sapiens | OX=9606 | GN=RPS19 | PE=1 | SV=2 | 99.20 | 238.51 | 2.40 | 1.27 |
| sp|P67809|YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 | Homo sapiens | OX=9606 | GN=YBX1 | PE=1 | SV=3 | 97.19 | 233.91 | 2.41 | 1.27 |
| tr|C9J4Z3|C9J4Z3_HUMAN 60S ribosomal protein L37a | Homo sapiens | OX=9606 | GN=RPL37A | PE=1 | SV=1 | 97.02 | 266.24 | 2.74 | 1.46 |
| sp|P84077|ARF1_HUMAN ADP-ribosylation factor 1 | Homo sapiens | OX=9606 | GN=ARF1 | PE=1 | SV=2 | 96.96 | 250.48 | 2.58 | 1.37 |
| sp|P52597|HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F | Homo sapiens | OX=9606 | GN=HNRNPF | PE=1 | SV=3 | 94.16 | 178.24 | 1.89 | 0.92 |
| sp|P63173|RL38_HUMAN 60S ribosomal protein L38 | Homo sapiens | OX=9606 | GN=RPL38 | PE=1 | SV=2 | 92.97 | 226.96 | 2.44 | 1.29 |
| tr|J3KPX7|J3KPX7_HUMAN Prohibitin-2 | Homo sapiens | OX=9606 | GN=PHB2 | PE=1 | SV=2 | 92.80 | 269.60 | 2.91 | 1.54 |
| sp|Q13162|PRDX4_HUMAN Peroxiredoxin-4 | Homo sapiens | OX=9606 | GN=PRDX4 | PE=1 | SV=1 | 92.41 | 246.06 | 2.66 | 1.41 |
| tr|A0A087WUS0|A0A087WUS0_HUMAN 40S ribosomal protein S24 | Homo sapiens | OX=9606 | GN=RPS24 | PE=1 | SV=1 | 91.04 | 256.86 | 2.82 | 1.50 |
| sp|O43760-2|SGN2_HUMAN Isoform 2 of Synaptogyrin-2 | Homo sapiens | OX=9606 | GN=SYNGR2 | PE=1 | SV=1 | 90.71 | 89.11 | 0.98 | -0.03 |
| sp|P32119|PRDX2_HUMAN Peroxiredoxin-2 | Homo sapiens | OX=9606 | GN=PRDX2 | PE=1 | SV=5 | 90.70 | 212.99 | 2.35 | 1.23 |
| sp|Q14019|COTL1_HUMAN Coactosin-like protein | Homo sapiens | OX=9606 | GN=COTL1 | PE=1 | SV=3 | 90.15 | 76.74 | 0.85 | -0.23 |
| Accession  | Description                                                                 | Oxidation | Redox | pH      | pI      |
|------------|------------------------------------------------------------------------------|-----------|-------|---------|---------|
| sp|P00441|SODC_HUMAN Superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD1 PE=1 SV=2 | 90.08     | 43.68 | 0.48    | -1.04   |
| sp|P55795|HNRH2_HUMAN Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNPH2 PE=1 SV=1 | 89.37     | 140.15| 1.57    | 0.65    |
| tr|D6R9P3|D6R9P3_HUMAN Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=1 | 89.15     | 204.21| 2.29    | 1.20    |
| sp|P84103-2|SRSF3_HUMAN Isoform 2 of Serine/arginine-rich splicing factor 3 OS=Homo sapiens OX=9606 GN=SRSF3 | 89.08     | 236.64| 2.66    | 1.41    |
| tr|M0R117|M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens OX=9606 GN=RPL18A PE=1 SV=1 | 88.95     | 187.23| 2.10    | 1.07    |
| sp|P62857|RS28_HUMAN 40S ribosomal protein S28 OS=Homo sapiens OX=9606 GN=RPS28 PE=1 SV=1 | 88.83     | 199.70| 2.25    | 1.17    |
| sp|P35613-2|BASI_HUMAN Isoform 2 of Basigin OS=Homo sapiens OX=9606 GN=BSG | 88.56     | 113.44| 1.28    | 0.36    |
| sp|P06703|S10A6_HUMAN Protein S100-A6 OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1 | 87.98     | 165.76| 1.88    | 0.91    |
| sp|P32969|RL9_HUMAN 60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1 | 87.89     | 187.85| 2.14    | 1.10    |
| tr|A0A1B0GV23|A0A1B0GV23_HUMAN Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 | 86.35     | 16.46 | 0.19    | -2.39   |
| sp|P07954-2|FUMH_HUMAN Isoform Cytoplasmic of Fumarate hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=FH | 85.61     | 178.32| 2.08    | 1.06    |
| tr|P8W1A4|P8W1A4_HUMAN Adenylate kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1 | 85.14     | 164.73| 1.93    | 0.95    |
| sp|P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens OX=9606 GN=PDIA4 PE=1 SV=2 | 84.18     | 248.95| 2.96    | 1.56    |
| sp|P50991|TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4 | 83.52     | 147.57| 1.77    | 0.82    |
| sp|P62280|RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens OX=9606 GN=RPS11 PE=1 SV=3 | 83.34     | 177.08| 2.12    | 1.09    |
| sp|P00505|AATM_HUMAN Aspartate aminotransferase, mitochondrial OS=Homo sapiens OX=9606 GN=GOT2 PE=1 SV=3 | 81.99     | 146.42| 1.79    | 0.84    |
| sp|P31689|DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens OX=9606 GN=DNJA1 PE=1 SV=2 | 81.43     | 150.89| 1.85    | 0.89    |
| sp|P55072|TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=4 | 80.27     | 13.13 | 0.16    | -2.61   |
| Accession   | Description                                                                 | Species          | Protein ID | Hs Gene ID | Score | Identities | Coverage | Value |
|-------------|-------------------------------------------------------------------------------|------------------|------------|------------|-------|------------|----------|-------|
| sp|P19338|NUCL_HUMAN Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3 | 80.05 | 196.72 | 2.46 | 1.30 |
| tr|A0A0B4J1Z1|A0A0B4J1Z1_HUMAN Serine/arginine-rich-splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 PE=1 SV=1 | 80.03 | 158.50 | 1.98 | 0.99 |
| sp|P26639|SYTC_HUMAN Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=TARS PE=1 SV=3 | 79.88 | 202.52 | 2.54 | 1.34 |
| sp|P62273|RS29_HUMAN 40S ribosomal protein S29 OS=Homo sapiens OX=9606 GN=RPS29 PE=1 SV=2 | 79.00 | 60.82 | 0.77 | -0.38 |
| sp|P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3 | 77.97 | 192.45 | 2.47 | 1.30 |
| sp|P40925|MDHC_HUMAN Isoform 3 of Malate dehydrogenase, cytoplasmic OS=Homo sapiens OX=9606 GN=MDH1 | 77.23 | 193.27 | 2.50 | 1.32 |
| sp|P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2 | 77.20 | 170.90 | 2.21 | 1.15 |
| sp|P40805|ARF5_HUMAN ADP-ribosylation factor 5 OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=2 | 77.08 | 515.69 | 6.69 | 2.74 |
| sp|P18085|ARF4_HUMAN ADP-ribosylation factor 4 OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=3 | 77.08 | 515.69 | 6.69 | 2.74 |
| sp|P15121|ALDR_HUMAN Aldose reductase OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1 SV=3 | 76.07 | 176.46 | 2.32 | 1.21 |
| sp|P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 | 75.99 | 128.33 | 1.69 | 0.76 |
| sp|P26373|RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RPL13 PE=1 SV=4 | 75.94 | 431.20 | 5.68 | 2.51 |
| sp|P38159|RBMX_HUMAN RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1 SV=3 | 75.91 | 73.89 | 0.97 | -0.04 |
| sp|P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 | 74.67 | 99.95 | 1.34 | 0.42 |
| sp|P25398|RS12_HUMAN 40S ribosomal protein S12 OS=Homo sapiens OX=9606 GN=RPS12 PE=1 SV=3 | 74.21 | 175.39 | 2.36 | 1.24 |
| sp|P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1 | 74.11 | 182.37 | 2.46 | 1.30 |
| sp|O75396|SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens OX=9606 GN=SEC22B PE=1 SV=4 | 74.04 | 24.74 | 0.33 | -1.58 |
| sp|P28066|PSA5_HUMAN Proteasome subunit alpha type-5 OS=Homo sapiens OX=9606 GN=PSMA5 PE=1 SV=3 | 73.63 | 75.11 | 1.02 | 0.03 |
| Accession   | Description                                                   | OS             | OX             | GN     | PE   | SV  | A   | R   | L   |
|-------------|--------------------------------------------------------------|----------------|----------------|--------|------|-----|-----|-----|-----|
| sp|P16401|H15_HUMAN Histone H1.5                                       | Homo sapiens   | 9606           | HIST1H1B | 1   | 3   | 73.31 | 66.74 | 0.91 | -0.14 |
| sp|P49368|TCPG_HUMAN T-complex protein 1 subunit gamma                 | Homo sapiens   | 9606           | HNRNPA0  | 1   | 4   | 73.08 | 184.43 | 2.52 | 1.34  |
| sp|P30086|PEBP1_HUMAN Phosphatidylethanolamine-binding protein 1      | Homo sapiens   | 9606           | PEBP1    | 1   | 3   | 72.98 | 202.02 | 2.77 | 1.47  |
| sp|Q13151|ROA0_HUMAN Heterogeneous nuclear ribonucleoprotein A0       | Homo sapiens   | 9606           | HNRNPA0  | 1   | 1   | 72.90 | 151.75 | 2.08 | 1.06  |
| sp|P51991|ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3       | Homo sapiens   | 9606           | HNRNPA3  | 1   | 2   | 72.49 | 170.79 | 2.36 | 1.24  |
| sp|Q04917|1433F_HUMAN 14-3-3 protein eta                              | Homo sapiens   | 9606           | YWHAH    | 1   | 4   | 71.82 | 211.89 | 2.95 | 1.56  |
| sp|Q01105|SET_HUMAN Protein SET                                        | Homo sapiens   | 9606           | SET      | 1   | 1   | 71.75 | 102.79 | 1.43 | 0.52  |
| sp|Q96AG4|LRC59_HUMAN Leucine-rich repeat-containing protein 59       | Homo sapiens   | 9606           | LRRC59   | 1   | 3   | 69.53 | 188.98 | 2.72 | 1.44  |
| sp|P11940|PABP1_HUMAN Polyadenylate-binding protein 1                  | Homo sapiens   | 9606           | PABPC1   | 1   | 2   | 69.34 | 132.64 | 1.91 | 0.94  |
| tr|E9PLL6|E9PLL6_HUMAN 60S ribosomal protein L27a                     | Homo sapiens   | 9606           | RPL27A   | 1   | 1   | 69.00 | 145.43 | 2.11 | 1.08  |
| sp|P49643|PRI2_HUMAN DNA primase large subunit                        | Homo sapiens   | 9606           | PRIM2    | 1   | 2   | 68.80 | 16.08  | 0.23 | -2.10 |
| sp|Q6EEV6|SUMO4_HUMAN Small ubiquitin-related modifier 4              | Homo sapiens   | 9606           | SUMO4    | 1   | 2   | 68.75 | 96.14  | 1.40 | 0.48  |
| tr|C9JNW5|C9JNW5_HUMAN 60S ribosomal protein L24                       | Homo sapiens   | 9606           | RPL24    | 1   | 1   | 68.61 | 242.59 | 3.54 | 1.82  |
| sp|P62917|RL8_HUMAN 60S ribosomal protein L8                          | Homo sapiens   | 9606           | RPL8     | 1   | 2   | 68.57 | 178.01 | 2.60 | 1.38  |
| sp|Q9H0U4|RAB1B_HUMAN Ras-related protein Rab-1B                     | Homo sapiens   | 9606           | RAB1B    | 1   | 1   | 68.30 | 182.91 | 2.68 | 1.42  |
| sp|P62820|RAB1A_HUMAN Ras-related protein Rab-1A                     | Homo sapiens   | 9606           | RAB1A    | 1   | 3   | 68.30 | 182.91 | 2.68 | 1.42  |
| sp|Q14974|IMB1_HUMAN Importin subunit beta-1                         | Homo sapiens   | 9606           | KPNB1    | 1   | 2   | 67.41 | 32.99  | 0.49 | -1.03 |
| Accession | Description | Peptide | Mw (kDa) | pI | M+H (ppm) |
|-----------|-------------|---------|----------|----|------------|
| sp|Q02790|FKBP4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens OX=9606 GN=FKBP4 PE=1 SV=3 | 67.32 | 121.01 | 1.80 | 0.85 |
| tr|A0A1C7CYX9|A0A1C7CYX9_HUMAN Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 PE=1 SV=1 | 64.96 | 30.79 | 0.47 | -1.08 |
| sp|P39748|FEN1_HUMAN Flap endonuclease 1 OS=Homo sapiens OX=9606 GN=FEN1 PE=1 SV=3 | 64.89 | 104.61 | 1.61 | 0.69 |
| sp|P35637-2|FUS_HUMAN Isoform Short of RNA-binding protein FUS OS=Homo sapiens OX=9606 GN=FUS | 64.17 | 98.28 | 1.53 | 0.62 |
| sp|O14818|PSA7_HUMAN Proteasome subunit alpha type-7 OS=Homo sapiens OX=9606 GN=PSMA7 PE=1 SV=1 | 63.74 | 178.98 | 2.81 | 1.49 |
| sp|P60866-2|RS20_HUMAN Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens OX=9606 GN=RPS20 | 63.56 | 185.66 | 2.92 | 1.55 |
| sp|P62879|GBB2_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens OX=9606 GN=GNB2 PE=1 SV=3 | 63.43 | 66.91 | 1.05 | 0.08 |
| sp|P62873-2|GBB1_HUMAN Isoform 2 of Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens OX=9606 GN=GNB1 | 63.43 | 23.19 | 0.37 | -1.45 |
| sp|Q9HAV0|GBB4_HUMAN Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens OX=9606 GN=GNB4 PE=1 SV=3 | 63.43 | 14.62 | 0.23 | -2.12 |
| sp|P12956|XRCC6_HUMAN X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=2 | 63.28 | 148.84 | 2.35 | 1.23 |
| tr|A0A0C4DG40|A0A0C4DG40_HUMAN Nesprin-1 OS=Homo sapiens OX=9606 GN=SYNE1 PE=1 SV=1 | 62.74 | 195.44 | 3.11 | 1.64 |
| sp|P29692|EF1D_HUMAN Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=5 | 62.66 | 216.01 | 3.45 | 1.79 |
| sp|P10599|THIO_HUMAN Thioredoxin OS=Homo sapiens OX=9606 GN=TXN PE=1 SV=3 | 62.27 | 150.47 | 2.42 | 1.27 |
| tr|H0Y5E5|H0Y5E5_HUMAN Plakophilin-3 (Fragment) OS=Homo sapiens OX=9606 GN=PKP3 PE=1 SV=1 | 61.89 | 193.91 | 3.13 | 1.65 |
| sp|Q12931-2|TRAP1_HUMAN Isoform 2 of Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens OX=9606 GN=TRAP1 | 61.39 | 150.52 | 2.45 | 1.29 |
| sp|P18077|RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens OX=9606 GN=RPL35A PE=1 SV=2 | 61.28 | 94.96 | 1.55 | 0.63 |
| Accession | Description                                    | OS   | OX   | GN   | PE  | SV  | Score | M.S.D | Score | M.S.D | Score | M.S.D |
|-----------|-----------------------------------------------|------|------|------|-----|-----|-------|-------|-------|-------|-------|-------|
| sp|P24534|EF1B_HUMAN Elongation factor 1-beta OS=Homo sapiens OX=9606 GN=EEF1B2 PE=1 SV=3 | Homo sapiens | 9606 | EEF1B2 | 1 | 3 | 60.56 | 147.00 | 2.43 | 1.28 |
| tr|A0A087WSW9|A0A087WSW9_HUMAN Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens OX=9606 GN=TXNRD1 PE=1 SV=1 | Homo sapiens | 9606 | TXNRD1 | 1 | 1 | 60.26 | 121.91 | 2.02 | 1.02 |
| tr|M0QYS1|M0QYS1_HUMAN 60S ribosomal protein L13a (Fragment) OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2 | Homo sapiens | 9606 | RPL13A | 1 | 2 | 60.24 | 156.34 | 2.60 | 1.38 |
| sp|P23381|SYWC_HUMAN Tryptophan-tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=WARS PE=1 SV=2 | Homo sapiens | 9606 | WARS | 1 | 2 | 60.24 | 107.39 | 1.78 | 0.83 |
| sp|P50395|GDIB_HUMAN Rab GDP dissociation inhibitor beta OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=2 | Homo sapiens | 9606 | GDI2 | 1 | 2 | 60.16 | 103.29 | 1.72 | 0.78 |
| sp|Q99497|PARK7_HUMAN Protein/nucleic acid de glycase DJ-1 OS=Homo sapiens OX=9606 GN=PARK7 PE=1 SV=2 | Homo sapiens | 9606 | PARK7 | 1 | 2 | 60.15 | 123.86 | 2.06 | 1.04 |
| tr|D3YTB1|D3YTB1_HUMAN 60S ribosomal protein L32 (Fragment) OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=1 | Homo sapiens | 9606 | RPL32 | 1 | 1 | 59.54 | 59.52 | 1.00 | 0.00 |
| tr|E9PBS1|E9PBS1_HUMAN Multifunctional protein ADE2 (Fragment) OS=Homo sapiens OX=9606 GN=PAICS PE=1 SV=1 | Homo sapiens | 9606 | PAICS | 1 | 1 | 58.71 | 143.50 | 2.44 | 1.29 |
| sp|P09972|ALDOC_HUMAN Fructose-bisphosphate aldolase C OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=2 | Homo sapiens | 9606 | ALDOC | 1 | 2 | 57.49 | 239.47 | 4.17 | 2.06 |
| tr|B4DJV2|B4DJV2_HUMAN Citrate synthase OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 | Homo sapiens | 9606 | CS | 1 | 1 | 57.39 | 105.29 | 1.83 | 0.88 |
| tr|H0YIC4|H0YIC4_HUMAN Citrate synthase (Fragment) OS=Homo sapiens OX=9606 GN=CS PE=1 SV=1 | Homo sapiens | 9606 | CS | 1 | 1 | 57.39 | 90.92 | 1.58 | 0.66 |
| tr|Q5VV89|Q5VV89_HUMAN Microsomal glutathione S-transferase 3 OS=Homo sapiens OX=9606 GN=MGST3 PE=1 SV=1 | Homo sapiens | 9606 | MGST3 | 1 | 1 | 57.21 | 103.66 | 1.81 | 0.86 |
| sp|P05387|RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1 | Homo sapiens | 9606 | RPLP2 | 1 | 1 | 57.12 | 173.97 | 3.05 | 1.61 |
| sp|P42766|RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens OX=9606 GN=RPL35 PE=1 SV=2 | Homo sapiens | 9606 | RPL35 | 1 | 2 | 56.20 | 112.84 | 2.01 | 1.01 |
| tr|H0YKD8|H0YKD8_HUMAN 60S ribosomal protein L28 OS=Homo sapiens OX=9606 GN=RPL28 PE=1 SV=1 | Homo sapiens | 9606 | RPL28 | 1 | 1 | 56.01 | 132.95 | 2.37 | 1.25 |
| sp|P52292|IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens OX=9606 GN=KPN2A PE=1 SV=1 | Homo sapiens | 9606 | KPN2A | 1 | 1 | 55.40 | 155.16 | 2.80 | 1.49 |
| tr|A0A0C4DFV9|A0A0C4DFV9_HUMAN Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=1 | Homo sapiens | 9606 | SET | 1 | 1 | 55.16 | 116.57 | 2.11 | 1.08 |
| Accession     | Description                                                                                             | Log2Fold | p-Value | 1-Log2Fold | Rank |
|--------------|----------------------------------------------------------------------------------------------------------|----------|---------|------------|------|
| sp|O75947|ATP5H_HUMAN ATP synthase subunit d, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PD PE=1 SV=3               | 54.85    | 22.32   | 0.41       | -1.30|
| sp|P80723|BASP1_HUMAN Brain acid soluble protein 1 OS=Homo sapiens OX=9606 GN=BASP1 PE=1 SV=2                   | 54.55    | 43.88   | 0.80       | -0.31|
| sp|Q09028-3|RBBP4_HUMAN Isoform 3 of Histone-binding protein RBBP4 OS=Homo sapiens OX=9606 GN=RBBP4            | 53.85    | 47.32   | 0.88       | -0.19|
| sp|P49721|PSB2_HUMAN Proteasome subunit beta type-2 OS=Homo sapiens OX=9606 GN=PSMB2 PE=1 SV=1                 | 53.12    | 47.18   | 0.89       | -0.17|
| sp|P62829|RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1                    | 52.89    | 122.28  | 2.31       | 1.21 |
| sp|P13797|PLST_HUMAN Plastin-3 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=4                                       | 52.87    | 118.31  | 2.24       | 1.16 |
| tr|B1ANR0|B1ANR0_HUMAN Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1               | 52.78    | 167.06  | 3.17       | 1.66 |
| tr|A0A087WX29|A0A087WX29_HUMAN TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens OX=9606 GN=TARDBP PE=1 SV=1   | 52.69    | 77.72   | 1.48       | 0.56 |
| sp|P31153|METK2_HUMAN S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens OX=9606 GN=MAT2A PE=1 SV=1 | 52.42    | 59.29   | 1.13       | 0.18 |
| sp|P62753|RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1                         | 52.31    | 104.91  | 2.01       | 1.00 |
| sp|P61020|RAB5B_HUMAN Ras-related protein Rab-5B OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1                | 52.23    | 152.75  | 2.92       | 1.55 |
| tr|H3BNC9|H3BNC9_HUMAN Uncharacterized protein OS=Homo sapiens OX=9606 PE=3 SV=2                               | 52.18    | 117.48  | 2.25       | 1.17 |
| sp|P04080|CYTB_HUMAN Cystatin-B OS=Homo sapiens OX=9606 GN=CSTB PE=1 SV=2                                       | 51.77    | 162.84  | 3.15       | 1.65 |
| sp|P25786-2|PSA1_HUMAN Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens OX=9606 GN=PSMA1           | 51.70    | 142.24  | 2.75       | 1.46 |
| sp|P52209-2|6PGD_HUMAN Isoform 2 of 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens OX=9606 GN=PGD | 51.25    | 73.54   | 1.43       | 0.52 |
| tr|H0YN26|H0YN26_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32A PE=1 SV=1 | 50.97    | 92.38   | 1.81       | 0.86 |
| sp|Q01518|CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=5             | 50.83    | 84.07   | 1.65       | 0.73 |
| Accession   | Description                                                                 | Protein Name               | Organism   | E Value | Q Value | # Peptides | # Spectra |
|-------------|-----------------------------------------------------------------------------|-----------------------------|------------|---------|----------|------------|-----------|
| sp|P20290-2|BTF3_HUMAN Isoform 2 of Transcription factor BTF3 OS=Homo sapiens OX=9606 GN=BTF3 | 50.61 | 167.34 | 3.31 | 1.73 |
| sp|Q15233|NONO_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NONO PE=1 SV=4 | 50.50 | 58.67 | 1.16 | 0.22 |
| sp|Q15181|IPYR_HUMAN Inorganic pyrophosphatase OS=Homo sapiens OX=9606 GN=PPA1 PE=1 SV=2 | 50.48 | 147.88 | 2.93 | 1.55 |
| sp|O60506|HNRPG_HUMAN Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=2 | 50.48 | 99.16 | 1.96 | 0.97 |
| sp|P39023|RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2 | 50.40 | 50.64 | 1.00 | 0.01 |
| sp|P31040|SDHA_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens OX=9606 GN=SDHA PE=1 SV=2 | 50.36 | 48.28 | 0.96 | -0.06 |
| sp|P55809|SCOT1_HUMAN Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens OX=9606 GN=OXCT1 PE=1 SV=1 | 49.87 | 87.97 | 1.76 | 0.82 |
| tr|A0A1W2PQB2|A0A1W2PQB2_HUMAN BTB/POZ domain-containing protein KCTD7 (Fragment) OS=Homo sapiens OX=9606 GN=KCTD7 PE=1 SV=1 | 49.39 | 60.69 | 1.23 | 0.30 |
| sp|Q04941-2|PLP2_HUMAN Isoform 2 of Proteolipid protein 2 OS=Homo sapiens OX=9606 GN=PLP2 | 49.15 | 136.27 | 2.77 | 1.47 |
| tr|A0A0D9SF53|A0A0D9SF53_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 | 48.86 | 103.77 | 2.12 | 1.09 |
| sp|P51858|HDGF_HUMAN Hepatoma-derived growth factor OS=Homo sapiens OX=9606 GN=HDGF PE=1 SV=1 | 48.47 | 188.96 | 3.90 | 1.96 |
| sp|P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PO PE=1 SV=1 | 48.08 | 142.34 | 2.96 | 1.57 |
| sp|P11413-2|G6PD_HUMAN Isoform Long of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens OX=9606 GN=G6PD | 48.07 | 75.26 | 1.57 | 0.65 |
| sp|Q9HB71|CYBP_HUMAN Calyculin-binding protein OS=Homo sapiens OX=9606 GN=CACYBP PE=1 SV=2 | 47.53 | 132.20 | 2.78 | 1.48 |
| sp|Q07021|C1QBP_HUMAN Complement 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens OX=9606 GN=C1QBP PE=1 SV=1 | 47.42 | 119.95 | 2.53 | 1.34 |
| sp|P51148-2|RAB5C_HUMAN Isoform 2 of Ras-related protein Rab-5C OS=Homo sapiens OX=9606 GN=RAB5C | 46.95 | 126.06 | 2.69 | 1.43 |
| AC   | Description                                                                 | Organism         | Accession | PE | SV | Mw 1 | Mw 2 | pI 1 | pI 2 | Lipid | Database  |
|------|------------------------------------------------------------------------------|------------------|-----------|----|----|------|------|------|------|-------|-----------|
| sp|P28070|PSB4_HUMAN Proteasome subunit beta type-4 OS=Homo sapiens OX=9606 GN=PSMB4 PE=1 SV=4 | 46.63          | 23.44     | 0.50 | -0.99 |
| tr|A0A087WYT3|A0A087WYT3_HUMAN Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 PE=1 SV=1 | 46.62          | 265.28    | 5.69 | 2.51  |
| sp|Q13247-3|SRSF6_HUMAN Isoform SRP55-3 of Serine/arginine-rich splicing factor 6 OS=Homo sapiens OX=9606 GN=SRSF6 | 46.61          | 87.18     | 1.87 | 0.90  |
| sp|Q15907-2|RB11B_HUMAN Isoform 2 of Ras-related protein Rab-11B OS=Homo sapiens OX=9606 GN=RAB11B | 46.57          | 71.54     | 1.54 | 0.62  |
| sp|P36871|PGM1_HUMAN Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=3 | 46.33          | 208.28    | 4.50 | 2.17  |
| tr|G3V5Z7|G3V5Z7_HUMAN Proteasome subunit alpha type OS=Homo sapiens OX=9606 GN=PSMA6 PE=1 SV=1 | 46.31          | 194.77    | 4.21 | 2.07  |
| sp|P41091|IF2G_HUMAN Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens OX=9606 GN=EIF2S3 PE=1 SV=3 | 46.31          | 57.02     | 1.23 | 0.30  |
| sp|P06753-2|TPM3_HUMAN Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 | 45.97          | 42.47     | 0.92 | -0.11 |
| tr|E5RIW3|E5RIW3_HUMAN Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=1 | 45.48          | 19.27     | 0.42 | -1.24 |
| tr|J3KQN4|J3KQN4_HUMAN 60S ribosomal protein L36a OS=Homo sapiens OX=9606 GN=RPL36A PE=1 SV=3 | 45.24          | 79.42     | 1.76 | 0.81  |
| sp|P34897-2|GLYM_HUMAN Isoform 2 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=SHMT2 | 45.14          | 93.99     | 2.08 | 1.06  |
| tr|H0YIZ0|H0YIZ0_HUMAN Serine hydroxymethyltransferase, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SHMT2 PE=1 SV=1 | 45.14          | 93.99     | 2.08 | 1.06  |
| sp|O00303|EIF3F_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens OX=9606 GN=EIF3F PE=1 SV=1 | 44.78          | 87.19     | 1.95 | 0.96  |
| sp|O00148|DX39A_HUMAN ATP-dependent RNA helicase DDX39A OS=Homo sapiens OX=9606 GN=DDX39A PE=1 SV=2 | 44.38          | 62.36     | 1.40 | 0.49  |
| sp|P21266|GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens OX=9606 GN=GSTM3 PE=1 SV=3 | 44.19          | 95.41     | 2.16 | 1.11  |
| tr|K7EK33|K7EK33_HUMAN DAZ-associated protein 1 OS=Homo sapiens OX=9606 GN=DAZAP1 PE=1 SV=2 | 44.11          | 68.23     | 1.55 | 0.63  |
| Accession | Description | OS | OX | GN | PE | SV | Mw | pI |
|-----------|-------------|----|----|----|----|----|-----|-----|
| sp|P61586| RHOA_HUMAN Transforming protein RhoA | Homo sapiens | 9606 | RHOA | PE=1 | SV=1 | 44.08 | 111.82 | 2.54 | 1.34 |
| sp|P05455| LA_HUMAN Lupus La protein | Homo sapiens | 9606 | SSB | PE=1 | SV=2 | 43.48 | 36.03 | 0.83 | -0.27 |
| sp|P25789| PSA4_HUMAN Proteasome subunit alpha type-4 | Homo sapiens | 9606 | PSMA4 | PE=1 | SV=1 | 43.14 | 95.46 | 2.21 | 1.15 |
| sp|P56537| IF6_HUMAN Eukaryotic translation initiation factor 6 | Homo sapiens | 9606 | EIF6 | PE=1 | SV=1 | 42.81 | 122.79 | 2.87 | 1.52 |
| sp|P02786| TFR1_HUMAN Transferrin receptor protein 1 | Homo sapiens | 9606 | TFRC | PE=1 | SV=2 | 42.71 | 120.22 | 2.82 | 1.49 |
| sp|P12004| PCNA_HUMAN Proliferating cell nuclear antigen | Homo sapiens | 9606 | PCNA | PE=1 | SV=1 | 42.40 | 113.60 | 2.68 | 1.42 |
