

Title: Tear Proteins Calcium binding protein A4 (S100A4) and Prolactin Induced Protein (PIP) are Potential Biomarkers for Thyroid Eye Disease

Authors: Chiaw-Ling Chng, Lay Leng Seah, Morgan Yang, Shen Yu Sunny, Siew Kwan Koh, Yan Gao, Lu Deng, Louis Tong, Roger Wilmer Beuerman, Lei Zhou

| Up regulated proteins | | |
|--------------------------------|---|----------------|
| Gene Symbol | Fold Change (geometric mean) | p-value |
| ALDH3A1 | 3.972 | 0.020 |
| RARRES1 | 2.193 | 0.019 |
| CHMP4B | 1.705 | 0.013 |
| Down regulated proteins | | |
| Gene Symbol | Fold Change (geometric mean) | p-value |
| TF | 0.092 | 0.003 |
| IGHG4 | 0.095 | 0.013 |
| ALB | 0.120 | 0.014 |
| LTF | 0.126 | 0.003 |
| APOA2 | 0.128 | 0.046 |
| SERPINA1 | 0.139 | 0.006 |
| A1BG | 0.164 | 0.035 |
| APOA1 | 0.173 | 0.043 |
| PLA2G2A | 0.178 | 0.040 |
| AGR2 | 0.184 | 0.030 |
| ORM1 | 0.188 | 0.027 |
| HPX | 0.206 | 0.015 |
| GC | 0.216 | 0.019 |
| PRDX5 | 0.271 | 0.036 |
| ITIH1 | 0.398 | 0.046 |
| LAP3 | 0.447 | 0.043 |
| SERPINC1 | 0.468 | 0.05 |
| AHSG | 0.530 | 0.031 |

Supplemental Table S1. Three up- and 18 down- regulated tear proteins in AITD vs normal controls (fold change > 1.5, or < 0.67, p value < 0.05).

| Up regulated proteins | | |
|--------------------------------|---|----------------|
| Gene Symbol | Fold Change (geometric mean) | p-value |
| LACRT | 4.605 | 0.031 |
| LYZ | 3.363 | 0.045 |
| MSLN | 3.285 | 0.028 |
| AZGP1 | 3.089 | 0.046 |
| CLU | 2.415 | 0.030 |
| Down regulated proteins | | |
| Gene Symbol | Fold Change (geometric mean) | p-value |
| ADH1C | 0.077 | 0.007 |
| PRR4 | 0.098 | 0.027 |
| FBP1 | 0.179 | 0.001 |
| PPIA | 0.284 | 0.021 |
| AKR1C1 | 0.303 | 0.036 |
| PFN2 | 0.305 | 0.022 |
| PSMB9 | 0.306 | 0.046 |
| LAP3 | 0.332 | 0.004 |
| ENO1 | 0.336 | 0.045 |
| CAPG | 0.346 | 0.033 |
| HSPA1B;HSPA1A | 0.354 | 0.010 |
| PRDX1 | 0.357 | 0.021 |
| A2M | 0.375 | 0.010 |
| ANXA3 | 0.388 | 0.011 |
| SELENBP1 | 0.390 | 0.013 |
| APRT | 0.397 | 0.026 |
| TPI1;TPI1P1 | 0.399 | 0.011 |
| CALML3 | 0.401 | 0.034 |
| LDHA | 0.404 | 0.033 |
| NQO1 | 0.404 | 0.044 |
| ALDH1A3 | 0.417 | 0.005 |
| S100A6 | 0.432 | 0.007 |
| PKM2 | 0.436 | 0.026 |
| ALDOA | 0.442 | 0.010 |
| TKT | 0.447 | 0.008 |
| HSPB1 | 0.448 | 0.034 |
| AKR1A1 | 0.450 | 0.043 |
| CAP1 | 0.469 | 0.047 |
| CCT8 | 0.469 | 0.031 |
| UGP2 | 0.495 | 0.040 |
| ANXA5 | 0.505 | 0.029 |

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|-------|-------|-------|
| PRDX2 | 0.506 | 0.044 |
| YWHAZ | 0.508 | 0.003 |
| PARK7 | 0.511 | 0.034 |
| YWHAB | 0.522 | 0.005 |
| GSTO1 | 0.534 | 0.019 |
| ORM1 | 0.544 | 0.043 |
| VCL | 0.548 | 0.014 |
| GBE1 | 0.560 | 0.037 |
| TYMP | 0.563 | 0.045 |
| SORD | 0.575 | 0.007 |
| HSPA8 | 0.593 | 0.032 |
| PGK1 | 0.594 | 0.030 |
| GSS | 0.608 | 0.020 |
| CMPK1 | 0.625 | 0.005 |
| SFN | 0.636 | 0.025 |

Supplemental Table S2. Five up- and 46 down- regulated tear proteins in mild TED vs normal controls (fold change > 1.5, or < 0.67, p value < 0.05).

| Up regulated proteins | | |
|--------------------------------|---|----------------|
| Gene Symbol | Fold Change (geometric mean) | p-value |
| PRR4;PRH2;PRH1 | 13.996 | 0.000 |
| LACRT | 7.122 | 0.002 |
| AZGP1 | 5.535 | 0.007 |
| LYZ | 4.891 | 0.029 |
| IGHA1 | 4.813 | 0.017 |
| CLU | 4.622 | 0.002 |
| MSLN | 4.406 | 0.023 |
| PIP | 4.188 | 0.023 |
| CST4 | 3.929 | 0.005 |
| PIGR | 3.316 | 0.041 |
| CHI3L2 | 3.078 | 0.007 |
| LGALS3BP | 2.658 | 0.005 |
| HSPG2 | 2.626 | 0.003 |
| IGJ | 2.251 | 0.049 |
| PLTP | 2.173 | 0.026 |
| C4orf40 | 2.152 | 0.027 |
| SCGB2A1 | 2.012 | 0.041 |
| TCN1 | 2.010 | 0.048 |
| IGKV2-30 | 1.994 | 0.032 |
| CST3 | 1.965 | 0.038 |
| IGLV3-19 | 1.895 | 0.049 |
| GOLM1 | 1.831 | 0.036 |
| IGKV3D-15 | 1.731 | 0.023 |
| IGLV1-47 | 1.614 | 0.021 |
| Down regulated proteins | | |
| Gene Symbol | Fold Change (geometric mean) | p-value |
| ANXA5 | 0.189 | 0.005 |
| IGHG2 | 0.210 | 0.035 |
| ENO1 | 0.231 | 0.005 |
| TPI1;TPI1P1 | 0.242 | 0.018 |
| PGK1 | 0.251 | 0.002 |
| AKR1C1 | 0.260 | 0.037 |
| PRDX5 | 0.277 | 0.010 |
| CAPG | 0.284 | 0.004 |
| ALDH1A1 | 0.287 | 0.015 |
| PRDX1 | 0.288 | 0.003 |
| HSPA1B;HSPA1A | 0.291 | 0.006 |
| PSMA1 | 0.319 | 0.028 |

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| ASS1 | 0.321 | 0.018 |
| S100A6 | 0.327 | 0.001 |
| S100A4 | 0.332 | 0.029 |
| PRDX5 | 0.337 | 0.015 |
| TAGLN2 | 0.352 | 0.006 |
| LDHA | 0.355 | 0.007 |
| ADH1C | 0.362 | 0.026 |
| SELENBP1 | 0.370 | 0.014 |
| ALDOA | 0.380 | 0.012 |
| PARK7 | 0.383 | 0.017 |
| SORD | 0.385 | 0.023 |
| PSMB9 | 0.391 | 0.038 |
| PEBP1 | 0.400 | 0.000 |
| AGR2 | 0.411 | 0.014 |
| LXN | 0.424 | 0.011 |
| LAP3 | 0.431 | 0.021 |
| PPP1R7 | 0.434 | 0.044 |
| ORM2 | 0.442 | 0.020 |
| NAPRT1 | 0.453 | 0.003 |
| YWHAZ | 0.460 | 0.024 |
| FGG | 0.493 | 0.005 |
| TALDO1 | 0.503 | 0.016 |
| AKR1A1 | 0.504 | 0.000 |
| HSPA8 | 0.518 | 0.024 |
| HSP90AA1 | 0.532 | 0.023 |
| YWHAB | 0.534 | 0.020 |
| PCBD1 | 0.540 | 0.025 |
| FBP1 | 0.568 | 0.032 |
| IDH1 | 0.576 | 0.019 |
| SLC9A3R1 | 0.643 | 0.049 |
| RAB1B | 0.654 | 0.037 |
| PYGL | 0.662 | 0.023 |

Supplemental Table S3. Twenty-four up- and 44 down- regulated tear proteins in severe TED vs normal controls (fold change > 1.5, or < 0.67, p value < 0.05).

| N | Accession # | Protein Name | Unused Score | Peptides (> 95% confidence) |
|----|-------------|---|--------------|-----------------------------|
| 1 | P02788 | Lactotransferrin GN=LTF PE=1 SV=6 | 383.29 | 624 |
| 2 | P02768 | Serum albumin GN=ALB PE=1 SV=2 | 276.39 | 494 |
| 3 | P01024 | Complement C3 GN=C3 PE=1 SV=2 | 181.52 | 132 |
| 4 | P98160 | Basement membrane-specific heparan sulfate proteoglycan core protein GN=HSPG2 PE=1 SV=4 | 149.27 | 80 |
| 5 | P01876 | Ig alpha-1 chain C region GN=IGHA1 PE=1 SV=2 | 148.04 | 222 |
| 6 | P01833 | Polymeric immunoglobulin receptor GN=PIGR PE=1 SV=4 | 134.68 | 200 |
| 7 | P31025 | Lipocalin-1 GN=LCN1 PE=1 SV=1 | 127.41 | 303 |
| 8 | P01877 | Ig alpha-2 chain C region GN=IGHA2 PE=1 SV=3 | 125.96 | 188 |
| 9 | P61626 | Lysozyme C GN=LYZ PE=1 SV=1 | 117.29 | 261 |
| 10 | P02787 | Serotransferrin GN=TF PE=1 SV=3 | 106.44 | 122 |
| 11 | Q9UGM3 | Deleted in malignant brain tumors 1 protein GN=DMBT1 PE=1 SV=2 | 93.12 | 88 |
| 12 | P00352 | Retinal dehydrogenase 1 GN=ALDH1A1 PE=1 SV=2 | 89.27 | 76 |
| 13 | P25311 | Zinc-alpha-2-glycoprotein GN=AZGP1 PE=1 SV=2 | 87.35 | 125 |
| 14 | P63261 | Actin, cytoplasmic 2 GN=ACTG1 PE=1 SV=1 | 78.99 | 106 |
| 15 | P21980 | Protein-glutamine gamma-glutamyltransferase 2 GN=TGM2 PE=1 SV=2 | 78.54 | 59 |
| 16 | P00450 | Ceruloplasmin GN=CP PE=1 SV=1 | 78.33 | 60 |
| 17 | P01023 | Alpha-2-macroglobulin GN=A2M PE=1 SV=3 | 77.53 | 43 |
| 18 | O43707 | Alpha-actinin-4 GN=ACTN4 PE=1 SV=2 | 76.54 | 50 |
| 19 | P60709 | Actin, cytoplasmic 1 GN=ACTB PE=1 SV=1 | 72.19 | 108 |

