

| Accession Number | Description | Fold Enrichment | UniquePeptideCount |
|------------------|--|-----------------|--------------------|
| Q15648 | Mediator of RNA polymerase II transcription subunit 1 | 4.41 | 6 |
| O95711 | E3 ubiquitin-protein ligase UBR5 | 1.91 | 2 |
| ORUXG8 | Butyrophilin-like protein 9 | 1.75 | 2 |
| Q96KN7 | X-linked retinitis pigmentosa GTPase regulator-interacting protein 1 | 1.58 | 2 |
| Q13765 | Nascent polypeptide-associated complex subunit alpha | 1.57 | 1 |
| Q96HL8 | SH3 domain-containing YSC84-like protein 1 | 1.23 | 1 |
| O723E5 | LisH domain-containing protein ARMC9 | 1.14 | 1 |
| UB84Z6 | Ubiquitin C | 1.12 | 2 |
| Q9NSD7 | Relaxin-3 receptor 1 | 1.11 | 2 |
| O95789 | Zinc finger MYM-type protein 6 | 1.09 | 1 |
| Q9BTV4 | Transmembrane protein 43 | 1.08 | 1 |
| P30101 | Protein disulfide-isomerase A3 | 1.08 | 2 |
| P19429 | Troponin I cardiac muscle | 1.07 | 2 |
| P60174 | Triosephosphate isomerase | 1.06 | 1 |
| P54284 | Voltage-dependent L-type calcium channel subunit beta-3 | 1.00 | 1 |
| P35637 | RNA-binding protein FUS | 0.99 | 3 |
| O15205 | Ubiquitin D | 0.95 | 1 |
| P81978 | Heterogeneous nuclear ribonucleoprotein K | 0.93 | 7 |
| Q9Y4F1 | FERM RhoGEF and pleckstrin domain-containing protein 1 | 0.92 | 1 |
| P00558 | Phosphoglycerate kinase 1 | 0.92 | 2 |
| P53396 | ATP-citrate synthase | 0.88 | 1 |
| P13509 | Tubulin beta-3 chain | 0.88 | 15 |
| O60391 | Glutamate receptor ionotropic NMDA 3B | 0.85 | 1 |
| P62937 | Peptidyl-prolyl cis-trans isomerase A | 0.84 | 2 |
| P28907 | ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1 | 0.84 | 1 |
| P52597 | Heterogeneous nuclear ribonucleoprotein F | 0.83 | 5 |
| P17707 | S-adenosylmethionine decarboxylase proenzyme | 0.83 | 2 |
| Q15436 | Protein transport protein Sec23A | 0.81 | 2 |
| ADP123 | Glucoside xylosyltransferase 2 | 0.81 | 1 |
| Q04828 | Aldo-keto reductase family 1 member C1 | 0.80 | 1 |
| Q86WA8 | Lon protease homolog 2 peroxisomal | 0.79 | 1 |
| Q9UHX1 | Poly(U)-binding-splicing factor PUF60 | 0.78 | 1 |
| O43175 | D-3-phosphoglycerate dehydrogenase | 0.76 | 2 |
| Q9HCC0 | Methylcrotonyl-CoA carboxylase beta chain mitochondrial | 0.76 | 1 |
| Q16647 | Prostacyclin synthase | 0.76 | 2 |
| Q13838 | Spliceosome RNA helicase DDX39B | 0.75 | 2 |
| P55796 | Puromycin-sensitive aminopeptidase | 0.74 | 1 |
| Q86VG8 | Kinesin-like protein KIFC3 | 0.74 | 6 |
| P32119 | Peroxiredoxin-2 | 0.74 | 2 |
| P01712 | Ig lambda chain V-II region WIN | 0.73 | 2 |
| E1P5S2 | RNA-binding region (RNP1 RRM) containing 2 isoform CRA_b | 0.72 | 1 |
| P14869 | Aspartate--RNA ligase cytoplasmic | 0.72 | 3 |
| O43497 | Voltage-dependent L-type calcium channel subunit alpha-1G | 0.72 | 1 |