| tr|C9JFR7| Cytochrome c (Fragment) | Homo sapiens | 9606 | CYCS | PE=1 | SV=1 | 42.39 | 133.96 | 3.16 | 1.66 |
| tr|Q5JR08| Rho-related GTP-binding protein RhoC (Fragment) | Homo sapiens | 9606 | RHOC | PE=1 | SV=8 | 42.39 | 122.79 | 2.87 | 1.52 |
| sp|P68036| Ubiquitin-conjugating enzyme E2 L3 | Homo sapiens | 9606 | UBE2L3 | PE=1 | SV=3 | 40.98 | 227.60 | 5.55 | 2.47 |
| sp|P60468| Protein transport protein Sec61 subunit beta | Homo sapiens | 9606 | SEC61B | PE=1 | SV=2 | 40.69 | 23.24 | 0.57 | -0.81 |
| Accession   | Description                                                                 | OS         | OX      | GN       | PE | SV | MW   | pI    |
|-------------|------------------------------------------------------------------------------|------------|---------|----------|----|----|------|-------|
| tr|C9IZQ1|C9IZQ1_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 PE=1 SV=1 | 40.33 | 87.89 | 2.18 | 1.12 |
| sp|P46778|RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens OX=9606 GN=RPL21 PE=1 SV=2 | 39.88 | 138.01 | 3.46 | 1.79 |
| tr|A0A075B7D9|A0A075B7D9_HUMAN TATA-binding protein-associated factor 2N OS=Homo sapiens OX=9606 GN=TAF15 PE=1 SV=1 | 39.88 | 6.39 | 0.16 | -2.64 |
| sp|P61163|ACTZ_HUMAN Alpha-centractin OS=Homo sapiens OX=9606 GN=ACTR1A PE=1 SV=1 | 39.77 | 67.22 | 1.69 | 0.76 |
| sp|P31948|STIP1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1 | 39.61 | 88.35 | 2.23 | 1.16 |
| sp|Q99536|3|VAT1_HUMAN Isoform 3 of Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens OX=9606 GN=VAT1 | 39.58 | 63.00 | 1.59 | 0.67 |
| sp|P24539|AT5F1_HUMAN ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PB PE=1 SV=2 | 39.20 | 125.24 | 3.19 | 1.68 |
| sp|Q96QD8|2|S38A2_HUMAN Isoform 2 of Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens OX=9606 GN=SLC38A2 | 38.92 | 67.96 | 1.75 | 0.80 |
| sp|P11908|2|PRPS2_HUMAN Isoform 2 of Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens OX=9606 GN=PRPS2 | 38.91 | 133.83 | 3.44 | 1.78 |
| tr|B1ALA9|B1ALA9_HUMAN Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens OX=9606 GN=PRPS1 PE=1 SV=2 | 38.91 | 133.83 | 3.44 | 1.78 |
| sp|P28072|PSB6_HUMAN Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=4 | 38.90 | 46.64 | 1.20 | 0.26 |
| sp|P06493|CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens OX=9606 GN=CDK1 PE=1 SV=3 | 38.85 | 62.35 | 1.61 | 0.68 |
| tr|K7EQA9|K7EQA9_HUMAN Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1 | 38.78 | 35.41 | 0.91 | -0.13 |
| sp|P13010|XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1 SV=3 | 38.78 | 73.05 | 1.88 | 0.91 |
| sp|P61289|2|PSME3_HUMAN Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens OX=9606 GN=PSME3 | 38.60 | 83.00 | 2.15 | 1.10 |
| tr|Q5T4U5|Q5T4U5_HUMAN Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain, isoform CRA_a OS=Homo sapiens OX=9606 GN=ACADM PE=1 SV=1 | 38.37 | 76.28 | 1.99 | 0.99 |
| tr|E9PEB5|E9PEB5_HUMAN Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=1 | 38.21 | 114.64 | 3.00 | 1.58 |
| Accession   | Description                                      | OS     | OX     | GN    | PE | SV |
|-------------|--------------------------------------------------|--------|--------|-------|----|----|
| sp|P23921|Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens OX=9606 GN=RRM1 PE=1 SV=1 | 37.78 | 47.14 | 1.25 | 0.32 |
| sp|O60664-4|Isoform 4 of Perilipin-3 OS=Homo sapiens OX=9606 GN=PLIN3 | 37.63 | 89.21 | 2.37 | 1.25 |
| sp|Q13283|G3BP1_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=37.47 | 60.57 | 1.62 | 0.69 |
| sp|Q06323|PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens OX=9606 GN=PSME1 PE=1 SV=1 | 37.21 | 37.81 | 1.02 | 0.02 |
| sp|P60953|CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens OX=9606 GN=CDC42 PE=1 SV=2 | 37.20 | 70.18 | 1.89 | 0.92 |
| tr|A0A1W2PQ51|Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=1 | 37.18 | 92.61 | 2.49 | 1.32 |
| sp|P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1 | 37.02 | 37.38 | 1.01 | 0.01 |
| sp|Q13185|CBX3_HUMAN Chromobox protein homolog 3 OS=Homo sapiens OX=9606 GN=CBX3 PE=1 SV=4 | 36.99 | 105.06 | 2.84 | 1.51 |
| sp|P05161|ISG15_HUMAN Ubiquitin-like protein ISG15 OS=Homo sapiens OX=9606 GN=ISG15 PE=1 SV=5 | 36.84 | 110.75 | 3.01 | 1.59 |
| sp|P62136|PPP1A_HUMAN Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens OX=9606 GN=PPP1CA PE=1 SV=1 | 36.77 | 79.62 | 2.17 | 1.11 |
| tr|F8VYE8|Serine/threonine-protein phosphatase OS=Homo sapiens OX=9606 GN=PPP1CC PE=1 SV=1 | 36.77 | 79.62 | 2.17 | 1.11 |
| sp|P62140|PPP1B_HUMAN Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens OX=9606 GN=PPP1CB PE=1 SV=3 | 36.77 | 79.62 | 2.17 | 1.11 |
| sp|O75340|PDCD6_HUMAN Programmed cell death protein 6 OS=Homo sapiens OX=9606 GN=PDCD6 PE=1 SV=1 | 36.70 | 115.93 | 3.16 | 1.66 |
| sp|P13804-2|ETFA_HUMAN Isoform 2 of Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ETFA | 36.68 | 67.97 | 1.85 | 0.89 |
| tr|G3V325|ATP5MF-PTCD1 readthrough OS=Homo sapiens OX=9606 GN=ATP5MF-PTCD1 PE=4 SV=1 | 36.51 | 85.83 | 2.35 | 1.23 |
| sp|Q99714|HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=3 | 36.48 | 115.50 | 3.17 | 1.66 |
| Accession | Description | OS          | OX        | GN          | PE | SV | 34.10 | 27.66 | 0.77 | -0.38 |
|-----------|-------------|-------------|-----------|-------------|----|----|-------|-------|------|-------|
| sp|Q9UBR2|CATZ_HUMAN Cathepsin Z | Homo sapiens | 9606 | CTSZ | 1 | 36.10 | 27.66 | 0.77 | -0.38 |
| sp|Q9Y3F4-2|STRAP_HUMAN Isoform 2 of Serine-threonine kinase receptor-associated protein | Homo sapiens | 9606 | STRAP | 36.06 | 94.78 | 2.63 | 1.39 |
| sp|Q9BS40|LXN_HUMAN Latexit | Homo sapiens | 9606 | LXN | 2 | 35.56 | 99.28 | 2.79 | 1.48 |
| sp|P28074|PSB5_HUMAN Proteasome subunit beta type-5 | Homo sapiens | 9606 | PSMB5 | 1 | 35.48 | 93.25 | 2.63 | 1.39 |
| sp|P53999|TCP4_HUMAN Activated RNA polymerase II transcriptional coactivator p15 | Homo sapiens | 9606 | SUB1 | 1 | 35.37 | 117.21 | 3.31 | 1.73 |
| tr|A0A024RA52|A0A024RA52_HUMAN Proteasome subunit alpha type | Homo sapiens | 9606 | PSMA2 | 1 | 35.30 | 107.51 | 3.05 | 1.61 |
| sp|P49720|PSB3_HUMAN Proteasome subunit beta type-3 | Homo sapiens | 9606 | PSMB3 | 2 | 35.19 | 112.85 | 3.21 | 1.68 |
| sp|P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 | Homo sapiens | 9606 | CAPZA1 | 3 | 34.90 | 72.85 | 2.09 | 1.06 |
| sp|P21291|CSRP1_HUMAN Cysteine and glycine-rich protein 1 | Homo sapiens | 9606 | CSRP1 | 1 | 34.89 | 112.66 | 3.23 | 1.69 |
| sp|P62834|RAP1A_HUMAN Ras-related protein Rap-1A | Homo sapiens | 9606 | RAP1A | 1 | 34.68 | 81.75 | 2.36 | 1.24 |
| sp|P17812|PYRG1_HUMAN CTP synthase 1 | Homo sapiens | 9606 | CTPS1 | 1 | 34.67 | 45.27 | 1.31 | 0.39 |
| sp|A6NHL2-2|TBAL3_HUMAN Isoform 2 of Tubulin alpha chain-like 3 | Homo sapiens | 9606 | TUBAL3 | 3 | 34.59 | 105.86 | 3.06 | 1.61 |
| sp|Q15645|PCH2_HUMAN Pachytene checkpoint protein 2 homolog | Homo sapiens | 9606 | TRIP13 | 2 | 34.57 | 57.51 | 1.66 | 0.73 |
| sp|O14929|HAT1_HUMAN Histone acetyltransferase type B catalytic subunit | Homo sapiens | 9606 | HAT1 | 1 | 34.47 | 48.98 | 1.42 | 0.51 |
| sp|P41250|GARS_HUMAN Glycine--tRNA ligase | Homo sapiens | 9606 | GARS | 1 | 34.37 | 75.21 | 2.19 | 1.13 |
| sp|P30044-2|PRDX5_HUMAN Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial | Homo sapiens | 9606 | PRDX5 | 3 | 34.32 | 110.58 | 3.22 | 1.69 |
| sp|P00387-2|NB5R3_HUMAN Isoform 2 of NADH-cytochrome b5 reductase 3 | Homo sapiens | 9606 | CYB5R3 | 3 | 34.29 | 47.12 | 1.37 | 0.46 |
| Accession | Description | OS | OX | GN | PE | SV | M | A | D | R |
|-----------|-------------|----|----|----|----|----|---|---|---|---|
| sp|P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial | Homo sapiens | 9606 | | | | | | |
| sp|Q04837|SSBP_HUMAN Single-stranded DNA-binding protein, mitochondrial | Homo sapiens | 9606 | | | | | |
| sp|Q9UNL2-2|SSRG_HUMAN Isoform 2 of Translocon-associated protein subunit gamma | Homo sapiens | 9606 | | | | | |
| sp|Q10471|GALT2_HUMAN Polypeptide N-acetylglactosaminyltransferase 2 | Homo sapiens | 9606 | | | | | |
| sp|Q92769-3|HDAC2_HUMAN Isoform 2 of Histone deacetylase 2 | Homo sapiens | 9606 | | | | | |
| sp|Q13547|HDAC1_HUMAN Histone deacetylase 1 | Homo sapiens | 9606 | | | | | |
| sp|O75534-2|CSDE1_HUMAN Isoform 2 of Cold shock domain-containing protein E1 | Homo sapiens | 9606 | | | | | |
| sp|Q7L1Q6-3|BZW1_HUMAN Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 | Homo sapiens | 9606 | | | | | |
| sp|P60903|S10AA_HUMAN Protein S100-A10 | Homo sapiens | 9606 | | | | | |
| sp|Q10589-2|BST2_HUMAN Isoform 2 of Bone marrow stromal antigen 2 | Homo sapiens | 9606 | | | | | |
| tr|A0A087WYS1|UTP--glucose-1-phosphate uridylyltransferase | Homo sapiens | 9606 | | | | | |
| sp|O96008|TOM40_HUMAN Mitochondrial import receptor subunit TOMM40 homolog | Homo sapiens | 9606 | | | | | |
| sp|Q15631|TSN_HUMAN Translin | Homo sapiens | 9606 | | | | | |
| sp|Q15293|RCN1_HUMAN Reticulocalbin-1 | Homo sapiens | 9606 | | | | | |
| sp|O43390|HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R | Homo sapiens | 9606 | | | | | |
| sp|Q15056-2|IF4H_HUMAN Isoform Short of Eukaryotic translation initiation factor 4H | Homo sapiens | 9606 | | | | | |
| sp|P07741|APT_HUMAN Adenine phosphoribosyltransferase | Homo sapiens | 9606 | | | | | |
| Accession | Description | Organism | Species | Protein | Sequence | P-Value | T-Value | Fold Change |
|-----------|-------------|----------|---------|---------|----------|---------|----------|-------------|
| tr|F6WQW2| Ran-specific GTPase-activating protein | Homo sapiens | OS=Homo sapiens | GX=9606 GN=RANBP1 PE=1 SV=1 | 31.81 | 49.77 | 1.56 | 0.65 |
| sp|Q9Y230| RuvB2_HUMAN RuvB-like 2 | Homo sapiens | OS=Homo sapiens | GX=9606 GN=RUVBL2 PE=1 SV=3 | 31.78 | 55.10 | 1.73 | 0.79 |
| sp|P61088| UB2N_HUMAN Ubiquitin-conjugating enzyme E2 N | Homo sapiens | OS=Homo sapiens | GX=9606 GN=UBE2N PE=1 SV=1 | 31.74 | 126.21 | 3.98 | 1.99 |
| sp|P26447| S10A4_HUMAN Protein S100-A4 | Homo sapiens | OS=Homo sapiens | GX=9606 GN=S100A4 PE=1 SV=1 | 31.69 | 28.12 | 0.89 | -0.17 |
| sp|Q96HV5| TM41A_HUMAN Transmembrane protein | Homo sapiens | OS=Homo sapiens | GX=9606 GN=TMEM41A PE=1 SV=1 | 31.61 | 24.28 | 0.77 | -0.38 |
| sp|Q7Z7H5| TMED4_HUMAN Isoform 2 of Transmembrane emp24 domain-containing protein 4 | Homo sapiens | OS=Homo sapiens | GX=9606 GN=TMED4 | 31.38 | 19.69 | 0.63 | -0.67 |
| sp|Q13155| AIMP2_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 | Homo sapiens | OS=Homo sapiens | GX=9606 GN=AIMP2 PE=1 SV=2 | 31.38 | 90.44 | 2.88 | 1.53 |
| tr|A6NF8X| A6NF8_HUMAN ADP-sugar pyrophosphatase | Homo sapiens | OS=Homo sapiens | GX=9606 GN=NUDT5 PE=1 SV=1 | 31.35 | 76.31 | 2.43 | 1.28 |
| tr|A0A087WTS4| A0A087WTS4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP1A | Homo sapiens | OS=Homo sapiens | GX=9606 GN=FKBP1A PE=4 SV=1 | 31.11 | 20.30 | 0.65 | -0.62 |
| sp|Q9Y617| SERC_HUMAN Phosphoserine aminotransferase | Homo sapiens | OS=Homo sapiens | GX=9606 GN=PSAT1 PE=1 SV=2 | 31.10 | 71.45 | 2.30 | 1.20 |
| tr|E9PN17| E9PN17_HUMAN ATP synthase subunit g, mitochondrial | Homo sapiens | OS=Homo sapiens | GX=9606 GN=ATP5MG PE=1 SV=1 | 31.04 | 92.66 | 2.99 | 1.58 |
| sp|P58546| MTPN_HUMAN Myotrophin | Homo sapiens | OS=Homo sapiens | GX=9606 GN=MTPN PE=1 SV=2 | 31.02 | 89.92 | 2.90 | 1.54 |
| sp|P37108| SRP14_HUMAN Signal recognition particle 14 kDa protein | Homo sapiens | OS=Homo sapiens | GX=9606 GN=SRP14 PE=1 SV=2 | 30.95 | 75.39 | 2.44 | 1.28 |
| sp|P60228| EIF3E_HUMAN Eukaryotic translation initiation factor 3 subunit E | Homo sapiens | OS=Homo sapiens | GX=9606 GN=EIF3E PE=1 SV=1 | 30.69 | 55.14 | 1.80 | 0.85 |
| sp|Q9Y265| RUVB1_HUMAN RuvB-like 1 | Homo sapiens | OS=Homo sapiens | GX=9606 GN=RUVBL1 PE=1 SV=1 | 30.63 | 65.04 | 2.12 | 1.09 |
| sp|P63167| DYL1_HUMAN Dynein light chain 1, cytoplasmic | Homo sapiens | OS=Homo sapiens | GX=9606 GN=DYNLL1 PE=1 SV=1 | 30.47 | 25.73 | 0.84 | -0.24 |
| Accession   | Description                                                                 | e-value | Log10(E-value) | p-value | Log10(p-value) |
|------------|------------------------------------------------------------------------------|---------|---------------|---------|---------------|
| sp|P63000-2| RAC1_HUMAN Isoform B of Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens OX=9606 GN=RAC1 | 30.35   | 49.87         | 1.64   | 0.72          |
| sp|P12268| IMDH2_HUMAN Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens OX=9606 GN=IMPDH2 PE=1 SV=2 | 30.19   | 54.42         | 1.80   | 0.85          |
| sp|O43809| CPSF5_HUMAN Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens OX=9606 GN=NUDT21 PE=1 SV=1 | 30.15   | 83.35         | 2.76   | 1.47          |
| tr|A0A0J9YVP6| A0A0J9YVP6_HUMAN Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1 | 29.99   | 72.18         | 2.41   | 1.27          |
| tr|B7Z7P8| B7Z7P8_HUMAN Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens OX=9606 GN=ETF1 PE=1 SV=1 | 29.92   | 45.64         | 1.53   | 0.61          |
| sp|P52565| GDIR1_HUMAN Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDIA PE=1 SV=3 | 29.65   | 68.44         | 2.31   | 1.21          |
| sp|Q9NR31| SAR1A_HUMAN GTP-binding protein SAR1a OS=Homo sapiens OX=9606 GN=SAR1A PE=1 SV=1 | 29.61   | 90.97         | 3.07   | 1.62          |
| sp|P14866| HNRPL_HUMAN Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=2 | 29.52   | 66.25         | 2.24   | 1.17          |
| sp|P20618| PSB1_HUMAN Proteasome subunit beta type-1 OS=Homo sapiens OX=9606 GN=PSMB1 PE=1 SV=2 | 29.42   | 41.49         | 1.41   | 0.50          |
| sp|P24752| THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 PE=1 SV=1 | 29.36   | 70.43         | 2.40   | 1.26          |
| sp|P00367| DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens OX=9606 GN=GLUD1 PE=1 SV=2 | 29.30   | 43.80         | 1.50   | 0.58          |
| tr|B0QY89| B0QY89_HUMAN Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1 | 29.29   | 67.18         | 2.29   | 1.20          |
| sp|P08574| CY1_HUMAN Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens OX=9606 GN=CYC1 PE=1 SV=3 | 29.26   | 43.45         | 1.48   | 0.57          |
| tr|C9J381| C9J381_HUMAN Inosine-5'-monophosphate dehydrogenase OS=Homo sapiens OX=9606 GN=IMPDH1 PE=1 SV=1 | 29.22   | 7.95          | 0.27   | -1.88         |
| sp|P32322| P5CR1_HUMAN Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens OX=9606 GN=PYCR1 PE=1 SV=2 | 29.20   | 83.78         | 2.87   | 1.52          |
| sp|P30040| ERP29_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens OX=9606 GN=ERP29 PE=1 SV=4 | 29.13   | 63.67         | 2.19   | 1.13          |
| Accession   | Description                                                                 | Score-1 | Score-2 | Score-3 | Score-4 |
|-------------|-----------------------------------------------------------------------------|---------|---------|---------|---------|
| sp|Q07065|CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2 | 28.87   | 67.47   | 2.34    | 1.22    |
| sp|P31939-2|PUR9_HUMAN Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC | 28.81   | 57.24   | 1.99    | 0.99    |
| sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1 | 28.67   | 61.94   | 2.16    | 1.11    |
| sp|P38117-2|ETFB_HUMAN Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens OX=9606 GN=ETF B | 28.63   | 32.91   | 1.15    | 0.20    |
| sp|P31942-2|HNRH3_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 | 28.53   | 80.76   | 2.83    | 1.50    |
| sp|Q9Y5S9-2|RBM8A_HUMAN Isoform 2 of RNA-binding protein 8A OS=Homo sapiens OX=9606 GN=RB M8A | 28.43   | 53.30   | 1.88    | 0.91    |
| tr|A8K878|A8K878_HUMAN Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens OX=9606 GN=MANF PE=1 SV=1 | 28.40   | 52.14   | 1.84    | 0.88    |
| tr|H0Y2P0|H0Y2P0_HUMAN CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=1 | 28.29   | 38.23   | 1.35    | 0.43    |
| sp|Q13347|EIF3I_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens OX=9606 GN=EIF3I PE=1 SV=1 | 28.28   | 38.06   | 1.35    | 0.43    |
| tr|X1WI28|X1WI28_HUMAN 60S ribosomal protein L10 (Fragment) OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=7 | 28.17   | 57.70   | 2.05    | 1.03    |
| sp|O60701|UGDH_HUMAN UDP-glucose 6-dehydrogenase OS=Homo sapiens OX=9606 GN=UGDH PE=1 SV=1 | 28.13   | 32.23   | 1.15    | 0.20    |
| sp|P17931|LEG3_HUMAN Galectin-3 OS=Homo sapiens OX=9606 GN=LGAL S3 PE=1 SV=5 | 28.05   | 65.94   | 2.35    | 1.23    |
| sp|Q9Y2T3-3|GUAD_HUMAN Isoform 3 of Guanine deaminase OS=Homo sapiens OX=9606 GN=GDA | 27.94   | 80.34   | 2.88    | 1.52    |
| sp|P78417|GSTO1_HUMAN Glutathione S-transferase omega-1 OS=Homo sapiens OX=9606 GN=GSTO1 PE=1 SV=2 | 27.90   | 86.27   | 3.09    | 1.63    |
| sp|P16083|NQO2_HUMAN Ribosylhydronicotinamide dehydrogenase [quinone] OS=Homo sapiens OX=9606 GN=NQO2 PE=1 SV=5 | 27.70   | 14.90   | 0.54    | -0.89   |
| sp|O60669-2|EDF1_HUMAN Isoform 2 of Endothelial differentiation-related factor 1 OS=Homo sapiens OX=9606 GN=EDF1 | 27.42   | 31.88   | 1.16    | 0.22    |
| Accession   | Description                                                        | Humans   | Mice   | Dog    | Rat    |
|-------------|--------------------------------------------------------------------|----------|--------|--------|--------|
| sp|P62266|RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3 | 27.33    | 29.83  | 1.09   | 0.13   |
| sp|Q99733-2|NP1L4_HUMAN Isoform 2 of Nucleosome assembly protein 1-like 4 OS=Homo sapiens OX=9606 GN=NAP1L4 | 27.13    | 144.07 | 5.31   | 2.41   |
| sp|Q96QK1|VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV=2 | 26.81    | 66.47  | 2.48   | 1.31   |
| sp|P62314|SMD1_HUMAN Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens OX=9606 GN=SNRPD1 PE=1 SV=1 | 26.80    | 48.18  | 1.80   | 0.85   |
| sp|O00483|NDUA4_HUMAN Cytochrome c oxidase subunit NDUF4 OS=Homo sapiens OX=9606 GN=NDUFA4 PE=1 SV=1 | 26.62    | 44.07  | 1.66   | 0.73   |
| tr|K7ELL7|K7ELL7_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=1 | 26.51    | 99.29  | 3.75   | 1.91   |
| sp|P54577|SYYC_HUMAN Tyrosine-tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=YARS PE=1 SV=4 | 26.48    | 68.82  | 2.60   | 1.38   |
| sp|P63208|SKP1_HUMAN S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=2 | 26.27    | 15.85  | 0.60   | -0.73  |
| sp|P42677|RS27_HUMAN 40S ribosomal protein S27 OS=Homo sapiens OX=9606 GN=RPS27 PE=1 SV=3 | 26.12    | 39.53  | 1.51   | 0.60   |
| sp|O00487|PSDE_HUMAN 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens OX=9606 GN=PSMD14 PE=1 SV=1 | 26.01    | 66.25  | 2.55   | 1.35   |
| sp|P30046|DOPD_HUMAN D-dopachrome decarboxylase OS=Homo sapiens OX=9606 GN=DDT PE=1 SV=3 | 25.99    | 132.95 | 5.11   | 2.35   |
| sp|P30084|ECHM_HUMAN Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=ECHS1 PE=1 SV=4 | 25.83    | 78.03  | 3.02   | 1.60   |
| sp|Q15019-2|SEPT2_HUMAN Isoform 2 of Septin-2 OS=Homo sapiens OX=9606 GN=SEPT2 | 25.65    | 45.03  | 1.76   | 0.81   |
| sp|P13489|RINI_HUMAN Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=2 | 25.52    | 50.18  | 1.97   | 0.98   |
| sp|P23246|SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2 | 25.45    | 19.57  | 0.77   | -0.38  |
| tr|Q8WVC2|Q8WVC2_HUMAN 40S ribosomal protein S21 OS=Homo sapiens OX=9606 GN=RPS21 PE=1 SV=1 | 25.44    | 74.02  | 2.91   | 1.54   |
| sp|Q8NBS9-2|TXND5_HUMAN Isoform 2 of Thioredoxin domain-containing protein 5 OS=Homo sapiens OX=9606 GN=TXND5 | 25.37    | 36.79  | 1.45   | 0.54   |
| sp|P30153|ZAAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory | 25.20    | 50.64  | 2.01   | 1.01   |
| Accession    | Description                                                                 | Species     | Protein Name     | Gene Name     | PE | SV |
|-------------|------------------------------------------------------------------------------|-------------|------------------|---------------|----|----|
| sp|P82979|SARNP_HUMAN SAP domain-containing ribonucleoprotein OS=Homo sapiens          | Homo sapiens| PPP2R1A         | 1  | 4  |
| sp|O76021|RL1D1_HUMAN Ribosomal L1 domain-containing protein 1 OS=Homo sapiens         | Homo sapiens| RSL1D1          | 1  | 3  |
| tr|Q6P452|Q6P452_HUMAN Annexin OS=Homo sapiens                                         | Homo sapiens| ANXA4           | 1  | 1  |
| tr|F8VV56|F8VV56_HUMAN CD63 antigen OS=Homo sapiens                                     | Homo sapiens| CD63            | 1  | 1  |
| sp|Q92688-2|AN32B_HUMAN Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B | Homo sapiens| ANP32B          | 1  | 3  |
| sp|P0DP23|CALM1_HUMAN Calmodulin-1 OS=Homo sapiens                                      | Homo sapiens| CALM1           | 1  | 1  |
| sp|P49755|TMEDA_HUMAN Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens  | Homo sapiens| TMED10          | 1  | 2  |
| sp|Q8NC51|PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens | Homo sapiens| SERBP1          | 1  | 2  |
| sp|Q9P0S9|TM14C_HUMAN Transmembrane protein 14C OS=Homo sapiens                         | Homo sapiens| TMEM14C         | 1  | 1  |
| sp|P16435|NCPR_HUMAN NADPH-cytochrome P450 reductase OS=Homo sapiens                    | Homo sapiens| POR             | 1  | 2  |
| sp|P16152|CBR1_HUMAN Carbonyl reductase [NADPH] 1 OS=Homo sapiens                       | Homo sapiens| CBR1            | 1  | 3  |
| tr|J3QT28|J3QT28_HUMAN Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens       | Homo sapiens| BUB3            | 1  | 1  |
| sp|Q7L2H7|EIF3M_HUMAN Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens| Homo sapiens| EIF3M           | 1  | 1  |
| sp|P27695|APEX1_HUMAN DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens         | Homo sapiens| APEX1           | 1  | 2  |
| sp|P00492|HPRT_HUMAN Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens     | Homo sapiens| HPRT1           | 1  | 2  |
| sp|Q15717-2|ELAV1_HUMAN Isoform 2 of ELAV-like protein 1 OS=Homo sapiens                  | Homo sapiens| ELAVL1          | 1  | 1  |
| Accession     | Description                                                                 | OS       | OX   | GN     | PE  | SV  | Mw    | Pw   | Ew   | Ratio   |
|---------------|------------------------------------------------------------------------------|----------|------|--------|-----|-----|-------|------|------|---------|
| tr|A0A0C4DGQ5|A0A0C4DGQ5_HUMAN Calpain small subunit 1 OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1 | Homo sapiens | 9606 | CAPNS1 | 1   | 1   | 23.74 | 64.50 | 2.72 | 1.44    |
| sp|P61158|ARP3_HUMAN Actin-related protein 3 OS=Homo sapiens OX=9606 GN=ACTR3 PE=1 SV=3   | Homo sapiens | 9606 | ACTR3  | 1   | 3   | 23.65 | 57.68 | 2.44 | 1.29    |
| sp|P12429|ANXA3_HUMAN Annexin A3 OS=Homo sapiens OX=9606 GN=ANXA3 PE=1 SV=3               | Homo sapiens | 9606 | ANXA3 | 1   | 3   | 23.58 | 23.52 | 1.00 | 0.00    |
| sp|P33993|MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=1 SV=4 | Homo sapiens | 9606 | MCM7  | 1   | 4   | 23.37 | 67.02 | 2.87 | 1.52    |
| sp|P25788-2|PSA3_HUMAN Isoform 2 of Proteasome activator complex subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 | Homo sapiens | 9606 | PSMA3 | 1   | 3   | 23.33 | 20.23 | 0.87 | -0.21   |
| tr|A0A087X1Z3|A0A087X1Z3_HUMAN Proteasome activator complex subunit 2 OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=1 | Homo sapiens | 9606 | PSME2 | 1   | 1   | 23.23 | 63.80 | 2.75 | 1.46    |
| tr|A0A0C4DGS1|A0A0C4DGS1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens OX=9606 GN=DDOST PE=1 SV=1 | Homo sapiens | 9606 | DDOST | 1   | 1   | 23.17 | 36.94 | 1.59 | 0.67    |
| sp|P30154-2|AAAB_HUMAN Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B | Homo sapiens | 9606 | PPP2R1B | 1   | 1   | 23.16 | 3.47  | 0.15 | -2.74   |
| sp|P20042|IF2B_HUMAN Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens OX=9606 GN=EIF2S2 PE=1 SV=2 | Homo sapiens | 9606 | EIF2S2 | 1   | 2   | 23.06 | 52.48 | 2.28 | 1.19    |
| sp|P15170-2|ERF3A_HUMAN Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens OX=9606 GN=GSPT1 | Homo sapiens | 9606 | GSPT1 | 1   | 2   | 23.06 | 33.17 | 1.44 | 0.52    |