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|----|--------|--|-------|-----|
| 20 | P14618 | Pyruvate kinase PKM GN=PKM PE=1 SV=4 | 71.71 | 66 |
| 21 | P08107 | Heat shock 70 kDa protein 1A/1B GN=HSPA1A PE=1 SV=5 | 69.56 | 52 |
| 22 | P06733 | Alpha-enolase GN=ENO1 PE=1 SV=2 | 64.63 | 78 |
| 23 | Q13228 | Selenium-binding protein 1 GN=SELENBP1 PE=1 SV=2 | 60.9 | 43 |
| 24 | P01857 | Ig gamma-1 chain C region GN=IGHG1 PE=1 SV=1 | 60.73 | 69 |
| 25 | P0C0L5 | Complement C4-B GN=C4B PE=1 SV=2 | 60.51 | 33 |
| 26 | Q16378 | Proline-rich protein 4 GN=PRR4 PE=1 SV=3 | 59.72 | 83 |
| 27 | P0C0L4 | Complement C4-A GN=C4A PE=1 SV=2 | 59.16 | 33 |
| 28 | P06396 | Gelsolin GN=GSN PE=1 SV=1 | 56.86 | 57 |
| 29 | P07355 | Annexin A2 GN=ANXA2 PE=1 SV=2 | 54.92 | 42 |
| 30 | Q9GZZ8 | Extracellular glycoprotein lacritin GN=LACRT PE=1 SV=1 | 54.72 | 129 |
| 31 | P04083 | Annexin A1 GN=ANXA1 PE=1 SV=2 | 54.52 | 62 |
| 32 | P22314 | Ubiquitin-like modifier-activating enzyme 1 GN=UBA1 PE=1 SV=3 | 54.51 | 32 |
| 33 | P07900 | Heat shock protein HSP 90-alpha GN=HSP90AA1 PE=1 SV=5 | 54.42 | 30 |
| 34 | P30740 | Leukocyte elastase inhibitor GN=SERPINB1 PE=1 SV=1 | 53.84 | 58 |
| 35 | Q13421 | Mesothelin GN=MSLN PE=1 SV=2 | 52.42 | 42 |
| 36 | P00738 | Haptoglobin GN=HP PE=1 SV=1 | 52.12 | 45 |
| 37 | P01009 | Alpha-1-antitrypsin GN=SERPINA1 PE=1 SV=3 | 50.47 | 42 |
| 38 | P01859 | Ig gamma-2 chain C region GN=IGHG2 PE=1 SV=2 | 50.03 | 57 |
| 39 | P50395 | Rab GDP dissociation inhibitor beta GN=GDI2 PE=1 SV=2 | 48.43 | 28 |
| 40 | P13639 | Elongation factor 2 GN=EEF2 PE=1 SV=4 | 48.35 | 29 |

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|----|--------|---|-------|----|
| 41 | P00338 | L-lactate dehydrogenase A chain GN=LDHA PE=1 SV=2 | 48.08 | 39 |
| 42 | P68104 | Elongation factor 1-alpha 1 GN=EEF1A1 PE=1 SV=1 | 47.19 | 37 |
| 43 | O75556 | Mammaglobin-B GN=SCGB2A1 PE=1 SV=1 | 46.5 | 99 |
| 44 | P14550 | Alcohol dehydrogenase [NADP(+)] GN=AKR1A1 PE=1 SV=3 | 45.81 | 32 |
| 45 | P01834 | Ig kappa chain C region GN=IGKC PE=1 SV=1 | 44.1 | 90 |
| 46 | Q09666 | Neuroblast differentiation-associated protein AHNAK GN=AHNAK PE=1 SV=2 | 43.9 | 25 |
| 47 | P08603 | Complement factor H GN=CFH PE=1 SV=4 | 43.43 | 24 |
| 48 | P22079 | Lactoperoxidase GN=LPO PE=1 SV=2 | 42.92 | 33 |
| 49 | P06703 | Protein S100-A6 GN=S100A6 PE=1 SV=1 | 42.77 | 58 |
| 50 | P20061 | Transcobalamin-1 GN=TCN1 PE=1 SV=2 | 42.12 | 32 |
| 51 | Q99935 | Proline-rich protein 1 GN=PROL1 PE=1 SV=2 | 41.95 | 48 |
| 52 | P15311 | Ezrin GN=EZR PE=1 SV=4 | 41.83 | 31 |
| 53 | P00558 | Phosphoglycerate kinase 1 GN=PGK1 PE=1 SV=3 | 41.5 | 38 |
| 54 | Q7Z406 | Myosin-14 GN=MYH14 PE=1 SV=2 | 41.25 | 22 |
| 55 | P02790 | Hemopexin GN=HPX PE=1 SV=2 | 41.17 | 32 |
| 56 | P55072 | Transitional endoplasmic reticulum ATPase GN=VCP PE=1 SV=4 | 41.12 | 24 |
| 57 | P04406 | Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH PE=1 SV=3 | 40.71 | 41 |
| 58 | P12273 | Prolactin-inducible protein GN=PIP PE=1 SV=1 | 39.88 | 78 |
| 59 | Q96KP4 | Cytosolic non-specific dipeptidase GN=CNDP2 PE=1 SV=2 | 39.87 | 27 |
| 60 | Q06830 | Peroxiredoxin-1 GN=PRDX1 PE=1 SV=1 | 39.75 | 42 |
| 61 | P10909 | Clusterin GN=CLU PE=1 SV=1 | 39.67 | 37 |

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|----|--------|--|-------|----|
| 62 | P07384 | Calpain-1 catalytic subunit GN=CAPN1 PE=1 SV=1 | 39.44 | 24 |
| 63 | P09211 | Glutathione S-transferase P GN=GSTP1 PE=1 SV=2 | 39.28 | 56 |
| 64 | Q04828 | Aldo-keto reductase family 1 member C1 GN=AKR1C1 PE=1 SV=1 | 39.24 | 25 |
| 65 | P68371 | Tubulin beta-4B chain GN=TUBB4B PE=1 SV=1 | 38.91 | 27 |
| 66 | P26447 | Protein S100-A4 GN=S100A4 PE=1 SV=1 | 38.84 | 38 |
| 67 | O95968 | Secretoglobin family 1D member 1 GN=SCGB1D1 PE=1 SV=1 | 38.7 | 45 |
| 68 | P08238 | Heat shock protein HSP 90-beta GN=HSP90AB1 PE=1 SV=4 | 38.45 | 26 |
| 69 | P01871 | Ig mu chain C region GN=IGHM PE=1 SV=3 | 38.44 | 35 |
| 70 | P04075 | Fructose-bisphosphate aldolase A GN=ALDOA PE=1 SV=2 | 38.19 | 36 |
| 71 | P52209 | 6-phosphogluconate dehydrogenase, decarboxylating GN=PGD PE=1 SV=3 | 37.95 | 26 |
| 72 | P13645 | Keratin, type I cytoskeletal 10 GN=KRT10 PE=1 SV=6 | 37.88 | 25 |
| 73 | P06737 | Glycogen phosphorylase, liver form GN=PYGL PE=1 SV=4 | 37.69 | 25 |
| 74 | P08727 | Keratin, type I cytoskeletal 19 GN=KRT19 PE=1 SV=4 | 37.63 | 26 |
| 75 | P13797 | Plastin-3 GN=PLS3 PE=1 SV=4 | 37.54 | 22 |
| 76 | P28838 | Cytosol aminopeptidase GN=LAP3 PE=1 SV=3 | 37.37 | 21 |
| 77 | P30041 | Peroxiredoxin-6 GN=PRDX6 PE=1 SV=3 | 37.36 | 32 |
| 78 | P01037 | Cystatin-SN GN=CST1 PE=1 SV=3 | 37.07 | 67 |
| 79 | P07437 | Tubulin beta chain GN=TUBB PE=1 SV=2 | 36.29 | 27 |
| 80 | P00326 | Alcohol dehydrogenase 1C GN=ADH1C PE=1 SV=2 | 35.84 | 21 |

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|----|--------|--|-------|----|
| 81 | P11142 | Heat shock cognate 71 kDa protein GN=HSPA8 PE=1 SV=1 | 35.65 | 33 |
| 82 | P02774 | Vitamin D-binding protein GN=GC PE=1 SV=1 | 35.61 | 22 |
| 83 | Q08380 | Galectin-3-binding protein GN=LGALS3BP PE=1 SV=1 | 34.99 | 31 |
| 84 | Q6XQN6 | Nicotinate phosphoribosyltransferase GN=NAPRT PE=1 SV=2 | 34.84 | 20 |
| 85 | P04792 | Heat shock protein beta-1 GN=HSPB1 PE=1 SV=2 | 34.67 | 42 |
| 86 | P05109 | Protein S100-A8 GN=S100A8 PE=1 SV=1 | 34.37 | 48 |
| 87 | P35579 | Myosin-9 GN=MYH9 PE=1 SV=4 | 34.33 | 18 |
| 88 | P13489 | Ribonuclease inhibitor GN=RNH1 PE=1 SV=2 | 34.02 | 21 |
| 89 | P46940 | Ras GTPase-activating-like protein IQGAP1 GN=IQGAP1 PE=1 SV=1 | 34.01 | 18 |
| 90 | P04264 | Keratin, type II cytoskeletal 1 GN=KRT1 PE=1 SV=6 | 33.9 | 23 |
| 91 | P01036 | Cystatin-S GN=CST4 PE=1 SV=3 | 33.87 | 59 |
| 92 | P00390 | Glutathione reductase, mitochondrial GN=GSR PE=1 SV=2 | 33.66 | 22 |
| 93 | P30838 | Aldehyde dehydrogenase, dimeric NADP- preferring GN=ALDH3A1 PE=1 SV=3 | 33.24 | 32 |
| 94 | P13647 | Keratin, type II cytoskeletal 5 GN=KRT5 PE=1 SV=3 | 33.03 | 21 |
| 95 | P98088 | Mucin-5AC (Fragments) GN=MUC5AC PE=1 SV=3 | 32.81 | 18 |
| 96 | P55786 | Puromycin-sensitive aminopeptidase GN=NPEPPS PE=1 SV=2 | 32.14 | 17 |
| 97 | Q06323 | Proteasome activator complex subunit 1 GN=PSME1 PE=1 SV=1 | 32 | 19 |
| 98 | P00751 | Complement factor B GN=CFB PE=1 SV=2 | 31.49 | 19 |
| 99 | P62258 | 14-3-3 protein epsilon GN=YWHAE PE=1 SV=1 | 31 | 29 |