| B4EDN9 | Glutamate dehydrogenase | 0.70 | 2 |
| J3QR09 | Ribosomal protein L19 | 0.69 | 1 |
| P10809 | 60 kDa heat shock protein mitochondrial | 0.69 | 13 |
| P05388 | 60S acidic ribosomal protein P0 | 0.68 | 2 |
| P07137 | Pofillin-1 | 0.68 | 2 |
| P48643 | T-complex protein 1 subunit epsilon | 0.67 | 3 |
| P62277 | 40S ribosomal protein S13 | 0.65 | 1 |
| O95793 | Double-stranded RNA-binding protein Staufen homolog 1 | 0.65 | 3 |
| P27694 | Replication protein A 70 kDa DNA-binding subunit | 0.64 | 2 |
| P23528 | Cofilin-1 | 0.63 | 1 |
| Q14103 | Heterogeneous nuclear ribonucleoprotein D0 | 0.63 | 3 |
| Q9H1C3 | Glycosyltransferase 8 domain-containing protein 2 | 0.62 | 1 |
| P31483 | Nucleolysin TIA-1 isoform p40 | 0.62 | 1 |
| P41252 | Isoleucine--tRNA ligase cytoplasmic | 0.62 | 2 |
| P63261 | Actin cytoplasmic 2 | 0.61 | 19 |
| R49411 | Elongation factor Tu mitochondrial | 0.58 | 8 |
| Q9P2E9 | Ribosome-binding protein 1 | 0.58 | 2 |
| O75369 | Filamin-B | 0.56 | 1 |
| Q3LXA3 | Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cycling) | 0.55 | 2 |
| Q7L014 | Probable ATP-dependent RNA helicase DDX46 | 0.55 | 1 |
| Q27325 | C-X-C motif chemokine 9 | 0.54 | 2 |
| Q5V7E0 | Putative elongation factor 1-alpha-like 3 | 0.53 | 7 |
| P56192 | Methionine--tRNA ligase cytoplasmic | 0.53 | 1 |
| P68371 | Tubulin beta-4B chain | 0.52 | 20 |
| P23396 | 40S ribosomal protein S3 | 0.51 | 3 |
| P06576 | ATP synthase subunit beta mitochondrial | 0.51 | 6 |
| Q96PK6 | RNA-binding protein 14 | 0.50 | 1 |
| Q8N6C5 | Immunoglobulin superfamily member 1 | 0.50 | 1 |
| P14618 | Pyruvate kinase PKM | 0.49 | 6 |
| P36542 | ATP synthase subunit gamma mitochondrial | 0.49 | 2 |
| O96EY1 | DnaJ homolog subfamily A member 3 mitochondrial | 0.49 | 2 |
| P22081 | Protein-L-isoaspartate(D-aspartate) O-methyltransferase | 0.48 | 16 |
| P02545 | Prelamin-A/C | 0.48 | 1 |
| P49327 | Fatty acid synthase | 0.48 | 5 |
| P06733 | Alpha-enolase | 0.47 | 9 |
| P62929 | 60S ribosomal protein L23 | 0.46 | 1 |
| P07437 | Tubulin beta chain | 0.46 | 18 |
| P38646 | Stress-70 protein mitochondrial | 0.45 | 3 |
| Q99623 | Prohibitin-2 n=7 Tax=Euarchontoglires RepID=PHB2_HUMAN | 0.45 | 2 |
| P05783 | Keratin type I cytoskeletal 18 | 0.45 | 16 |
| P49368 | T-complex protein 1 subunit gamma | 0.44 | 1 |
| Q13268 | Dehydrogenase/reductase SDR family member 2 mitochondrial | 0.43 | 8 |
| Q92841 | Probable ATP-dependent RNA helicase DDX17 | 0.43 | 2 |
| Q06520 | Bile salt sulfotransferase | 0.43 | 1 |
| P07237 | Protein disulfide-isomerase | 0.43 | 2 |
| P44496 | Glyceraldehyde-3-phosphate dehydrogenase | 0.43 | 4 |
| P04075 | Fructose-bisphosphate aldolase A | 0.43 | 3 |
| P68363 | Tubulin alpha-1B chain | 0.42 | 14 |