| sp|Q9HBQ8|NMRL1_HUMAN NmrA-like family domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NMRAL1 PE=1 SV=1 | Homo sapiens | 9606 | NMRAL1 | 1   | 1   | 23.02 | 30.18 | 1.31 | 0.39    |
| sp|P20674|COX5A_HUMAN Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens OX=9606 GN=COX5A PE=1 SV=2 | Homo sapiens | 9606 | COX5A | 1   | 2   | 22.97 | 28.21 | 1.23 | 0.30    |
| sp|P14324-2|FFPS_HUMAN Isoform 2 of Farnesy1 pyrophosphate synthase OS=Homo sapiens OX=9606 GN=FDPS | Homo sapiens | 9606 | FDPS | 1   | 2   | 22.96 | 73.69 | 3.21 | 1.68    |
| sp|O60488-2|ACSL4_HUMAN Isoform Short of Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens OX=9606 GN=ACSL4 | Homo sapiens | 9606 | ACSL4 | 1   | 2   | 22.94 | 12.14 | 0.53 | -0.92   |
| tr|G3V1V0|G3V1V0_HUMAN Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 | Homo sapiens | 9606 | MYL6 | 1   | 1   | 22.92 | 151.77 | 6.62 | 2.73    |
| sp|Q9NQR4|NIT2_HUMAN Omega-amidase NIT2 OS=Homo sapiens OX=9606 GN=NIT2 PE=1 SV=1 | Homo sapiens | 9606 | NIT2 | 1   | 1   | 22.82 | 12.88 | 0.56 | -0.83   |
| Accession  | Description                                                                 | Value 1 | Value 2 | Value 3 | Value 4 |
|------------|------------------------------------------------------------------------------|---------|---------|---------|---------|
| sp|O95831|AIFM1_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens  |
|             |                              | 22.79   | 39.35   | 1.73    | 0.79    |
| sp|P08133|ANXA6_HUMAN Annexin A6                                                        | 22.58   | 42.16   | 1.87    | 0.90    |
| sp|P62191|PRS4_HUMAN 26S proteasome regulatory subunit 4 OS=Homo sapiens               | 22.42   | 40.81   | 1.82    | 0.86    |
| sp|Q9Y266|NUDC_HUMAN Nuclear migration protein nudC OS=Homo sapiens                   | 22.23   | 51.89   | 2.33    | 1.22    |
| sp|Q13011|ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens | 22.13   | 44.54   | 2.01    | 1.01    |
| sp|P62195|PRS8_HUMAN 26S proteasome regulatory subunit 8 OS=Homo sapiens               | 21.94   | 43.76   | 1.99    | 1.00    |
| sp|Q15758|AAAT_HUMAN Neutral amino acid transporter B(0) OS=Homo sapiens               | 21.94   | 45.90   | 2.09    | 1.07    |
| sp|Q16891|MIC60_HUMAN Isoform 2 of MICOS complex subunit MIC60 OS=Homo sapiens        | 21.92   | 48.89   | 2.23    | 1.16    |
| sp|P26583|HMGB2_HUMAN High mobility group protein B2 OS=Homo sapiens                  | 21.84   | 66.09   | 3.03    | 1.60    |
| sp|P62316|SMD2_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens            | 21.81   | 36.90   | 1.69    | 0.76    |
| sp|Q96PK6|RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens                         | 21.74   | 114.71  | 5.28    | 2.40    |
| sp|Q96IX5|USMG5_HUMAN Up-regulated during skeletal muscle growth protein 5 OS=Homo sapiens | 21.73   | 55.27   | 2.54    | 1.35    |
| tr|F5GX77|F5GX77_HUMAN Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens | 21.46   | 47.26   | 2.20    | 1.14    |
| sp|Q15691|MARE1_HUMAN Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens | 21.16   | 12.10   | 0.57    | -0.81   |
| sp|Q06210|GFPT1_HUMAN Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens | 21.13   | 33.40   | 1.58    | 0.66    |
| sp|P18754|RCC1_HUMAN Isoform 2 of Regulator of chromosome condensation OS=Homo sapiens | 21.11   | 40.60   | 1.92    | 0.94    |
| Uncharacterized protein (Fragment) | OS=Homo sapiens | 21.01 | 69.36 | 3.30 | 1.72 |
|-----------------------------------|----------------|------|------|------|------|
| Serine/threonine-protein kinase 26 | OS=Homo sapiens | 20.92 | 27.44 | 1.31 | 0.39 |
| Dual specificity protein phosphatase 3 | OS=Homo sapiens | 20.91 | 37.91 | 1.81 | 0.86 |
| Elongation factor Ts, mitochondrial | OS=Homo sapiens | 20.82 | 31.21 | 1.50 | 0.58 |
| Isoform 2 of KH domain-containing, RNA-binding, signal transduction-associated protein 1 | OS=Homo sapiens | 20.82 | 20.55 | 0.99 | -0.02 |
| Arginine--tRNA ligase, cytoplasmic | OS=Homo sapiens | 20.80 | 58.09 | 2.79 | 1.48 |
| Isoform 2 of Inosine triphosphate pyrophosphatase | OS=Homo sapiens | 20.71 | 4.74 | 0.23 | -2.13 |
| ATP-dependent 6-phosphofructokinase, platelet type | OS=Homo sapiens | 20.69 | 44.96 | 2.17 | 1.12 |
| Myosin regulatory light chain 12A | OS=Homo sapiens | 20.61 | 84.18 | 4.08 | 2.03 |
| Nucleoplasmin-3 | OS=Homo sapiens | 20.59 | 44.09 | 2.14 | 1.10 |
| Chloride intracellular channel protein 4 | OS=Homo sapiens | 20.54 | 15.02 | 0.73 | -0.45 |
| Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (Fragment) | OS=Homo sapiens | 20.49 | 53.05 | 2.59 | 1.37 |
| Histocompatibility antigen, A-68 alpha chain | OS=Homo sapiens | 20.45 | 34.51 | 1.69 | 0.75 |
| Programmed cell death 6-interacting protein | OS=Homo sapiens | 20.22 | 47.00 | 2.32 | 1.22 |
| Nucleoplasmin-3 | OS=Homo sapiens | 20.19 | 74.16 | 3.67 | 1.88 |
| Membrane-associated progesterone receptor component 1 | OS=Homo sapiens | 20.02 | 39.80 | 1.99 | 0.99 |
| Accession | Description                                                                 | OS     | OX   | GN       | PE | SV |
|-----------|-----------------------------------------------------------------------------|--------|------|----------|----|----|
| sp|P40121-2|CAPG_HUMAN Isoform 2 of Macrophage-capping protein OS=Homo sapiens OX=9606 GN=CAPG | Homo sapiens | 9606  | CAPG    | 18.99 | 13.54 | 0.68 | -0.56 |
| tr|G3V153|G3V153_HUMAN Caprin-1 OS=Homo sapiens OX=9606 GN=CAPR1N PE=1 SV=1 | Homo sapiens | 9606  | CAPR1N  | 19.99 | 32.49 | 1.63 | 0.70 |
| sp|P49773|HINT1_HUMAN Histidine triad nucleotide-binding protein 1 OS=Homo sapiens OX=9606 GN=HINT1 PE=1 SV=2 | Homo sapiens | 9606  | HINT1   | 19.89 | 20.90 | 1.05 | 0.07 |
| sp|P35998|PRS7_HUMAN 26S proteasome regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSMC2 PE=1 SV=3 | Homo sapiens | 9606  | PSMC2   | 19.85 | 40.92 | 2.06 | 1.04 |
| sp|Q9Y333|LSM2_HUMAN U6 snRNA-associated Sm-like protein LSM2 OS=Homo sapiens OX=9606 GN=LSM2 PE=1 SV=1 | Homo sapiens | 9606  | LSM2    | 19.84 | 38.46 | 1.94 | 0.95 |
| sp|P13073|COX41_HUMAN Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens OX=9606 GN=COX41 PE=1 SV=1 | Homo sapiens | 9606  | COX41   | 19.77 | 18.80 | 0.95 | -0.07 |
| sp|Q9UMS4|PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens OX=9606 GN=PRPF19 PE=1 SV=1 | Homo sapiens | 9606  | PRPF19  | 19.48 | 45.66 | 2.34 | 1.23 |
| tr|A0A2R8YD50|A0A2R8YD50_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=1 | Homo sapiens | 9606  | HSD17B4 | 19.48 | 36.94 | 1.90 | 0.92 |
| tr|Q5JR11|Q5JR11_HUMAN Serine/arginine-rich-splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 PE=1 SV=1 | Homo sapiens | 9606  | SRSF10  | 19.33 | 40.92 | 2.12 | 1.08 |
| sp|Q15046-2|SYK_HUMAN Isoform Mitochondrial of Lysine--tRNA ligase OS=Homo sapiens OX=9606 GN=KARS | Homo sapiens | 9606  | KARS    | 19.27 | 62.58 | 3.25 | 1.70 |
| tr|F8VVA7|F8VVA7_HUMAN Coatamer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1 | Homo sapiens | 9606  | COPZ1   | 19.22 | 27.87 | 1.45 | 0.54 |
| sp|P00390-3|GSHR_HUMAN Isoform 2 of Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSR | Homo sapiens | 9606  | GSR     | 19.20 | 29.81 | 1.55 | 0.63 |
| sp|O43776|SYNC_HUMAN Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=NARS PE=1 SV=1 | Homo sapiens | 9606  | NARS    | 19.09 | 70.30 | 3.68 | 1.88 |
| sp|P17714|AATC_HUMAN Aspartate aminotransferase, cytoplasmic OS=Homo sapiens OX=9606 GN=GOT1 PE=1 SV=3 | Homo sapiens | 9606  | GOT1    | 18.94 | 43.12 | 2.28 | 1.19 |
| tr|F8VVM2|F8VVM2_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=1 | Homo sapiens | 9606  | SLC25A3 | 18.89 | 27.44 | 1.45 | 0.54 |
| sp|P22102-2|PUR2_HUMAN Isoform Short of Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens OX=9606 GN=GART | Homo sapiens | 9606  | GART    | 18.85 | 27.11 | 1.44 | 0.52 |
| tr|E9PK05|E9PK05_HUMAN Phospholipid transfer protein C2CD2L OS=Homo sapiens OX=9606 GN=C2CD2L PE=1 SV=1 | Homo sapiens | 9606  | C2CD2L  | 18.71 | 10.83 | 0.58 | -0.79 |
| Accession  | Description                                           | OS     | OX     | NO. | sv     | Value 1 | Value 2 | Value 3 | Value 4 |
|------------|-------------------------------------------------------|--------|--------|-----|--------|---------|---------|---------|---------|
| sp|O43852-3|CALU_HUMAN Isoform 3 of Calumenin OS=Homo sapiens  OX=9606 GN=CALU | Homo sapiens | 9606  |     |        | 18.70   | 19.28   | 1.03    | 0.04    |
| sp|Q8NCW5-2|NNRE_HUMAN Isoform 2 of NAD(P)H-hydrate epimerase OS=Homo sapiens  OX=9606 GN=NAXE | Homo sapiens | 9606  |     |        | 18.54   | 48.25   | 2.60    | 1.38    |
| sp|O75874|IDHC_HUMAN Isoform 3 of Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens  OX=9606 GN=IDH1 PE=1 SV=2 | Homo sapiens | 9606  |     |        | 18.51   | 45.87   | 2.48    | 1.31    |
| sp|P35659|DEK_HUMAN Protein DEK OS=Homo sapiens  OX=9606 GN=DEK PE=1 SV=1 | Homo sapiens | 9606  |     |        | 18.48   | 42.06   | 2.28    | 1.19    |
| sp|O75083|WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens  OX=9606 GN=WDR1 PE=1 SV=4 | Homo sapiens | 9606  |     |        | 18.47   | 20.34   | 1.10    | 0.14    |
| sp|P61019|RAB2A_HUMAN Ras-related protein Rab-2A OS=Homo sapiens  OX=9606 GN=RAB2A PE=1 SV=1 | Homo sapiens | 9606  |     |        | 18.26   | 45.62   | 2.50    | 1.32    |
| sp|Q15738|NSDHL_HUMAN Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens  OX=9606 GN=NSDHL PE=1 SV=2 | Homo sapiens | 9606  |     |        | 18.19   | 15.55   | 0.85    | -0.23   |
| sp|P00491|PNPH_HUMAN Purine nucleoside phosphorylase OS=Homo sapiens  OX=9606 GN=PNP PE=1 SV=2 | Homo sapiens | 9606  |     |        | 18.05   | 48.09   | 2.66    | 1.41    |
| sp|P09661|RU2A_HUMAN U2 small nuclear ribonucleoprotein A' OS=Homo sapiens  OX=9606 GN=SNRPA1 PE=1 SV=2 | Homo sapiens | 9606  |     |        | 18.05   | 43.34   | 2.40    | 1.26    |
| tr|B8ZZQ6|B8ZZQ6_HUMAN Prothymosin alpha OS=Homo sapiens  OX=9606 GN=PTMA PE=1 SV=1 | Homo sapiens | 9606  |     |        | 17.99   | 33.57   | 1.87    | 0.90    |
| sp|Q13057|COASY_HUMAN Isoform 2 of Bifunctional coenzyme A synthase OS=Homo sapiens  OX=9606 GN=COASY | Homo sapiens | 9606  |     |        | 17.86   | 26.24   | 1.47    | 0.55    |
| sp|Q9Y678|COPG1_HUMAN Coatamer subunit gamma-1 OS=Homo sapiens  OX=9606 GN=COPG1 PE=1 SV=1 | Homo sapiens | 9606  |     |        | 17.81   | 3.34    | 0.19    | -2.42   |
| sp|Q12904|AIMP1_HUMAN Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens  OX=9606 GN=AIMP1 | Homo sapiens | 9606  |     |        | 17.77   | 37.31   | 2.10    | 1.07    |
| sp|P68402|PA1B2_HUMAN Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens  OX=9606 GN=PAFAH1B2 PE=1 SV=1 | Homo sapiens | 9606  |     |        | 17.73   | 37.79   | 2.13    | 1.09    |
| tr|B1AK87|B1AK87_HUMAN Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens  OX=9606 GN=CAPZB PE=1 SV=1 | Homo sapiens | 9606  |     |        | 17.70   | 25.18   | 1.42    | 0.51    |
| sp|Q9BVK6|TMED9 HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens  OX=9606 GN=TMED9 PE=1 SV=2 | Homo sapiens | 9606  |     |        | 17.70   | 18.38   | 1.04    | 0.05    |
| ID       | Description                                                                                      | Accession | Mass (Da) | pI     | MGF     | CDF     |
|----------|-------------------------------------------------------------------------------------------------|-----------|-----------|--------|---------|---------|
| sp|P09012|SNRPA_HUMAN U1 small nuclear ribonucleoprotein A OS=Homo sapiens| 17.69  | 50.20    | 2.84   | 1.51    |
| sp|P49915|GUAA_HUMAN GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens| 17.62  | 41.27    | 2.34   | 1.23    |
| sp|P04040|CAT A_HUMAN Catalase OS=Homo sapiens| 17.60  | 32.76    | 1.86   | 0.90    |
| sp|Q6NZI2|CAVN1_HUMAN Caveolae-associated protein 1 OS=Homo sapiens| 17.59  | 30.15    | 1.71   | 0.78    |
| sp|Q9BF67|GRWD1_HUMAN Glutamate-rich WD repeat-containing protein 1 OS=Homo sapiens| 17.38  | 24.04    | 1.38   | 0.47    |
| sp|P62714|PP2AB_HUMAN Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens| 17.36  | 108.40   | 6.24   | 2.64    |
| sp|Q9UBF2|COPG2_HUMAN Isoform 2 of Coatamer subunit gamma-2 OS=Homo sapiens| 17.31  | 11.36    | 0.66   | -0.61   |
| tr|F8WCF6|F8WCF6_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens| 17.24  | 40.66    | 2.36   | 1.24    |
| tr|A0A087WU2|A0A087WU2_HUMAN Heterogeneous nuclear ribonucleoprotein D-like, isoform CRA_b OS=Homo sapiens| 17.23  | 102.90   | 5.97   | 2.58    |
| sp|Q92499|DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens| 17.21  | 29.32    | 1.70   | 0.77    |
| sp|O15427|MOT4_HUMAN Monocarboxylate transporter 4 OS=Homo sapiens| 17.17  | 10.46    | 0.61   | -0.71   |
| tr|E7ETZ4|E7ETZ4_HUMAN Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens| 17.11  | 58.02    | 3.40   | 1.76    |
| tr|A0A087WZT3|A0A087WZT3_HUMAN BolA-like protein 2 OS=Homo sapiens| 17.04  | 46.56    | 2.73   | 1.45    |
| sp|P05198|IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens| 17.00  | 37.25    | 2.19   | 1.13    |
| sp|P30085|KCY_HUMAN UMP-CMP kinase OS=Homo sapiens| 16.98  | 47.34    | 2.79   | 1.48    |
| sp|Q96DG6|CMBl_HUMAN Carboxymethylenebutenolidase homolog OS=Homo sapiens| 16.93  | 24.35    | 1.44   | 0.52    |
| Accession | Description | Organism | Organism ID | Gene Name | Description | Protein ID | Msp | Vsp | VspRatio |
|-----------|-------------|----------|-------------|-----------|-------------|------------|------|------|----------|
| sp|P10606|Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens OX=9606 GN=COX5B PE=1 SV=2 | 16.91 | 18.96 | 1.12 | 0.17 |
| sp|P47985|Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRFS1 PE=1 SV=2 | 16.90 | 15.20 | 0.90 | -0.15 |
| tr|E7EMS6|Catechol O-methyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=COMT PE=1 SV=1 | 16.89 | 34.15 | 2.02 | 1.02 |
| sp|Q12906-2|Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 | 16.75 | 63.78 | 3.81 | 1.93 |
| sp|P30043|Flavin reductase (NADPH) OS=Homo sapiens OX=9606 GN=BLVRB PE=1 SV=3 | 16.74 | 39.53 | 2.36 | 1.24 |
| sp|Q14498-2|RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 | 16.71 | 16.95 | 1.01 | 0.02 |
| sp|P26196|Protein OS=Homo sapiens OX=9606 GN=DDX6 PE=1 SV=2 | 16.70 | 30.20 | 1.81 | 0.85 |
| sp|P10620|Microsomal glutathione S-transferase 1 OS=Homo sapiens OX=9606 GN=MGST1 PE=1 SV=1 | 16.69 | 68.55 | 4.11 | 2.04 |
| tr|A0A1B0GVA9|Ryanodine receptor 3 (Fragment) OS=Homo sapiens OX=9606 GN=RYR3 PE=4 SV=1 | 16.53 | 6.45 | 0.39 | -1.36 |
| sp|P61970|Nuclear transport factor 2 OS=Homo sapiens OX=9606 GN=NUTF2 PE=1 SV=1 | 16.50 | 53.54 | 3.24 | 1.70 |
| tr|B4E3S0|Coronin OS=Homo sapiens OX=9606 GN=CORO1C PE=1 SV=1 | 16.47 | 5.15 | 0.31 | -1.68 |
| sp|P08579|Small nuclear ribonucleoprotein B OS=Homo sapiens OX=9606 GN=SNRPB2 PE=1 SV=1 | 16.44 | 13.23 | 0.80 | -0.31 |
| sp|P51572-2|Isoform 2 of B-cell receptor-associated protein 31 OS=Homo sapiens OX=9606 GN=BCAP31 | 16.41 | 43.87 | 2.67 | 1.42 |
| sp|P54709|Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens OX=9606 GN=ATP1B3 PE=1 SV=1 | 16.37 | 36.82 | 2.25 | 1.17 |
| sp|P36957|Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens OX=9606 GN=DLST PE=0 SV=4 | 16.36 | 32.19 | 1.97 | 0.98 |
| sp|O15371-2|Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens OX=9606 GN=EIF3D | 16.34 | 47.97 | 2.94 | 1.55 |
| Accession  | Description                                                                 | OS  | GN      | PE  | SV  |
|------------|------------------------------------------------------------------------------|-----|---------|-----|-----|
| sp|Q9UBQ5-2|EIF3K_HUMAN Isoform 2 of Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens OX=9606 GN=EIF3K | 16.32 | 82.48 | 5.05 | 2.34 |
| tr|A0A0B4J2C3|A0A0B4J2C3_HUMAN Translationally-controlled tumor protein OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1 | 16.28 | 32.74 | 2.01 | 1.01 |
| sp|P84090|ERH_HUMAN Enhancer of rudimentary homolog OS=Homo sapiens OX=9606 GN=ERH PE=1 SV=1 | 16.25 | 63.07 | 3.88 | 1.96 |
| sp|P51571|SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens OX=9606 GN=SSR4 PE=1 SV=1 | 16.24 | 70.17 | 4.32 | 2.11 |
| tr|A0A0C4DFL7|A0A0C4DFL7_HUMAN Lanosterol 14-alpha demethylase OS=Homo sapiens OX=9606 GN=CYP51A1 PE=1 SV=1 | 16.21 | 4.76 | 0.29 | -1.77 |
| sp|P14923|PLAK_HUMAN Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3 | 16.07 | 10.90 | 0.68 | -0.56 |
| sp|Q14847-2|LASP1_HUMAN Isoform 2 of LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 | 16.01 | 17.89 | 1.12 | 0.16 |
| sp|O60684|IMAT_HUMAN Importin subunit alpha-7 OS=Homo sapiens OX=9606 GN=KPN6 PE=1 SV=1 | 16.00 | 31.25 | 1.95 | 0.97 |
| sp|O95816-2|BAG2_HUMAN Isoform 2 of BAG family molecular chaperone regulator 2 OS=Homo sapiens OX=9606 GN=BAG2 | 15.93 | 10.85 | 0.68 | -0.55 |
| sp|Q92979|NEP1_HUMAN Ribosomal RNA small subunit methyltransferase NEP1 OS=Homo sapiens OX=9606 GN=EMG1 PE=1 SV=4 | 15.83 | 43.63 | 2.76 | 1.46 |
| sp|Q9BS26|ERP44_HUMAN Endoplasmic reticulum resident protein 44 OS=Homo sapiens OX=9606 GN=ERP44 PE=1 SV=1 | 15.72 | 27.28 | 1.73 | 0.79 |
| tr|G5EA30|G5EA30_HUMAN CUG triplet repeat, RNA binding protein 1, isoform CRA_c OS=Homo sapiens OX=9606 GN=CELF1 PE=1 SV=1 | 15.70 | 24.67 | 1.57 | 0.65 |
| sp|O76003|GLRX3_HUMAN Glutaredoxin-3 OS=Homo sapiens OX=9606 GN=GLRX3 PE=1 SV=2 | 15.63 | 89.33 | 5.72 | 2.51 |
| sp|O76070|SYUG_HUMAN Gamma-synuclein OS=Homo sapiens OX=9606 GN=SNCG PE=1 SV=2 | 15.57 | 61.41 | 3.94 | 1.98 |
| tr|A0A0D9SFS3|A0A0D9SFS3_HUMAN 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=OGDH PE=1 SV=1 | 15.47 | 69.67 | 4.50 | 2.17 |
| sp|P20700|LMNB1_HUMAN Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2 | 15.36 | 27.43 | 1.79 | 0.84 |
| Accession | Description | OS | OX | GN | PE | SV | Score |
|-----------|-------------|----|----|----|----|----|-------|
| sp|Q9BPW8|NIPS1_HUMAN|Protein NipSnap homolog 1|Homo sapiens|9606|NIPSNAP1|1|1|15.33|2.34|0.15|-2.72|
| sp|O00232|PSD12_HUMAN|26S proteasome non-ATPase regulatory subunit 12|Homo sapiens|9606|PSMD12|1|3|15.26|53.34|3.49|1.81|
| sp|A6NDG6|PGP_HUMAN|Glycerol-3-phosphate phosphatase|Homo sapiens|9606|PGP|1|1|15.19|49.75|3.28|1.71|
| sp|Q7RTV0|PHF5A_HUMAN|PHD finger-like domain-containing protein 5A|Homo sapiens|9606|PHF5A|1|1|15.18|10.15|0.67|-0.58|
| sp|P30520|PURB2_HUMAN|Adenylosuccinate synthetase isozyme 2|Homo sapiens|9606|ADSS|1|3|15.15|30.23|2.00|1.00|
| tr|I3L0A0|HCG2044781|OS|Homo sapiens|9606|TMEM189-UBE2V1|4|1|14.99|44.44|2.97|1.57|
| tr|E9PKG1|E9PKG1_HUMAN|Protein arginine N-methyltransferase 1|Homo sapiens|9606|PRMT1|1|1|14.92|30.43|2.04|1.03|
| sp|Q86YZ3|HORN_HUMAN|Hornerin|Homo sapiens|9606|HRNR|1|2|14.89|10.78|0.72|-0.47|
| sp|O75531|BAF_HUMAN|Barrier-to-autointegration factor OS|Homo sapiens|9606|BANF1|1|1|14.88|36.19|2.43|1.28|
| sp|P55735|SEC13_HUMAN|Protein SEC13 homolog|Homo sapiens|9606|SEC13|1|3|14.81|28.47|1.92|0.94|
| sp|Q13595-2|TRA2A_HUMAN|Isoform Short of Transformer-2 protein homolog alpha|Homo sapiens|9606|TRA2A|1|2|14.79|10.03|0.68|-0.56|
| sp|P31949|S10AB_HUMAN|Protein S100-A11|Homo sapiens|9606|S100A11|1|2|14.70|81.69|5.56|2.47|
| sp|P47897|SYQ_HUMAN|Glutamine--tRNA ligase OS|Homo sapiens|9606|QARS|1|1|14.70|54.41|3.70|1.89|
| tr|F8VXJ7|F8VXJ7_HUMAN|Protein canopy homolog 2 (Fragment)|Homo sapiens|9606|CNPY2|1|1|14.66|15.86|1.08|0.11|
| sp|Q9H2P9|DPH5_HUMAN|Isoform 4 of Diphthine methyl ester synthase|Homo sapiens|9606|DPH5|1|1|14.64|30.44|2.08|1.06|
| sp|O00764|PDXK_HUMAN|Pyridoxal kinase OS|Homo sapiens|9606|PDXK|1|1|14.63|3.94|0.27|-1.89|
| sp|Q7Z333-3|SETX_HUMAN|Isoform 3 of Probable helicase senataxin OS|Homo sapiens|9606|SETX|1|1|14.55|30.78|2.12|1.08|
| sp|P17655|CAN2_HUMAN|Calpain-2 catalytic subunit OS|Homo sapiens|9606|CAPN2|1|6|14.51|35.79|2.47|1.30|
| Accession | Description | OS: Homo sapiens | GN | PE | SV |
|-----------|-------------|-----------------|----|----|----|
| sp|Q9BUL8|PDC10_HUMAN Programmed cell death protein 10 | 9606 | 1 | 1 |
| sp|O75489|NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial | 9606 | 1 | 1 |
| tr|A0A1B0GTJ7|A0A1B0GTJ7_HUMAN Adenyllosuccinate lyase | 9606 | 1 | 1 |
| sp|Q16401|PSMD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 | 9606 | 1 | 3 |
| sp|O75489|NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial | 9606 | 1 | 1 |
| sp|Q00688|FKBP3_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP3 | 9606 | 1 | 1 |
| sp|Q96C19|EFHD2_HUMAN EF-hand domain-containing protein D2 | 9606 | 1 | 1 |
| sp|P42765|ADCA2_HUMAN Aconitate hydratase, mitochondrial | 9606 | 1 | 1 |
| sp|Q3MHD2-2|LSM12_HUMAN Isoform 2 of Protein LSM12 homolog | 9606 | 1 | 1 |
| sp|Q96EY1-2|DNJA3_HUMAN Isoform 2 of DnaJ homolog subfamily A member 3, mitochondrial | 9606 | 1 | 1 |
| tr|J3KNQ4|J3KNQ4_HUMAN Alpha-parvin | 9606 | 1 | 1 |
| sp|P30405|PPIF_HUMAN Peptidyl-prolyl cis-trans isomerase F, mitochondrial | 9606 | 1 | 1 |
| sp|Q9Y310|RTCB_HUMAN tRNA-splicing ligase RtcB homolog | 9606 | 1 | 1 |
| sp|Q16795|NDUA9_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha | 9606 | 1 | 1 |
| Accession   | Description                                                                 | Species   | Gene    | SwissProtID | Description                       | PE | SV | E-value | q-value | Log2 Fold |
|-------------|-----------------------------------------------------------------------------|-----------|---------|-------------|-----------------------------------|----|----|---------|---------|-----------|
| sp|P61081|UBC12_HUMAN NEDD8-conjugating enzyme Ubc12| Homo sapiens | OX=9606 | GN=NDUFA9 | PE=1 SV=2 | 13.93 | 35.83 | 2.57 | 1.36 |
| sp|P12081-4|SYHC_HUMAN Isoform 4 of Histidine-ribosomal protein ligase, cytoplasmic| Homo sapiens | OX=9606 | GN=UBE2M | PE=1 SV=1 | 13.92 | 28.71 | 2.06 | 1.04 |
| tr|G3V5T9|G3V5T9_HUMAN Cyclin-dependent kinase 2| Homo sapiens | OX=9606 | GN=CDK2 | PE=1 SV=1 | 13.91 | 22.33 | 1.60 | 0.68 |
| sp|Q9UHV9|PFD2_HUMAN Prefoldin subunit 2| Homo sapiens | OX=9606 | GN=PFDN2 | PE=1 SV=1 | 13.79 | 61.40 | 4.45 | 2.15 |
| tr|H0YFD6|H0YFD6_HUMAN Trifunctional enzyme subunit alpha, mitochondrial| Homo sapiens | OX=9606 | GN=HADHA | PE=1 SV=2 | 13.73 | 34.70 | 2.53 | 1.34 |
| sp|Q08945|SSRP1_HUMAN FACT complex subunit SSRP1| Homo sapiens | OX=9606 | GN=SSRP1 | PE=1 SV=1 | 13.69 | 8.53 | 0.62 | -0.68 |
| tr|A0A0A0MRF6|A0A0A0MRF6_HUMAN A-kinase anchor protein 9| Homo sapiens | OX=9606 | GN=AKAP9 | PE=1 SV=1 | 13.67 | 11.30 | 0.83 | -0.27 |
| tr|A0A0A0MRJ6|A0A0A0MRJ6_HUMAN Protein-isoaspartate O-methyltransferase| Homo sapiens | OX=9606 | GN=PCMT1 | PE=1 SV=1 | 13.58 | 69.77 | 5.14 | 2.36 |
| sp|Q9UBI6|GBG12_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12| Homo sapiens | OX=9606 | GN=GNG12 | PE=1 SV=3 | 13.56 | 10.77 | 0.79 | -0.33 |
| tr|J3KQ32|J3KQ32_HUMAN Obg-like ATPase 1| Homo sapiens | OX=9606 | GN=OLA1 | PE=1 SV=1 | 13.55 | 15.84 | 1.17 | 0.22 |
| tr|F8W7Q4|F8W7Q4_HUMAN Protein FAM162A| Homo sapiens | OX=9606 | GN=FAM162A | PE=1 SV=1 | 13.48 | 87.69 | 6.50 | 2.70 |
| sp|P20073-2|ANXA7_HUMAN Isoform 2 of Annexin A7| Homo sapiens | OX=9606 | GN=ANXA7 | PE=1 SV=1 | 13.39 | 49.26 | 3.68 | 1.88 |
| sp|P54866-2|P5CS_HUMAN Isoform Short of Delta-1-pyrroline-5-carboxylate synthase| Homo sapiens | OX=9606 | GN=ALDH18A1 | PE=1 SV=1 | 13.37 | 20.75 | 1.55 | 0.63 |
| sp|Q92937-2|TNPO1_HUMAN Isoform 2 of Transportin-1| Homo sapiens | OX=9606 | GN=TNPO1 | PE=1 SV=1 | 13.36 | 27.03 | 2.02 | 1.02 |
| tr|F5H4X0|F5H4X0_HUMAN Scavenger receptor class B member 1| Homo sapiens | OX=9606 | GN=SCARB1 | PE=1 SV=1 | 13.32 | 13.51 | 1.01 | 0.02 |
| tr|B4DR61|B4DR61_HUMAN cDNA FLJ59739, highly similar to Protein transport protein Sec61| Homo sapiens | OX=9606 | GN=HEX | PE=1 SV=1 | 13.23 | 6.23 | 0.47 | -1.09 |
| Entrez| KEGG| EC  | UniProt| Name                                      | Description                                                                 | Organism  | Source | Peptide Start | Peptide Stop | Match Count | Pvalue |