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|-----|--------|---|-------|----|
| 100 | P01008 | Antithrombin-III GN=SERPINC1 PE=1 SV=1 | 30.74 | 20 |
| 101 | P47895 | Aldehyde dehydrogenase family 1 member A3 GN=ALDH1A3 PE=1 SV=2 | 30.59 | 19 |
| 102 | P63104 | 14-3-3 protein zeta/delta GN=YWHAZ PE=1 SV=1 | 30.51 | 33 |
| 103 | P60174 | Triosephosphate isomerase GN=TPI1 PE=1 SV=3 | 30.46 | 33 |
| 104 | P30044 | Peroxiredoxin-5, mitochondrial GN=PRDX5 PE=1 SV=4 | 30.22 | 32 |
| 105 | P07237 | Protein disulfide-isomerase GN=P4HB PE=1 SV=3 | 30.08 | 18 |
| 106 | P01011 | Alpha-1-antichymotrypsin GN=SERPINA3 PE=1 SV=2 | 30.01 | 22 |
| 107 | O75083 | WD repeat-containing protein 1 GN=WDR1 PE=1 SV=4 | 29.55 | 17 |
| 108 | P20810 | Calpastatin GN=CAST PE=1 SV=4 | 29.44 | 17 |
| 109 | Q9H4A4 | Aminopeptidase B GN=RNPEP PE=1 SV=2 | 29.38 | 16 |
| 110 | Q01518 | Adenylyl cyclase-associated protein 1 GN=CAP1 PE=1 SV=5 | 29.32 | 19 |
| 111 | P36952 | Serpin B5 GN=SERPINB5 PE=1 SV=2 | 29.19 | 19 |
| 112 | P01591 | Immunoglobulin J chain GN=IGJ PE=1 SV=4 | 28.95 | 32 |
| 113 | Q01469 | Fatty acid-binding protein, epidermal GN=FABP5 PE=1 SV=3 | 28.2 | 23 |
| 114 | P19971 | Thymidine phosphorylase GN=TYMP PE=1 SV=2 | 28.19 | 20 |
| 115 | P00966 | Argininosuccinate synthase GN=ASS1 PE=1 SV=2 | 28.18 | 19 |
| 116 | P0CG06 | Ig lambda-3 chain C regions GN=IGLC3 PE=1 SV=1 | 28.18 | 64 |
| 117 | B9A064 | Immunoglobulin lambda-like polypeptide 5 GN=IGLL5 PE=2 SV=2 | 27.99 | 62 |
| 118 | P61769 | Beta-2-microglobulin GN=B2M PE=1 SV=1 | 27.59 | 24 |

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|-----|--------|--|-------|----|
| 119 | P62937 | Peptidyl-prolyl cis-trans isomerase A GN=PPIA PE=1 SV=2 | 26.65 | 31 |
| 120 | P08758 | Annexin A5 GN=ANXA5 PE=1 SV=2 | 26.5 | 20 |
| 121 | P18206 | Vinculin GN=VCL PE=1 SV=4 | 26.27 | 17 |
| 122 | P31947 | 14-3-3 protein sigma GN=SFN PE=1 SV=1 | 25.99 | 25 |
| 123 | P06702 | Protein S100-A9 GN=S100A9 PE=1 SV=1 | 25.97 | 80 |
| 124 | P09960 | Leukotriene A-4 hydrolase GN=LTA4H PE=1 SV=2 | 25.92 | 14 |
| 125 | O75874 | Isocitrate dehydrogenase [NADP] cytoplasmic GN=IDH1 PE=1 SV=2 | 25.8 | 16 |
| 126 | P68363 | Tubulin alpha-1B chain GN=TUBA1B PE=1 SV=1 | 25.69 | 17 |
| 127 | P19013 | Keratin, type II cytoskeletal 4 GN=KRT4 PE=1 SV=4 | 25.55 | 16 |
| 128 | P09467 | Fructose-1,6-bisphosphatase 1 GN=FBP1 PE=1 SV=5 | 25.38 | 17 |
| 129 | P16152 | Carbonyl reductase [NADPH] 1 GN=CBR1 PE=1 SV=3 | 25.18 | 15 |
| 130 | P18136 | Ig kappa chain V-III region HIC PE=2 SV=2 | 25.01 | 31 |
| 131 | P50995 | Annexin A11 GN=ANXA11 PE=1 SV=1 | 24.86 | 13 |
| 132 | P02647 | Apolipoprotein A-I GN=APOA1 PE=1 SV=1 | 24.81 | 17 |
| 133 | Q8WUM4 | Programmed cell death 6-interacting protein GN=PDCCD6IP PE=1 SV=1 | 24.61 | 14 |
| 134 | P30101 | Protein disulfide-isomerase A3 GN=PDIA3 PE=1 SV=4 | 24.56 | 13 |
| 135 | P02749 | Beta-2-glycoprotein 1 GN=APOH PE=1 SV=3 | 24.35 | 18 |
| 136 | P04217 | Alpha-1B-glycoprotein GN=A1BG PE=1 SV=4 | 24.29 | 15 |
| 137 | P05787 | Keratin, type II cytoskeletal 8 GN=KRT8 PE=1 SV=7 | 24.05 | 14 |
| 138 | P02763 | Alpha-1-acid glycoprotein 1 GN=ORM1 PE=1 SV=1 | 24 | 18 |

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|-----|--------|--|-------|----|
| 139 | O60437 | Periplakin GN=PPL PE=1 SV=4 | 23.88 | 13 |
| 140 | Q96DA0 | Zymogen granule protein 16 homolog B GN=ZG16B PE=1 SV=3 | 23.72 | 19 |
| 141 | P17655 | Calpain-2 catalytic subunit GN=CAPN2 PE=1 SV=6 | 23.69 | 14 |
| 142 | P80303 | Nucleobindin-2 GN=NUCB2 PE=1 SV=2 | 23.46 | 16 |
| 143 | P29401 | Transketolase GN=TKT PE=1 SV=3 | 23.45 | 15 |
| 144 | P0CG05 | Ig lambda-2 chain C regions GN=IGLC2 PE=1 SV=1 | 23.24 | 63 |
| 145 | P61158 | Actin-related protein 3 GN=ACTR3 PE=1 SV=3 | 23.19 | 14 |
| 146 | P07858 | Cathepsin B GN=CTSB PE=1 SV=3 | 23.1 | 17 |
| 147 | O60664 | Perilipin-3 GN=PLIN3 PE=1 SV=3 | 22.58 | 15 |
| 148 | P02671 | Fibrinogen alpha chain GN=FGA PE=1 SV=2 | 22.57 | 14 |
| 149 | P40394 | Alcohol dehydrogenase class 4 mu/sigma chain GN=ADH7 PE=1 SV=2 | 22.54 | 19 |
| 150 | P36871 | Phosphoglucomutase-1 GN=PGM1 PE=1 SV=3 | 22.49 | 13 |
| 151 | O00299 | Chloride intracellular channel protein 1 GN=CLIC1 PE=1 SV=4 | 22.32 | 16 |
| 152 | P02766 | Transthyretin GN=TTR PE=1 SV=1 | 22.18 | 17 |
| 153 | P07602 | Prosaposin GN=PSAP PE=1 SV=2 | 22.07 | 13 |
| 154 | P43490 | Nicotinamide phosphoribosyltransferase GN=NAMPT PE=1 SV=1 | 21.96 | 12 |
| 155 | P07203 | Glutathione peroxidase 1 GN=GPX1 PE=1 SV=4 | 21.91 | 12 |
| 156 | P06744 | Glucose-6-phosphate isomerase GN=GPI PE=1 SV=4 | 21.9 | 19 |
| 157 | Q14624 | Inter-alpha-trypsin inhibitor heavy chain H4 GN=ITIH4 PE=1 SV=4 | 21.71 | 12 |
| 158 | P17931 | Galectin-3 GN=LGALS3 PE=1 SV=5 | 21.67 | 27 |

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|-----|--------|---|-------|----|
| 159 | P07339 | Cathepsin D GN=CTSD PE=1 SV=1 | 21.49 | 14 |
| 160 | Q9NY33 | Dipeptidyl peptidase 3 GN=DPP3 PE=1 SV=2 | 20.82 | 13 |
| 161 | P31939 | Bifunctional purine biosynthesis protein PURH GN=ATIC PE=1 SV=3 | 20.8 | 11 |
| 162 | Q86VP6 | Cullin-associated NEDD8-dissociated protein 1 GN=CAND1 PE=1 SV=2 | 20.77 | 12 |
| 163 | P40121 | Macrophage-capping protein GN=CAPG PE=1 SV=2 | 20.71 | 15 |
| 164 | P23528 | Cofilin-1 GN=CFL1 PE=1 SV=3 | 20.69 | 15 |
| 165 | P18669 | Phosphoglycerate mutase 1 GN=PGAM1 PE=1 SV=2 | 20.66 | 18 |
| 166 | P48637 | Glutathione synthetase GN=GSS PE=1 SV=1 | 20.46 | 12 |
| 167 | P37802 | Transgelin-2 GN=TAGLN2 PE=1 SV=3 | 20.39 | 23 |
| 168 | O00151 | PDZ and LIM domain protein 1 GN=PDLIM1 PE=1 SV=4 | 20.37 | 14 |
| 169 | O95834 | Echinoderm microtubule-associated protein- like 2 GN=EML2 PE=1 SV=1 | 20.35 | 10 |
| 170 | O95336 | 6-phosphogluconolactonase GN=PGLS PE=1 SV=2 | 20.15 | 13 |
| 171 | P22392 | Nucleoside diphosphate kinase B GN=NME2 PE=1 SV=1 | 20.14 | 14 |
| 172 | P40925 | Malate dehydrogenase, cytoplasmic GN=MDH1 PE=1 SV=4 | 20.03 | 17 |
| 173 | O00391 | Sulfhydryl oxidase 1 GN=QSOX1 PE=1 SV=3 | 20.01 | 10 |
| 174 | Q99497 | Protein DJ-1 GN=PARK7 PE=1 SV=2 | 20 | 16 |
| 175 | O75891 | Cytosolic 10-formyltetrahydrofolate dehydrogenase GN=ALDH1L1 PE=1 SV=2 | 20 | 13 |
| 176 | P13646 | Keratin, type I cytoskeletal 13 GN=KRT13 PE=1 SV=4 | 19.75 | 22 |
| 177 | P01042 | Kininogen-1 GN=KNG1 PE=1 SV=2 | 19.73 | 12 |
| 178 | P00747 | Plasminogen GN=PLG PE=1 SV=2 | 19.73 | 11 |

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|-----|--------|--|-------|----|
| 179 | P05155 | Plasma protease C1 inhibitor GN=SERPING1 PE=1 SV=2 | 19.71 | 15 |
| 180 | P80188 | Neutrophil gelatinase-associated lipocalin GN=LCN2 PE=1 SV=2 | 19.69 | 23 |
| 181 | Q9Y6U3 | Adseverin GN=SCIN PE=1 SV=4 | 19.68 | 11 |
| 182 | Q02818 | Nucleobindin-1 GN=NUCB1 PE=1 SV=4 | 19.59 | 11 |
| 183 | Q8NBJ4 | Golgi membrane protein 1 GN=GOLM1 PE=1 SV=1 | 19.56 | 11 |
| 184 | Q16851 | UTP--glucose-1-phosphate uridylyltransferase GN=UGP2 PE=1 SV=5 | 19.44 | 10 |
| 185 | Q15181 | Inorganic pyrophosphatase GN=PPA1 PE=1 SV=2 | 19.43 | 12 |
| 186 | P30085 | UMP-CMP kinase GN=CMPK1 PE=1 SV=3 | 19.4 | 14 |
| 187 | Q9HC38 | Glyoxalase domain-containing protein 4 GN=GLOD4 PE=1 SV=1 | 19.07 | 11 |
| 188 | P52565 | Rho GDP-dissociation inhibitor 1 GN=ARHGDI1 PE=1 SV=3 | 18.98 | 15 |
| 189 | P12429 | Annexin A3 GN=ANXA3 PE=1 SV=3 | 18.89 | 11 |
| 190 | P34932 | Heat shock 70 kDa protein 4 GN=HSPA4 PE=1 SV=4 | 18.8 | 10 |
| 191 | P07195 | L-lactate dehydrogenase B chain GN=LDHB PE=1 SV=2 | 18.71 | 15 |
| 192 | P04632 | Calpain small subunit 1 GN=CAPNS1 PE=1 SV=1 | 18.63 | 15 |
| 193 | Q71U36 | Tubulin alpha-1A chain GN=TUBA1A PE=1 SV=1 | 18.54 | 15 |
| 194 | P36955 | Pigment epithelium-derived factor GN=SERPINF1 PE=1 SV=4 | 18.49 | 11 |
| 195 | P11021 | 78 kDa glucose-regulated protein GN=HSPA5 PE=1 SV=2 | 18.39 | 15 |
| 196 | P09525 | Annexin A4 GN=ANXA4 PE=1 SV=4 | 18.32 | 12 |
| 197 | P02814 | Submaxillary gland androgen-regulated protein 3B GN=SMR3B PE=1 SV=2 | 18.08 | 26 |