| P17987 | T-complex protein 1 subunit alpha | 0.41 | 1 |
| O00571 | ATP-dependent RNA helicase DDX3X | 0.40 | 5 |
| P31943 | Heterogeneous nuclear ribonucleoprotein H | 0.39 | 6 |
| P14625 | Endoplasmic | 0.38 | 4 |
| P45880 | Voltage-dependent anion-selective channel protein 2 | 0.38 | 1 |
| Q06830 | Peroxiredoxin-1 | 0.37 | 2 |
| Q567R6 | Single-stranded DNA-binding protein | 0.37 | 1 |
| Q15984 | Protein disulfide-isomerase A6 | 0.37 | 2 |
| Q9N216 | Insulin-like growth factor 2 mRNA-binding protein 1 | 0.36 | 2 |
| P01024 | Complement C3 | 0.36 | 1 |
| Q15365 | Poly(rC)-binding protein 1 | 0.36 | 3 |
| Q14847 | LIM and SH3 domain protein 1 | 0.35 | 2 |
| P11021 | 78 kDa glucose-regulated protein | 0.34 | 18 |
| P54136 | Arginine--tRNA ligase cytoplasmic | 0.33 | 2 |
| D3DPG0 | Titin isoform CRA_a | 0.33 | 2 |
| O75379 | Vesicle-associated membrane protein 4 | 0.30 | 1 |
| O60701 | UDP-glucose 6-dehydrogenase | 0.29 | 4 |
| P63244 | Guanine nucleotide-binding protein subunit beta-2-like 1 | 0.28 | 1 |
| P02679 | Fibrinogen gamma chain | 0.28 | 4 |
| P05141 | ADP/ATP translocase 2 | 0.25 | 2 |
| P60842 | Eukaryotic initiation factor 4A-I | 0.24 | 1 |
| P05787 | Keratin type II cytoskeletal 8 | 0.24 | 13 |
| Q1KMD3 | Heterogeneous nuclear ribonucleoprotein U-like protein 2 | 0.24 | 1 |
| P11142 | Heat shock cognate 71 kDa protein | 0.23 | 4 |
| P02769 | Serum albumin | 0.23 | 64 |
| P08107 | Heat shock 70 kDa protein 1A1B | 0.22 | 3 |
| P31942 | Heterogeneous nuclear ribonucleoprotein H3 | 0.21 | 1 |
| P51659 | Peroxisomal multifunctional enzyme type 2 | 0.21 | 12 |
| P07814 | Bifunctional glutamateproline--tRNA ligase | 0.21 | 5 |
| P07900 | Heat shock protein HSP 90-alpha | 0.21 | 1 |
| P15924 | Desmoplakin | 0.20 | 6 |
| A2NUT2 | Lambda-chain (AA_20 to 215) | 0.20 | 2 |
| P02671 | Fibrinogen alpha chain | 0.19 | 4 |
| P06727 | Keratin type I cytoskeletal 19 | 0.19 | 3 |
| Q13151 | Heterogeneous nuclear ribonucleoprotein A0 | 0.18 | 2 |
| P19474 | E3 ubiquitin-protein ligase TRIM21 | 0.16 | 4 |
| Q00839 | Heterogeneous nuclear ribonucleoprotein U | 0.16 | 2 |
| P08238 | Heat shock protein HSP 90-beta | 0.15 | 2 |
| P52272 | Heterogeneous nuclear ribonucleoprotein M | 0.13 | 1 |
| P04264 | Keratin type II cytoskeletal 1 | 0.13 | 13 |
| Q15058 | Kinesin-like protein KIF14 | 0.13 | 7 |
| Q149N6 | Dedicator of cytokinesis 4 | 0.12 | 4 |
| P06748 | Nucleophosmin | 0.12 | 1 |
| P02768 | Serum albumin | 0.12 | 4 |
| P35906 | Keratin type II cytoskeletal 2 epidermal | 0.12 | 8 |
| P35527 | Keratin type I cytoskeletal 9 | 0.10 | 6 |
| P13645 | Keratin type I cytoskeletal 10 | 0.07 | 4 |
| Q9BUJ2 | Heterogeneous nuclear ribonucleoprotein U-like protein 1 | 0.06 | 1 |