|-------|------|-----|-------|-----------------|-----------------------------------------------------------------------------|------------|--------|---------------|--------------|-------------|--------|
| tr|B1AJY5|B1AJY5_HUMAN|26S proteasome non-ATPase regulatory subunit 10| Homo sapiens OS=9606 GN=PSMD10 PE=1 SV=1 | 13.23 | 12.63 | 0.95 | -0.07 |
| sp|Q9UDH8-2|SEPT9_HUMAN|Isoform 2 of Septin-9| Homo sapiens OS=9606 GN=SEPT9 | 13.21 | 14.16 | 1.07 | 0.10 |
| sp|P29966|MARC5_HUMAN|Myristoylated alanine-rich C-kinase substrate| Homo sapiens OS=9606 GN=MARCS PE=1 SV=4 | 13.16 | 9.90 | 0.75 | -0.41 |
| tr|H7BYV1|H7BYV1_HUMAN|Interferon-induced transmembrane protein 2 (Fragment)| Homo sapiens OS=9606 GN=IFITM2 PE=4 SV=1 | 13.07 | 49.00 | 3.75 | 1.91 |
| sp|Q15637-2|SF01_HUMAN|Splicing factor 1| Homo sapiens OS=9606 GN=SF1 | 13.04 | 20.32 | 1.56 | 0.64 |
| tr|A0A2R8Y3N3|A0A2R8Y3N3_HUMAN|Probable histidine--tRNA ligase, mitochondrial| Homo sapiens OS=9606 GN=HARS2 PE=1 SV=1 | 13.01 | 25.08 | 1.93 | 0.95 |
| tr|B4DUC8|B4DUC8_HUMAN|S-methyl-5'-thioadenosine phosphorylase| Homo sapiens OS=9606 GN=MTAP PE=1 SV=1 | 12.97 | 68.25 | 5.26 | 2.40 |
| sp|Q13501-2|SQSTM_HUMAN|Sequestosome-1| Homo sapiens OS=9606 GN=SQSTM1 | 12.92 | 33.10 | 2.56 | 1.36 |
| sp|P61106|RAB14_HUMAN|Ras-related protein Rab-14| Homo sapiens OS=9606 GN=RAB14 PE=4 SV=4 | 12.87 | 14.93 | 1.16 | 0.21 |
| sp|O00592-2|PODXL_HUMAN|Podocalyxin| Homo sapiens OS=9606 GN=PODXL | 12.85 | 30.42 | 2.37 | 1.24 |
| sp|P43490|NAMPT_HUMAN|Nicotinamide phosphoribosyltransferase| Homo sapiens OS=9606 GN=NAMPT PE=1 SV=1 | 12.79 | 31.84 | 2.49 | 1.32 |
| sp|Q14914-2|PTGR1_HUMAN|Prostaglandin reductase 1| Homo sapiens OS=9606 GN=PTGR1 | 12.77 | 15.02 | 1.18 | 0.23 |
| sp|P45973|CBX5_HUMAN|Chromobox protein homolog 5| Homo sapiens OS=9606 GN=CBX5 PE=1 SV=1 | 12.73 | 18.05 | 1.42 | 0.50 |
| sp|P43121|MUC18_HUMAN|Cell surface glycoprotein MUC18| Homo sapiens OS=9606 GN=MCAM PE=1 SV=2 | 12.72 | 29.01 | 2.28 | 1.19 |
| tr|M0QXB4|M0QXB4_HUMAN|Coatomer protein complex, subunit epsilon, isoform CRA_g| Homo sapiens OS=9606 GN=COPE PE=1 SV=1 | 12.65 | 49.03 | 3.88 | 1.95 |
| sp|Q8N4V1-2|MMGT1_HUMAN|Membrane magnesium transporter 1| Homo sapiens OS=9606 GN=MMGT1 | 12.57 | 45.78 | 3.64 | 1.86 |
| Accession  | Gene Name                        | Organism       | Protein Name                        | Peptide Coverage | Spectrum Coverage | Peptide Score | Spectrum Score | Charge | Mass 1  | Mass 2  | Mass 3  | Mass 4  |
|------------|---------------------------------|----------------|-------------------------------------|------------------|-------------------|--------------|----------------|--------|----------|----------|----------|----------|
| sp|Q9HCN8|SDF2L_HUMAN Stromal cell-derived factor 2-like protein 1 OS=Homo sapiens OX=9606 GN=SDF2L1 PE=1 SV=2 | 12.57 | 41.01 | 3.26 | 1.71 |
| sp|Q9BY43-2|CHM4A_HUMAN Isoform 2 of Charged multivesicular body protein 4a OS=Homo sapiens OX=9606 GN=CHMP4A | 12.56 | 44.92 | 3.58 | 1.84 |
| sp|O75629|CREG1_HUMAN Protein CREG1 OS=Homo sapiens OX=9606 GN=CREG1 PE=1 SV=1 | 12.54 | 27.20 | 2.17 | 1.12 |
| sp|P53007|TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A1 PE=1 SV=2 | 12.51 | 28.81 | 2.30 | 1.20 |
| tr|H0YIB4|H0YIB4_HUMAN Serine/arginine-rich-splicing factor 9 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF9 PE=1 SV=8 | 12.46 | 0.95 | 0.08 | -3.72 |
| tr|H7C2Q8|H7C2Q8_HUMAN EBNA1 binding protein 2, isoform CRA_d OS=Homo sapiens OX=9606 GN=EBNA1BP2 PE=1 SV=1 | 12.44 | 15.94 | 1.28 | 0.36 |
| tr|A0A087WZN1|A0A087WZN1_HUMAN Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Homo sapiens OX=9606 GN=IDH3B PE=1 SV=1 | 12.35 | 8.09 | 0.65 | -0.61 |
| sp|P0DN79|CBSL_HUMAN Cystathionine beta-synthase-like protein OS=Homo sapiens OX=9606 GN=CBSL PE=1 SV=1 | 12.35 | 20.48 | 1.66 | 0.73 |
| tr|A0A1B0GTG2|A0A1B0GTG2_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1 | 12.34 | 27.87 | 2.26 | 1.18 |
| sp|Q14166|TTL12_HUMAN Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens OX=9606 GN=TTL12 PE=1 SV=2 | 12.31 | 27.51 | 2.24 | 1.16 |
| tr|G5E9R5|G5E9R5_HUMAN Acid phosphatase 1, soluble, isoform CRA_d OS=Homo sapiens OX=9606 GN=ACP1 PE=1 SV=1 | 12.25 | 34.72 | 2.84 | 1.50 |
| sp|Q9BRA2|TXD17_HUMAN Thioredoxin domain-containing protein 17 OS=Homo sapiens OX=9606 GN=TXNDC17 PE=1 SV=1 | 12.23 | 44.80 | 3.66 | 1.87 |
| tr|F5GZQ3|F5GZQ3_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=1 | 12.23 | 25.98 | 2.12 | 1.09 |
| sp|Q8TDN6|BRX1_HUMAN Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRX1 PE=1 SV=2 | 12.15 | 19.08 | 1.57 | 0.65 |
| tr|B1AHB1|B1AHB1_HUMAN DNA helicase OS=Homo sapiens OX=9606 GN=MCM5 PE=1 SV=1 | 12.02 | 11.20 | 0.93 | -0.10 |
| sp|Q96EK6|GNA1_HUMAN Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens OX=9606 GN=GNPNAT1 PE=1 SV=1 | 12.02 | 35.08 | 2.92 | 1.55 |
| tr|E7EX17|E7EX17_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=1 | 11.98 | 23.39 | 1.95 | 0.97 |
| Accession   | Description                                                                 | OS             | OX     | GN      | PE  | SV  | Type | Value   |
|-------------|------------------------------------------------------------------------------|----------------|--------|---------|-----|-----|------|---------|
| sp|Q9NQ88|Fructose-2,6-bisphosphatase TIGAR| Homo sapiens   | 9606   | TIGAR  | 1   | 1   |       | 11.95  |
| sp|O95292|Vesicle-associated membrane protein-associated protein B/C| Homo sapiens   | 9606   | VAPB  | 1   | 3   |       | 11.92  |
| tr|Q5T5C7|Serine--tRNA ligase, cytoplasmic| Homo sapiens   | 9606   | SARS  | 1   | 1   |       | 11.90  |
| tr|F8VQE1|LIM domain and actin-binding protein 1| Homo sapiens   | 9606   | LIMA1 | 1   | 1   |       | 11.87  |
| sp|P63096|Guanine nucleotide-binding protein G(i) subunit alpha-1| Homo sapiens   | 9606   | GNAI1 | 1   | 2   |       | 11.86  |
| tr|D6RHJ3|Calnexin (Fragment)| Homo sapiens   | 9606   | CANX  | 1   | 8   |       | 11.86  |
| sp|P31930|Cytochrome b-c1 complex subunit 1, mitochondrial| Homo sapiens   | 9606   | UQCRC1| 1   | 3   |       | 11.85  |
| sp|Q14165|Malectin| Homo sapiens   | 9606   | MLEC  | 1   | 1   |       | 11.84  |
| sp|P40261|Nicotinamide N-methyltransferase| Homo sapiens   | 9606   | NNMT  | 1   | 1   |       | 11.76  |
| sp|P10301|Ras-related protein R-Ras| Homo sapiens   | 9606   | RRAS  | 1   | 1   |       | 11.76  |
| sp|P33991|DNA replication licensing factor MCM4| Homo sapiens   | 9606   | MCM4  | 1   | 5   |       | 11.64  |
| sp|O95336|6-phosphogluconolactonase| Homo sapiens   | 9606   | PGLS  | 1   | 2   |       | 11.63  |
| tr|M0R0I3|Endophilin-A2 (Fragment)| Homo sapiens   | 9606   | SH3GL1| 1   | 1   |       | 11.62  |
| sp|P0DN76|Splicing factor U2AF 35 kDa subunit-like protein| Homo sapiens   | 9606   | U2AF1L5| 1   | 1   |       | 11.58  |
| sp|P11172|Uridine 5'-monophosphate synthase| Homo sapiens   | 9606   | UMPS  | 1   | 1   |       | 11.58  |
| sp|O95340-2|Isoform B of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase| Homo sapiens   | 9606   | PAPSS2| 1   | 1   |       | 11.57  |
| Accession | Description | OS | GN | PE | SV | Unique ID | Gene Name | Unique ID | Gene Name | Unique ID | Gene Name | Unique ID | Gene Name | Unique ID | Gene Name | Unique ID | Gene Name | Unique ID | Gene Name | Unique ID | Gene Name | Unique ID | Gene Name |
|-----------|-------------|----|----|----|----|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| sp|O96019|ACL6A_HUMAN Actin-like protein 6A OS=Homo sapiens OX=9606 GN=ACTL6A PE=1 SV=1 | 11.55 | 18.35 | 1.59 | 0.67 |
| tr|J3KN29|J3KN29_HUMAN 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=1 | 11.55 | 3.30 | 0.29 | -1.81 |
| tr|H0Y368|H0Y368_HUMAN Dolichol-phosphate mannosyltransferase subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=DPM1 PE=1 SV=1 | 11.53 | 14.32 | 1.24 | 0.31 |
| sp|Q05682|CALD1_HUMAN Caldesmon OS=Homo sapiens OX=9606 GN=CALD1 PE=1 SV=3 | 11.53 | 10.53 | 0.91 | -0.13 |
| tr|I3L1Y9|I3L1Y9_HUMAN FLYWCH family member 2 OS=Homo sapiens OX=9606 GN=FLYWCH2 PE=1 SV=1 | 11.37 | 8.49 | 0.75 | -0.42 |
| sp|Q96RS6-2|NUDC1_HUMAN Isoform 2 of NudC domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NUDCD1 | 11.28 | 12.89 | 1.14 | 0.19 |
| sp|Q15388|TOM20_HUMAN Mitochondrial import receptor subunit TOM20 homolog OS=Homo sapiens OX=9606 GN=TOMM20 PE=1 SV=1 | 11.26 | 32.83 | 2.92 | 1.54 |
| sp|Q9H4A4|AMPB_HUMAN Aminopeptidase B OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=2 | 11.21 | 20.00 | 1.78 | 0.84 |
| sp|Q9UN7E|CHIP_HUMAN E3 ubiquitin-protein ligase CHIP OS=Homo sapiens OX=9606 GN=STUB1 PE=1 SV=2 | 11.19 | 28.09 | 2.51 | 1.33 |
| sp|P49189|AL9A1_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1 PE=1 SV=3 | 11.19 | 17.72 | 1.58 | 0.66 |
| sp|P42025|ACTY_HUMAN Beta-centractin OS=Homo sapiens OX=9606 GN=ACTR1B PE=1 SV=1 | 11.15 | 2.25 | 0.20 | -2.31 |
| sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=M6PR PE=1 SV=1 | 11.07 | 23.30 | 2.10 | 1.07 |
| sp|O15144|ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1 | 10.96 | 28.95 | 2.64 | 1.40 |
| tr|K7ERJ1|K7ERJ1_HUMAN Thymidine kinase (Fragment) OS=Homo sapiens OX=9606 GN=TK1 PE=1 SV=1 | 10.96 | 34.67 | 3.16 | 1.66 |
| sp|Q9Y2V2|CHSP1_HUMAN Calcium-regulated heat-stable protein 1 OS=Homo sapiens OX=9606 GN=CARHSP1 PE=1 SV=2 | 10.95 | 43.25 | 3.95 | 1.98 |
| sp|P11233|RALA_HUMAN Ras-related protein Ras-OS=Homo sapiens OX=9606 GN=RALA PE=1 SV=1 | 10.92 | 3.52 | 0.32 | -1.63 |
| tr|A0A286YEY5|A0A286YEY5_HUMAN MICOS complex subunit (Fragment) OS=Homo sapiens OX=9606 GN=CHCHD3 PE=1 SV=1 | 10.87 | 2.05 | 0.19 | -2.41 |
| Accession | Description                                           | OS       | OX    | GN    | PE | SV | E_value | Q_value | Delta Q | P_value |
|-----------|-------------------------------------------------------|----------|------|-------|----|----|---------|---------|---------|----------|
| sp|Q07960|RHG01_HUMAN Rho GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=ARHGAP1 PE=1 SV=1 | 10.87    | 19.66| 1.81  | 0.85 |
| sp|P36507|MP2K2_HUMAN Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens OX=9606 GN=MAP2K2 PE=1 SV=1 | 10.86    | 14.52| 1.34  | 0.42 |
| sp|Q02750|MP2K1_HUMAN Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens OX=9606 GN=MAP2K1 PE=1 SV=2 | 10.86    | 14.13| 1.30  | 0.38 |
| tr|H0Y2V1|H0Y2V1_HUMAN Microtubule-associated protein (Fragment) OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1 | 10.77    | 14.46| 1.34  | 0.42 |
| tr|G3V1C3|G3V1C3_HUMAN Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 PE=1 SV=1 | 10.76    | 43.20| 4.02  | 2.01 |
| tr|R4GMR5|R4GMR5_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens OX=9606 GN=PSMD8 PE=1 SV=1 | 10.74    | 31.90| 2.97  | 1.57 |
| sp|Q53EL6|PDCD4_HUMAN Isoform 2 of Programmed cell death protein 4 OS=Homo sapiens OX=9606 GN=PDCD4 | 10.70    | 16.50| 1.54  | 0.63 |
| tr|H0Y8X4|H0Y8X4_HUMAN 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 (Fragment) OS=Homo sapiens OX=9606 GN=DNPH1 PE=1 SV=1 | 10.69    | 37.47| 3.51  | 1.81 |
| tr|B1AMS2|B1AMS2_HUMAN Septin 6, isoform CRA_b OS=Homo sapiens OX=9606 GN=SEPT6 PE=1 SV=1 | 10.66    | 25.47| 2.39  | 1.26 |
| sp|Q9H074|PAIP1_HUMAN Isoform 2 of Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens OX=9606 GN=PAIP1 | 10.66    | 14.96| 1.40  | 0.49 |
| sp|P38606|VATA_HUMAN Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens OX=9606 GN=ATP6V1A | 10.66    | 14.67| 1.38  | 0.46 |
| sp|Q96IZ0|PAWR_HUMAN PRKC apoptosis WT1 regulator protein OS=Homo sapiens OX=9606 GN=PAWR PE=1 SV=1 | 10.62    | 1.48 | 0.14  | -2.84 |
| sp|Q15646|OASL_HUMAN 2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens OX=9606 GN=OASL PE=1 SV=2 | 10.56    | 9.82 | 0.93  | -0.10 |
| sp|P52943|CRIP2_HUMAN Cysteine-rich protein 2 OS=Homo sapiens OX=9606 GN=CRIP2 PE=1 SV=1 | 10.54    | 36.74| 3.48  | 1.80 |
| sp|P27694|RFA1_HUMAN Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RFA1 PE=1 SV=2 | 10.53    | 11.77| 1.12  | 0.16 |
| tr|K7ENG2|K7ENG2_HUMAN U2 snRNP auxiliary factor large subunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=1 SV=1 | 10.51    | 35.32| 3.36  | 1.75 |
| Accession | Description                                                                 | Species | OS  | GN          | PE  | SV  | PMF  | SPM  | DPM  | RAST  |
|-----------|-------------------------------------------------------------------------------|---------|-----|-------------|-----|-----|------|------|------|-------|
| sp|Q9NZ45|CISD1_HUMAN CDGSH iron-sulfur domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CISD1 PE=1 SV=1 | Homo sapiens | Homo sapiens | 9606 | CISD1 | 1 | 10.51 | 33.47 | 3.19 | 1.67 |
| sp|P61086|UBE2K_HUMAN Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens OX=9606 GN=UBE2K PE=1 SV=3 | Homo sapiens | Homo sapiens | 9606 | UBE2K | 1 | 10.45 | 18.14 | 1.74 | 0.80 |
| sp|Q969X5|ERGI1_HUMAN Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens OX=9606 GN=ERGIC1 PE=1 SV=1 | Homo sapiens | Homo sapiens | 9606 | ERGIC1 | 1 | 10.44 | 30.69 | 2.94 | 1.56 |
| sp|P51665|PSMD7_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSMD7 PE=1 SV=2 | Homo sapiens | Homo sapiens | 9606 | PSMD7 | 1 | 10.44 | 29.73 | 2.85 | 1.51 |
| sp|Q9Y224|RTRAF_HUMAN RNA transcription, translation and transport factor OS=Homo sapiens OX=9606 GN=RTRAF PE=1 SV=1 | Homo sapiens | Homo sapiens | 9606 | RTRAF | 1 | 10.40 | 30.65 | 2.95 | 1.56 |
| sp|O43143|DHX15_HUMAN Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens OX=9606 GN=DHX15 PE=1 SV=2 | Homo sapiens | Homo sapiens | 9606 | DHX15 | 1 | 10.30 | 15.47 | 1.50 | 0.59 |
| sp|P13861|KAP2_HUMAN Isoform 2 of cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR2A | Homo sapiens | Homo sapiens | 9606 | PRKAR2A | 1 | 10.30 | 14.46 | 1.40 | 0.49 |
| tr|E9PEX6|E9PEX6_HUMAN Dihydrolipoyl dehydrogenase OS=Homo sapiens OX=9606 GN=DLD PE=1 SV=1 | Homo sapiens | Homo sapiens | 9606 | DLD | 1 | 10.25 | 17.22 | 1.68 | 0.75 |
| sp|O95433|AHSA1_HUMAN Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens OX=9606 GN=AHSA1 PE=1 SV=1 | Homo sapiens | Homo sapiens | 9606 | AHSA1 | 1 | 10.24 | 46.85 | 4.58 | 2.19 |
| sp|P16949|STMN1_HUMAN Isoform 2 of Stathmin OS=Homo sapiens OX=9606 GN=STMN1 | Homo sapiens | Homo sapiens | 9606 | STMN1 | 1 | 10.23 | 29.94 | 2.93 | 1.55 |
| sp|P51970|NDUA8_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Homo sapiens OX=9606 GN=NDUFA8 PE=1 SV=3 | Homo sapiens | Homo sapiens | 9606 | NDUFA8 | 1 | 10.22 | 20.62 | 2.02 | 1.01 |
| sp|P21912|SDHB_HUMAN Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens OX=9606 GN=SDHB PE=1 SV=3 | Homo sapiens | Homo sapiens | 9606 | SDHB | 1 | 10.20 | 23.98 | 2.35 | 1.23 |
| sp|P46060|RAGP1_HUMAN Ran GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RANGAP1 PE=1 SV=1 | Homo sapiens | Homo sapiens | 9606 | RANGAP1 | 1 | 10.15 | 22.34 | 2.20 | 1.14 |
| tr|D6RBV2|D6RBV2_HUMAN Vesicular integral-membrane protein VIP36 OS=Homo sapiens OX=9606 GN=LMAN2 PE=1 SV=1 | Homo sapiens | Homo sapiens | 9606 | LMAN2 | 1 | 10.11 | 21.69 | 2.15 | 1.10 |
| sp|Q96HE7|ERO1A_HUMAN ERO1-like protein alpha OS=Homo sapiens OX=9606 GN=ERO1A PE=1 SV=2 | Homo sapiens | Homo sapiens | 9606 | ERO1A | 1 | 10.10 | 10.60 | 1.05 | 0.07 |
| Accession  | Gene Name                   | Description                                                                 | MAF   | BAF   | AD    | AC    |
|------------|-----------------------------|------------------------------------------------------------------------------|-------|-------|-------|-------|
| sp|P48507|GSH0_HUMAN Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens OX=9606 GN=GCLM PE=1 SV=1 | 10.06 | 26.96 | 2.68  | 1.42  |
| sp|P42166|LAP2A_HUMAN Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2 | 10.04 | 15.27 | 1.52  | 0.61  |
| sp|Q9BFWF3|RBM4_HUMAN RNA-binding protein 4 OS=Homo sapiens OX=9606 GN=RBM4 PE=1 SV=1 | 9.98  | 31.57 | 3.16  | 1.66  |
| sp|P52294|IMA5_HUMAN Importin subunit alpha-5 OS=Homo sapiens OX=9606 GN=KPNA1 PE=1 SV=3 | 9.97  | 22.33 | 2.24  | 1.16  |
| tr|J3QLE5|J3QLE5_HUMAN Small nuclear ribonucleoprotein-associated protein N (Fragment) OS=Homo sapiens OX=9606 GN=SNRPN PE=1 SV=1 | 9.96  | 69.50 | 6.98  | 2.80  |
| sp|Q9NUQ9|FA49B_HUMAN Protein FAM49B OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1 | 9.92  | 27.86 | 2.81  | 1.49  |
| tr|E5RFX4|E5RFX4_HUMAN Lymphokine-activated killer T-cell-activated protein kinase (Fragment) OS=Homo sapiens OX=9606 GN=PBK PE=1 SV=2 | 9.92  | 36.72 | 3.70  | 1.89  |
| sp|Q9Y2Z4|SYYM_HUMAN Tyrosine--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=YARS2 PE=1 SV=2 | 9.88  | 2.84  | 0.29  | -1.80 |
| tr|F5GX39|F5GX39_HUMAN Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=TMED2 PE=1 SV=1 | 9.88  | 7.22  | 0.73  | -0.45 |
| sp|Q15370|ELOB_HUMAN Isoform 2 of Elongin-B OS=Homo sapiens OX=9606 GN=ELOB | 9.87  | 14.18 | 1.44  | 0.52  |
| sp|O94925|GLSK_HUMAN Isoform 3 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS | 9.83  | 14.76 | 1.50  | 0.59  |
| sp|P82933|RT09_HUMAN 28S ribosomal protein S9, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS9 PE=1 SV=2 | 9.79  | 20.24 | 2.07  | 1.05  |
| sp|Q9H7Z7|PGES2_HUMAN Prostaglandin E synthase 2 OS=Homo sapiens OX=9606 GN=PTGES2 PE=1 SV=1 | 9.77  | 22.84 | 2.34  | 1.23  |
| sp|P62304|RUXE_HUMAN Small nuclear ribonucleoprotein E OS=Homo sapiens OX=9606 GN=SNRPE PE=1 SV=1 | 9.74  | 27.02 | 2.78  | 1.47  |
| tr|B4DLR8|B4DLR8_HUMAN NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens OX=9606 GN=NQO1 PE=1 SV=1 | 9.73  | 7.93  | 0.81  | -0.30 |
| tr|H0YKU1|H0YKU1_HUMAN Tropomodulin-3 (Fragment) OS=Homo sapiens OX=9606 GN=TMOD3 PE=1 SV=1 | 9.68  | 25.52 | 2.64  | 1.40  |
| tr|C9JK13|C9JK13_HUMAN Caveolin (Fragment) OS=Homo sapiens OX=9606 GN=CAV1 PE=1 SV=1 | 9.68  | 21.04 | 2.17  | 1.12  |
| Accession   | Description                                                                 | OS      | S100A1    | S100A1     | S100A1     |
|-------------|------------------------------------------------------------------------------|---------|-----------|-----------|-----------|
| sp|P25815|S100P_HUMAN Protein S100-P | Homo sapiens | 9606 | GN=S100P PE=1 SV=2 | 9.64 | 30.57 | 3.17 | 1.66 |
| sp|Q6NUO4-2|TM214_HUMAN Isoform 2 of Transmembrane protein 214 | Homo sapiens | 9606 | GN=TMEM214 | 9.59 | 0.44 | 0.05 | -4.46 |
| sp|Q9UBT2|SAE2_HUMAN SUMO-activating enzyme subunit 2 | Homo sapiens | 9606 | GN=UBA2 PE=1 SV=2 | 9.56 | 1.92 | 0.20 | -2.32 |
| sp|Q15008-4|PSMD6_HUMAN Isoform 4 of 26S proteasome non-ATPase regulatory subunit 6 | Homo sapiens | 9606 | GN=PSMD6 | 9.53 | 13.49 | 1.42 | 0.50 |
| sp|Q7L5N1|CSN6_HUMAN COP9 signalosome complex subunit 6 | Homo sapiens | 9606 | GN=COP6 PE=1 SV=1 | 9.51 | 15.41 | 1.62 | 0.70 |
| tr|A0A2U3TZL5|A0A2U3TZL5_HUMAN CD59 glycoprotein (Fragment) | Homo sapiens | 9606 | GN=CD59 PE=4 SV=1 | 9.51 | 16.02 | 1.69 | 0.75 |
| sp|Q9UJS0-2|CMC2_HUMAN Isoform 2 of Calcium-binding mitochondrial carrier protein Aralar2 | Homo sapiens | 9606 | GN=SLC25A13 | 9.46 | 15.01 | 1.59 | 0.67 |
| sp|O14745|NHRF1_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF1 | Homo sapiens | 9606 | GN=SLC9A3R1 PE=4 SV=4 | 9.41 | 6.40 | 0.68 | -0.56 |
| sp|P51151|RAB9A_HUMAN Ras-related protein Rab-9A | Homo sapiens | 9606 | GN=RAB9A PE=1 SV=1 | 9.41 | 26.99 | 2.87 | 1.52 |
| tr|A0A1W2PNR9|A0A1W2PNR9_HUMAN Immediate early response 3-interacting protein 1 | Homo sapiens | 9606 | GN=IER3IP1 PE=1 SV=1 | 9.36 | 24.35 | 2.60 | 1.38 |
| tr|J3QRG6|J3QRG6_HUMAN Cyclin-dependent kinase inhibitor 2A | Homo sapiens | 9606 | GN=CDKN2A PE=1 SV=1 | 9.35 | 34.60 | 3.70 | 1.89 |
| sp|Q96B26|EXOS8_HUMAN Exosome complex component RRP43 | Homo sapiens | 9606 | GN=EXOSC8 PE=1 SV=1 | 9.35 | 20.79 | 2.22 | 1.15 |
| sp|Q9Y2Z0-2|SGT1_HUMAN Isoform 2 of Protein SGT1 homolog | Homo sapiens | 9606 | GN=SUGT1 | 9.33 | 15.87 | 1.70 | 0.77 |
| sp|Q6NUK1-2|SCMC1_HUMAN Isoform 2 of Calcium-binding mitochondrial carrier protein SCaMC-1 | Homo sapiens | 9606 | GN=SLC25A24 | 9.29 | 12.73 | 1.37 | 0.45 |
| sp|P50995-2|ANX11_HUMAN Isoform 2 of Annexin A11 | Homo sapiens | 9606 | GN=ANXA11 | 9.24 | 18.41 | 1.99 | 0.99 |
| sp|Q13868|EXOS2_HUMAN Exosome complex component RRP4 | Homo sapiens | 9606 | GN=EXOSC2 PE=1 SV=2 | 9.23 | 22.76 | 2.47 | 1.30 |
| Accession | Description                                                                 | Score | Log2 Fold Change | Ratio | Q Value |
|-----------|------------------------------------------------------------------------------|-------|------------------|-------|---------|
| sp|Q9UDY8|MALT1_HUMAN Mucosa-associated lymphoid tissue lymphoma translocation protein 1 OS=Homo sapiens OX=9606 GN=MALT1 PE=1 SV=1 | 9.21 | 20.54 | 2.23 | 1.16 |
| sp|Q9Y383|LC7L2_HUMAN Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens OX=9606 GN=LUC7L2 PE=1 SV=2 | 9.13 | 8.37 | 0.92 | -0.13 |
| tr|A0A0A6YYA0|A0A0A6YYA0_HUMAN Protein TMED7-TICAM2 OS=Homo sapiens OX=9606 GN=TMED7-TICAM2 PE=3 SV=1 | 9.10 | 13.72 | 1.51 | 0.59 |
| sp|Q9UJZ1-2|STP1L2_HUMAN Isoform 2 of Stomatin-like protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=STPML2 | 9.07 | 20.22 | 2.23 | 1.16 |
| tr|D6W5Y5|D6W5Y5_HUMAN Cold inducible RNA binding protein, isoform CRA_c OS=Homo sapiens OX=9606 GN=CIRBP PE=1 SV=1 | 9.07 | 15.84 | 1.75 | 0.80 |
| sp|Q7L9L4-2|MOB1B_HUMAN Isoform 2 of MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B | 9.05 | 14.07 | 1.55 | 0.64 |
| sp|P53004|BIEA_HUMAN Biliverdin reductase A OS=Homo sapiens OX=9606 GN=BLVRA PE=1 SV=2 | 9.03 | 34.15 | 3.78 | 1.92 |
| sp|Q5JWF2-2|GNAS1_HUMAN Isoform XLas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens OX=9606 GN=GNAS | 9.03 | 26.05 | 2.89 | 1.53 |
| sp|Q9161|NCBP1_HUMAN Nuclear cap-binding protein subunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1 | 9.01 | 12.92 | 1.43 | 0.52 |
| sp|Q9NPD8|UBE2T_HUMAN Ubiquitin-conjugating enzyme E2 T OS=Homo sapiens OX=9606 GN=UBE2T PE=1 SV=1 | 9.01 | 24.85 | 2.76 | 1.46 |
| sp|P49257|LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens OX=9606 GN=LMAN1 PE=1 SV=2 | 8.97 | 23.28 | 2.59 | 1.38 |
| sp|O60493|SNX3_HUMAN Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 PE=1 SV=3 | 8.96 | 33.86 | 3.78 | 1.92 |
| sp|Q9H444|CHM4B_HUMAN Charged multivesicular body protein 4b OS=Homo sapiens OX=9606 GN=CHM4B PE=1 SV=1 | 8.95 | 6.21 | 0.69 | -0.53 |
| sp|P55010|IF5_HUMAN Eukaryotic translation initiation factor 5 OS=Homo sapiens OX=9606 GN=EIF5 PE=1 SV=2 | 8.91 | 10.35 | 1.16 | 0.22 |
| tr|M0QYZ2|M0QYZ2_HUMAN AP complex subunit sigma OS=Homo sapiens OX=9606 GN=AP2S1 PE=1 SV=1 | 8.84 | 8.57 | 0.97 | -0.05 |
| sp|Q15785|TOM34_HUMAN Mitochondrial import receptor subunit TOM34 OS=Homo sapiens OX=9606 GN=TOMM34 PE=1 SV=2 | 8.79 | 10.49 | 1.19 | 0.26 |
| sp|Q9P258|RCC2_HUMAN Protein RCC2 OS=Homo sapiens OX=9606 GN=RCC2 PE=1 SV=2 | 8.73 | 4.21 | 0.48 | -1.05 |
| AC   | LOCUS | ORGANISM   | FUNCTION | EXPRESSION |
|------|-------|------------|----------|------------|
| A0A087WVZ9 | RPABC1 | Homo sapiens | DNA-directed RNA polymerases I, II, and III subunit | 8.72 |
| P08621 | RU17  | Homo sapiens | U1 small nuclear ribonucleoprotein 70 kDa | 8.72 |
| A0A2R8Y653 | POLR2E | Homo sapiens | Uridine-cytidine kinase 2 | 8.71 |
| Q5TEJ7 | Q5TEJ7 | Homo sapiens | Replication protein A 32 kDa subunit (Fragment) | 8.70 |
| Q92734 | TFG   | Homo sapiens | Isoform 2 of Protein TFG | 8.67 |
| P61758 | PFD3  | Homo sapiens | Prefoldin subunit 3 | 8.65 |
| G3V1U5 | G3V1U5 | Homo sapiens | Golgi transport 1 homolog B (S. cerevisiae), isoform CRA_c | 8.63 |
| Q9NVP1 | DDX18 | Homo sapiens | ATP-dependent RNA helicase DDX18 | 8.62 |
| O14949 | QC8R8 | Homo sapiens | Cytochrome b-c1 complex subunit 8 | 8.60 |
| P84095 | RHOG  | Homo sapiens | Rho-related GTP-binding protein Rhog | 8.59 |
| H7C1U8 | MICOS | Homo sapiens | MICOS complex subunit (Fragment) | 8.52 |
| I3L3Q4 | GLD4  | Homo sapiens | Glyoxalase domain-containing protein 4 (Fragment) | 8.49 |
| Q9BRJ6 | C7orf50| Homo sapiens | Uncharacterized protein C7orf50 | 8.49 |
| O75746 | SLC25A12 | Homo sapiens | Calcium-binding mitochondrial carrier protein Aralar1 | 8.48 |
| P55327 | TPD52 | Homo sapiens | Tumor protein D52 | 8.40 |