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|-----|--------|--|-------|----|
| 198 | P30086 | Phosphatidylethanolamine-binding protein 1 GN=PEBP1 PE=1 SV=3 | 18.06 | 16 |
| 199 | P31946 | 14-3-3 protein beta/alpha GN=YWHAB PE=1 SV=3 | 18 | 22 |
| 200 | P00734 | Prothrombin GN=F2 PE=1 SV=2 | 18 | 9 |
| 201 | P18510 | Interleukin-1 receptor antagonist protein GN=IL1RN PE=1 SV=1 | 17.92 | 14 |
| 202 | P21281 | V-type proton ATPase subunit B, brain isoform GN=ATP6V1B2 PE=1 SV=3 | 17.84 | 10 |
| 203 | P63241 | Eukaryotic translation initiation factor 5A-1 GN=EIF5A PE=1 SV=2 | 17.8 | 11 |
| 204 | P01601 | Ig kappa chain V-I region HK101 (Fragment) PE=4 SV=1 | 17.75 | 17 |
| 205 | P02765 | Alpha-2-HS-glycoprotein GN=AHSG PE=1 SV=1 | 17.56 | 16 |
| 206 | P15104 | Glutamine synthetase GN=GLUL PE=1 SV=4 | 17.39 | 10 |
| 207 | P01034 | Cystatin-C GN=CST3 PE=1 SV=1 | 17.21 | 14 |
| 208 | Q13938 | Calcyphosin GN=CAPS PE=1 SV=1 | 17.19 | 9 |
| 209 | P45974 | Ubiquitin carboxyl-terminal hydrolase 5 GN=USP5 PE=1 SV=2 | 17.16 | 9 |
| 210 | P62158 | Calmodulin GN=CALM1 PE=1 SV=2 | 17.15 | 14 |
| 211 | P02679 | Fibrinogen gamma chain GN=FGG PE=1 SV=3 | 17.15 | 10 |
| 212 | P60981 | Dextrin GN=DSTN PE=1 SV=3 | 16.85 | 10 |
| 213 | P01764 | Ig heavy chain V-III region VH26 PE=1 SV=1 | 16.71 | 25 |
| 214 | Q96C19 | EF-hand domain-containing protein D2 GN=EFHD2 PE=1 SV=1 | 16.65 | 9 |
| 215 | P61160 | Actin-related protein 2 GN=ACTR2 PE=1 SV=1 | 16.51 | 9 |
| 216 | P18135 | Ig kappa chain V-III region HAH PE=2 SV=1 | 16.47 | 23 |
| 217 | P02675 | Fibrinogen beta chain GN=FGB PE=1 SV=2 | 16.43 | 9 |

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|-----|--------|---|-------|----|
| 218 | Q15782 | Chitinase-3-like protein 2 GN=CHI3L2 PE=1 SV=1 | 16.39 | 10 |
| 219 | P08729 | Keratin, type II cytoskeletal 7 GN=KRT7 PE=1 SV=5 | 16.33 | 13 |
| 220 | P04080 | Cystatin-B GN=CSTB PE=1 SV=2 | 16.09 | 17 |
| 221 | P23526 | Adenosylhomocysteinase GN=AHCY PE=1 SV=4 | 16.05 | 10 |
| 222 | P67936 | Tropomyosin alpha-4 chain GN=TPM4 PE=1 SV=3 | 16.01 | 11 |
| 223 | P50990 | T-complex protein 1 subunit theta GN=CCT8 PE=1 SV=4 | 16.01 | 8 |
| 224 | Q00796 | Sorbitol dehydrogenase GN=SORD PE=1 SV=4 | 16 | 10 |
| 225 | P78371 | T-complex protein 1 subunit beta GN=CCT2 PE=1 SV=4 | 16 | 8 |
| 226 | P01766 | Ig heavy chain V-III region BRO PE=1 SV=1 | 16 | 35 |
| 227 | P01019 | Angiotensinogen GN=AGT PE=1 SV=1 | 15.77 | 8 |
| 228 | P31949 | Protein S100-A11 GN=S100A11 PE=1 SV=2 | 15.6 | 33 |
| 229 | P32119 | Peroxiredoxin-2 GN=PRDX2 PE=1 SV=5 | 15.58 | 22 |
| 230 | P55058 | Phospholipid transfer protein GN=PLTP PE=1 SV=1 | 15.52 | 11 |
| 231 | P27797 | Calreticulin GN=CALR PE=1 SV=1 | 15.35 | 9 |
| 232 | P37837 | Transaldolase GN=TALDO1 PE=1 SV=2 | 15.34 | 8 |
| 233 | P17987 | T-complex protein 1 subunit alpha GN=TCP1 PE=1 SV=1 | 15.13 | 8 |
| 234 | O75369 | Filamin-B GN=FLNB PE=1 SV=2 | 15.12 | 8 |
| 235 | Q9UL46 | Proteasome activator complex subunit 2 GN=PSME2 PE=1 SV=4 | 15.02 | 11 |
| 236 | P21964 | Catechol O-methyltransferase GN=COMT PE=1 SV=2 | 14.97 | 11 |
| 237 | P17858 | ATP-dependent 6-phosphofructokinase, liver type GN=PFKL PE=1 SV=6 | 14.97 | 11 |

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|-----|--------|---|-------|----|
| 238 | P30153 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform GN=PPP2R1A PE=1 SV=4 | 14.94 | 9 |
| 239 | Q06210 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 GN=GFPT1 PE=1 SV=3 | 14.86 | 8 |
| 240 | P08670 | Vimentin GN=VIM PE=1 SV=4 | 14.74 | 9 |
| 241 | P47756 | F-actin-capping protein subunit beta GN=CAPZB PE=1 SV=4 | 14.74 | 11 |
| 242 | Q16719 | Kynureninase GN=KYNU PE=1 SV=1 | 14.57 | 9 |
| 243 | P35527 | Keratin, type I cytoskeletal 9 GN=KRT9 PE=1 SV=3 | 14.53 | 8 |
| 244 | P60660 | Myosin light polypeptide 6 GN=MYL6 PE=1 SV=2 | 14.49 | 13 |
| 245 | O00764 | Pyridoxal kinase GN=PDXK PE=1 SV=1 | 14.48 | 9 |
| 246 | P47755 | F-actin-capping protein subunit alpha-2 GN=CAPZA2 PE=1 SV=3 | 14.48 | 8 |
| 247 | P19827 | Inter-alpha-trypsin inhibitor heavy chain H1 GN=ITIH1 PE=1 SV=3 | 14.33 | 9 |
| 248 | P14314 | Glucosidase 2 subunit beta GN=PRKCSH PE=1 SV=2 | 14.22 | 9 |
| 249 | P02750 | Leucine-rich alpha-2-glycoprotein GN=LRG1 PE=1 SV=2 | 14.18 | 9 |
| 250 | P52907 | F-actin-capping protein subunit alpha-1 GN=CAPZA1 PE=1 SV=3 | 14.16 | 9 |
| 251 | P13798 | Acylamino-acid-releasing enzyme GN=APEH PE=1 SV=4 | 14.14 | 8 |
| 252 | Q96G03 | Phosphoglucomutase-2 GN=PGM2 PE=1 SV=4 | 14.12 | 9 |
| 253 | P11413 | Glucose-6-phosphate 1-dehydrogenase GN=G6PD PE=1 SV=4 | 14.08 | 8 |
| 254 | P60842 | Eukaryotic initiation factor 4A-I GN=EIF4A1 PE=1 SV=1 | 14.03 | 9 |
| 255 | P10599 | Thioredoxin GN=TXN PE=1 SV=3 | 14.01 | 11 |

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| 256 | P07737 | Profilin-1 GN=PFN1 PE=1 SV=2 | 14 | 18 |
| 257 | O95994 | Anterior gradient protein 2 homolog GN=AGR2 PE=1 SV=1 | 14 | 14 |
| 258 | Q14914 | Prostaglandin reductase 1 GN=PTGR1 PE=1 SV=2 | 14 | 8 |
| 259 | P52566 | Rho GDP-dissociation inhibitor 2 GN=ARHGDI2 PE=1 SV=3 | 14 | 9 |
| 260 | P04196 | Histidine-rich glycoprotein GN=HRG PE=1 SV=1 | 14 | 9 |
| 261 | P02748 | Complement component C9 GN=C9 PE=1 SV=2 | 14 | 7 |
| 262 | O60547 | GDP-mannose 4,6 dehydratase GN=GMD5 PE=1 SV=1 | 13.8 | 8 |
| 263 | O00534 | von Willebrand factor A domain-containing protein 5A GN=VWA5A PE=2 SV=2 | 13.79 | 8 |
| 264 | Q13813 | Spectrin alpha chain, non-erythrocytic 1 GN=SPTAN1 PE=1 SV=3 | 13.77 | 10 |
| 265 | P20618 | Proteasome subunit beta type-1 GN=PSMB1 PE=1 SV=2 | 13.73 | 9 |
| 266 | P31941 | DNA dC->dU-editing enzyme APOBEC-3A GN=APOBEC3A PE=1 SV=3 | 13.7 | 10 |
| 267 | P13796 | Plastin-2 GN=LCP1 PE=1 SV=6 | 13.69 | 13 |
| 268 | Q9ULZ3 | Apoptosis-associated speck-like protein containing a CARD GN=PYCARD PE=1 SV=2 | 13.64 | 7 |
| 269 | P61978 | Heterogeneous nuclear ribonucleoprotein K GN=HNRNPK PE=1 SV=1 | 13.48 | 7 |
| 270 | Q14651 | Plastin-1 GN=PLS1 PE=1 SV=2 | 13.45 | 12 |
| 271 | P05388 | 60S acidic ribosomal protein P0 GN=RPLP0 PE=1 SV=1 | 13.41 | 7 |
| 272 | P30046 | D-dopachrome decarboxylase GN=DDT PE=1 SV=3 | 13.38 | 8 |
| 273 | P01768 | Ig heavy chain V-III region CAM PE=1 SV=1 | 13.33 | 15 |
| 274 | P46459 | Vesicle-fusing ATPase GN=NSF PE=1 SV=3 | 13.29 | 8 |