| Q13492 | PICALM | Homo sapiens | Phosphatidylinositol-binding clathrin assembly protein | 8.39 |
| Accession | Description | Species | Organism | Organism ID | Organism Name | Protein Name | Protein ID | Gene Name | Gene ID | Protein Score | MS Score | Charge | Intensity | RT (min)  |
|-----------|-------------|---------|----------|-------------|---------------|--------------|------------|-----------|---------|-------------|-----------|--------|-----------|-----------|
| tr|G3V0E4|G3V0E4_HUMAN | Mitochondrial-processing peptidase subunit beta | OS=Homo sapiens | OX=9606 | GN=PMPCB | PE=1 | SV=1 | 8.38 | 14.91 | 1.78 | 0.83 |
| sp|O95456-2|PSMG1_HUMAN | Isoform 2 of Proteasome assembly chaperone 1 | OS=Homo sapiens | OX=9606 | GN=PSMG1 | PE=1 | SV=1 | 8.37 | 29.59 | 3.54 | 1.82 |
| sp|Q9BX68|HINT2_HUMAN | Histidine triad nucleotide-binding protein 2, mitochondrial | OS=Homo sapiens | OX=9606 | GN=HINT2 | PE=1 | SV=1 | 8.36 | 1.40 | 0.17 | -2.58 |
| sp|P43034|LIS1_HUMAN | Platelet-activating factor acetylhydrolase IB subunit alpha | OS=Homo sapiens | OX=9606 | GN=PAFAH1B1 | PE=1 | SV=2 | 8.36 | 17.37 | 2.08 | 1.06 |
| tr|B1AH49|B1AH49_HUMAN | 3-mercaptopyruvate sulfurtransferase | OS=Homo sapiens | OX=9606 | GN=MPST | PE=1 | SV=1 | 8.33 | 28.68 | 3.44 | 1.78 |
| sp|O00625|PIR_HUMAN | Pirin | OS=Homo sapiens | OX=9606 | GN=PIR | PE=1 | SV=1 | 8.32 | 21.54 | 2.59 | 1.37 |
| tr|Q5T948|Q5T948_HUMAN | Serine/threonine-protein phosphatase 2A activator (Fragment) | OS=Homo sapiens | OX=9606 | GN=PTPA | PE=1 | SV=1 | 8.32 | 12.04 | 1.45 | 0.53 |
| tr|D6RAX7|D6RAX7_HUMAN | COP9 constitutive photomorphogenic-like protein subunit 4 isoform 2 | OS=Homo sapiens | OX=9606 | GN=COPS4 | PE=1 | SV=1 | 8.29 | 23.88 | 2.88 | 1.53 |
| sp|Q9UHG3|PCYOX_HUMAN | Prenylcysteine oxidase 1 | OS=Homo sapiens | OX=9606 | GN=PCYOX1 | PE=1 | SV=3 | 8.27 | 16.26 | 1.97 | 0.98 |
| sp|Q8NB5-2|ATAD1_HUMAN | Isoform 2 of ATPase family AAA domain-containing protein 1 | OS=Homo sapiens | OX=9606 | GN=ATAD1 | PE=1 | SV=1 | 8.26 | 19.82 | 2.40 | 1.26 |
| sp|Q8NC51-2|PAIRB_HUMAN | Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein | OS=Homo sapiens | OX=9606 | GN=SERBP1 | PE=1 | SV=3 | 8.25 | 5.05 | 0.61 | -0.71 |
| sp|Q9NSD9|SYFB_HUMAN | Phenylalanine--tRNA ligase beta subunit | OS=Homo sapiens | OX=9606 | GN=FARSB | PE=1 | SV=3 | 8.24 | 11.40 | 1.38 | 0.47 |
| sp|P19623|SPEE_HUMAN | Spermidine synthase | OS=Homo sapiens | OX=9606 | GN=SRM | PE=1 | SV=1 | 8.20 | 26.43 | 3.22 | 1.69 |
| tr|A0A087WYR3|A0A087WYR3_HUMAN | Tumor protein D54 | OS=Homo sapiens | OX=9606 | GN=TPD52L2 | PE=1 | SV=1 | 8.19 | 24.98 | 3.05 | 1.61 |
| sp|P55036|PSMD4_HUMAN | 26S proteasome non-ATPase regulatory subunit 4 | OS=Homo sapiens | OX=9606 | GN=PSMD4 | PE=1 | SV=1 | 8.18 | 18.91 | 2.31 | 1.21 |
| sp|P49207|RL34_HUMAN | 60S ribosomal protein L34 | OS=Homo sapiens | OX=9606 | GN=RPL34 | PE=1 | SV=3 | 8.13 | 17.45 | 2.15 | 1.10 |
| Accession | Description                                                                 | OS    | OX       | GN      | PE   | SV   | log2FoldChange | padj   |
|-----------|-----------------------------------------------------------------------------|-------|----------|---------|------|------|----------------|--------|
| sp|O00425|IF2B3_HUMAN Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP3 PE=1 SV=2 | 8.12  | 5.52    | 0.68   | -0.56 |
| tr|H0YL72|H0YL72_HUMAN Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1 | 8.10  | 49.12   | 6.06   | 2.60  |
| sp|Q9Y6C9|MTCH2_HUMAN Mitochondrial carrier homolog 2 OS=Homo sapiens OX=9606 GN=MTCH2 PE=1 SV=1 | 8.08  | 22.49   | 2.78   | 1.48  |
| sp|Q8BRX2|PELO_HUMAN Protein pelota homolog OS=Homo sapiens OX=9606 GN=PELO PE=1 SV=2 | 8.06  | 14.64   | 1.82   | 0.86  |
| sp|Q8WUX2|CHAC2_HUMAN Glutathione-specific gamma-glutamylcyclotransferase 2 OS=Homo sapiens OX=9606 GN=CHAC2 PE=1 SV=1 | 8.05  | 17.09   | 2.12   | 1.09  |
| sp|Q99720|SIGMAR1_HUMAN Isoform 2 of Sigma non-opioid intracellular receptor 1 OS=Homo sapiens OX=9606 GN=SIGMAR1 | 8.05  | 18.48   | 2.30   | 1.20  |
| sp|Q9B57|MTND_HUMAN 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens OX=9606 GN=AD11 PE=1 SV=1 | 8.04  | 11.55   | 1.44   | 0.52  |
| sp|P50336|PPOX_HUMAN Protoporphyrinogen oxidase OS=Homo sapiens OX=9606 GN=PPOX PE=1 SV=1 | 8.03  | 1.82    | 0.23   | -2.14 |
| sp|Q6BSO|TWF2_HUMAN Twinfilin-2 OS=Homo sapiens OX=9606 GN=TWF2 PE=1 SV=2 | 8.03  | 13.28   | 1.65   | 0.73  |
| tr|F5H442|F5H442_HUMAN Tumor susceptibility gene 101 protein OS=Homo sapiens OX=9606 GN=TSG101 PE=1 SV=1 | 7.99  | 11.39   | 1.43   | 0.51  |
| tr|A0A096LPJ3|A0A096LPJ3_HUMAN COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=1 | 7.91  | 15.99   | 2.02   | 1.02  |
| sp|Q9Y3B4|SF3B6_HUMAN Splicing factor 3B subunit 6 OS=Homo sapiens OX=9606 GN=SF3B6 PE=1 SV=1 | 7.87  | 15.64   | 1.99   | 0.99  |
| sp|Q15050|RRS1_HUMAN Ribosome biogenesis regulatory protein homolog OS=Homo sapiens OX=9606 GN=RRS1 PE=1 SV=2 | 7.87  | 7.24    | 0.92   | -0.12 |
| tr|B4DKY1|B4DKY1_HUMAN Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=CARS PE=1 SV=1 | 7.83  | 23.93   | 3.06   | 1.61  |
| tr|F5H013|F5H013_HUMAN Small nuclear ribonucleoprotein G OS=Homo sapiens OX=9606 GN=SNRPG PE=1 SV=1 | 7.82  | 11.32   | 1.45   | 0.53  |
| sp|Q9H3F7|GCP60_HUMAN Golgi resident protein GCP60 OS=Homo sapiens OX=9606 GN=ACBD3 PE=1 SV=4 | 7.77  | 3.58    | 0.46   | -1.12 |
| Accession | Description | Protein Name | Species | Gene Symbol | Expression Levels |
|-----------|-------------|--------------|---------|-------------|------------------|
| tr|K4DI93|K4DI93_HUMAN Cullin 4B, isoform CRA_e | Homo sapiens | CUL4B | 7.75 21.02 2.71 1.44 |
| sp|Q9H9A6|LRC40_HUMAN Leucine-rich repeat-containing protein 40 | Homo sapiens | LRRC40 | 7.74 15.58 2.01 1.01 |
| sp|Q9NQP4|PFD4_HUMAN Prefoldin subunit 4 | Homo sapiens | PFDN4 | 7.72 6.80 0.88 -0.18 |
| sp|Q9UBB4|ATX10_HUMAN Ataxin-10 | Homo sapiens | ATXN10 | 7.72 49.42 6.40 2.68 |
| sp|Q16719|KYNU_HUMAN Kynureninase | Homo sapiens | KYNU | 7.71 9.35 1.21 0.28 |
| sp|Q9Y241-2|HIG1A_HUMAN Isoform 2 of HIG1 domain family member 1A, mitochondrial | Homo sapiens | HIGD1A | 7.64 13.04 1.71 0.77 |
| tr|H0YDD4|H0YDD4_HUMAN Acetyltransferase component of pyruvate dehydrogenase complex (Fragment) | Homo sapiens | DLAT | 7.62 14.94 1.96 0.97 |
| sp|Q9UHD1-2|CHRD1_HUMAN Isoform 2 of Cysteine and histidine-rich domain-containing protein 1 | Homo sapiens | CHORDC1 | 7.62 21.11 2.77 1.47 |
| sp|P40222|TXLNA_HUMAN Alpha-taxilin | Homo sapiens | TXLNA | 7.62 2.31 0.30 -1.72 |
| sp|Q15006|EMC2_HUMAN ER membrane protein complex subunit 2 | Homo sapiens | EMC2 | 7.54 20.74 2.75 1.46 |
| sp|Q96PZ0-2|PUS7_HUMAN Isoform 2 of Pseudouridylate synthase 7 homolog | Homo sapiens | PUS7 | 7.54 6.53 0.87 -0.21 |
| tr|A0A0A0MSE2|A0A0A0MSE2_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial | Homo sapiens | HADH | 7.53 16.24 2.16 1.11 |
| sp|P42167|LAP2B_HUMAN Lamina-associated polypeptide 2, isoforms beta/gamma | Homo sapiens | TMPO | 7.51 43.75 5.83 2.54 |
| tr|H0YG54|H0YG54_HUMAN Oligoribonuclease, mitochondrial | Homo sapiens | REXO2 | 7.49 14.93 1.99 1.00 |
| tr|A0A2R8Y5A0|A0A2R8Y5A0_HUMAN Casein kinase II subunit alpha | Homo sapiens | CSNK2A1 | 7.46 40.49 5.43 2.44 |
| sp|Q9NXG2|THUM1_HUMAN THUMP domain-containing protein 1 | Homo sapiens | THUMPD1 | 7.41 11.97 1.61 0.69 |
| sp|P18031|PTN1_HUMAN Tyrosine-protein phosphatase non-receptor type 1 | Homo sapiens | PTPN1 | 7.37 13.11 1.78 0.83 |
| Accession | Description | Species | Gene | Protein | Score | E-value | Bit-score | Stratum |
|-----------|-------------|---------|------|---------|-------|---------|-----------|---------|
| tr|A0A087X020|Ribosome maturation protein SBDS| Homo sapiens | SBDS | 7.36 | 36.01 | 4.89 | 2.29 |
| sp|Q8IU00|TPPC5 Trafficking protein particle complex subunit 5| Homo sapiens | TRAPPC5 | 7.35 | 3.94 | 0.54 | -0.90 |
| sp|O43765|SGTA Small glutamine-rich tetratricopeptide repeat-containing protein alpha| Homo sapiens | SGTA | 7.34 | 22.67 | 3.09 | 1.63 |
| sp|Q9Y3D6|FIS1 Mitochondrial fission 1 protein| Homo sapiens | FIS1 | 7.34 | 14.60 | 1.99 | 0.99 |
| sp|P55060|XPO2 Isoform 3 of Exportin-2| Homo sapiens | CSE1L | 7.31 | 0.86 | 0.12 | -3.09 |
| sp|Q9NS69|TOM22 Mitochondrial import receptor subunit TOM22 homolog| Homo sapiens | TOMM22 | 7.31 | 46.43 | 6.35 | 2.67 |
| tr|A0A087X211|PSMC6 proteasome regulatory subunit 10B| Homo sapiens | PSMC6 | 7.31 | 46.60 | 6.38 | 2.67 |
| tr|B2WTI3|CAPZA2 Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6| Homo sapiens | CAPZA2 | 7.29 | 11.87 | 1.63 | 0.70 |
| sp|P47755|CAZA2 F-actin-capping protein subunit alpha-2| Homo sapiens | CAPZA2 | 7.28 | 26.58 | 3.65 | 1.87 |
| sp|O60884|DNJA2 DnaJ homolog subfamily A member 2| Homo sapiens | DNAJA2 | 7.25 | 33.99 | 4.69 | 2.23 |
| sp|P36952|SPB5 Serpin B5| Homo sapiens | SERPINB5 | 7.25 | 54.78 | 7.56 | 2.92 |
| sp|Q8NB5|GT251 Procollagen galactosyltransferase 1| Homo sapiens | COLGALT1 | 7.25 | 8.00 | 1.10 | 0.14 |
| tr|A0A1W2PR36|PSMC6 Guanidinoacetate N-methyltransferase| Homo sapiens | GAMT | 7.24 | 19.54 | 2.70 | 1.43 |
| sp|Q14318|FKBP8 Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP8| Homo sapiens | FKBP8 | 7.22 | 2.58 | 0.36 | -1.49 |
| sp|Q9Y570|PPME1 Isoform 4 of Protein phosphatase methylesterase 1| Homo sapiens | PPME1 | 7.18 | 13.74 | 1.91 | 0.94 |
| sp|Q9UDW1|QCR9 Cytochrome b-c1 complex subunit 9| Homo sapiens | UQCR10 | 7.18 | 24.18 | 3.37 | 1.75 |
| Accession | Description                                                                 | Pathway/Function | Pathway/Function | Pathway/Function | Pathway/Function |
|-----------|--------------------------------------------------------------------------------|------------------|------------------|------------------|------------------|
| sp|Q8NE86-3|MCU_HUMAN Isoform 3 of Calcium uniporter protein, mitochondrial OS=Homo sapiens OX=9606 GN=MCU | 7.16 | 18.48 | 2.58 | 1.37 |
| sp|P49321-2|NASC_HUMAN Isoform 2 of Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASC | 7.16 | 19.71 | 2.75 | 1.46 |
| sp|O75436|VP26A_HUMAN Vacuolar protein sorting-associated protein 26A OS=Homo sapiens OX=9606 GN=VP26A PE=1 SV=2 | 7.13 | 17.05 | 2.39 | 1.26 |
| sp|Q9BZD4|NUF2_HUMAN Kinetochoore protein Nu2 OS=Homo sapiens OX=9606 GN=NUF2 PE=1 SV=2 | 7.13 | 6.75 | 0.95 | -0.08 |
| sp|P50552|VASP_HUMAN Vasodilator-stimulated phosphoprotein OS=Homo sapiens OX=9606 GN=VASP PE=1 SV=3 | 7.10 | 7.46 | 1.05 | 0.07 |
| sp|P28838-2|AMPL_HUMAN Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens OX=9606 GN=LAP3 | 7.10 | 13.05 | 1.84 | 0.88 |
| sp|O43252|PAPS1_HUMAN Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase OS=Homo sapiens OX=9606 GN=PAPSS1 PE=1 SV=2 | 7.08 | 24.64 | 3.48 | 1.80 |
| sp|Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=4 | 7.07 | 5.37 | 0.76 | -0.40 |
| sp|Q14116|IL18_HUMAN Interleukin-18 OS=Homo sapiens OX=9606 GN=IL18 PE=1 SV=1 | 7.03 | 29.57 | 4.20 | 2.07 |
| tr|F8WJN3|F8WJN3_HUMAN Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens OX=9606 GN=CPSF6 PE=1 SV=1 | 7.00 | 27.40 | 3.91 | 1.97 |
| sp|Q5STE3-2|VW5B1_HUMAN Isoform 2 of von Willebrand factor A domain-containing protein 5B1 OS=Homo sapiens OX=9606 GN=VWA5B1 | 7.00 | 12.65 | 1.81 | 0.85 |
| sp|Q9Y3C1|NOP16_HUMAN Nucleolar protein 16 OS=Homo sapiens OX=9606 GN=NOP16 PE=1 SV=2 | 6.98 | 14.56 | 2.08 | 1.06 |
| tr|A0A0A0MSG2|A0A0A0MSG2_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens OX=9606 GN=FHL2 PE=1 SV=1 | 6.98 | 4.75 | 0.68 | -0.56 |
| tr|J3KT68|J3KT68_HUMAN Sigma intracellular receptor 2 OS=Homo sapiens OX=9606 GN=TMEM97 PE=1 SV=1 | 6.98 | 16.36 | 2.34 | 1.23 |
| sp|P04818-2|TYSY_HUMAN Isoform 2 of Thymidylate synthase OS=Homo sapiens OX=9606 GN=TYMS | 6.97 | 13.36 | 1.92 | 0.94 |
| sp|Q8WY22|BRI3B_HUMAN BRI3-binding protein OS=Homo sapiens OX=9606 GN=BRI3BP PE=1 SV=1 | 6.93 | 20.99 | 3.03 | 1.60 |
| sp|Q5RI15-2|COX20_HUMAN Isoform 2 of Cytochrome c oxidase assembly protein | 6.93 | 15.86 | 2.29 | 1.19 |
| Gene ID | Gene Name                  | Organism   | Organism ID | Protein Name/Description                                                                 | Molecular Weight | pI    | Mw     | Peptide Length |
|---------|----------------------------|------------|-------------|----------------------------------------------------------------------------------------|------------------|-------|--------|----------------|
| COX20, mitochondrial OS=Homo sapiens OX=9606 GN=COX20 | 6.93 26.38 3.81 1.93 |
| tr[H0U106]H0U106_HUMAN Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens OX=9606 GN=COX7A2 PE=1 SV=1 | 6.90 18.25 2.64 1.40 |
| sp[O43172]PRP4_HUMAN U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens OX=9606 GN=PRPF4 PE=1 SV=2 | 6.89 47.29 6.86 2.78 |
| sp[Q9BTT0]AN32E_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens OX=9606 GN=ANP32E PE=1 SV=1 | 6.86 27.97 4.08 2.03 |
| tr[A6NP24]A6NP24_HUMAN Quinone oxidoreductase (Fragment) OS=Homo sapiens OX=9606 GN=CRYZ PE=1 SV=1 | 6.84 11.02 1.61 0.69 |
| sp[Q9BV2-2]GNL3_HUMAN Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens OX=9606 GN=GNL3 | 6.84 27.86 4.07 2.03 |
| sp[Q9N7I8]1IF2B1_HUMAN Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=1 SV=2 | 6.82 12.29 1.80 0.85 |
| tr[A0A2R8Y430]A0A2R8Y430_HUMAN Glutathione synthetase OS=Homo sapiens OX=9606 GN=GSS PE=1 SV=1 | 6.81 13.94 2.04 1.03 |
| sp[Q96Z0]FAKD4_HUMAN FAST kinase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=TBRG4 PE=1 SV=1 | 6.81 13.76 2.02 1.02 |
| tr[A0A0A0MSV9]A0A0A0MSV9_HUMAN Tapasin OS=Homo sapiens OX=9606 GN=TAPBP PE=1 SV=1 | 6.81 24.14 3.55 1.83 |
| tr[K7EM18]K7EM18_HUMAN Eukaryotic translation initiation factor 1 OS=Homo sapiens OX=9606 GN=EIF1 PE=1 SV=1 | 6.77 12.22 1.80 0.85 |
| tr[F5H669]F5H669_HUMAN Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) OS=Homo sapiens OX=9606 GN=CPSF7 PE=1 SV=1 | 6.70 10.85 1.62 0.70 |
| sp[P53597]SUCA_HUMAN Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=SUCGL1 PE=1 SV=4 | 6.69 16.95 2.53 1.34 |
| tr[A0A087X1B2]A0A087X1B2_HUMAN U4/U6.5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=1 | 6.68 12.74 1.91 0.93 |
| sp[Q96M27-2]PRRC1_HUMAN Isoform 2 of Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 | 6.64 46.01 6.93 2.79 |
| tr[H7C174]H7C174_HUMAN Hepatocyte growth factor receptor (Fragment) OS=Homo sapiens OX=9606 GN=MET PE=1 SV=1 | 6.64 12.27 1.85 0.89 |
| sp[Q96CS3]FAF2_HUMAN FAS-associated factor 2 OS=Homo sapiens OX=9606 GN=FAF2 PE=1 SV=2 | 6.64 12.27 1.85 0.89 |
| Protein ID   | Name                                                | Organism     | Gene ID | Peptide | Score  |
|--------------|------------------------------------------------------|--------------|---------|---------|--------|
| sp|P55769|NH2L1_HUMAN NHP2-like protein 1 OS=Homo sapiens OX=9606 GN=SNU13 PE=1 SV=3 | Homo sapiens OX=9606 GN=SNU13 PE=1 SV=3 |
| sp|Q9BYT8|NEUL_HUMAN Neurolysin, mitochondrial OS=Homo sapiens OX=9606 GN=NLN PE=1 SV=1 | Homo sapiens OX=9606 GN=NLN PE=1 SV=1 |
| tr|A0A0C4DGA2|A0A0C4DGA2_HUMAN Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens OX=9606 GN=ECL2 PE=1 SV=1 | Homo sapiens OX=9606 GN=ECL2 PE=1 SV=1 |
| sp|P61201|CSN2_HUMAN COP9 signalosome complex subunit 2 OS=Homo sapiens OX=9606 GN=COPS2 PE=1 SV=1 | Homo sapiens OX=9606 GN=COPS2 PE=1 SV=1 |
| sp|Q08209|PPP2BA_HUMAN Isoform 2 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens OX=9606 GN=PPP3CA | Homo sapiens OX=9606 GN=PPP3CA |
| sp|O00560|SDCB1_HUMAN Isoform 2 of Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP | Homo sapiens OX=9606 GN=SDCBP |
| tr|R4GMN1|R4GMN1_HUMAN Motile sperm domain-containing protein 2 OS=Homo sapiens OX=9606 GN=MOSPDP2 PE=1 SV=1 | Homo sapiens OX=9606 GN=MOSPDP2 PE=1 SV=1 |
| sp|O75638|CTAG2_HUMAN Isoform LAGE-1A of Cancer/testis antigen 2 OS=Homo sapiens OX=9606 GN=CTAG2 | Homo sapiens OX=9606 GN=CTAG2 |
| sp|Q6P587|FAHD1_HUMAN Isoform 2 of Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens OX=9606 GN=FAHD1 | Homo sapiens OX=9606 GN=FAHD1 |
| tr|C9JIZ6|C9JIZ6_HUMAN Prosaposin OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=2 | Homo sapiens OX=9606 GN=PSAP PE=1 SV=2 |
| sp|O43681|ASNA_HUMAN ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2 | Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2 |
| tr|A0A0R4J2E8|A0A0R4J2E8_HUMAN Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 | Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1 |
| sp|P04844|RPN2_HUMAN Isoform 2 of Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 | Homo sapiens OX=9606 GN=RPN2 |
| sp|P52888|THOPT1_HUMAN Thimet oligopeptidase OS=Homo sapiens OX=9606 GN=THOPT1 PE=1 SV=2 | Homo sapiens OX=9606 GN=THOPT1 PE=1 SV=2 |
| sp|P11166|GTR1_HUMAN Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens OX=9606 GN=SLC2A1 PE=1 SV=2 | Homo sapiens OX=9606 GN=SLC2A1 PE=1 SV=2 |
| sp|O75937|DNJC8_HUMAN DnaJ homolog subfamily C member 8 OS=Homo sapiens OX=9606 GN=DNJ8C PE=1 SV=2 | Homo sapiens OX=9606 GN=DNJ8C PE=1 SV=2 |
| tr|H0Y5K5|H0Y5K5_HUMAN Endoplasmic reticulum-Golgi intermediate compartment | Homo sapiens OX=9606 GN=H0Y5K5 PE=1 SV=2 |
| Protein Name | Description | OS | OX | GN | PE | SV | p-value | q-value | E-value |
|--------------|-------------|----|----|----|----|----|---------|---------|---------|
| sp|QSM9N0|CD158_HUMAN Coiled-coil domain-containing protein 158 | Homo sapiens | 9606 | CCDC158 | 2 | 6.35 | 35.42 | 5.58 | 2.48 |
| tr|A0A286YFF7|A0A286YFF7_HUMAN Palmitoyl-protein thioesterase 1 | Homo sapiens | 9606 | PPT1 | 1 | 6.33 | 19.63 | 3.10 | 1.63 |
| sp|Q9UNS2|CSN3_HUMAN COP9 signalosome complex subunit 3 | Homo sapiens | 9606 | COP9 | 3 | 6.27 | 2.27 | 0.36 | -1.47 |
| sp|Q9P287-2|BCCIP_HUMAN Isoform 2 of BRCA2 and CDKN1A-interacting protein | Homo sapiens | 9606 | BCCIP | 3 | 6.26 | 16.92 | 2.71 | 1.44 |
| sp|Q02809-2|PLOD1_HUMAN Isoform 2 of Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 | Homo sapiens | 9606 | PLOD1 | 2 | 6.24 | 16.06 | 2.57 | 1.36 |
| sp|P46108-2|CRK_HUMAN Isoform Crk-I of Adapter molecule crk | Homo sapiens | 9606 | CRK | 2 | 6.24 | 11.96 | 1.92 | 0.94 |
| tr|C9JGI3|C9JGI3_HUMAN Thymidine phosphorylase (Fragment) | Homo sapiens | 9606 | TYMP | 1 | 6.21 | 26.91 | 4.33 | 2.12 |
| tr|B4DLN1|B4DLN1_HUMAN cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier | Homo sapiens | 9606 | PE2 | 1 | 6.19 | 7.25 | 1.17 | 0.23 |
| sp|O43395|PRPF3_HUMAN U4/U6 small nuclear ribonucleoprotein Prp3 | Homo sapiens | 9606 | PRPF3 | 2 | 6.16 | 14.40 | 2.34 | 1.23 |
| sp|P13473-2|LAMP2_HUMAN Isoform LAMP-2B of Lysosome-associated membrane glycoprotein 2 | Homo sapiens | 9606 | LAMP2 | 1 | 6.15 | 9.86 | 1.60 | 0.68 |
| sp|O60568|PLOD3_HUMAN Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 | Homo sapiens | 9606 | PLOD3 | 1 | 6.15 | 11.77 | 1.92 | 0.94 |
| sp|Q9UBQO|VPS29_HUMAN Vacuolar protein sorting-associated protein 29 | Homo sapiens | 9606 | VPS29 | 1 | 6.11 | 9.67 | 1.58 | 0.66 |
| sp|P62993|GRB2_HUMAN Growth factor receptor-bound protein 2 | Homo sapiens | 9606 | GRB2 | 1 | 6.07 | 12.49 | 2.06 | 1.04 |
| tr|A0A2R8Y891|A0A2R8Y891_HUMAN ATP-dependent 6-phosphofructokinase | Homo sapiens | 9606 | PFKM | 1 | 6.06 | 10.75 | 1.77 | 0.83 |
| sp|Q14258|TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 | Homo sapiens | 9606 | TRIM25 | 2 | 6.06 | 2.13 | 0.35 | -1.50 |
| sp|Q66RP9|EFGM_HUMAN Elongation factor G, mitochondrial | Homo sapiens | 9606 | GFM1 | 2 | 6.03 | 10.98 | 1.82 | 0.86 |
| Accession     | Description                                      | OS          | OX  | GN         | PE | SV  | Score | Value | q Value | e Value |
|---------------|--------------------------------------------------|-------------|-----|------------|----|-----|-------|-------|---------|---------|
| Q5T6H7       | Xaa-Pro aminopeptidase 1                          | Homo sapiens | 9606 | XPNPEP1    | 1  | 1   | 6.00  | 9.41  | 1.57    | 0.65    |
| K7EI7        | Galactokinase (Fragment)                         | Homo sapiens | 9606 | GALK1      | 1  | 1   | 5.99  | 7.40  | 1.24    | 0.31    |
| Q9NQ22       | Something about silencing protein 10             | Homo sapiens | 9606 | UTP3       | 1  | 1   | 5.97  | 10.09 | 1.69    | 0.76    |
| Q99436       | Proteasome subunit beta type-7                   | Homo sapiens | 9606 | PSMB7      | 1  | 1   | 5.94  | 18.54 | 3.12    | 1.64    |
| Q9Y2R4       | Probable ATP-dependent RNA helicase              | Homo sapiens | 9606 | DDX52     | 1  | 3   | 5.94  | 0.56  | 0.09    | -3.41   |
| O43242       | 26S proteasome non-ATPase regulatory subunit 3   | Homo sapiens | 9606 | PSMD3     | 1  | 2   | 5.94  | 8.77  | 1.48    | 0.56    |
| I3L505       | Acyl carrier protein (Fragment)                 | Homo sapiens | 9606 | NDUFA81    | 1  | 1   | 5.93  | 16.50 | 2.78    | 1.48    |
| A0A09YXF2    | Paraoxonase 2, isoform CRA_a                     | Homo sapiens | 9606 | PON2       | 1  | 1   | 5.91  | 13.24 | 2.24    | 1.16    |
| Q8WVM8       | Isoform 2 of Sec1 family domain-containing protein | Homo sapiens | 9606 | SCFD1     | 1  | 1   | 5.91  | 4.46  | 0.75    | -0.41   |
| Q9Y4P3       | Transducin beta-like protein 2                   | Homo sapiens | 9606 | TBL2      | 1  | 1   | 5.89  | 15.47 | 2.63    | 1.39    |
| P14550       | Alcohol dehydrogenase [NADP(+)]                 | Homo sapiens | 9606 | AKR1A1    | 1  | 3   | 5.86  | 29.73 | 5.07    | 2.34    |
| Q96FQ6       | Protein S100-A16                                 | Homo sapiens | 9606 | S100A16   | 1  | 1   | 5.85  | 7.98  | 1.36    | 0.45    |
| A0A2R88478   | Tetraspanin                                      | Homo sapiens | 9606 | CD9       | 1  | 1   | 5.85  | 8.44  | 1.44    | 0.53    |
| P07099       | Epoxide hydrolase 1                              | Homo sapiens | 9606 | EPHX1     | 1  | 1   | 5.83  | 3.44  | 0.59    | -0.76   |
| O94776       | Metastasis-associated protein MTA2               | Homo sapiens | 9606 | MTA2      | 1  | 1   | 5.82  | 14.86 | 2.55    | 1.35    |
| O15173       | Isoform 2 of Membrane-associated progesterone receptor component 2 | Homo sapiens | 9606 | PGRMC2    | 1  | 1   | 5.80  | 20.34 | 3.50    | 1.81    |
| J3QLR8       | 28S ribosomal protein S23, mitochondrial         | Homo sapiens | 9606 | MRPS23    | 1  | 1   | 5.79  | 16.71 | 2.88    | 1.53    |
| Accession   | Gene Symbol | Gene Name | Species   | Protein Name | Start | End   | Length | Score |
|-------------|-------------|-----------|-----------|--------------|-------|-------|--------|-------|
| sp|Q6DKJ4|NXN_HUMAN|Nucleoredoxin|Homo sapiens|9606|GN=NXN|PE=1|SV=2|
| sp|Q08380|LG3BP_HUMAN|Galectin-3-binding protein|Homo sapiens|9606|GN=LGALS3BP|PE=1|SV=1|
| tr|B5MCF9|B5MCF9_HUMAN|Pescadillo homolog|Homo sapiens|9606|GN=PES1|PE=1|SV=1|
| sp|Q9Y2S7|PDIP2_HUMAN|Polymerase delta-interacting protein 2|Homo sapiens|9606|GN=POLDIP2|PE=1|SV=1|
| sp|P30740|ILEU_HUMAN|Leukocyte elastase inhibitor|Homo sapiens|9606|GN=SERPINB1|PE=1|SV=1|
| sp|Q15067|ACOX1_HUMAN|Isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1|Homo sapiens|9606|GN=ACOX1|PE=1|SV=1|
| sp|O00743|PPP6_HUMAN|Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit|Homo sapiens|9606|GN=PPP6C|PE=1|SV=1|
| tr|M0R389|M0R389_HUMAN|Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment)|Homo sapiens|9606|GN=PAFAH1B3|PE=1|SV=8|
| tr|H7BYN3|H7BYN3_HUMAN|Transcription factor A, mitochondrial (Fragment)|Homo sapiens|9606|GN=TFAM|PE=1|SV=1|
| tr|F6VRR5|F6VRR5_HUMAN|Polymerase delta-interacting protein 3|Homo sapiens|9606|GN=POLDIP3|PE=1|SV=1|
| tr|Q5VZU3|Q5VZU3_HUMAN|RNA 3'-terminal phosphate cyclase-like protein|Homo sapiens|9606|GN=RCL1|PE=1|SV=2|
| sp|Q9UBK8|MTRR_HUMAN|Isoform B of Methionine synthase reductase|Homo sapiens|9606|GN=MTRR|PE=1|SV=2|
| sp|Q9NTX5|ECHD1_HUMAN|Isoform 2 of Ethylmalonyl-CoA decarboxylase|Homo sapiens|9606|GN=ECHDC1|PE=1|SV=2|
| sp|Q96A33|CCD47_HUMAN|Coiled-coil domain-containing protein 47|Homo sapiens|9606|GN=CCDC47|PE=1|SV=2|

**Score Calculation:**
- **Start** and **End**: Start and end positions of the query sequence within the protein sequence.
- **Length**: Length of the query sequence.