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| 275 | Q14515 | SPARC-like protein 1 GN=SPARCL1 PE=1 SV=2 | 13.25 | 7 |
| 276 | O15144 | Actin-related protein 2/3 complex subunit 2 GN=ARPC2 PE=1 SV=1 | 13.23 | 7 |
| 277 | Q9BRF8 | Serine/threonine-protein phosphatase CPPED1 GN=CPPED1 PE=1 SV=3 | 13.21 | 9 |
| 278 | P40926 | Malate dehydrogenase, mitochondrial GN=MDH2 PE=1 SV=3 | 13.2 | 7 |
| 279 | P01617 | Ig kappa chain V-II region TEW PE=1 SV=1 | 13.1 | 19 |
| 280 | P01610 | Ig kappa chain V-I region WEA PE=1 SV=1 | 13.07 | 19 |
| 281 | P04004 | Vitronectin GN=VTN PE=1 SV=1 | 13.02 | 8 |
| 282 | P31151 | Protein S100-A7 GN=S100A7 PE=1 SV=4 | 13.01 | 10 |
| 283 | P40227 | T-complex protein 1 subunit zeta GN=CCT6A PE=1 SV=3 | 12.97 | 7 |
| 284 | P07741 | Adenine phosphoribosyltransferase GN=APRT PE=1 SV=2 | 12.93 | 9 |
| 285 | P47989 | Xanthine dehydrogenase/oxidase GN=XDH PE=1 SV=4 | 12.88 | 7 |
| 286 | P06309 | Ig kappa chain V-II region GM607 (Fragment) PE=4 SV=1 | 12.87 | 22 |
| 287 | Q14247 | Src substrate cortactin GN=CTTN PE=1 SV=2 | 12.85 | 7 |
| 288 | P02511 | Alpha-crystallin B chain GN=CRYAB PE=1 SV=2 | 12.81 | 8 |
| 289 | O14818 | Proteasome subunit alpha type-7 GN=PSMA7 PE=1 SV=1 | 12.71 | 7 |
| 290 | Q14894 | Ketimine reductase mu-crystallin GN=CRYM PE=1 SV=1 | 12.65 | 7 |
| 291 | P06576 | ATP synthase subunit beta, mitochondrial GN=ATP5B PE=1 SV=3 | 12.46 | 6 |
| 292 | Q15435 | Protein phosphatase 1 regulatory subunit 7 GN=PPP1R7 PE=1 SV=1 | 12.31 | 7 |
| 293 | P01781 | Ig heavy chain V-III region GAL PE=1 SV=1 | 12.16 | 14 |

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| 294 | Q9NQW7 | Xaa-Pro aminopeptidase 1 GN=XPNPEP1 PE=1 SV=3 | 12.06 | 6 |
| 295 | Q12792 | Twinfilin-1 GN=TWF1 PE=1 SV=3 | 12 | 6 |
| 296 | Q96FW1 | Ubiquitin thioesterase OTUB1 GN=OTUB1 PE=1 SV=2 | 12 | 6 |
| 297 | P35754 | Glutaredoxin-1 GN=GLRX PE=1 SV=2 | 12 | 9 |
| 298 | P27482 | Calmodulin-like protein 3 GN=CALML3 PE=1 SV=2 | 12 | 7 |
| 299 | P09651 | Heterogeneous nuclear ribonucleoprotein A1 GN=HNRNPA1 PE=1 SV=5 | 12 | 7 |
| 300 | O75368 | SH3 domain-binding glutamic acid-rich-like protein GN=SH3BGRL PE=1 SV=1 | 11.92 | 6 |
| 301 | P38606 | V-type proton ATPase catalytic subunit A GN=ATP6V1A PE=1 SV=2 | 11.88 | 6 |
| 302 | P11216 | Glycogen phosphorylase, brain form GN=PYGB PE=1 SV=5 | 11.86 | 9 |
| 303 | P22626 | Heterogeneous nuclear ribonucleoproteins A2/B1 GN=HNRNPA2B1 PE=1 SV=2 | 11.85 | 7 |
| 304 | P49189 | 4-trimethylaminobutyraldehyde dehydrogenase GN=ALDH9A1 PE=1 SV=3 | 11.84 | 8 |
| 305 | P12955 | Xaa-Pro dipeptidase GN=PEPD PE=1 SV=3 | 11.8 | 7 |
| 306 | P62140 | Serine/threonine-protein phosphatase PP1- beta catalytic subunit GN=PPP1CB PE=1 SV=3 | 11.77 | 7 |
| 307 | Q96C23 | Aldose 1-epimerase GN=GALM PE=1 SV=1 | 11.72 | 6 |
| 308 | Q14697 | Neutral alpha-glucosidase AB GN=GANAB PE=1 SV=3 | 11.68 | 8 |
| 309 | Q14240 | Eukaryotic initiation factor 4A-II GN=EIF4A2 PE=1 SV=2 | 11.62 | 8 |
| 310 | P46926 | Glucosamine-6-phosphate isomerase 1 GN=GNPDA1 PE=1 SV=1 | 11.52 | 6 |
| 311 | Q15293 | Reticulocalbin-1 GN=RCN1 PE=1 SV=1 | 11.4 | 7 |
| 312 | P05164 | Myeloperoxidase GN=MPO PE=1 SV=1 | 11.38 | 7 |

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| 313 | P31948 | Stress-induced-phosphoprotein 1 GN=STIP1 PE=1 SV=1 | 11.19 | 7 |
| 314 | P61586 | Transforming protein RhoA GN=RHOA PE=1 SV=1 | 11.15 | 7 |
| 315 | P50991 | T-complex protein 1 subunit delta GN=CCT4 PE=1 SV=4 | 11.12 | 7 |
| 316 | P68402 | Platelet-activating factor acetylhydrolase IB subunit beta GN=PFAFH1B2 PE=1 SV=1 | 11.04 | 7 |
| 317 | Q14974 | Importin subunit beta-1 GN=KPNB1 PE=1 SV=2 | 10.99 | 6 |
| 318 | P27348 | 14-3-3 protein theta GN=YWHAQ PE=1 SV=1 | 10.97 | 15 |
| 319 | P04179 | Superoxide dismutase [Mn], mitochondrial GN=SOD2 PE=1 SV=2 | 10.96 | 8 |
| 320 | P19105 | Myosin regulatory light chain 12A GN=MYL12A PE=1 SV=2 | 10.92 | 7 |
| 321 | P31150 | Rab GDP dissociation inhibitor alpha GN=GDI1 PE=1 SV=2 | 10.82 | 19 |
| 322 | P34896 | Serine hydroxymethyltransferase, cytosolic GN=SHMT1 PE=1 SV=1 | 10.73 | 6 |
| 323 | P49902 | Cytosolic purine 5'-nucleotidase GN=NT5C2 PE=1 SV=1 | 10.72 | 7 |
| 324 | P17174 | Aspartate aminotransferase, cytoplasmic GN=GOT1 PE=1 SV=3 | 10.68 | 6 |
| 325 | P48147 | Prolyl endopeptidase GN=PREP PE=1 SV=2 | 10.65 | 7 |
| 326 | P00441 | Superoxide dismutase [Cu-Zn] GN=SOD1 PE=1 SV=2 | 10.55 | 7 |
| 327 | Q8N474 | Secreted frizzled-related protein 1 GN=SFRP1 PE=1 SV=1 | 10.55 | 8 |
| 328 | O14745 | Na(+)/H(+) exchange regulatory cofactor NHE- RF1 GN=SLC9A3R1 PE=1 SV=4 | 10.54 | 6 |
| 329 | P05546 | Heparin cofactor 2 GN=SERPIND1 PE=1 SV=3 | 10.46 | 7 |
| 330 | Q9UBC9 | Small proline-rich protein 3 GN=SPRR3 PE=1 SV=2 | 10.45 | 6 |

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| 331 | P23381 | Tryptophan--tRNA ligase, cytoplasmic GN=WARS PE=1 SV=2 | 10.37 | 7 |
| 332 | P25788 | Proteasome subunit alpha type-3 GN=PSMA3 PE=1 SV=2 | 10.31 | 6 |
| 333 | O43852 | Calumenin GN=CALU PE=1 SV=2 | 10.26 | 6 |
| 334 | O15143 | Actin-related protein 2/3 complex subunit 1B GN=ARPC1B PE=1 SV=3 | 10.21 | 6 |
| 335 | P56537 | Eukaryotic translation initiation factor 6 GN=EIF6 PE=1 SV=1 | 10.21 | 8 |
| 336 | P25815 | Protein S100-P GN=S100P PE=1 SV=2 | 10.14 | 11 |
| 337 | Q9UNZ2 | NSFL1 cofactor p47 GN=NSFL1C PE=1 SV=2 | 10.11 | 7 |
| 338 | P62136 | Serine/threonine-protein phosphatase PP1- alpha catalytic subunit GN=PPP1CA PE=1 SV=1 | 10.11 | 7 |
| 339 | Q15365 | Poly(rC)-binding protein 1 GN=PCBP1 PE=1 SV=2 | 10.09 | 7 |
| 340 | Q96S96 | Phosphatidylethanolamine-binding protein 4 GN=PEBP4 PE=1 SV=3 | 10.08 | 6 |
| 341 | P19961 | Alpha-amylase 2B GN=AMY2B PE=1 SV=1 | 10.04 | 6 |
| 342 | Q02809 | Procollagen-lysine,2-oxoglutarate 5- dioxygenase 1 GN=PLOD1 PE=1 SV=2 | 10.04 | 5 |
| 343 | P35606 | Coatomer subunit beta' GN=COPB2 PE=1 SV=2 | 10.03 | 5 |
| 344 | Q9UN36 | Protein NDRG2 GN=NDRG2 PE=1 SV=2 | 10.02 | 6 |
| 345 | Q04917 | 14-3-3 protein eta GN=YWHAH PE=1 SV=4 | 10 | 13 |
| 346 | Q9Y5Z4 | Heme-binding protein 2 GN=HEBP2 PE=1 SV=1 | 10 | 8 |
| 347 | P05387 | 60S acidic ribosomal protein P2 GN=RPLP2 PE=1 SV=1 | 10 | 5 |
| 348 | P01700 | Ig lambda chain V-I region HA PE=1 SV=1 | 10 | 7 |
| 349 | Q13126 | S-methyl-5'-thioadenosine phosphorylase GN=MTAP PE=1 SV=2 | 10 | 6 |

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| 350 | P01033 | Metalloproteinase inhibitor 1 GN=TIMP1 PE=1 SV=1 | 10 | 7 |
| 351 | P60953 | Cell division control protein 42 homolog GN=CDC42 PE=1 SV=2 | 10 | 6 |
| 352 | Q9BR76 | Coronin-1B GN=CORO1B PE=1 SV=1 | 10 | 8 |
| 353 | P01772 | Ig heavy chain V-III region KOL PE=1 SV=1 | 10 | 14 |
| 354 | Q9H0W9 | Ester hydrolase C11orf54 GN=C11orf54 PE=1 SV=1 | 10 | 5 |
| 355 | P60900 | Proteasome subunit alpha type-6 GN=PSMA6 PE=1 SV=1 | 10 | 5 |
| 356 | P11766 | Alcohol dehydrogenase class-3 GN=ADH5 PE=1 SV=4 | 10 | 6 |
| 357 | P28062 | Proteasome subunit beta type-8 GN=PSMB8 PE=1 SV=3 | 10 | 5 |
| 358 | P49773 | Histidine triad nucleotide-binding protein 1 GN=HINT1 PE=1 SV=2 | 10 | 5 |
| 359 | P01594 | Ig kappa chain V-I region AU PE=1 SV=1 | 10 | 16 |
| 360 | P01777 | Ig heavy chain V-III region TEI PE=1 SV=1 | 10 | 31 |
| 361 | P08134 | Rho-related GTP-binding protein RhoC GN=RHOC PE=1 SV=1 | 10 | 6 |
| 362 | P30043 | Flavin reductase (NADPH) GN=BLVRB PE=1 SV=3 | 9.96 | 7 |
| 363 | Q9Y678 | Coatomer subunit gamma-1 GN=COPG1 PE=1 SV=1 | 9.92 | 5 |
| 364 | P17812 | CTP synthase 1 GN=CTPS1 PE=1 SV=2 | 9.92 | 6 |
| 365 | P19823 | Inter-alpha-trypsin inhibitor heavy chain H2 GN=ITIH2 PE=1 SV=2 | 9.91 | 6 |
| 366 | P04745 | Alpha-amylase 1 GN=AMY1A PE=1 SV=2 | 9.89 | 6 |
| 367 | P19652 | Alpha-1-acid glycoprotein 2 GN=ORM2 PE=1 SV=2 | 9.86 | 13 |
| 368 | P35908 | Keratin, type II cytoskeletal 2 epidermal GN=KRT2 PE=1 SV=2 | 9.82 | 11 |