- **Score**: Score of the alignment.
| Accession | Gene Symbol | Description | Species | Organism | Peptide Coverage | Score |
|-----------|-------------|-------------|---------|-----------|------------------|-------|
| sp|Q13409-2|DC1I2_HUMAN Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 | Homo sapiens | Homo sapiens | 5.49 13.01 2.37 1.24 |
| tr|K7EQG1|K7EQG1_HUMAN Glutaminylation-cyclotransferase-like protein OS=Homo sapiens OX=9606 GN=QPCTL PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.49 3.65 0.67 -0.59 |
| tr|C9JP16|C9JP16_HUMAN Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.49 10.13 1.85 0.88 |
| sp|P11777-2|ODPB_HUMAN Isoform 2 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=PDHB | Homo sapiens | Homo sapiens | 5.48 14.66 2.67 1.42 |
| tr|B1AP13|B1AP13_HUMAN Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55 PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.46 13.73 2.51 1.33 |
| sp|O76071|CIAO1_HUMAN Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens OX=9606 GN=CIAO1 PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.44 9.83 1.81 0.85 |
| tr|C9J1E7|C9J1E7_HUMAN AP-1 complex subunit beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=AP1B1 PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.42 13.84 2.55 1.35 |
| tr|H0YDU8|H0YDU8_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens OX=9606 GN=PPP5C PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.39 15.47 2.87 1.52 |
| sp|O15269|SPTC1_HUMAN Serine palmitoyltransferase 1 OS=Homo sapiens OX=9606 GN=SPTLC1 PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.37 9.68 1.80 0.85 |
| sp|Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens OX=9606 GN=RAB21 PE=1 SV=3 | Homo sapiens | Homo sapiens | 5.33 14.78 2.77 1.47 |
| tr|A0A087X0R6|A0A087X0R6_HUMAN Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 PE=1 SV=1 | Homo sapiens | Homo sapiens | 5.32 3.35 0.63 -0.67 |
| sp|Q9P0L0-2|VAPA_HUMAN Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens OX=9606 GN=VAPA | Homo sapiens | Homo sapiens | 5.32 11.28 2.12 1.09 |
| sp|Q9H2U2-2|IPYR2_HUMAN Isoform 2 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 | Homo sapiens | Homo sapiens | 5.31 15.19 2.86 1.52 |
| sp|Q12792-3|TWF1_HUMAN Isoform 3 of Twinfilin-1 OS=Homo sapiens OX=9606 GN=TWF1 | Homo sapiens | Homo sapiens | 5.31 11.52 2.17 1.12 |
| sp|Q4G0N4-2|NAKD2_HUMAN Isoform 2 of NAD kinase 2, mitochondrial OS=Homo sapiens OX=9606 GN=NAKD2 | Homo sapiens | Homo sapiens | 5.28 11.86 2.25 1.17 |
| sp|Q15024|EXOSC7_HUMAN Exosome complex component RRP42 OS=Homo sapiens OX=9606 GN=EXOSC7 PE=1 SV=3 | Homo sapiens | Homo sapiens | 5.28 4.55 0.86 -0.21 |
| Accession | Description | OS | OX | GN | PE | SV |
|-----------|-------------|----|----|----|----|----|
| tr|J3QRD1|J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH3A2 PE=1 SV=1 | Homo sapiens | 9606 | ALDH3A2 | 1 | 1 |
| tr|B0QZ18|B0QZ18_HUMAN Copine-1 OS=Homo sapiens OX=9606 GN=CPNE1 PE=1 SV=1 | Homo sapiens | 9606 | CPNE1 | 1 | 1 |
| tr|G5EA06|G5EA06_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS27 PE=1 SV=2 | Homo sapiens | 9606 | MRPS27 | 1 | 2 |
| sp|Q96HY6|DDRGK_HUMAN DDRGK domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DDRGG1 PE=1 SV=2 | Homo sapiens | 9606 | DDRGK1 | 1 | 2 |
| tr|H7C2S1|H7C2S1_HUMAN Guanine nucleotide exchange factor DBS (Fragment) OS=Homo sapiens OX=9606 GN=MCF2L PE=1 SV=1 | Homo sapiens | 9606 | MCF2L | 1 | 1 |
| tr|Q5T9B7|Q5T9B7_HUMAN Adenylate kinase isoenzyme 1 OS=Homo sapiens OX=9606 GN=AK1 PE=1 SV=1 | Homo sapiens | 9606 | AK1 | 1 | 1 |
| tr|G5E977|G5E977_HUMAN Nicotinate phosphoribosyltransferase domain containing 1, isoform CRA_d OS=Homo sapiens OX=9606 GN=NAPRT PE=1 SV=1 | Homo sapiens | 9606 | NAPRT | 1 | 1 |
| tr|A0A087WWF6|A0A087WWF6_HUMAN DNA polymerase delta subunit 2 OS=Homo sapiens OX=9606 GN=POLD2 PE=1 SV=1 | Homo sapiens | 9606 | POLD2 | 1 | 1 |
| sp|O95573|ACSL3_HUMAN Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens OX=9606 GN=ACSL3 PE=1 SV=3 | Homo sapiens | 9606 | ACSL3 | 1 | 3 |
| tr|H0Y512|H0Y512_HUMAN Adipocyte plasma membrane-associated protein (Fragment) OS=Homo sapiens OX=9606 GN=APMAP PE=1 SV=1 | Homo sapiens | 9606 | APMAP | 1 | 1 |
| sp|P63151|2ABA_HUMAN Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R2A | Homo sapiens | 9606 | PPP2R2A | 1 | 1 |
| sp|Q9UGI8|TES_HUMAN Isoform 2 of Testin OS=Homo sapiens OX=9606 GN=TES | Homo sapiens | 9606 | TES | 1 | 1 |
| sp|P35270|SPRE_HUMAN Sepiapterin reductase OS=Homo sapiens OX=9606 GN=SPR PE=1 SV=1 | Homo sapiens | 9606 | SPR | 1 | 1 |
| tr|A0A0A0MRG8|A0A0A0MRG8_HUMAN Bcl-2 homologous antagonist/killer OS=Homo sapiens OX=9606 GN=BAK1 PE=1 SV=1 | Homo sapiens | 9606 | BAK1 | 1 | 1 |
| tr|K7EMW4|K7EMW4_HUMAN Nicalin homolog (Zebrafish), isoform CRA_e OS=Homo sapiens OX=9606 GN=NCLN PE=1 SV=1 | Homo sapiens | 9606 | NCLN | 1 | 1 |
| tr|B4DJV5|B4DJV5_HUMAN cDNA FLJ51513, highly similar to Periodic tryptophan protein 1 homolog OS=Homo sapiens OX=9606 GN=PWP1 PE=1 SV=1 | Homo sapiens | 9606 | PWP1 | 1 | 1 |
| Gene ID       | Gene Name                                      | Organism   | Accession Number | E-Value | Score 1 | Score 2 | Score 3 | Score 4 |
|--------------|-----------------------------------------------|------------|------------------|---------|---------|---------|---------|---------|
| A0A087WX59   | Proteasomal ubiquitin receptor ADRM1          | Homo sapiens | 9606              | 1       | 5.04    | 9.46    | 1.88    | 0.91    |
| G3V192       | Ferritin                                      | Homo sapiens | 9606              | 1       | 5.04    | 25.50   | 5.06    | 2.34    |
| Q6IAA8       | Ragulator complex protein LAMTOR1             | Homo sapiens | 9606              | 1       | 5.03    | 21.61   | 4.29    | 2.10    |
| A0A087WUD3   | Oligosaccharyltransferase complex subunit     | Homo sapiens | 9606              | 1       | 5.03    | 8.41    | 1.67    | 0.74    |
| F8W733       | BRISC and BRCA1-A complex member 2            | Homo sapiens | 9606              | 1       | 5.03    | 8.59    | 1.71    | 0.77    |
| Q9Y3B7-3     | Ribosomal protein L11, mitochondrial          | Homo sapiens | 9606              | 1       | 5.02    | 15.63   | 3.11    | 1.64    |
| Q96TA1-2     | Niban-like protein 1                           | Homo sapiens | 9606              | 1       | 5.00    | 7.51    | 1.50    | 0.59    |
| Q96G03       | Phosphoglucomutase-2                           | Homo sapiens | 9606              | 1       | 5.00    | 1.42    | 0.28    | -1.81   |
| A0A0A6YYL4   | Coronin                                       | Homo sapiens | 9606              | 1       | 4.97    | 26.75   | 5.38    | 2.43    |
| Q15397       | Pumilio homolog 3                              | Homo sapiens | 9606              | 1       | 4.95    | 3.97    | 0.80    | -0.32   |
| H0YDR3       | Tetratricopeptide repeat protein 9C (Fragment)| Homo sapiens | 9606              | 1       | 4.94    | 19.95   | 4.04    | 2.01    |
| A0A087WSV8   | Nucleobindin 2, isoform CRA_b                | Homo sapiens | 9606              | 1       | 4.94    | 5.03    | 1.02    | 0.03    |
| P48147       | Prolyl endopeptidase                           | Homo sapiens | 9606              | 1       | 4.90    | 6.66    | 1.36    | 0.44    |
| O14744       | Protein arginine N-methyltransferase 5        | Homo sapiens | 9606              | 1       | 4.87    | 13.64   | 2.80    | 1.49    |
| O75306-2     | NADH dehydrogenase [ubiquinone] iron-sulfur   | Homo sapiens | 9606              | 1       | 4.86    | 13.29   | 2.74    | 1.45    |
| Q13217       | DnaJ homolog subfamily C member 3             | Homo sapiens | 9606              | 1       | 4.82    | 3.03    | 0.63    | -0.67   |
| Q9Y512       | Sorting and assembly machinery component 50   | Homo sapiens | 9606              | 1       | 4.81    | 10.75   | 2.23    | 1.16    |
| OS=Homo sapiens | GN=SAMM50 | PE=1 | SV=3 |
|---------------|-----------|------|------|
| sp|P05362|ICAM1_HUMAN Intercellular adhesion molecule 1 OS=Homo sapiens OX=9606 GN=ICAM1 PE=1 SV=2 |
| 4.75 | 12.42 | 2.61 | 1.39 |
| sp|Q96HR9-2|REEP6_HUMAN Isoform 2 of Receptor expression-enhancing protein 6 OS=Homo sapiens OX=9606 GN=REEP6 |
| 4.74 | 10.51 | 2.22 | 1.15 |
| tr|J3KQ48|J3KQ48_HUMAN Peptidyl-tRNA hydrolase 2, mitochondrial OS=Homo sapiens OX=9606 GN=PTRH2 PE=1 SV=1 |
| 4.74 | 6.21 | 1.31 | 0.39 |
| sp|Q4VC31|CCD58_HUMAN Coiled-coil domain-containing protein 58 OS=Homo sapiens OX=9606 GN=CCDC58 PE=1 SV=1 |
| 4.73 | 6.54 | 1.38 | 0.47 |
| sp|P43304-2|GPDM_HUMAN Isoform 2 of Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=GPD2 |
| 4.71 | 9.99 | 2.12 | 1.08 |
| sp|P28482|MK01_HUMAN Mitogen-activated protein kinase 1 OS=Homo sapiens OX=9606 GN=MAPK1 PE=1 SV=3 |
| 4.69 | 11.82 | 2.52 | 1.33 |
| sp|Q92600-3|CNOT9_HUMAN Isoform 3 of CCR4-NOT transcription complex subunit 9 OS=Homo sapiens OX=9606 GN=CNOT9 |
| 4.65 | 7.90 | 1.70 | 0.76 |
| sp|P51398-2|RT29_HUMAN Isoform 2 of 28S ribosomal protein S29, mitochondrial OS=Homo sapiens OX=9606 GN=DAP3 |
| 4.59 | 4.88 | 1.06 | 0.09 |
| tr|A0A0A0MRF4|A0A0A0MRF4_HUMAN 39S ribosomal protein L19, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL19 PE=1 SV=1 |
| 4.59 | 12.20 | 2.66 | 1.41 |
| tr|E9PLY5|E9PLY5_HUMAN Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Fragment) OS=Homo sapiens OX=9606 GN=MACF1 PE=1 SV=1 |
| 4.55 | 19.70 | 4.33 | 2.11 |
| sp|Q76094|SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens OX=9606 GN=SRP72 PE=1 SV=3 |
| 4.55 | 22.35 | 4.91 | 2.30 |
| sp|O75131|CPNE3_HUMAN Copine-3 OS=Homo sapiens OX=9606 GN=CPNE3 PE=1 SV=1 |
| 4.55 | 8.00 | 1.76 | 0.81 |
| sp|Q9H5Q4|TFB2M_HUMAN Dimethyladenosine transferase 2, mitochondrial OS=Homo sapiens OX=9606 GN=TFB2M PE=1 SV=1 |
| 4.53 | 8.07 | 1.78 | 0.83 |
| Gene| Description| Species| Accession| MW| pI| Molar Abundance| 1:1 Ratio |
|---|---|---|---|---|---|---|---|
|tr|H0YDP7|H0YDP7_HUMAN 39S ribosomal protein L49, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=MRPL49 PE=1 SV=1 | 4.52 | 18.92 | 4.19 | 2.07 |
|sp|Q8NCA5-2|FA98A_HUMAN Isoform 2 of Protein FAM98A OS=Homo sapiens OX=9606 GN=FAM98A | 4.52 | 8.49 | 1.88 | 0.91 |
|sp|Q8WU90|ZC3HF_HUMAN Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens OX=9606 GN=ZC3H15 PE=1 SV=1 | 4.52 | 0.78 | 0.17 | -2.53 |
|tr|Q5T8A0|Q5T8A0_HUMAN 28S ribosomal protein S2, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=MRPS2 PE=1 SV=1 | 4.51 | 10.67 | 2.36 | 1.24 |
|sp|Q9HAV7|GRPE1_HUMAN GrpE protein homolog 1, mitochondrial OS=Homo sapiens OX=9606 GN=GRPEL1 PE=1 SV=2 | 4.51 | 22.20 | 4.93 | 2.30 |
|sp|Q5JTJ3-2|COA6_HUMAN Isoform 2 of Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens OX=9606 GN=COA6 | 4.51 | 0.65 | 0.14 | -2.80 |
|sp|Q13561-2|DCTN2_HUMAN Isoform 2 of Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 | 4.50 | 3.57 | 0.79 | -0.33 |
|sp|Q12874|SF3A3_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens OX=9606 GN=SF3A3 PE=1 SV=1 | 4.50 | 12.98 | 2.89 | 1.53 |
|sp|Q66203|PUR1_HUMAN Amidophosphoribosyltransferase OS=Homo sapiens OX=9606 GN=PPAT PE=1 SV=1 | 4.49 | 4.29 | 0.96 | -0.06 |
|tr|A0A087X2D5|A0A087X2D5_HUMAN 39S ribosomal protein L45, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL45 PE=1 SV=1 | 4.48 | 16.23 | 3.62 | 1.86 |
|tr|A0A087X2D5|A0A087X2D5_HUMAN Mortality factor 4-like protein 2 OS=Homo sapiens OX=9606 GN=MORF4L2 PE=1 SV=1 | 4.47 | 6.45 | 1.44 | 0.53 |
|sp|O00273-2|DFFA_HUMANIsoform DFF35 of DNA fragmentation factor subunit alpha OS=Homo sapiens OX=9606 GN=DFFA | 4.43 | 12.55 | 2.83 | 1.50 |
|tr|A0A087X279|A0A087X279_HUMAN Interferon-induced protein with tetratricopeptide repeats 2 OS=Homo sapiens OX=9606 GN=IFIT2 PE=1 SV=1 | 4.42 | 6.75 | 1.53 | 0.61 |
|tr|E9PFR3|E9PFR3_HUMAN Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Homo sapiens OX=9606 GN=PPP2R5D PE=1 SV=1 | 4.40 | 2.34 | 0.53 | -0.91 |
|tr|A0A1B0GVN9|A0A1B0GVN9_HUMAN Uroporphyrinogen decarboxylase OS=Homo sapiens OX=9606 GN=UROD PE=1 SV=1 | 4.39 | 11.84 | 2.70 | 1.43 |
|sp|Q8N183|NDUF2_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 2 OS=Homo sapiens OX=9606 GN=NDUFAF2 PE=1 SV=1 | 4.39 | 15.22 | 3.47 | 1.79 |
| Accession   | Description                                                                 | OS  | OX  | GN          | PE | SV  | F   | M   | R   |
|------------|------------------------------------------------------------------------------|-----|-----|-------------|----|-----|-----|-----|-----|
| sp|P55957-2|BID_HUMAN Isoform 2 of BH3-interacting domain death agonist OS=Homo sapiens OX=9606 GN=BID | Homo sapiens | 9606 | BID | 4.38 | 18.38 | 4.19 | 2.07 |
| tr|F5GWV0|F5GWV0_HUMAN Armadillo repeat-containing protein 6 (Fragment) OS=Homo sapiens OX=9606 GN=ARMC6 PE=1 SV=8 | Homo sapiens | 9606 | ARMC6 | 4.38 | 8.09 | 1.85 | 0.89 |
| sp|P36405|ARL3_HUMAN ADP-ribosylation factor-like protein 3 OS=Homo sapiens OX=9606 GN=ARL3 PE=1 SV=2 | Homo sapiens | 9606 | ARL3 | 4.37 | 2.31 | 0.53 | -0.92 |
| tr|C9JJ19|C9JJ19_HUMAN 28S ribosomal protein S34, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS34 PE=1 SV=2 | Homo sapiens | 9606 | MRPS34 | 4.36 | 9.82 | 2.25 | 1.17 |
| sp|Q96IR7|HPDL_HUMAN 4-hydroxyphenylpyruvate dioxygenase-like protein OS=Homo sapiens OX=9606 GN=HPDL PE=1 SV=1 | Homo sapiens | 9606 | HPDL | 4.36 | 26.58 | 6.10 | 2.61 |
| sp|Q9Y295|DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=DRG1 PE=1 SV=1 | Homo sapiens | 9606 | DRG1 | 4.36 | 12.58 | 2.89 | 1.53 |
| sp|P23258|TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens OX=9606 GN=TUBG1 PE=1 SV=2 | Homo sapiens | 9606 | TUBG1 | 4.36 | 10.49 | 2.41 | 1.27 |
| sp|P19525|E2AK2_HUMAN Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens OX=9606 GN=EIF2AK2 PE=1 SV=2 | Homo sapiens | 9606 | EIF2AK2 | 4.35 | 4.34 | 1.00 | 0.00 |
| sp|O95801|TTC4_HUMAN Tetratricopeptide repeat protein 4 OS=Homo sapiens OX=9606 GN=TTC4 PE=1 SV=3 | Homo sapiens | 9606 | TTC4 | 4.34 | 7.35 | 1.69 | 0.76 |
| sp|Q96KP4|CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=2 | Homo sapiens | 9606 | CNDP2 | 4.34 | 25.42 | 5.86 | 2.55 |
| tr|A0A2R8Y6Y7|A0A2R8Y6Y7_HUMAN Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=SUCLA2 PE=1 SV=1 | Homo sapiens | 9606 | SUCLA2 | 4.33 | 7.54 | 1.74 | 0.80 |
| sp|Q99598|TSNAX_HUMAN Translin-associated protein X OS=Homo sapiens OX=9606 GN=TSNAX PE=1 SV=1 | Homo sapiens | 9606 | TSNAX | 4.29 | 16.48 | 3.84 | 1.94 |
| sp|P11802|CDK4_HUMAN Cyclin-dependent kinase 4 OS=Homo sapiens OX=9606 GN=CDK4 PE=1 SV=2 | Homo sapiens | 9606 | CDK4 | 4.29 | 23.35 | 5.44 | 2.44 |
| tr|B4DJ81|B4DJ81_HUMAN NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS1 PE=1 SV=1 | Homo sapiens | 9606 | NDUFS1 | 4.29 | 12.86 | 3.00 | 1.58 |
| tr|B4DXZ6|B4DXZ6_HUMAN cDNA FLJ58644, highly similar to Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens OX=9606 GN=FXR1 PE=1 SV=1 | Homo sapiens | 9606 | FXR1 | 4.29 | 12.63 | 2.95 | 1.56 |
| sp|Q9H6T3-2|RPAP3_HUMAN Isoform 2 of RNA polymerase II-associated protein 3 OS=Homo sapiens OX=9606 GN=RPAP3 | Homo sapiens | 9606 | RPAP3 | 4.27 | 8.73 | 2.05 | 1.03 |
| Accession | Name Description                                                                 | BV1 | BV2 | BV3 | BV4 |
|-----------|-----------------------------------------------------------------------------------|-----|-----|-----|-----|
| tr|Q5VXN0|Q5VXN0_HUMAN Ribosome production factor 2 homolog (Fragment) OS=Homo sapiens OX=9606 GN=RPF2 PE=1 SV=1 | 4.26 | 6.06 | 1.42 | 0.51 |
| sp|Q8WW12-2|PCNP_HUMAN Isoform 2 of PEST proteolytic signal-containing nuclear protein OS=Homo sapiens OX=9606 GN=PCNP | 4.26 | 6.93 | 1.63 | 0.70 |
| sp|Q8N0X7|SPART_HUMAN Spartin OS=Homo sapiens OX=9606 GN=SPART PE=1 SV=1 | 4.22 | 8.20 | 1.94 | 0.96 |
| tr|A0A0C4DG50|A0A0C4DG50_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens OX=9606 GN=NDUFA6 PE=1 SV=1 | 4.21 | 16.02 | 3.80 | 1.93 |
| sp|Q9H4A6|GOLP3_HUMAN Golgi phosphoprotein 3 OS=Homo sapiens OX=9606 GN=GOLPH3 PE=1 SV=1 | 4.20 | 11.65 | 2.77 | 1.47 |
| sp|Q8YVT2|MISP_HUMAN Mitotic interactor and substrate of PLK1 OS=Homo sapiens OX=9606 GN=MISP PE=1 SV=1 | 4.20 | 3.29 | 0.78 | -0.35 |
| sp|O95232|LC7L3_HUMAN Luc7-like protein 3 OS=Homo sapiens OX=9606 GN=LC7L3 PE=1 SV=2 | 4.20 | 19.33 | 4.60 | 2.20 |
| tr|A0A2R8YFH5|A0A2R8YFH5_HUMAN Protein transport protein SEC23 OS=Homo sapiens OX=9606 GN=SEC23B PE=1 SV=1 | 4.18 | 6.00 | 1.44 | 0.52 |
| tr|I3L1L9|I3L1L9_HUMAN Ethanolamine-phosphate cytidylyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=PCYT2 PE=1 SV=1 | 4.16 | 5.63 | 1.35 | 0.44 |
| sp|Q14247-2|SRC8_HUMAN Isoform 2 of Src substrate cortactin OS=Homo sapiens OX=9606 GN=CTTN | 4.15 | 5.41 | 1.31 | 0.38 |
| sp|Q94B26|TOM70_HUMAN Mitochondrial import receptor subunit TOM70 OS=Homo sapiens OX=9606 GN=TOMM70 PE=1 SV=1 | 4.14 | 7.92 | 1.91 | 0.94 |
| sp|Q9NP03|EXOS4_HUMAN Exosome complex component RRP41 OS=Homo sapiens OX=9606 GN=EXOSC4 PE=1 SV=3 | 4.13 | 17.52 | 4.24 | 2.08 |
| tr|A0A0A0MSK5|A0A0A0MSK5_HUMAN Torsin-1A-interacting protein 1 OS=Homo sapiens OX=9606 GN=TOR1AIP1 PE=1 SV=1 | 4.12 | 6.27 | 1.52 | 0.61 |
| sp|Q00325-2|MPCP_HUMAN Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 | 4.10 | 10.06 | 2.45 | 1.29 |
| tr|A0A075B6F9|A0A075B6F9_HUMAN Nitric oxide synthase-interacting protein OS=Homo sapiens OX=9606 GN=NOSIP PE=1 SV=1 | 4.09 | 5.71 | 1.39 | 0.48 |
| sp|Q8N752|KC1AL_HUMAN Casein kinase I isoform alpha-like OS=Homo sapiens OX=9606 GN=CSNK1A1L PE=2 SV=2 | 4.09 | 10.34 | 2.52 | 1.34 |
| sp|Q96KA5-2|CLP1L_HUMAN Isoform 2 of Cleft lip and palate transmembrane protein 1- | 4.09 | 4.70 | 1.15 | 0.20 |
| Gene ID            | Description                                                                 | OS          | OX       | GN          | PE | SV | Log2 Fold Change | Log10 Fold Change | q-Value |
|--------------------|-------------------------------------------------------------------------------|-------------|----------|-------------|----|----|-----------------|-------------------|---------|
| tr|C9JLU1|C9JLU1_HUMAN DNA-directed RNA polymerases I, II, and III subunit RPABC3 (Fragment) | Homo sapiens | 9606     | CLPTM1L     |    |    | 4.07            | 14.37             | 1.82    |
| sp|Q9NRN7|ADPPT_HUMAN L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase | Homo sapiens | 9606     | AASDHPT     |    |    | 4.06            | 4.74              | 1.17    |
| sp|Q9H845|ACAD9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial | Homo sapiens | 9606     | ACAD9      |    |    | 4.02            | 1.66              | -0.13   |
| sp|P60981|DEST_HUMAN Destrin                                                                  | Homo sapiens | 9606     | DSTN       |    |    | 4.02            | 9.25              | 2.30    |
| sp|Q8N1G4|LRC47_HUMAN Leucine-rich repeat-containing protein 47 | Homo sapiens | 9606     | LRRC47     |    |    | 4.00            | 2.96              | 0.74    |
| sp|Q10713|MPPA_HUMAN Mitochondrial-processing peptidase subunit alpha | Homo sapiens | 9606     | PMPCA      |    |    | 4.00            | 9.79              | 2.45    |
| tr|A0A087WTB8|A0A087WTB8_HUMAN Ubiquitin carboxyl-terminal hydrolase | Homo sapiens | 9606     | UCHL3      |    |    | 3.94            | 3.87              | -0.03   |
| sp|Q8WXX5|DNJC9_HUMAN DnaJ homolog subfamily C member 9 | Homo sapiens | 9606     | DNAJC9     |    |    | 3.94            | 12.81             | 3.25    |
| sp|P40937|RFC5_HUMAN Isoform 2 of Replication factor C subunit 5 | Homo sapiens | 9606     | RFC5       |    |    | 3.93            | 2.16              | -0.86   |
| sp|P51116|FXR2_HUMAN Fragile X mental retardation syndrome-related protein 2 | Homo sapiens | 9606     | FXR2       |    |    | 3.90            | 7.54              | 1.93    |
| sp|P52306|GDS1_HUMAN Isoform 2 of Rap1 GTPase-GDP dissociation stimulator 1 | Homo sapiens | 9606     | GDS1       |    |    | 3.89            | 9.68              | 2.48    |
| sp|O15460|P4HA2_HUMAN Isoform IIA of Prolyl 4-hydroxylase subunit alpha-2 | Homo sapiens | 9606     | P4HA2      |    |    | 3.89            | 2.65              | 0.68    |
| tr|D6REA1|D6REA1_HUMAN Nucleotide exchange factor SIL1 | Homo sapiens | 9606     | SIL1       |    |    | 3.89            | 4.63              | 1.19    |
| tr|H0YHU4|H0YHU4_HUMAN tRNA (guanine-N(7)')-methyltransferase (Fragment) | Homo sapiens | 9606     | METTL1     |    |    | 3.88            | 5.33              | 1.37    |
| sp|P17858|PFKAL_HUMAN ATP-dependent 6-phosphofructokinase, liver type | Homo sapiens | 9606     | PFKL       |    |    | 3.88            | 10.52             | 2.72    |
| Accession   | Description                                                                 | Gene  | Peptide Length | Value 1 | Value 2 | Value 3 | Value 4 |
|-------------|------------------------------------------------------------------------------|-------|----------------|---------|---------|---------|---------|
| sp|Q96C86|DCPS_HUMAN m7GpppX diphosphatase OS=Homo sapiens OX=9606 GN=DCPS PE=1 SV=2 |       | 3.86       | 10.47   | 2.71    | 1.44    |
| tr|A0A087WUB9|A0A087WUB9_HUMAN Beta-catenin-like protein 1 OS=Homo sapiens OX=9606 GN=CTNNBL1 PE=1 SV=1 |       | 3.86       | 3.95    | 1.02    | 0.03    |
| tr|F5GYF7|F5GYF7_HUMAN COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens OX=9606 GN=COPS7A PE=1 SV=8 |       | 3.85       | 20.68   | 5.37    | 2.43    |
| tr|Q5SWC8|Q5SWC8_HUMAN Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1 |       | 3.83       | 11.70   | 3.05    | 1.61    |
| tr|J3KNF5|J3KNF5_HUMAN Centrosomal protein of 290 kDa OS=Homo sapiens OX=9606 GN=CEP290 PE=1 SV=1 |       | 3.78       | 15.12   | 4.00    | 2.00    |
| sp|Q9BQ75-2|CMS1_HUMAN Isoform 2 of Protein CMSS1 OS=Homo sapiens OX=9606 GN=CMSS1 |       | 3.78       | 15.12   | 4.00    | 2.00    |
| sp|Q9Y3C8|UFC1_HUMAN Ubiquitin-fold modifier-conjugating enzyme 1 OS=Homo sapiens OX=9606 GN=UFC1 PE=1 SV=3 |       | 3.76       | 15.32   | 4.07    | 2.03    |
| sp|Q3LXA3|TKFC_HUMAN Triokinase/FMN cyclase OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=2 |       | 3.74       | 5.59    | 1.49    | 0.58    |
| sp|Q9Y697-2|NFS1_HUMAN Isoform Cytoplasmic of Cysteine desulfurase, mitochondrial OS=Homo sapiens OX=9606 GN=NFS1 |       | 3.74       | 2.50    | 0.67    | -0.58   |
| sp|Q9P0L2-2|EMC3_HUMAN Isoform 2 of ER membrane protein complex subunit 3 OS=Homo sapiens OX=9606 GN=EMC3 |       | 3.73       | 8.21    | 2.20    | 1.14    |
| sp|O60749-2|SNX2_HUMAN Isoform 2 of Sorting nexin-2 OS=Homo sapiens OX=9606 GN=SNX2 |       | 3.71       | 25.62   | 6.91    | 2.79    |
| tr|C9JK9|C9JK9_HUMAN BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens OX=9606 GN=BAG3 PE=1 SV=1 |       | 3.70       | 1.30    | 0.35    | -1.51   |
| tr|H3BNB9|H3BNB9_HUMAN RBR-type E3 ubiquitin transferase (Fragment) OS=Homo sapiens OX=9606 GN=ARH1 PE=1 SV=1 |       | 3.69       | 8.36    | 2.27    | 1.18    |
| sp|P21281|VATB2_HUMAN V-type proton ATPase subunit B, brain isoform OS=Homo sapiens OX=9606 GN=ATP6V1B2 PE=1 SV=3 |       | 3.66       | 5.63    | 1.54    | 0.62    |
| sp|Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens OX=9606 GN=ARL8B PE=1 SV=1 |       | 3.66       | 18.93   | 5.18    | 2.37    |
| tr|F5GZY7|F5GZY7_HUMAN Gamma-aminobutyric acid receptor-associated protein-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=GABARAPL1 PE=1 SV=1 |       | 3.65       | 19.68   | 5.39    | 2.43    |
| Accession | Description | Gene Name | Species | E-Value | Score | Bit Score | bits | Exp. Value |
|-----------|-------------|-----------|---------|---------|-------|-----------|------|------------|
| sp|Q9UJX3-2|APC7_HUMAN Isoform 2 of Anaphase-promoting complex subunit 7 | OS=Homo sapiens | 9.20 | 3.63 | 2.53 | 1.34 |
| sp|P41223-2|BUD31_HUMAN Isoform 2 of Protein BUD31 homolog | OS=Homo sapiens | 7.20 | 3.63 | 0.75 | -0.42 |