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| 369 | P30520 | Adenylosuccinate synthetase isozyme 2 GN=ADSS PE=1 SV=3 | 9.8 | 6 |
| 370 | P43652 | Afamin GN=AFM PE=1 SV=1 | 9.69 | 6 |
| 371 | Q14376 | UDP-glucose 4-epimerase GN=GALE PE=1 SV=2 | 9.68 | 6 |
| 372 | Q92743 | Serine protease HTRA1 GN=HTRA1 PE=1 SV=1 | 9.64 | 5 |
| 373 | P49721 | Proteasome subunit beta type-2 GN=PSMB2 PE=1 SV=1 | 9.64 | 5 |
| 374 | P49720 | Proteasome subunit beta type-3 GN=PSMB3 PE=1 SV=2 | 9.46 | 6 |
| 375 | P51149 | Ras-related protein Rab-7a GN=RAB7A PE=1 SV=1 | 9.41 | 5 |
| 376 | Q96TA1 | Niban-like protein 1 GN=FAM129B PE=1 SV=3 | 9.37 | 8 |
| 377 | P43034 | Platelet-activating factor acetylhydrolase IB subunit alpha GN=PAFAH1B1 PE=1 SV=2 | 9.36 | 6 |
| 378 | P05090 | Apolipoprotein D GN=APOD PE=1 SV=1 | 9.35 | 6 |
| 379 | Q04760 | Lactoylglutathione lyase GN=GLO1 PE=1 SV=4 | 9.34 | 7 |
| 380 | P13010 | X-ray repair cross-complementing protein 5 GN=XRCC5 PE=1 SV=3 | 9.3 | 5 |
| 381 | P28325 | Cystatin-D GN=CST5 PE=1 SV=1 | 9.29 | 6 |
| 382 | P49368 | T-complex protein 1 subunit gamma GN=CCT3 PE=1 SV=4 | 9.29 | 6 |
| 383 | P04746 | Pancreatic alpha-amylase GN=AMY2A PE=1 SV=2 | 9.29 | 5 |
| 384 | P21399 | Cytoplasmic aconitate hydratase GN=ACO1 PE=1 SV=3 | 9.27 | 6 |
| 385 | P28066 | Proteasome subunit alpha type-5 GN=PSMA5 PE=1 SV=3 | 9.2 | 5 |
| 386 | Q96HC4 | PDZ and LIM domain protein 5 GN=PDLIM5 PE=1 SV=5 | 9.2 | 6 |

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| 387 | Q99933 | BAG family molecular chaperone regulator 1 GN=BAG1 PE=1 SV=4 | 9.19 | 5 |
| 388 | P25787 | Proteasome subunit alpha type-2 GN=PSMA2 PE=1 SV=2 | 9.11 | 6 |
| 389 | P25789 | Proteasome subunit alpha type-4 GN=PSMA4 PE=1 SV=1 | 9.11 | 5 |
| 390 | O43776 | Asparagine--tRNA ligase, cytoplasmic GN=NARS PE=1 SV=1 | 8.94 | 5 |
| 391 | O43396 | Thioredoxin-like protein 1 GN=TXNL1 PE=1 SV=3 | 8.9 | 5 |
| 392 | P53004 | Biliverdin reductase A GN=BLVRA PE=1 SV=2 | 8.84 | 5 |
| 393 | Q9P2T1 | GMP reductase 2 GN=GMPR2 PE=1 SV=1 | 8.75 | 5 |
| 394 | P02760 | Protein AMBP GN=AMBP PE=1 SV=1 | 8.66 | 6 |
| 395 | Q9H0U4 | Ras-related protein Rab-1B GN=RAB1B PE=1 SV=1 | 8.62 | 6 |
| 396 | P49788 | Retinoic acid receptor responder protein 1 GN=RARRES1 PE=1 SV=2 | 8.55 | 5 |
| 397 | Q15366 | Poly(rC)-binding protein 2 GN=PCBP2 PE=1 SV=1 | 8.5 | 5 |
| 398 | P12956 | X-ray repair cross-complementing protein 6 GN=XRCC6 PE=1 SV=2 | 8.49 | 5 |
| 399 | P62820 | Ras-related protein Rab-1A GN=RAB1A PE=1 SV=3 | 8.47 | 5 |
| 400 | P06727 | Apolipoprotein A-IV GN=APOA4 PE=1 SV=3 | 8.46 | 5 |
| 401 | P78417 | Glutathione S-transferase omega-1 GN=GSTO1 PE=1 SV=2 | 8.31 | 6 |
| 402 | P28799 | Granulins GN=GRN PE=1 SV=2 | 8.31 | 5 |
| 403 | P23284 | Peptidyl-prolyl cis-trans isomerase B GN=PPIB PE=1 SV=2 | 8.3 | 6 |
| 404 | Q53FA7 | Quinone oxidoreductase PIG3 GN=TP53I3 PE=1 SV=2 | 8.26 | 5 |
| 405 | P35237 | Serpin B6 GN=SERPINB6 PE=1 SV=3 | 8.25 | 7 |

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| 406 | P14174 | Macrophage migration inhibitory factor GN=MIF PE=1 SV=4 | 8.21 | 9 |
| 407 | Q01105 | Protein SET GN=SET PE=1 SV=3 | 8.21 | 6 |
| 408 | Q9UJ70 | N-acetyl-D-glucosamine kinase GN=NAGK PE=1 SV=4 | 8.18 | 4 |
| 409 | Q13217 | DnaJ homolog subfamily C member 3 GN=DNAJC3 PE=1 SV=1 | 8.17 | 5 |
| 410 | P23083 | Ig heavy chain V-I region V35 PE=1 SV=1 | 8.16 | 9 |
| 411 | P07108 | Acyl-CoA-binding protein GN=DBI PE=1 SV=2 | 8.14 | 7 |
| 412 | P54727 | UV excision repair protein RAD23 homolog B GN=RAD23B PE=1 SV=1 | 8.14 | 6 |
| 413 | P02652 | Apolipoprotein A-II GN=APOA2 PE=1 SV=1 | 8.09 | 6 |
| 414 | P20073 | Annexin A7 GN=ANXA7 PE=1 SV=3 | 8.09 | 5 |
| 415 | P22352 | Glutathione peroxidase 3 GN=GPX3 PE=1 SV=2 | 8.09 | 5 |
| 416 | P48643 | T-complex protein 1 subunit epsilon GN=CCT5 PE=1 SV=1 | 8.07 | 5 |
| 417 | P08263 | Glutathione S-transferase A1 GN=GSTA1 PE=1 SV=3 | 8.07 | 5 |
| 418 | Q32P51 | Heterogeneous nuclear ribonucleoprotein A1- like 2 GN=HNRNPA1L2 PE=2 SV=2 | 8.07 | 4 |
| 419 | O43488 | Aflatoxin B1 aldehyde reductase member 2 GN=AKR7A2 PE=1 SV=3 | 8.06 | 5 |
| 420 | O75223 | Gamma-glutamylcyclotransferase GN=GGCT PE=1 SV=1 | 8.03 | 6 |
| 421 | P50502 | Hsc70-interacting protein GN=ST13 PE=1 SV=2 | 8.02 | 4 |
| 422 | Q96IU4 | Alpha/beta hydrolase domain-containing protein 14B GN=ABHD14B PE=1 SV=1 | 8.01 | 4 |
| 423 | O95171 | Sciellin GN=SCEL PE=1 SV=2 | 8.01 | 4 |
| 424 | P55263 | Adenosine kinase GN=ADK PE=1 SV=2 | 8.01 | 5 |
| 425 | Q6ZVX7 | F-box only protein 50 GN=NCCRP1 PE=1 | 8 | 6 |

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| | | SV=1 | | |
| 426 | P62987 | Ubiquitin-60S ribosomal protein L40 GN=UBA52 PE=1 SV=2 | 8 | 6 |
| 427 | P33241 | Lymphocyte-specific protein 1 GN=LSP1 PE=1 SV=1 | 8 | 4 |
| 428 | P55957 | BH3-interacting domain death agonist GN=BID PE=1 SV=1 | 8 | 4 |
| 429 | Q9NZT1 | Calmodulin-like protein 5 GN=CALML5 PE=1 SV=2 | 8 | 5 |
| 430 | P62328 | Thymosin beta-4 GN=TMSB4X PE=1 SV=2 | 8 | 11 |
| 431 | P29692 | Elongation factor 1-delta GN=EEF1D PE=1 SV=5 | 8 | 4 |
| 432 | Q9UJU6 | Drebrin-like protein GN=DBNL PE=1 SV=1 | 8 | 4 |
| 433 | P63151 | Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform GN=PPP2R2A PE=1 SV=1 | 8 | 4 |
| 434 | P09429 | High mobility group protein B1 GN=HMGB1 PE=1 SV=3 | 8 | 4 |
| 435 | O95436 | Sodium-dependent phosphate transport protein 2B GN=SLC34A2 PE=1 SV=3 | 8 | 4 |
| 436 | P36405 | ADP-ribosylation factor-like protein 3 GN=ARL3 PE=1 SV=2 | 8 | 4 |
| 437 | Q9BRA2 | Thioredoxin domain-containing protein 17 GN=TXNDC17 PE=1 SV=1 | 8 | 4 |
| 438 | Q9UHY7 | Enolase-phosphatase E1 GN=ENOPH1 PE=1 SV=1 | 8 | 4 |
| 439 | P80748 | Ig lambda chain V-III region LOI PE=1 SV=1 | 8 | 8 |
| 440 | P01743 | Ig heavy chain V-I region HG3 PE=4 SV=1 | 8 | 8 |
| 441 | P13716 | Delta-aminolevulinic acid dehydratase GN=ALAD PE=1 SV=1 | 8 | 4 |
| 442 | Q08623 | Pseudouridine-5'-monophosphatase GN=HDHD1 PE=1 SV=3 | 8 | 4 |
| 443 | P84077 | ADP-ribosylation factor 1 GN=ARF1 PE=1 | 8 | 5 |