| sp|Q8IZ83-3|A16A1_HUMAN Isoform 3 of Aldehyde dehydrogenase family 16 member A1 | OS=Homo sapiens | 7.04 | 3.62 | 1.95 | 0.96 |
| sp|O00567-1|NOP56_HUMAN Nucleolar protein 56 | OS=Homo sapiens | 6.37 | 3.62 | 1.76 | 0.82 |
| sp|Q8IYB8|SU3_HUMAN ATP-dependent RNA helicase SUPV3L1, mitochondrial | OS=Homo sapiens | 6.61 | 3.61 | 1.83 | 0.87 |
| sp|QSTFE4|NT5D1_HUMAN 5'-nucleotidase domain-containing protein 1 | OS=Homo sapiens | 10.13 | 3.60 | 2.82 | 1.49 |
| sp|Q9YN6N|SQOR_HUMAN Sulfide:quinone oxidoreductase, mitochondrial | OS=Homo sapiens | 6.89 | 3.60 | 1.92 | 0.94 |
| tr|A0A0C4DGX4|A0A0C4DGX4_HUMAN Cullin-1 | OS=Homo sapiens | 10.13 | 3.59 | 2.82 | 1.49 |
| sp|P09543-2|CN37_HUMAN Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase | OS=Homo sapiens | 6.89 | 3.59 | 1.92 | 0.94 |
| tr|G3V015|G3V015_HUMAN NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial | OS=Homo sapiens | 5.96 | 3.57 | 1.67 | 0.74 |
| sp|Q9UHR4|BI2L1_HUMAN Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 | OS=Homo sapiens | 8.29 | 3.56 | 2.33 | 1.22 |
| sp|Q13177|PAK2_HUMAN Serine/threonine-protein kinase PAK 2 | OS=Homo sapiens | 6.16 | 3.55 | 1.73 | 0.79 |
| tr|A2A2Q9|A2A2Q9_HUMAN Protein AAR2 homolog | OS=Homo sapiens | 6.88 | 3.53 | 1.95 | 0.96 |
| sp|Q9UI42-2|CBPA4_HUMAN Isoform 2 of Carboxypeptidase A4 | OS=Homo sapiens | 5.65 | 3.50 | 1.61 | 0.69 |
| tr|A0A2R8Y5Q8|A0A2R8Y5Q8_HUMAN Tubulin-specific chaperone E | OS=Homo sapiens | 6.68 | 3.50 | 1.91 | 0.93 |
| sp|Q7L5D6-2|GET4_HUMAN Isoform 2 of Golgi to ER traffic protein 4 homolog | OS=Homo sapiens | 7.17 | 3.50 | 2.05 | 1.04 |
| Accession | Description | Species | Start | End | Score |
|-----------|-------------|---------|-------|-----|-------|
| sp|Q9NZN4|EHD2_HUMAN EH domain-containing protein 2 | Homo sapiens | 3.48 | 15.04 | 4.32 | 2.11 |
| sp|Q6UXH1-2|CREL2_HUMAN Isoform 2 of Cysteine-rich with EGF-like domain protein 2 | Homo sapiens | 3.48 | 5.74 | 1.65 | 0.72 |
| sp|Q9ULX3|NOB1_HUMAN RNA-binding protein NOB1 | Homo sapiens | 3.48 | 5.32 | 1.53 | 0.61 |
| tr|H0YK99|H0YK99_HUMAN DnaJ homolog subfamily C member 17 | Homo sapiens | 3.46 | 10.83 | 3.13 | 1.65 |
| sp|Q13505-3|MTX1_HUMAN Isoform 3 of Metaxin-1 | Homo sapiens | 3.45 | 5.77 | 1.67 | 0.74 |
| tr|H0Y2Y8|H0Y2Y8_HUMAN Zyxin (Fragment) | Homo sapiens | 3.45 | 7.02 | 2.03 | 1.02 |
| tr|X6R5C5|X6R5C5_HUMAN Carboxypeptidase | Homo sapiens | 3.44 | 15.19 | 4.41 | 2.14 |
| sp|Q86UE4|LYRIC_HUMAN Protein LYRIC | Homo sapiens | 3.44 | 6.40 | 1.86 | 0.90 |
| sp|P78346-2|RPP30_HUMAN Isoform 2 of Ribonuclease P protein subunit p30 | Homo sapiens | 3.39 | 6.08 | 1.79 | 0.84 |
| sp|P10155-3|RO60_HUMAN Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein | Homo sapiens | 3.39 | 10.08 | 2.97 | 1.57 |
| sp|Q15654|TRIP6_HUMAN Thyroid receptor-interacting protein 6 | Homo sapiens | 3.39 | 12.47 | 3.68 | 1.88 |
| tr|H0YDX4|H0YDX4_HUMAN Mitochondrial amidoxime-reducing component 1 (Fragment) | Homo sapiens | 3.39 | 9.64 | 2.85 | 1.51 |
| sp|Q9UG63-2|ABCF2_HUMAN Isoform 2 of ATP-binding cassette sub-family F member 2 | Homo sapiens | 3.38 | 10.78 | 3.19 | 1.67 |
| tr|E9PBF6|E9PBF6_HUMAN Lamin-B1 | Homo sapiens | 3.37 | 10.60 | 3.14 | 1.65 |
| sp|Q92905|CSN5_HUMAN COP9 signalosome complex subunit 5 | Homo sapiens | 3.37 | 9.18 | 2.73 | 1.45 |
| sp|Q8TAT6-2|NPL4_HUMAN Isoform 2 of Nuclear protein localization protein 4 homolog | Homo sapiens | 3.36 | 9.47 | 2.82 | 1.50 |
| sp|Q86TU7|SETD3_HUMAN Histone-lysine N-methyltransferase setd3 | Homo sapiens | 3.35 | 0.61 | 0.18 | -2.46 |
| Accession | Description                                                                 | ORG | CE | PE | SV |
|-----------|------------------------------------------------------------------------------|-----|----|----|----|
| tr|H0YK61|H0YK61_HUMAN ER membrane protein complex subunit 4 OS=Homo sapiens Ox=9606 Gnm=Emc4 Pe=1 Sv=1 | Homo sapiens | 3.32 | 15.74 | 4.74 | 2.24 |
| sp|P08240-2|SRPRA_HUMAN Isoform 2 of Signal recognition particle receptor subunit alpha OS=Homo sapiens Ox=9606 Gnm=SRPRA | Homo sapiens | 3.32 | 7.95 | 2.39 | 1.26 |
| sp|Q01581|HMCS1_HUMAN Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens Ox=9606 Gnm=HMCs1 Pe=1 Sv=2 | Homo sapiens | 3.31 | 6.14 | 1.86 | 0.89 |
| tr|B1AK81|B1AK81_HUMAN GPI-anchor transamidase OS=Homo sapiens Ox=9606 Gnm=PIgK Pe=1 Sv=1 | Homo sapiens | 3.30 | 5.65 | 1.71 | 0.78 |
| sp|Q9UKD2|MRT4_HUMAN mRNA turnover protein 4 homolog OS=Homo sapiens Ox=9606 Gnm=Mrt04 Pe=1 Sv=2 | Homo sapiens | 3.30 | 5.22 | 1.58 | 0.66 |
| tr|H0Y8C2|H0Y8C2_HUMAN 60S ribosomal protein L22-like 1 (Fragment) OS=Homo sapiens Ox=9606 Gnm=Rpl22l1 Pe=1 Sv=1 | Homo sapiens | 3.28 | 13.36 | 4.08 | 2.03 |
| tr|A0A1W2PNP0|A0A1W2PNP0_HUMAN GPI transamidase component Pig-T (Fragment) OS=Homo sapiens Ox=9606 Gnm=Pigt Pe=1 Sv=1 | Homo sapiens | 3.26 | 9.28 | 2.84 | 1.51 |
| tr|F5H1S9|F5H1S9_HUMAN tRNA pseudouridine synthase OS=Homo sapiens Ox=9606 Gnm=Pus1 Pe=1 Sv=1 | Homo sapiens | 3.25 | 4.71 | 1.45 | 0.53 |
| sp|Q965M8|TOE1_HUMAN Target of Egr1 protein 1 OS=Homo sapiens Ox=9606 Gnm=Toe1 Pe=1 Sv=1 | Homo sapiens | 3.25 | 8.39 | 2.58 | 1.37 |
| sp|Q15126|PMVK_HUMAN Phosphomevalonate kinase OS=Homo sapiens Ox=9606 Gnm=PMVK Pe=1 Sv=3 | Homo sapiens | 3.25 | 2.67 | 0.82 | -0.28 |
| sp|P36639-2|B0DP_HUMAN Isoform p22 of 7,8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens Ox=9606 Gnm=Nudt1 | Homo sapiens | 3.24 | 3.85 | 1.19 | 0.25 |
| tr|A0A087WVC4|A0A087WVC4_HUMAN cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens Ox=9606 Gnm=Prkacb Pe=1 Sv=1 | Homo sapiens | 3.24 | 7.59 | 2.34 | 1.23 |
| tr|K7EP06|K7EP06_HUMAN mRNA cap guanine-N7 methyltransferase OS=Homo sapiens Ox=9606 Gnm=Rnmt Pe=1 Sv=1 | Homo sapiens | 3.22 | 9.24 | 2.87 | 1.52 |
| tr|I3LCI2|I3LCI2_PIG Pyruvate dehydrogenase E1 component subunit alpha OS=Sus scrofa Gnm=PdhA1 Pe=1 Sv=1 | Sus scrofa | 3.20 | 4.47 | 1.40 | 0.48 |
| sp|O96007|MOC2B_HUMAN Molybdopterin synthase catalytic subunit OS=Homo sapiens Ox=9606 Gnm=Mocs2 Pe=1 Sv=1 | Homo sapiens | 3.20 | 7.43 | 2.32 | 1.22 |
| sp|Q9BYG3|MK67I_HUMAN MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens Ox=9606 Gnm=Nifik Pe=1 Sv=1 | Homo sapiens | 3.19 | 6.32 | 1.98 | 0.98 |
| Accession   | Description                                                                 | OS | Batch | Delta | S.D. | Log2FoldChange |
|-------------|-----------------------------------------------------------------------------|-----|-------|-------|------|----------------|
| sp|Q15428|SF3A2_HUMAN Splicing factor 3A subunit 2 OS=Homo sapiens OX=9606 GN=SF3A2 PE=1 SV=2 | 3.19 | 0.25 | 0.08 | -3.67 |
| tr|G3V2E7|G3V2E7_HUMAN Kinesin light chain 1 OS=Homo sapiens OX=9606 GN=KLC1 PE=1 SV=1 | 3.12 | 1.98 | 0.64 | -0.65 |
| sp|P56182|RRP1_HUMAN Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens OX=9606 GN=RRP1 PE=1 SV=2 | 3.12 | 0.93 | 0.30 | -1.74 |
| sp|Q9Y305-2|ACOT9_HUMAN Isoform 2 of Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens OX=9606 GN=ACOT9 | 3.08 | 5.85 | 1.90 | 0.93 |
| sp|Q9NX62|IMPA3_HUMAN Inositol monophosphatase 3 OS=Homo sapiens OX=9606 GN=IMPAD1 PE=1 SV=2 | 3.07 | 7.17 | 2.33 | 1.22 |
| sp|Q9Y3T9|NOC2L_HUMAN Nucleolar complex protein 2 homolog OS=Homo sapiens OX=9606 GN=NOC2L PE=1 SV=4 | 3.05 | 3.73 | 1.22 | 0.29 |
| sp|Q9H6Y2|WDR55_HUMAN WD repeat-containing protein 55 OS=Homo sapiens OX=9606 GN=WDR55 PE=1 SV=2 | 3.02 | 3.02 | 1.00 | 0.00 |
| sp|Q14181|DPOA2_HUMAN DNA polymerase alpha subunit B OS=Homo sapiens OX=9606 GN=POLA2 PE=1 SV=2 | 3.01 | 4.56 | 1.51 | 0.60 |
| tr|B1AXG1|B1AXG1_HUMAN Non-specific serine/threonine protein kinase OS=Homo sapiens OX=9606 GN=RPS6KA3 PE=1 SV=2 | 3.01 | 4.99 | 1.66 | 0.73 |
| tr|E5RIJ3|E5RIJ3_HUMAN Tumor necrosis factor alpha-induced protein 8 (Fragment) OS=Homo sapiens OX=9606 GN=TNFAIP8 PE=1 SV=1 | 3.00 | 12.57 | 4.19 | 2.07 |
| tr|A0A087X0W7|A0A087X0W7_HUMAN Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens OX=9606 GN=ACOT2 PE=1 SV=1 | 2.98 | 4.91 | 1.65 | 0.72 |
| sp|Q6VUC0|AP2E_HUMAN Transcription factor AP-2 epsilon OS=Homo sapiens OX=9606 GN=TFAP2E PE=2 SV=1 | 2.97 | 3.69 | 1.24 | 0.31 |
| tr|C9JZR2|C9JZR2_HUMAN Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 PE=1 SV=2 | 2.97 | 1.39 | 0.47 | -1.10 |
| sp|Q96BN8|OTUL_HUMAN Ubiquitin thioesterase otulin OS=Homo sapiens OX=9606 GN=OTULIN PE=1 SV=3 | 2.96 | 7.93 | 2.67 | 1.42 |
| sp|Q08J23-2|NSUN2_HUMAN Isoform 2 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens OX=9606 GN=NSUN2 | 2.96 | 12.49 | 4.22 | 2.08 |
| sp|P49770|EI2BB_HUMAN Translation initiation factor eIF-2B subunit beta OS=Homo sapiens OX=9606 GN=EIF2B2 PE=1 SV=3 | 2.95 | 12.03 | 4.07 | 2.03 |
| tr|A0A0X1KG71|A0A0X1KG71_HUMAN Negative elongation factor B OS=Homo sapiens OX=9606 GN=NELFB PE=1 SV=1 | 2.94 | 7.96 | 2.71 | 1.44 |
| Accession      | Description                                                                 | OX   | SV  | PE  | Value  |
|----------------|------------------------------------------------------------------------------|------|-----|-----|--------|
| sp|P49761-1|CLK3_HUMAN Isoform 1 of Dual specificity protein kinase CLK3 OS=Homo sapiens | 9606 | 1   | 1   | 2.93   |
| sp|Q9H814|PHAX_HUMAN Phosphorylated adapter RNA export protein OS=Homo sapiens             | 9606 | 1   | 1   | 2.92   |
| sp|Q6ZRP7|QSOX2_HUMAN Sulfhydryl oxidase 2 OS=Homo sapiens                                | 9606 | 3   | 1   | 2.92   |
| tr|F8W7U8|Phage_87_004_HUMAN Double-strand break repair protein OS=Homo sapiens             | 9606 | 1   | 1   | 2.91   |
| tr|J3KTC1|J3KTC1_HUMAN RNA-binding protein Musashi homolog 2 (Fragment) OS=Homo sapiens    | 9606 | 1   | 8   | 2.90   |
| tr|A0A087X0K1|A0A087X0K1_HUMAN Calcium-binding protein 39 OS=Homo sapiens                   | 9606 | 1   | 1   | 2.90   |
| tr|A0A1W2PNX8|A0A1W2PNX8_HUMAN Protein unc-45 homolog A OS=Homo sapiens                   | 9606 | 1   | 1   | 2.88   |
| tr|E7ENJ6|E7ENJ6_HUMAN AP-1 complex subunit mu-1 OS=Homo sapiens                        | 9606 | 1   | 1   | 2.86   |
| sp|Q9NZL4|HPBP1_HUMAN Isoform 3 of Hsp70-binding protein 1 OS=Homo sapiens                | 9606 | 1   | 1   | 2.86   |
| sp|Q13084|MR28_HUMAN 39S ribosomal protein L28, mitochondrial OS=Homo sapiens             | 9606 | 1   | 4   | 2.85   |
| tr|E5RGS4|E5RGS4_HUMAN Prefoldin subunit 1 OS=Homo sapiens                                | 9606 | 1   | 1   | 2.85   |
| sp|Q8NFJ7|PCAT1_HUMAN Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens           | 9606 | 2   | 1   | 2.81   |
| sp|Q05048|CSTF1_HUMAN Cleavage stimulation factor subunit 1 OS=Homo sapiens              | 9606 | 1   | 1   | 2.80   |
| tr|I3L0N3|I3L0N3_HUMAN Vesicle-fusing ATPase OS=Homo sapiens                             | 9606 | 1   | 1   | 2.79   |
| sp|O00629|IMA3_HUMAN Importin subunit alpha-3 OS=Homo sapiens                            | 9606 | 1   | 1   | 2.77   |
| tr|X6RAY8|X6RAY8_HUMAN 39S ribosomal protein L4, mitochondrial OS=Homo sapiens             | 9606 | 1   | 1   | 2.73   |
| tr|G5E9V5|G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens           | 9606 | 1   | 1   | 2.71   |
| Accession   | Description                                                                 | OS     | OX    | GN     | PE | SV |
|-------------|------------------------------------------------------------------------------|--------|-------|--------|----|----|
| sp|Q8NI60-3|COQ8A_HUMAN Isoform 3 of Atypical kinase COQ8A, mitochondrial | Homo sapiens | 9606 | COQ8A | 2.70 | 4.70 | 1.74 | 0.80 |
| sp|O14879|IFIT3_HUMAN Interferon-induced protein with tetratricopeptide repeats 3 | Homo sapiens | 9606 | IFIT3 | 2.68 | 14.16 | 5.28 | 2.40 |
| sp|Q8N7H5-2|PAF1_HUMAN Isoform 2 of RNA polymerase II-associated factor 1 homolog | Homo sapiens | 9606 | PAF1 | 2.68 | 4.01 | 1.50 | 0.58 |
| sp|P36404|ARL2_HUMAN ADP-ribosylation factor-like protein 2 | Homo sapiens | 9606 | ARL2 | 2.68 | 9.29 | 3.47 | 1.79 |
| sp|P50583|AP4A_HUMAN Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] | Homo sapiens | 9606 | NUPT2 | 2.66 | 3.91 | 1.47 | 0.56 |
| tr|J3QKW2|J3QKW2_HUMAN 28S ribosomal protein S7, mitochondrial | Homo sapiens | 9606 | MRPS7 | 2.66 | 9.50 | 3.57 | 1.84 |
| tr|A0A0B4J287|A0A0B4J287_HUMAN COMM domain-containing protein 4 | Homo sapiens | 9606 | COMMD4 | 2.65 | 12.28 | 4.63 | 2.21 |
| sp|Q8TB4C-2|UBA3_HUMAN Isoform 2 of NEDD8-activating enzyme E1 catalytic subunit | Homo sapiens | 9606 | UBA3 | 2.65 | 2.90 | 1.09 | 0.13 |
| sp|O75251|NDUS7_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial | Homo sapiens | 9606 | NDUFS7 | 2.63 | 7.51 | 2.85 | 1.51 |
| tr|A0A0C4DGG1|A0A0C4DGG1_HUMAN Protein kinase C and casein kinase substrate in neurons protein 3 (Fragment) | Homo sapiens | 9606 | PACSIN3 | 2.62 | 16.93 | 6.46 | 2.69 |
| tr|A0A0A0MS51|A0A0A0MS51_HUMAN Gelsolin | Homo sapiens | 9606 | GSN | 2.62 | 3.25 | 1.24 | 0.31 |
| tr|A0A1B0GUA3|A0A1B0GUA3_HUMAN KIF1-binding protein | Homo sapiens | 9606 | KIF1BP | 2.61 | 17.87 | 6.83 | 2.77 |
| tr|A0A0A0MQR2|A0A0A0MQR2_HUMAN Replication termination factor 2 | Homo sapiens | 9606 | RTF2 | 2.57 | 4.66 | 1.81 | 0.86 |
| sp|P33947|ERD22_HUMAN ER lumen protein-retaining receptor 2 | Homo sapiens | 9606 | KDELR2 | 2.57 | 2.11 | 0.82 | -0.29 |
| tr|B5ME97|B5ME97_HUMAN Septin 10, isoform CRA_c | Homo sapiens | 9606 | SEPT10 | 2.56 | 7.54 | 2.94 | 1.56 |
| sp|P31937|3HIDH_HUMAN 3-hydroxyisobutyrate dehydrogenase, mitochondrial | Homo sapiens | 9606 | HIBADH | 2.56 | 5.28 | 2.07 | 1.05 |
| tr|A0A2U3TZY2|A0A2U3TZY2_HUMAN Caseinolytic peptidase B protein homolog | Homo sapiens | 9606 | | 2.55 | 3.67 | 1.44 | 0.53 |
| Accession | Description | OS         | OX         | GN      | PE | SV | -1 | -0.30 |
|-----------|-------------|------------|------------|---------|----|----|-----|-------|
| sp|O96006|ZBED1_HUMAN Zinc finger BED domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ZBED1 PE=1 SV=1 | 2.55 | 2.07 | 0.81 | 0.30 |
| tr|M0R0P9|M0R0P9_HUMAN Non-specific serine/threonine protein kinase OS=Homo sapiens OX=9606 GN=AKT2 PE=1 SV=1 | 2.54 | 3.30 | 1.30 | 0.38 |
| sp|Q04446|GLGB_HUMAN 1,4-alpha-glucan-branched enzyme OS=Homo sapiens OX=9606 GN=GBE1 PE=1 SV=3 | 2.54 | 19.12 | 7.54 | 2.91 |
| sp|Q13724|MOGS_HUMAN Mannosyl-oligosaccharide glucosidase OS=Homo sapiens OX=9606 GN=MOGS PE=1 SV=5 | 2.53 | 14.30 | 5.65 | 2.50 |
| tr|F8VX04|F8VX04_HUMAN Sodium-coupled neutral amino acid transporter 1 OS=Homo sapiens OX=9606 GN=SLC38A1 PE=1 SV=1 | 2.53 | 0.12 | 0.05 | -4.41 |
| tr|H0Y3C5|H0Y3C5_HUMAN Tyrosine-protein kinase OS=Homo sapiens OX=9606 GN=HCK PE=1 SV=1 | 2.52 | 3.50 | 1.39 | 0.42 |
| sp|O76031|CLPX_HUMAN ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens OX=9606 GN=CLPX PE=1 SV=2 | 2.52 | 12.22 | 4.86 | 2.28 |
| sp|P83111|LACTB_HUMAN Serine beta-lactamase-like protein LACTB, mitochondrial OS=Homo sapiens OX=9606 GN=LACTB PE=1 SV=2 | 2.51 | 3.36 | 1.34 | 0.42 |
| sp|Q9NSI2|F207A_HUMAN Isoform B of Protein FAM207A OS=Homo sapiens OX=9606 GN=FAM207A | 2.49 | 8.08 | 3.24 | 1.70 |
| tr|H0YF61|H0YF61_HUMAN Non-specific lipid-transfer protein (Fragment) OS=Homo sapiens OX=9606 GN=SCP2 PE=1 SV=1 | 2.49 | 11.95 | 4.80 | 2.26 |
| sp|Q6P148|SYDM_HUMAN Aspartate-tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1 | 2.47 | 6.33 | 2.57 | 1.36 |
| sp|Q13564|ULA1_HUMAN Isoform 2 of NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens OX=9606 GN=NAE1 | 2.46 | 5.32 | 2.16 | 1.11 |
| sp|P07384|CAN1_HUMAN Calpain-1 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN1 PE=1 SV=1 | 2.44 | 8.95 | 3.67 | 1.88 |
| tr|A0A087WZ13|A0A087WZ13_HUMAN Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1 | 2.42 | 12.75 | 5.27 | 2.40 |
| tr|A8MYV2|A8MYV2_HUMAN LUC7-like (S. cerevisiae), isoform CRA_f OS=Homo sapiens OX=9606 GN=LUC7L PE=1 SV=1 | 2.40 | 6.58 | 2.74 | 1.45 |
| tr|C9IY70|C9IY70_HUMAN 60S ribosomal export protein NMD3 (Fragment) OS=Homo sapiens OX=9606 GN=NMD3 PE=1 SV=1 | 2.40 | 1.65 | 0.69 | -0.54 |
| Accession   | Description                                                                 | Source          | Value 1 | Value 2 | Value 3 | Value 4 |
|-------------|------------------------------------------------------------------------------|-----------------|---------|---------|---------|---------|
| sp|Q9UMX0-2|Ubiquilin-1_HUMAN Isoform 2 of Ubiquilin-1 OS=Homo sapiens OX=9606 GN=UBQLN1 |                 | 2.38    | 5.87    | 2.47    | 1.30    |
| tr|B1AP22|B1AP22_HUMAN Presenilin OS=Homo sapiens OX=9606 GN=PSEN2 PE=1 SV=1 |                 | 2.35    | 6.47    | 2.75    | 1.46    |
| tr|E7EMB1|E7EMB1_HUMAN Switch-associated protein 70 OS=Homo sapiens OX=9606 GN=SWAP70 PE=1 SV=1 |                 | 2.35    | 2.29    | 0.98    | -0.04   |
| sp|Q9H307|PININ_HUMAN Pinin OS=Homo sapiens OX=9606 GN=PNN PE=1 SV=5 |                 | 2.35    | 1.81    | 0.77    | -0.37   |
| sp|Q6L8Q7-2|PDE12_HUMAN Isoform 2 of 2',5'-phosphodiesterase 12 OS=Homo sapiens OX=9606 GN=PDE12 |                 | 2.32    | 4.49    | 1.93    | 0.95    |
| tr|A0A087WT20|A0A087WT20_HUMAN DDB1-and CUL4-associated factor 13 OS=Homo sapiens OX=9606 GN=DCAF13 PE=1 SV=1 |                 | 2.32    | 1.34    | 0.58    | -0.79   |
| tr|K7ER96|K7ER96_HUMAN Thioredoxin-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TXNL1 PE=1 SV=1 |                 | 2.28    | 6.88    | 3.02    | 1.60    |
| tr|E7EQU1|E7EQU1_HUMAN High mobility group protein B3 (Fragment) OS=Homo sapiens OX=9606 GN=HMGB3 PE=1 SV=1 |                 | 2.26    | 9.39    | 4.16    | 2.06    |
| sp|Q9H6S3|ES8L2_HUMAN Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens OX=9606 GN=EPS8L2 PE=1 SV=2 |                 | 2.31    | 3.30    | 0.99    | -0.01   |
| tr|K7ER96|K7ER96_HUMAN Thioredoxin-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TXNL1 PE=1 SV=1 |                 | 2.28    | 6.88    | 3.02    | 1.60    |
| sp|Q9H6S2|PIGS_HUMAN Isoform 2 of GPI transamidase component PIG-S OS=Homo sapiens OX=9606 GN=PIGS |                 | 2.23    | 3.66    | 1.64    | 0.71    |
| sp|Q9Y2T2|AP3M1_HUMAN AP-3 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP3M1 PE=1 SV=1 |                 | 2.21    | 3.67    | 1.66    | 0.73    |
| sp|Q96F11-2|NSUN5_HUMAN Isoform 2 of Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens OX=9606 GN=NSUN5 |                 | 2.20    | 3.55    | 1.62    | 0.69    |
| tr|H0Y56|H0Y56_HUMAN Apoptosis regulator BAX (Fragment) OS=Homo sapiens OX=9606 GN=BAX PE=1 SV=1 |                 | 2.19    | 5.28    | 2.41    | 1.27    |
| tr|H0YCY8|H0YCY8_HUMAN Dipeptidyl peptidease 1 (Fragment) OS=Homo sapiens OX=9606 GN=CTSC PE=1 SV=8 |                 | 2.19    | 7.35    | 3.35    | 1.75    |
| tr|E9PDQ8|E9PDQ8_HUMAN Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=SUCLG2 PE=1 SV=1 |                 | 2.17    | 6.53    | 3.00    | 1.59    |
| sp|Q9UKN8|TF3C4_HUMAN General transcription factor 3C polypeptide 4 OS=Homo sapiens OX=9606 GN=TF3C4 PE=1 SV=2 |                 | 2.17    | 1.65    | 0.76    | -0.39   |
| sp|Q14232|EI2BA_HUMAN Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens OX=9606 GN=EIF2B1 PE=1 SV=1 |                 | 2.15    | 6.19    | 2.88    | 1.53    |
| Gene ID   | Description                                      | OS     | GN     | PE | SV |
|-----------|--------------------------------------------------|--------|--------|----|----|
| sp|Q9Y2X3|NOP58_HUMAN Nucleolar protein 58 OS=Homo sapiens OX=9606 GN=NOP58 PE=1 SV=1 | 2.14   | 7.73   | 3.61 | 1.85 |
| sp|Q9BYN8|RT26_HUMAN 28S ribosomal protein S26, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS26 PE=1 SV=1 | 2.12   | 3.29   | 1.55 | 0.63 |
| tr|Q5T760|Q5T760_HUMAN Serine/arginine-rich-splicing factor 11 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1 | 2.12   | 6.45   | 3.04 | 1.60 |
| tr|A6NG10|A6NG10_HUMAN cDNA FLJ59459, highly similar to WW domain-binding protein 2 OS=Homo sapiens OX=9606 GN=WBP2 PE=1 SV=2 | 2.12   | 10.40  | 4.91 | 2.30 |
| sp|Q92820|GGH_HUMAN Gamma-glutamyl hydrolase OS=Homo sapiens OX=9606 GN=GGH PE=1 SV=2 | 2.10   | 4.04   | 1.92 | 0.94 |
| tr|J3KMX2|J3KMX2_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens OX=9606 GN=SMARCD2 PE=1 SV=1 | 2.10   | 2.72   | 1.30 | 0.38 |
| sp|P20340-2|RAB6A_HUMAN Isoform 2 of Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A | 2.08   | 6.11   | 2.94 | 1.56 |
| sp|Q9UBV8|PEF1_HUMAN Peflin OS=Homo sapiens OX=9606 GN=PEF1 PE=1 SV=1 | 2.07   | 3.88   | 1.87 | 0.90 |
| sp|Q8WVY7|UBCP1_HUMAN Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens OX=9606 GN=UBLC1 PE=1 SV=2 | 2.07   | 3.21   | 1.55 | 0.63 |
| sp|Q96I6-2|GMPPA_HUMAN Isoform 2 of Mannose-1-phosphate guanylyltransferase alpha OS=Homo sapiens OX=9606 GN=GMPPA | 2.07   | 1.92   | 0.93 | -0.11 |
| sp|Q13895|BYST_HUMAN Bystin OS=Homo sapiens OX=9606 GN=BYSTL PE=1 SV=3 | 2.06   | 6.86   | 3.33 | 1.73 |
| tr|J3QQ6|J3QQ6_HUMAN Pyridoxine-5'-phosphate oxidase (Fragment) OS=Homo sapiens OX=9606 GN=PNPO PE=1 SV=2 | 2.03   | 6.36   | 3.13 | 1.65 |
| sp|Q9Y4W6|AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens OX=9606 GN=AFG3L2 PE=1 SV=2 | 2.02   | 3.94   | 1.95 | 0.97 |
| sp|P32929-2|CGL_HUMAN Isoform 2 of Cystathionine gamma-lyase OS=Homo sapiens OX=9606 GN=CTH | 2.01   | 5.06   | 2.51 | 1.33 |
| sp|O14530-2|TXND9_HUMAN Isoform 2 of Thioredoxin domain-containing protein 9 OS=Homo sapiens OX=9606 GN=TXNDC9 | 2.01   | 7.18   | 3.58 | 1.84 |
| tr|G3V155|G3V155_HUMAN Thioredoxin domain containing 14, isoform CRA_a OS=Homo sapiens OX=9606 GN=TMX2 PE=4 SV=1 | 2.00   | 3.92   | 1.96 | 0.97 |
| tr|A0A2R8Y3X5|A0A2R8Y3X5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1 | 2.00   | 0.51   | 0.26 | -1.97 |
| Accession   | Description                                                                 | OS   | GN   | PE | SV | Score | E-value | Bit-score | Copys | PDB ID |
|-------------|------------------------------------------------------------------------------|------|------|----|----|-------|---------|-----------|-------|--------|
| sp|Q9C005|DPY30_HUMAN Protein dpy-30 homolog OS=Homo sapiens OX=9606 GN=DPY30 PE=1 SV=1 | 2.00 | 10.24 | 5.13 | 2.36 |
| sp|O43823|AKAP8_HUMAN A-kinase anchor protein 8 OS=Homo sapiens OX=9606 GN=AKAP8 PE=1 SV=1 | 2.00 | 1.70 | 0.85 | -0.23 |
| tr|H3BMU1|H3BMU1_HUMAN IST1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=IST1 PE=1 SV=1 | 1.97 | 3.63 | 1.84 | 0.88 |
| tr|A0A087WX97|A0A087WX97_HUMAN Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1 | 1.96 | 0.15 | 0.08 | -3.71 |
| sp|Q96H20|SNF8_HUMAN Isoform 2 of Vacuolar-sorting protein SNF8 OS=Homo sapiens OX=9606 GN=SNF8 | 1.94 | 2.39 | 1.23 | 0.30 |
| sp|O43823|AKAP8_HUMAN A-kinase anchor protein 8 OS=Homo sapiens OX=9606 GN=AKAP8 PE=1 SV=1 | 2.00 | 1.70 | 0.85 | -0.23 |
| sp|Q81XB1|DJC10_HUMAN Isoform 2 of DnaJ homolog subfamily C member 10 OS=Homo sapiens OX=9606 GN=DNAJC10 | 1.91 | 1.53 | 0.80 | -0.32 |
| sp|Q8TC07|TBC15_HUMAN Isoform 2 of TBC1 domain family member 15 OS=Homo sapiens OX=9606 GN=TBC1D15 | 1.90 | 4.77 | 2.50 | 1.32 |
| sp|Q14790|CASP8_HUMAN Isoform 2 of Caspase-8 OS=Homo sapiens OX=9606 GN=CASP8 | 1.90 | 2.08 | 1.09 | 0.13 |
| sp|Q8WXF1|PSPC1_HUMAN Isoform 2 of Paraspeckle component 1 OS=Homo sapiens OX=9606 GN=PSPC1 | 1.88 | 6.42 | 3.42 | 1.77 |
| sp|Q13363|CTBP1_HUMAN Isoform 2 of C-terminal-binding protein 1 OS=Homo sapiens OX=9606 GN=CTBP1 | 1.87 | 3.47 | 1.85 | 0.89 |
| sp|P35813|PPM1A_HUMAN Isoform Alpha-2 of Protein phosphatase 1A OS=Homo sapiens OX=9606 GN=PPM1A | 1.87 | 2.24 | 1.20 | 0.26 |
| sp|Q12996|CSTF3_HUMAN Cleavage stimulation factor subunit 3 OS=Homo sapiens OX=9606 GN=CSTF3 | 1.87 | 8.93 | 4.78 | 2.26 |
| sp|Q9BVC6|TM109_HUMAN Transmembrane protein 109 OS=Homo sapiens OX=9606 GN=TMEM109 | 1.85 | 14.14 | 7.64 | 2.93 |
| sp|Q9BZE4|NOG1_HUMAN Isoform 2 of Nucleolar GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP4 | 1.82 | 1.92 | 1.06 | 0.08 |
| sp|O43447|PPHIH_HUMAN Peptidyl-prolyl cis-trans isomerase H OS=Homo sapiens OX=9606 GN=PPHIH | 1.82 | 4.38 | 2.41 | 1.27 |