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| | | SV=2 | | |
| 444 | P67775 | Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform GN=PPP2CA PE=1 SV=1 | 8 | 4 |
| 445 | P05452 | Tetranectin GN=CLEC3B PE=1 SV=3 | 8 | 4 |
| 446 | P04208 | Ig lambda chain V-I region WAH PE=1 SV=1 | 8 | 6 |
| 447 | Q15084 | Protein disulfide-isomerase A6 GN=PDIA6 PE=1 SV=1 | 7.93 | 5 |
| 448 | Q14508 | WAP four-disulfide core domain protein 2 GN=WFDC2 PE=1 SV=2 | 7.92 | 5 |
| 449 | O43865 | Putative adenosylhomocysteinase 2 GN=AHCYL1 PE=1 SV=2 | 7.91 | 4 |
| 450 | P46108 | Adapter molecule crk GN=CRK PE=1 SV=2 | 7.89 | 4 |
| 451 | P29373 | Cellular retinoic acid-binding protein 2 GN=CRABP2 PE=1 SV=2 | 7.77 | 4 |
| 452 | P01031 | Complement C5 GN=C5 PE=1 SV=4 | 7.76 | 4 |
| 453 | Q16881 | Thioredoxin reductase 1, cytoplasmic GN=TXNRD1 PE=1 SV=3 | 7.75 | 4 |
| 454 | P61088 | Ubiquitin-conjugating enzyme E2 N GN=UBE2N PE=1 SV=1 | 7.72 | 6 |
| 455 | Q13630 | GDP-L-fucose synthase GN=TSTA3 PE=1 SV=1 | 7.7 | 5 |
| 456 | Q9UBQ7 | Glyoxylate reductase/hydroxypyruvate reductase GN=GRHPR PE=1 SV=1 | 7.69 | 6 |
| 457 | Q8IZ83 | Aldehyde dehydrogenase family 16 member A1 GN=ALDH16A1 PE=1 SV=2 | 7.66 | 5 |
| 458 | O43175 | D-3-phosphoglycerate dehydrogenase GN=PHGDH PE=1 SV=4 | 7.64 | 4 |
| 459 | Q9NQR4 | Omega-amidase NIT2 GN=NIT2 PE=1 SV=1 | 7.62 | 5 |
| 460 | Q10567 | AP-1 complex subunit beta-1 GN=AP1B1 PE=1 SV=2 | 7.62 | 4 |
| 461 | O75351 | Vacuolar protein sorting-associated protein 4B GN=VPS4B PE=1 SV=2 | 7.52 | 4 |

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| 462 | P63244 | Guanine nucleotide-binding protein subunit beta-2-like 1 GN=GNB2L1 PE=1 SV=3 | 7.5 | 4 |
| 463 | Q9NTK5 | Obg-like ATPase 1 GN=OLA1 PE=1 SV=2 | 7.47 | 4 |
| 464 | P08865 | 40S ribosomal protein SA GN=RPSA PE=1 SV=4 | 7.47 | 4 |
| 465 | P14625 | Endoplasmic reticulum chaperone GN=HSP90B1 PE=1 SV=1 | 7.45 | 4 |
| 466 | Q01813 | ATP-dependent 6-phosphofructokinase, platelet type GN=PFKP PE=1 SV=2 | 7.4 | 5 |
| 467 | Q9UEW8 | STE20/SPS1-related proline-alanine-rich protein kinase GN=STK39 PE=1 SV=3 | 7.39 | 4 |
| 468 | P58107 | Epiplakin GN=EPPK1 PE=1 SV=2 | 7.34 | 5 |
| 469 | O00584 | Ribonuclease T2 GN=RNASET2 PE=1 SV=2 | 7.33 | 4 |
| 470 | P02538 | Keratin, type II cytoskeletal 6A GN=KRT6A PE=1 SV=3 | 7.32 | 14 |
| 471 | P08571 | Monocyte differentiation antigen CD14 GN=CD14 PE=1 SV=2 | 7.32 | 5 |
| 472 | Q15056 | Eukaryotic translation initiation factor 4H GN=EIF4H PE=1 SV=5 | 7.27 | 4 |
| 473 | Q99832 | T-complex protein 1 subunit eta GN=CCT7 PE=1 SV=2 | 7.22 | 5 |
| 474 | Q9UKK9 | ADP-sugar pyrophosphatase GN=NUDT5 PE=1 SV=1 | 7.22 | 4 |
| 475 | P06314 | Ig kappa chain V-IV region B17 PE=2 SV=1 | 7.07 | 16 |
| 476 | Q8TAX9 | Gasdermin-B GN=GSDMB PE=1 SV=2 | 7.02 | 4 |
| 477 | Q96PD5 | N-acetylmuramoyl-L-alanine amidase GN=PGLYRP2 PE=1 SV=1 | 7 | 5 |
| 478 | P61970 | Nuclear transport factor 2 GN=NUTF2 PE=1 SV=1 | 7 | 5 |
| 479 | Q9Y5P6 | Mannose-1-phosphate guanylyltransferase beta GN=GMPPB PE=1 SV=2 | 6.99 | 4 |
| 480 | P28070 | Proteasome subunit beta type-4 GN=PSMB4 PE=1 SV=4 | 6.87 | 6 |

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| 481 | P61981 | 14-3-3 protein gamma GN=YWHAG PE=1 SV=2 | 6.8 | 10 |
| 482 | P34096 | Ribonuclease 4 GN=RNASE4 PE=1 SV=3 | 6.77 | 4 |
| 483 | P24666 | Low molecular weight phosphotyrosine protein phosphatase GN=ACP1 PE=1 SV=3 | 6.76 | 4 |
| 484 | P09228 | Cystatin-SA GN=CST2 PE=1 SV=1 | 6.75 | 32 |
| 485 | Q14764 | Major vault protein GN=MVP PE=1 SV=4 | 6.73 | 4 |
| 486 | Q07960 | Rho GTPase-activating protein 1 GN=ARHGAP1 PE=1 SV=1 | 6.69 | 4 |
| 487 | P19338 | Nucleolin GN=NCL PE=1 SV=3 | 6.68 | 5 |
| 488 | P62826 | GTP-binding nuclear protein Ran GN=RAN PE=1 SV=3 | 6.68 | 4 |
| 489 | P48668 | Keratin, type II cytoskeletal 6C GN=KRT6C PE=1 SV=3 | 6.68 | 10 |
| 490 | P29508 | Serpin B3 GN=SERPINB3 PE=1 SV=2 | 6.66 | 6 |
| 491 | P00491 | Purine nucleoside phosphorylase GN=PNP PE=1 SV=2 | 6.61 | 4 |
| 492 | P59998 | Actin-related protein 2/3 complex subunit 4 GN=ARPC4 PE=1 SV=3 | 6.6 | 5 |
| 493 | P62714 | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform GN=PPP2CB PE=1 SV=1 | 6.6 | 5 |
| 494 | P61019 | Ras-related protein Rab-2A GN=RAB2A PE=1 SV=1 | 6.59 | 4 |
| 495 | Q8WWI1 | LIM domain only protein 7 GN=LMO7 PE=1 SV=3 | 6.59 | 4 |
| 496 | Q9NR45 | Sialic acid synthase GN=NANS PE=1 SV=2 | 6.57 | 5 |
| 497 | P62979 | Ubiquitin-40S ribosomal protein S27a GN=RPS27A PE=1 SV=2 | 6.56 | 5 |
| 498 | P49354 | Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha GN=FNNTA PE=1 SV=1 | 6.55 | 4 |
| 499 | P61758 | Prefoldin subunit 3 GN=VBP1 PE=1 SV=3 | 6.55 | 4 |

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| 500 | P09210 | Glutathione S-transferase A2 GN=GSTA2 PE=1 SV=4 | 6.51 | 4 |
| 501 | P32455 | Interferon-induced guanylate-binding protein 1 GN=GBP1 PE=1 SV=2 | 6.42 | 3 |
| 502 | Q99954 | Submaxillary gland androgen-regulated protein 3A GN=SMR3A PE=2 SV=2 | 6.39 | 8 |
| 503 | P25786 | Proteasome subunit alpha type-1 GN=PSMA1 PE=1 SV=1 | 6.38 | 5 |
| 504 | Q9ULA0 | Aspartyl aminopeptidase GN=DNPEP PE=1 SV=1 | 6.3 | 4 |
| 505 | O43242 | 26S proteasome non-ATPase regulatory subunit 3 GN=PSMD3 PE=1 SV=2 | 6.25 | 4 |
| 506 | O95747 | Serine/threonine-protein kinase OSR1 GN=OXSR1 PE=1 SV=1 | 6.25 | 3 |
| 507 | Q14103 | Heterogeneous nuclear ribonucleoprotein D0 GN=HNRNPD PE=1 SV=1 | 6.21 | 3 |
| 508 | P49591 | Serine--tRNA ligase, cytoplasmic GN=SARS PE=1 SV=3 | 6.18 | 4 |
| 509 | P30048 | Thioredoxin-dependent peroxide reductase, mitochondrial GN=PRDX3 PE=1 SV=3 | 6.14 | 5 |
| 510 | Q3LXA3 | Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) GN=DAK PE=1 SV=2 | 6.11 | 4 |
| 511 | Q96NY7 | Chloride intracellular channel protein 6 GN=CLIC6 PE=2 SV=3 | 6.1 | 4 |
| 512 | P61204 | ADP-ribosylation factor 3 GN=ARF3 PE=1 SV=2 | 6.09 | 5 |
| 513 | P26641 | Elongation factor 1-gamma GN=EEF1G PE=1 SV=3 | 6.08 | 3 |
| 514 | Q13510 | Acid ceramidase GN=ASAH1 PE=1 SV=5 | 6.08 | 4 |
| 515 | P68036 | Ubiquitin-conjugating enzyme E2 L3 GN=UBE2L3 PE=1 SV=1 | 6.06 | 5 |
| 516 | O95865 | N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 GN=DDAH2 PE=1 SV=1 | 6.05 | 4 |

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| 517 | P31146 | Coronin-1A GN=CORO1A PE=1 SV=4 | 6.04 | 3 |
| 518 | P52895 | Aldo-keto reductase family 1 member C2 GN=AKR1C2 PE=1 SV=3 | 6.04 | 21 |
| 519 | P03973 | Antileukoproteinase GN=SLPI PE=1 SV=2 | 6.03 | 5 |
| 520 | Q9Y490 | Talin-1 GN=TLN1 PE=1 SV=3 | 6.03 | 3 |
| 521 | P63010 | AP-2 complex subunit beta GN=AP2B1 PE=1 SV=1 | 6.03 | 4 |
| 522 | Q6MZM9 | Proline-rich protein 27 GN=PRR27 PE=1 SV=1 | 6.02 | 5 |
| 523 | P01776 | Ig heavy chain V-III region WAS PE=1 SV=1 | 6.02 | 20 |
| 524 | P62942 | Peptidyl-prolyl cis-trans isomerase FKBP1A GN=FKBP1A PE=1 SV=2 | 6.01 | 5 |
| 525 | P61086 | Ubiquitin-conjugating enzyme E2 K GN=UBE2K PE=1 SV=3 | 6.01 | 3 |
| 526 | Q13561 | Dynactin subunit 2 GN=DCTN2 PE=1 SV=4 | 6.01 | 3 |
| 527 | P35221 | Catenin alpha-1 GN=CTNNA1 PE=1 SV=1 | 6.01 | 3 |
| 528 | Q9NTX5 | Ethylmalonyl-CoA decarboxylase GN=ECHDC1 PE=1 SV=2 | 6.01 | 3 |
| 529 | Q16543 | Hsp90 co-chaperone Cdc37 GN=CDC37 PE=1 SV=1 | 6.01 | 3 |
| 530 | Q7Z7M9 | Polypeptide N- acetylgalactosaminyltransferase 5 GN=GALNT5 PE=1 SV=1 | 6.01 | 3 |
| 531 | P01602 | Ig kappa chain V-I region HK102 (Fragment) GN=IGKV1-5 PE=4 SV=1 | 6.01 | 6 |
| 532 | P01717 | Ig lambda chain V-IV region Hil PE=1 SV=1 | 6 | 4 |
| 533 | P30050 | 60S ribosomal protein L12 GN=RPL12 PE=1 SV=1 | 6 | 3 |
| 534 | P58546 | Myotrophin GN=MTPN PE=1 SV=2 | 6 | 4 |
| 535 | P08294 | Extracellular superoxide dismutase [Cu-Zn] GN=SOD3 PE=1 SV=2 | 6 | 3 |
| 536 | P06331 | Ig heavy chain V-II region ARH-77 PE=4 SV=1 | 6 | 5 |