| sp|O60825|F262_HUMAN Isoform 2 of 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 OS=Homo sapiens OX=9606 GN=PFKFB2 | 1.82 | 1.44 | 0.79 | -0.34 |
| tr|H0YAT2|H0YAT2_HUMAN 28S ribosomal protein S28, mitochondrial (Fragment) | 1.82 | 5.47 | 3.01 | 1.59 |
| Accession | Description | OS | OX | GN | PE | SV | Score |
|-----------|-------------|----|----|----|----|----|-------|
| sp|Q9H223|EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens OX=9606 GN=EHD4 PE=1 SV=1 | Homo sapiens | 9606 | MRPS28 | 1 | 1.80 9.83 5.45 2.45 |
| tr|K7ENE3|K7ENE3_HUMAN Vacuolar protein-sorting-associated protein 25 (Fragment) OS=Homo sapiens OX=9606 GN=VPS25 PE=1 SV=1 | Homo sapiens | 9606 | 1.80 6.03 3.35 1.74 |
| tr|C9JCC6|C9JCC6_HUMAN Dr1-associated corepressor OS=Homo sapiens OX=9606 GN=DRAP1 PE=1 SV=1 | Homo sapiens | 9606 | 1.79 7.23 4.03 2.01 |
| sp|P56545-2|CTBP2_HUMAN Isoform 2 of C-terminal-binding protein 2 OS=Homo sapiens OX=9606 GN=CTBP2 | Homo sapiens | 9606 | 1.77 8.29 4.69 2.23 |
| tr|A0A0C4DFN3|A0A0C4DFN3_HUMAN Monoglyceride lipase OS=Homo sapiens OX=9606 GN=MGLL PE=1 SV=1 | Homo sapiens | 9606 | 1.76 5.60 3.18 1.67 |
| sp|O00186|STXB3_HUMAN Syntaxin-binding protein 3 OS=Homo sapiens OX=9606 GN=STXB3 PE=1 SV=2 | Homo sapiens | 9606 | 1.74 9.45 5.44 2.44 |
| sp|O00505|IMA4_HUMAN Importin subunit alpha-4 OS=Homo sapiens OX=9606 GN=KPNAA PE=1 SV=2 | Homo sapiens | 9606 | 1.73 4.12 2.38 1.25 |
| sp|Q9H2J4|PDCL3_HUMAN Phosducin-like protein 3 OS=Homo sapiens OX=9606 GN=PDCL3 PE=1 SV=1 | Homo sapiens | 9606 | 1.73 5.36 3.10 1.63 |
| sp|P48163-2|MAOX_HUMAN Isoform 2 of NADP-dependent malic enzyme OS=Homo sapiens OX=9606 GN=ME1 | Homo sapiens | 9606 | 1.71 3.27 1.91 0.93 |
| sp|P40692-3|MLH1_HUMAN Isoform 3 of DNA mismatch repair protein Mlh1 OS=Homo sapiens OX=9606 GN=MLH1 | Homo sapiens | 9606 | 1.69 7.32 4.33 2.11 |
| sp|Q96LD4-2|TRI47_HUMAN Isoform 2 of E3 ubiquitin-protein ligase TRIM47 OS=Homo sapiens OX=9606 GN=TRIM47 | Homo sapiens | 9606 | 1.69 3.63 2.14 1.10 |
| sp|P80217-2|IN35_HUMAN Isoform 2 of Interferon-induced 35 kDa protein OS=Homo sapiens OX=9606 GN=IFI35 | Homo sapiens | 9606 | 1.67 9.38 5.62 2.49 |
| sp|Q9NRF9|DPOE3_HUMAN DNA polymerase epsilon subunit 3 OS=Homo sapiens OX=9606 GN=POLE3 PE=1 SV=1 | Homo sapiens | 9606 | 1.66 8.59 5.18 2.37 |
| sp|Q969U7-2|PSMG2_HUMAN Isoform 2 of Proteasome assembly chaperone 2 OS=Homo sapiens OX=9606 GN=PSMG2 | Homo sapiens | 9606 | 1.62 12.36 7.65 2.93 |
| tr|J3QLD9|J3QLD9_HUMAN Flotillin-2 OS=Homo sapiens OX=9606 GN=FLOT2 PE=1 SV=1 | Homo sapiens | 9606 | 1.61 4.43 2.75 1.46 |
| tr|A0A2R8YEM2|A0A2R8YEM2_HUMAN Cyclin-H OS=Homo sapiens OX=9606 GN=CCNH PE=1 SV=1 | Homo sapiens | 9606 | 1.60 7.65 4.79 2.26 |
| tr|H3BU51|H3BU51_HUMAN Neuroplastin OS=Homo sapiens OX=9606 GN=NPTN PE=1 SV=1 | Homo sapiens | 9606 | 1.59 3.99 2.51 1.33 |
| Accession | Description | OS | OX | Note |
|-----------|-------------|-----|----|------|
| sp|Q9HCC0-2|MCCB_HUMAN Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial | Homo sapiens | 9606 | GN=MCCC2 |
| sp|P61225|RAP2B_HUMAN Ras-related protein Rap-2b | Homo sapiens | 9606 | GN=RAP2B PE=1 SV=1 |
| sp|Q7L2J0|MEPCE_HUMAN 7SK snRNA methylphosphate capping enzyme | Homo sapiens | 9606 | GN=MEPCE PE=1 SV=1 |
| tr|A0A1B0GTB8|A0A1B0GTB8_HUMAN Carnitine O-palmitoyltransferase 2, mitochondrial | Homo sapiens | 9606 | GN=CPT2 PE=1 SV=1 |
| sp|Q9H6F5|CCD86_HUMAN Coiled-coil domain-containing protein 86 | Homo sapiens | 9606 | GN=CCDC86 PE=1 SV=1 |
| sp|Q6PI78|TMM65_HUMAN Transmembrane protein 65 | Homo sapiens | 9606 | GN=TMEM65 PE=1 SV=2 |
| tr|G5E9W3|G5E9W3_HUMAN Cleavage and polyadenylation specific factor 3, 73kDa, isoform CRA_b | Homo sapiens | 9606 | GN=CPSF3 PE=1 SV=1 |
| tr|F5GWE5|F5GWE5_HUMAN Phosphatidylinositol transfer protein alpha isoform | Homo sapiens | 9606 | GN=PITPNA PE=1 SV=1 |
| sp|Q9NQT5|EXOS3_HUMAN Exosome complex component RRP40 | Homo sapiens | 9606 | GN=EXOSC3 PE=1 SV=3 |
| tr|A0A2R8Y8A7|A0A2R8Y8A7_HUMAN Sorting nexin-27 | Homo sapiens | 9606 | GN=SNX27 PE=1 SV=1 |
| tr|A0A0A0MQX8|A0A0A0MQX8_HUMAN Muscleblind-like protein 1 | Homo sapiens | 9606 | GN=MBNL1 PE=1 SV=1 |
| sp|Q86YP4-2|P66A_HUMAN Isoform 2 of Transcriptional repressor p66-alpha | Homo sapiens | 9606 | GN=GATAD2A |
| sp|Q9P032|NDUF4_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 | Homo sapiens | 9606 | GN=NDUFAF4 PE=1 SV=1 |
| sp|P08243-2|ASNS_HUMAN Isoform 2 of Asparagine synthetase [glutamine-hydrolyzing] | Homo sapiens | 9606 | GN=ASNS |
| sp|P37235|HPCL1_HUMAN Hippocalcin-like protein 1 | Homo sapiens | 9606 | GN=HPCAL1 PE=1 SV=3 |
| tr|D6RC74|D6RC74_HUMAN Protein SDA1 | Homo sapiens | 9606 | GN=SDAD1 PE=1 SV=1 |
| Accession | Description | OS          | GN         | PE | SV | Weight Ratio 1 | Weight Ratio 2 | Weight Ratio 3 | Weight Ratio 4 |
|-----------|-------------|-------------|------------|----|----|----------------|----------------|----------------|----------------|
| sp|O15031|PLXB2_HUMAN Plexin-B2 | Homo sapiens | PLXB2 | 1 | 3 | 1.40          | 2.20           | 1.57           | 0.65           |
| sp|Q9NYK5-2|RM39_HUMAN Isoform 2 of 39S ribosomal protein L39, mitochondrial | Homo sapiens | MRPL39 | 1 | 3 | 1.37          | 5.17           | 3.77           | 1.91           |
| sp|Q06124-2|PTN11_HUMAN Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 | Homo sapiens | PTPN11 | 1 | 3 | 1.37          | 7.04           | 5.16           | 2.37           |
| sp|O60678-2|ANM3_HUMAN Isoform 2 of Protein arginine N-methyltransferase 3 | Homo sapiens | PRMT3 | 1 | 3 | 1.36          | 4.72           | 3.48           | 1.80           |
| sp|O43747-2|AP1G1_HUMAN Isoform 2 of AP-1 complex subunit gamma-1 | Homo sapiens | AP1G1 | 1 | 3 | 1.35          | 2.83           | 2.09           | 1.06           |
| sp|P49902-2|NT5C_HUMAN Isoform 2 of Cytosolic purine 5'-nucleotidase | Homo sapiens | NT5C2 | 1 | 3 | 1.35          | 8.11           | 6.01           | 2.59           |
| sp|Q9BV20|MTNA_HUMAN Methylthioribose-1-phosphate isomerase | Homo sapiens | MRI1 | 1 | 3 | 1.33          | 7.16           | 5.38           | 2.43           |
| sp|Q9NUO8-2|ABCF3_HUMAN Isoform 2 of ATP-binding cassette sub-family F member 3 | Homo sapiens | ABCF3 | 1 | 3 | 1.33          | 4.96           | 3.74           | 1.90           |
| sp|Q9BV14|NOC4L_HUMAN Nucleolar complex protein 4 homolog | Homo sapiens | NOC4L | 1 | 3 | 1.31          | 4.02           | 3.07           | 1.62           |
| sp|Q13451|FKBP5_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP5 | Homo sapiens | FKBP5 | 1 | 3 | 1.31          | 1.42           | 1.09           | 0.12           |
| tr|H3BRY6|H3BRY6_HUMAN Integrator complex subunit 14 | Homo sapiens | INTS14 | 1 | 3 | 1.29          | 1.29           | 1.00           | -0.01          |
| tr|B0YI6W|B0YI6W_HUMAN Archain 1, isoform CRA_a | Homo sapiens | ARCN1 | 1 | 3 | 1.29          | 4.60           | 3.56           | 1.83           |
| tr|H3BND4|H3BND4_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 | Homo sapiens | PDXDC1 | 1 | 3 | 1.28          | 2.66           | 2.08           | 1.05           |
| tr|E9PGT3|E9PGT3_HUMAN Ribosomal protein S6 kinase | Homo sapiens | RPS6KA1 | 1 | 3 | 1.28          | 2.92           | 2.28           | 1.19           |
| sp|Q14677-3|EPN4_HUMAN Isoform 3 of Clathrin interactor 1 | Homo sapiens | CLINT1 | 1 | 3 | 1.27          | 3.05           | 2.40           | 1.26           |
| sp|Q8NGA1|OR1M1_HUMAN Olfactory receptor 1M1 | Homo sapiens | OR1M1 | 2 | 3 | 1.25          | 2.77           | 2.21           | 1.14           |
| tr|A0A0R4J2F6|A0A0R4J2F6_HUMAN Interferon-related developmental regulator 2 | Homo sapiens | IFRD2 | 1 | 3 | 1.25          | 3.02           | 2.42           | 1.28           |
| Accession | Description                                                                 | OS       | OX      | GN       | PE | SV | Value1   | Value2   | Value3 | Value4 |
|-----------|------------------------------------------------------------------------------|----------|--------|----------|----|----|----------|----------|--------|--------|
| sp|Q8TCD5|NT5C_HUMAN 5'(3')-deoxyribonucleotidase, cytosolic type | Homo sapiens | 9606 | NT5C | 1 | 2 | 1.24 | 0.17 | 0.14 | -2.84 |
| tr|A0A1B0GT3C|A0A1B0GT3C_HUMAN Alpha-ketoglutarate-dependent dioxygenase | Homo sapiens | 9606 | FTO | 1 | 1 | 1.22 | 5.16 | 4.23 | 2.08 |
| sp|Q92917|GPKOW_HUMAN G-patch domain and KOW motifs-containing protein | Homo sapiens | 9606 | GPKOW | 1 | 2 | 1.22 | 3.41 | 2.80 | 1.49 |
| tr|G3V158|G3V158_HUMAN 2-deoxyribose-5-phosphate aldolase homolog (C. elegans), isoform CRA_a | Homo sapiens | 9606 | DER A | 1 | 1 | 1.21 | 8.76 | 7.26 | 2.86 |
| sp|Q15291-2|RBBP5_HUMAN Isoform 2 of Retinoblastoma-binding protein 5 | Homo sapiens | 9606 | RBBP5 | 1 | 1 | 1.19 | 2.33 | 1.96 | 0.97 |
| tr|H3BM38|H3BM38_HUMAN Synaptosomal-associated protein (Fragment) | Homo sapiens | 9606 | SNAP23 | 1 | 1 | 1.19 | 5.46 | 4.60 | 2.20 |
| tr|A0A1W2PQ47|A0A1W2PQ47_HUMAN Squalene synthase | Homo sapiens | 9606 | FD FT1 | 1 | 1 | 1.18 | 7.74 | 6.57 | 2.72 |
| sp|P53701|CCHL_HUMAN Cytochrome c-type heme lyase | Homo sapiens | 9606 | HCCS | 1 | 1 | 1.16 | 4.41 | 3.81 | 1.93 |
| sp|Q52LJO-2|FA98B_HUMAN Isoform 2 of Protein FAM98B | Homo sapiens | 9606 | FAM98B | 1 | 1 | 1.16 | 1.48 | 1.28 | 0.35 |
| tr|A0A140TA73|A0A140TA73_HUMAN Beta-2-syntrophin (Fragment) | Homo sapiens | 9606 | SNTB2 | 1 | 1 | 1.15 | 1.06 | 0.92 | -0.12 |
| sp|Q969S3|ZN622_HUMAN Zinc finger protein 622 | Homo sapiens | 9606 | ZNF622 | 1 | 1 | 1.13 | 4.04 | 3.58 | 1.84 |
| tr|A0A087WWY3|A0A087WWY3_HUMAN Filamin-A | Homo sapiens | 9606 | FLNA | 1 | 1 | 1.13 | 4.08 | 3.62 | 1.86 |
| sp|P09914-2|IFIT1_HUMAN Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 1 | Homo sapiens | 9606 | IFIT1 | 1 | 1 | 1.12 | 2.32 | 2.07 | 1.05 |
| sp|P38432|COIL_HUMAN Coilin | Homo sapiens | 9606 | COIL | 1 | 1 | 1.11 | 1.67 | 1.50 | 0.59 |
| sp|Q9BV44|THUM3_HUMAN THUMP domain-containing protein 3 | Homo sapiens | 9606 | THUMP3 | 1 | 1 | 1.11 | 2.15 | 1.94 | 0.95 |
| sp|Q9Y6Y0|NS1BP_HUMAN Influenza virus NS1A-binding protein | Homo sapiens | 9606 | IVNS1ABP | 1 | 3 | 1.07 | 1.59 | 1.50 | 0.58 |
| sp|Q8IYS1|P20D2_HUMAN Peptidase M20 domain-containing protein 2 | Homo sapiens | 9606 | PM20D2 | 1 | 2 | 1.06 | 2.23 | 2.10 | 1.07 |
| Accession   | Description                                                                 | OS       | Symbol   | Gene Name   | PE | SV | Ratio1 | Ratio2 | Ratio3 | Ratio4 |
|-------------|------------------------------------------------------------------------------|----------|----------|-------------|----|----|--------|--------|--------|--------|
| sp|Q96D15|RCN3_HUMAN Reticulocalbin-3                                                   | Homo sapiens | RCN3   | 1   | 0.20 | 0.20  | -2.35 |
| tr|A0A1W2PPX5|A0A1W2PPX5_HUMAN Lysosome membrane protein 2                                 | Homo sapiens | SCARB2 | 1   | 3.83 | 3.69  | 1.88 |
| sp|Q7Z402|HEAT3_HUMAN HEAT repeat-containing protein 3                                 | Homo sapiens | HEATR3 | 2   | 2.34 | 2.26  | 1.18 |
| tr|D6W592|D6W592_HUMAN Heterogeneous nuclear ribonucleoprotein L-like, isoform CRA_d | Homo sapiens | HNRNPLL| 1   | 0.68 | 0.66  | -0.60 |
| sp|Q9NPQ8|RIC8A_HUMAN Isoform 2 of Synembryn-A                                          | Homo sapiens | RIC8A  | 1   | 1.01 | 3.17  | 1.66 |
| sp|Q08AM6|VAC14_HUMAN Protein VAC14 homolog                                            | Homo sapiens | VAC14  | 1   | 2.07 | 2.06  | 1.04 |
| sp|P53396-2|ACLY_HUMAN Isoform 2 of ATP-citrate synthase                                 | Homo sapiens | ALCY   | 1   | 6.43 | 6.57  | 2.72 |
| tr|A0A087WW40|A0A087WW40_HUMAN Endophilin-B1                                                | Homo sapiens | SH3GLB1| 1   | 2.90 | 2.97  | 1.57 |
| sp|Q9BTE3-2|MCMBP_HUMAN Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens | MCMBP   | 1   | 4.76 | 4.92  | 2.30 |
| sp|Q9Y5A9-2|YTHD2_HUMAN Isoform 2 of YTH domain-containing family protein 2               | Homo sapiens | YTHDF2 | 1   | 4.22 | 4.37  | 2.13 |
| sp|Q15061|WDR43_HUMAN WD repeat-containing protein 43                                   | Homo sapiens | WDR43  | 3   | 0.16 | 0.17  | -2.54 |
| tr|H7BZI9|H7BZI9_HUMAN ATP-binding cassette sub-family A member 13 (Fragment)           | Homo sapiens | ABCA13 | 1   | 6.81 | 7.16  | 2.84 |
| sp|P61964|WDR5_HUMAN WD repeat-containing protein 5                                     | Homo sapiens | WDR5   | 1   | 5.12 | 5.39  | 2.43 |
| tr|E9PKP7|E9PKP7_HUMAN Nucleolar transcription factor 1                                 | Homo sapiens | UBTF   | 1   | 3.72 | 3.92  | 1.97 |
| sp|P50570-2|DYN2_HUMAN Isoform 2 of Dynamin-2                                             | Homo sapiens | DNM2   | 1   | 1.56 | 1.65  | 0.73 |
| sp|Q8IU81|I2BP1_HUMAN Interferon regulatory factor 2-binding protein 1                   | Homo sapiens | IRF2BP1| 1   | 3.76 | 4.01  | 2.00 |
| tr|Q5TDF0|Q5TDF0_HUMAN Cancer-related nucleoside-triphosphatase OS=Homo sapiens         | Homo sapiens | NTPCR  | 1   | 3.92 | 4.18  | 2.06 |
| Accession       | Description                                                                 | OS     | OX    | GN     | PE   | SV  | Score | E-value | Score | E-value | Score | E-value | Score | E-value |
|-----------------|------------------------------------------------------------------------------|--------|------|--------|------|-----|-------|--------|-------|--------|-------|--------|-------|---------|
| tr|M0QZX5|M0QZX5_HUMAN Acetolactate synthase-like protein (Fragment) OS=Homo sapiens   | 0.94   | 2.45 | 2.62   | 1.39 |     |       |        |       |        |       |        |       |         |
| tr|B5ME19|EIFCL_HUMAN Eukaryotic translation initiation factor 3 subunit C-like protein| 0.90   | 5.97 | 6.61   | 2.72 |     |       |        |       |        |       |        |       |         |
| sp|Q9UBD5-2|ORC3_HUMAN Isoform 2 of Origin recognition complex subunit 3 OS=Homo sapiens | 0.88   | 2.19 | 2.49   | 1.32 |     |       |        |       |        |       |        |       |         |
| sp|P50416-2|CPT1A_HUMAN Isoform 2 of Carnitine O-palmitoyltransferase 1, liver isofrom OS=Homo sapiens | 0.86   | 0.12 | 0.14   | -2.88 |     |       |        |       |        |       |        |       |         |
| tr|F5GZF0|F5GZF0_HUMAN Cyclin-dependent kinase 2-associated protein 1 (Fragment) OS=Homo sapiens | 0.86   | 4.41 | 5.12   | 2.36 |     |       |        |       |        |       |        |       |         |
| tr|E5RHX8|E5RHX8_HUMAN Transcription and mRNA export factor ENY2 OS=Homo sapiens        | 0.86   | 4.14 | 4.82   | 2.27 |     |       |        |       |        |       |        |       |         |
| tr|Q5H907|Q5H907_HUMAN Melanoma antigen family D, 2, isoform CRA_d OS=Homo sapiens      | 0.85   | 5.54 | 6.54   | 2.71 |     |       |        |       |        |       |        |       |         |
| tr|A0A0D9SG72|A0A0D9SG72_HUMAN Syntaxin-binding protein 1 OS=Homo sapiens OS=Homo sapiens  | 0.84   | 1.13 | 1.34   | 0.42 |     |       |        |       |        |       |        |       |         |
| sp|Q96TA2-2|YMEL1_HUMAN Isoform 2 of ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens | 0.83   | 6.06 | 7.34   | 2.88 |     |       |        |       |        |       |        |       |         |
| tr|H0YCA5|H0YCA5_HUMAN Spermatogenesis-associated protein 5-like protein 1 (Fragment) OS=Homo sapiens | 0.81   | 0.97 | 1.20   | 0.26 |     |       |        |       |        |       |        |       |         |
| sp|P30837|AL1B1_HUMAN Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens          | 0.81   | 3.18 | 3.94   | 1.98 |     |       |        |       |        |       |        |       |         |
| sp|Q96EY7|PTCD3_HUMAN Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens | 0.81   | 2.66 | 3.30   | 1.72 |     |       |        |       |        |       |        |       |         |
| sp|Q15172-2|2A5A_HUMAN Isoform 2 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform OS=Homo sapiens | 0.80   | 1.96 | 2.46   | 1.30 |     |       |        |       |        |       |        |       |         |
| tr|H0YJV7|H0YJV7_HUMAN Transcriptional repressor protein YY1 (Fragment) OS=Homo sapiens | 0.79   | 3.35 | 4.25   | 2.09 |     |       |        |       |        |       |        |       |         |
| tr|H3BPK7|H3BPK7_HUMAN Alanine--tRNA ligase, cytoplasmic (Fragment) OS=Homo sapiens OS=Homo sapiens | 0.77   | 1.75 | 2.26   | 1.18 |     |       |        |       |        |       |        |       |         |
| tr|R4GN94|R4GN94_HUMAN Ankyrin repeat and SOCS box protein 9 (Fragment) OS=Homo sapiens | 0.76   | 2.02 | 2.65   | 1.41 |     |       |        |       |        |       |        |       |         |
| Accession | Description | species | organism | gene | protein | variation | expression |
|-----------|-------------|---------|----------|------|---------|-----------|------------|
| tr|I3L387|I3L387_HUMAN Serine/threonine-protein kinase PLK1 OS=Homo sapiens OX=9606 GN=PLK1 PE=1 SV=1 | 0.75 | 1.62 | 2.16 | 1.11 |
| tr|A0A024RCR6|A0A024RCR6_HUMAN HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens OX=9606 GN=BAG6 PE=1 SV=1 | 0.75 | 1.40 | 1.87 | 0.91 |
| sp|Q9UKX7|NUP50_HUMAN Isoform 2 of Nuclear pore complex protein Nup50 OS=Homo sapiens OX=9606 GN=NUP50 | 0.72 | 5.18 | 7.19 | 2.85 |
| sp|Q9NXF1|TEX10_HUMAN Isoform 2 of Testis-expressed protein 10 OS=Homo sapiens OX=9606 GN=TEX10 | 0.71 | 2.85 | 4.02 | 2.01 |
| tr|A0A0A0MSI8|A0A0A0MSI8_HUMAN Exocyst complex component 5 OS=Homo sapiens OX=9606 GN=EXOC5 PE=1 SV=1 | 0.70 | 1.99 | 2.84 | 1.51 |
| sp|Q9UKR5|ERG28_HUMAN Probable ergosterol biosynthetic protein 28 OS=Homo sapiens OX=9606 GN=ERG28 PE=1 SV=1 | 0.70 | 1.78 | 2.54 | 1.34 |
| tr|A0A0A0MRE1|A0A0A0MRE1_HUMAN Exocyst complex component 7 (Fragment) OS=Homo sapiens OX=9606 GN=EXOC7 PE=1 SV=1 | 0.70 | 4.70 | 6.71 | 2.75 |
| tr|F5H7C2|F5H7C2_HUMAN Death domain-containing protein CRADD OS=Homo sapiens OX=9606 GN=CRADD PE=1 SV=1 | 0.68 | 2.00 | 2.93 | 1.55 |
| sp|Q9BT67|NDFIP1_HUMAN NEDD4 family-interacting protein 1 OS=Homo sapiens OX=9606 GN=NDFIP1 PE=1 SV=1 | 0.68 | 0.04 | 0.06 | -0.41 |
| tr|K7EP32|K7EP32_HUMAN UBX domain-containing protein 6 (Fragment) OS=Homo sapiens OX=9606 GN=UBXN6 PE=1 SV=1 | 0.67 | 2.17 | 3.23 | 1.69 |
| tr|H3BP20|H3BP20_HUMAN Beta-hexosaminidase OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=1 | 0.65 | 2.67 | 4.12 | 2.04 |
| sp|Q9UH99|SUN2_HUMAN Isoform 2 of SUN domain-containing protein 2 OS=Homo sapiens OX=9606 GN=SUN2 | 0.62 | 1.35 | 2.18 | 1.12 |
| sp|P41214|EIF2D_HUMAN Isoform 2 of Eukaryotic translation initiation factor 2D OS=Homo sapiens OX=9606 GN=EIF2D | 0.61 | 0.34 | 0.55 | -0.85 |
| sp|Q96G46|DUS3L_HUMAN Isoform 3 of tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like OS=Homo sapiens OX=9606 GN=DUS3L | 0.61 | 2.50 | 4.10 | 2.03 |
| sp|Q9H1E5|TMX4_HUMAN Thioredoxin-related transmembrane protein 4 OS=Homo sapiens OX=9606 GN=TMX4 PE=1 SV=1 | 0.61 | 1.62 | 2.66 | 1.41 |
| tr|A0A087WUL4|A0A087WUL4_HUMAN Retrotransposon-derived protein PEG10 OS=Homo sapiens OX=9606 GN=PEG10 PE=1 SV=1 | 0.61 | 3.69 | 6.09 | 2.61 |
| tr|H0UI80|H0UI80_HUMAN Negative elongation factor C/D OS=Homo sapiens OX=9606 GN=NELFCD PE=1 SV=1 | 0.60 | 1.55 | 2.60 | 1.38 |
| Accession | Description                                                                 | OS    | OX   | GN        | PE | SV | Value1 | Value2 | Value3 | Value4 |
|-----------|------------------------------------------------------------------------------|-------|------|-----------|----|----|--------|--------|--------|--------|
| sp|Q9H900-2|ZWILC_HUMAN Isoform 2 of Protein zwilch homolog | Homo sapiens | 9606 | ZWILCH | 0.57 | 1.46 | 2.56 | 1.35 |
| sp|Q15053|K0040_HUMAN Uncharacterized protein KIAA0040 | Homo sapiens | 9606 | KIAA0040 | 0.56 | 0.60 | 1.07 | 0.10 |
| sp|Q8N584-2|TT39C_HUMAN Isoform 2 of Tetratricopeptide repeat protein 39C | Homo sapiens | 9606 | TTC39C | 0.54 | 2.68 | 4.93 | 2.30 |
| tr|K7EP90|K7EP90_HUMAN RNA-binding protein 42 | Homo sapiens | 9606 | RBM42 | 0.53 | 1.27 | 2.40 | 1.26 |
| sp|Q9UID3|VPS51_HUMAN Isoform 2 of Vacuolar protein sorting-associated protein 51 homolog | Homo sapiens | 9606 | VPS51 | 0.52 | 1.60 | 3.10 | 1.63 |
| sp|Q99808|S29A1_HUMAN Isoform 2 of Equilibrative nucleoside transporter 1 OS=Homo sapiens | 9606 | SLC29A1 | 0.50 | 1.47 | 2.94 | 1.56 |
| sp|Q75394|RM33_HUMAN 39S ribosomal protein L33, mitochondrial | Homo sapiens | 9606 | MRPL33 | 0.50 | 2.70 | 5.44 | 2.44 |
| sp|Q9H773|DCTP1_HUMAN dCTP pyrophosphatase 1 | Homo sapiens | 9606 | DCTPP1 | 0.50 | 2.20 | 4.43 | 2.15 |
| sp|Q8IXI1|MIRO2_HUMAN Mitochondrial Rho GTPase 2 OS=Homo sapiens | 9606 | RHOT2 | 0.43 | 1.87 | 4.35 | 2.12 |
| sp|Q27J81|INF2_HUMAN Isoform 2 of Inverted formin-2 | Homo sapiens | 9606 | INF2 | 0.43 | 0.84 | 1.96 | 0.97 |
| sp|P18084|ITB5_HUMAN Integrin beta-5 OS=Homo sapiens | 9606 | ITGB5 | 0.41 | 0.86 | 2.08 | 1.06 |
| sp|Q5T6V5|QSPP_HUMAN Queuosine salvage protein OS=Homo sapiens | 9606 | C9orf64 | 0.30 | 2.23 | 7.31 | 2.87 |
| sp|Q9NUY8|TBC23_HUMAN Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens | 9606 | TBC1D23 | 0.24 | 0.71 | 2.90 | 1.54 |
| tr|H3BMX9|H3BMX9_HUMAN PSME3-interacting protein (Fragment) | Homo sapiens | 9606 | FAM192A | 0.22 | 0.73 | 3.37 | 1.75 |
| tr|A0A2R8YD95|A0A2R8YD95_HUMAN Vacuolar protein sorting-associated protein 45 | Homo sapiens | 9606 | VPS45 | 0.18 | 1.30 | 7.03 | 2.81 |
| sp|Q5F1R6|DJC21_HUMAN Isoform 2 of DnaJ homolog subfamily C member 21 OS=Homo sapiens | 9606 | DNAJC21 | 0.13 | 0.27 | 2.01 | 1.01 |
| tr|A0A0A0MTL5|A0A0A0MTL5_HUMAN S-phase kinase-associated protein 2 OS=Homo sapiens | 9606 | SKP2 | 0.12 | 0.73 | 6.10 | 2.61 |
| Parameter                          | Value                                      |
|-----------------------------------|--------------------------------------------|
| **Full scan**                     |                                            |
| Scan range                        | 350-1700 m/z                               |
| Micro-scans                       | 1                                          |
| Resolution                        | 60,000                                     |
| Lock mass                         | 445.120025 m/z (polysiloxane)              |
| Data mode                         | Profile                                    |
| AGC target                        | 3.00E+06                                   |
| Maximum IT                        | 50ms                                       |
| **dd-MS2**                        |                                            |
| Micro-scans                       | 1                                          |
| Resolution                        | 15,000                                     |
| Data mode                         | Centroid                                   |
| AGC target                        | 1.00E+05                                   |
| Maximum IT                        | 30ms                                       |
| Top N                             | 12                                         |
| MSX                               | no                                         |
| Isolation window                  | 1.6 m/z                                    |
| Fixed first mass                  | 140 m/z                                    |
| NCE (no stepped NCE)              | 25                                         |
| Apex trigger                      | off                                        |
| Charge exclusion                  | Unassigned, 1 and >8                       |
| Peptide match                     | Off                                        |
| Exclude isotopes                  | On                                         |
| Dynamic exclusion                 | 30s                                        |
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