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| 537 | Q9P1F3 | Costars family protein ABRACL GN=ABRACL PE=1 SV=1 | 6 | 6 |
| 538 | P04430 | Ig kappa chain V-I region BAN PE=1 SV=1 | 6 | 9 |
| 539 | P49327 | Fatty acid synthase GN=FASN PE=1 SV=3 | 6 | 4 |
| 540 | P62888 | 60S ribosomal protein L30 GN=RPL30 PE=1 SV=2 | 6 | 3 |
| 541 | P01780 | Ig heavy chain V-III region JON PE=1 SV=1 | 6 | 9 |
| 542 | P62837 | Ubiquitin-conjugating enzyme E2 D2 GN=UBE2D2 PE=1 SV=1 | 6 | 3 |
| 543 | P04220 | Ig mu heavy chain disease protein PE=1 SV=1 | 6 | 27 |
| 544 | P13693 | Translationally-controlled tumor protein GN=TPT1 PE=1 SV=1 | 6 | 3 |
| 545 | P10768 | S-formylglutathione hydrolase GN=ESD PE=1 SV=2 | 6 | 3 |
| 546 | P04040 | Catalase GN=CAT PE=1 SV=3 | 6 | 3 |
| 547 | P61020 | Ras-related protein Rab-5B GN=RAB5B PE=1 SV=1 | 6 | 3 |
| 548 | P06753 | Tropomyosin alpha-3 chain GN=TPM3 PE=1 SV=2 | 6 | 5 |
| 549 | P61916 | Epididymal secretory protein E1 GN=NPC2 PE=1 SV=1 | 6 | 4 |
| 550 | Q5SRE7 | Phytanoyl-CoA dioxygenase domain-containing protein 1 GN=PHYHD1 PE=1 SV=2 | 6 | 3 |
| 551 | P07711 | Cathepsin L1 GN=CTSL PE=1 SV=2 | 6 | 3 |
| 552 | P63208 | S-phase kinase-associated protein 1 GN=SKP1 PE=1 SV=2 | 6 | 3 |
| 553 | P40306 | Proteasome subunit beta type-10 GN=PSMB10 PE=1 SV=1 | 6 | 4 |
| 554 | O75363 | Breast carcinoma-amplified sequence 1 GN=BCAS1 PE=1 SV=2 | 6 | 3 |
| 555 | Q99574 | Neuroserpin GN=SERPINI1 PE=1 SV=1 | 6 | 3 |
| 556 | Q9H299 | SH3 domain-binding glutamic acid-rich-like | 6 | 3 |

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|-----|--------|--|---|---|
| | | protein 3 GN=SH3BGRL3 PE=1 SV=1 | | |
| 557 | P61163 | Alpha-centractin GN=ACTR1A PE=1 SV=1 | 6 | 3 |
| 558 | P31943 | Heterogeneous nuclear ribonucleoprotein H GN=HNRNPH1 PE=1 SV=4 | 6 | 3 |
| 559 | P55327 | Tumor protein D52 GN=TPD52 PE=1 SV=2 | 6 | 3 |
| 560 | Q8N335 | Glycerol-3-phosphate dehydrogenase 1-like protein GN=GPD1L PE=1 SV=1 | 6 | 3 |
| 561 | Q99598 | Translin-associated protein X GN=TSNAX PE=1 SV=1 | 6 | 3 |
| 562 | Q14011 | Cold-inducible RNA-binding protein GN=CIRBP PE=1 SV=1 | 6 | 3 |
| 563 | P20930 | Filaggrin GN=FLG PE=1 SV=3 | 6 | 3 |
| 564 | P46976 | Glycogenin-1 GN=GYG1 PE=1 SV=4 | 6 | 3 |
| 565 | Q9BS40 | Latexin GN=LXN PE=1 SV=2 | 6 | 3 |
| 566 | Q15642 | Cdc42-interacting protein 4 GN=TRIP10 PE=1 SV=3 | 6 | 3 |
| 567 | P22102 | Trifunctional purine biosynthetic protein adenosine-3 GN=GART PE=1 SV=1 | 6 | 3 |
| 568 | Q9UBG3 | Cornulin GN=CRNN PE=1 SV=1 | 6 | 3 |
| 569 | P24158 | Myeloblastin GN=PRTN3 PE=1 SV=3 | 6 | 3 |
| 570 | P62834 | Ras-related protein Rap-1A GN=RAP1A PE=1 SV=1 | 6 | 3 |
| 571 | P16403 | Histone H1.2 GN=HIST1H1C PE=1 SV=2 | 6 | 3 |
| 572 | P62805 | Histone H4 GN=HIST1H4A PE=1 SV=2 | 6 | 3 |
| 573 | P51148 | Ras-related protein Rab-5C GN=RAB5C PE=1 SV=2 | 6 | 3 |
| 574 | Q9NRX4 | 14 kDa phosphohistidine phosphatase GN=PHPT1 PE=1 SV=1 | 6 | 3 |
| 575 | P49419 | Alpha-aminoadipic semialdehyde dehydrogenase GN=ALDH7A1 PE=1 SV=5 | 6 | 3 |
| 576 | Q8IZP2 | Putative protein FAM10A4 GN=ST13P4 PE=5 | 6 | 4 |

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| | | SV=1 | | |
| 577 | O60784 | Target of Myb protein 1 GN=TOM1 PE=1 SV=2 | 6 | 3 |
| 578 | Q9BRK5 | 45 kDa calcium-binding protein GN=SDF4 PE=1 SV=1 | 5.94 | 3 |
| 579 | O60888 | Protein CutA GN=CUTA PE=1 SV=2 | 5.93 | 4 |
| 580 | P07686 | Beta-hexosaminidase subunit beta GN=HEXB PE=1 SV=3 | 5.92 | 3 |
| 581 | P02753 | Retinol-binding protein 4 GN=RBP4 PE=1 SV=3 | 5.89 | 4 |
| 582 | P02533 | Keratin, type I cytoskeletal 14 GN=KRT14 PE=1 SV=4 | 5.89 | 11 |
| 583 | P07996 | Thrombospondin-1 GN=THBS1 PE=1 SV=2 | 5.83 | 4 |
| 584 | O15511 | Actin-related protein 2/3 complex subunit 5 GN=ARPC5 PE=1 SV=3 | 5.82 | 3 |
| 585 | P61224 | Ras-related protein Rap-1b GN=RAP1B PE=1 SV=1 | 5.8 | 3 |
| 586 | Q9BZQ8 | Protein Niban GN=FAM129A PE=1 SV=1 | 5.77 | 5 |
| 587 | P22234 | Multifunctional protein ADE2 GN=PAICS PE=1 SV=3 | 5.74 | 4 |
| 588 | P25774 | Cathepsin S GN=CTSS PE=1 SV=3 | 5.73 | 4 |
| 589 | P00505 | Aspartate aminotransferase, mitochondrial GN=GOT2 PE=1 SV=3 | 5.72 | 3 |
| 590 | Q5TDH0 | Protein DDI1 homolog 2 GN=DDI2 PE=1 SV=1 | 5.72 | 4 |
| 591 | Q14847 | LIM and SH3 domain protein 1 GN=LASP1 PE=1 SV=2 | 5.7 | 3 |
| 592 | P04003 | C4b-binding protein alpha chain GN=C4BPA PE=1 SV=2 | 5.7 | 3 |
| 593 | P20591 | Interferon-induced GTP-binding protein Mx1 GN=MX1 PE=1 SV=4 | 5.7 | 3 |
| 594 | P05120 | Plasminogen activator inhibitor 2 GN=SERPINB2 PE=1 SV=2 | 5.69 | 5 |

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| 595 | P63000 | Ras-related C3 botulinum toxin substrate 1 GN=RAC1 PE=1 SV=1 | 5.66 | 4 |
| 596 | Q8NCW5 | NAD(P)H-hydrate epimerase GN=APOA1BP PE=1 SV=2 | 5.66 | 3 |
| 597 | Q9H4G0 | Band 4.1-like protein 1 GN=EPB41L1 PE=1 SV=2 | 5.64 | 3 |
| 598 | P62491 | Ras-related protein Rab-11A GN=RAB11A PE=1 SV=3 | 5.6 | 4 |
| 599 | P05455 | Lupus La protein GN=SSB PE=1 SV=2 | 5.54 | 3 |
| 600 | P26038 | Moesin GN=MSN PE=1 SV=3 | 5.45 | 13 |
| 601 | Q96HN2 | Putative adenosylhomocysteinase 3 GN=AHCYL2 PE=1 SV=1 | 5.41 | 4 |
| 602 | O15305 | Phosphomannomutase 2 GN=PMM2 PE=1 SV=1 | 5.37 | 3 |
| 603 | Q07654 | Trefoil factor 3 GN=TFF3 PE=1 SV=1 | 5.36 | 3 |
| 604 | Q96CN7 | Isochorismatase domain-containing protein 1 GN=ISOC1 PE=1 SV=3 | 5.28 | 3 |
| 605 | Q92817 | Envoplakin GN=EVPL PE=1 SV=3 | 5.28 | 3 |
| 606 | Q9H444 | Charged multivesicular body protein 4b GN=CHMP4B PE=1 SV=1 | 5.25 | 4 |
| 607 | Q12765 | Secernin-1 GN=SCRN1 PE=1 SV=2 | 5.25 | 4 |
| 608 | P11940 | Polyadenylate-binding protein 1 GN=PABPC1 PE=1 SV=2 | 5.18 | 3 |
| 609 | Q9BPY8 | Homeodomain-only protein GN=HOPX PE=1 SV=1 | 5.17 | 3 |
| 610 | P00568 | Adenylate kinase isoenzyme 1 GN=AK1 PE=1 SV=3 | 5.15 | 4 |
| 611 | Q96L46 | Calpain small subunit 2 GN=CAPNS2 PE=2 SV=2 | 5.1 | 4 |
| 612 | P68366 | Tubulin alpha-4A chain GN=TUBA4A PE=1 SV=1 | 5.05 | 15 |
| 613 | Q9UMR2 | ATP-dependent RNA helicase DDX19B GN=DDX19B PE=1 SV=1 | 5.02 | 3 |

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|-----|--------|--|------|----|
| 614 | Q9H6S3 | Epidermal growth factor receptor kinase substrate 8-like protein 2 GN=EPS8L2 PE=1 SV=2 | 4.99 | 3 |
| 615 | Q86X76 | Nitrilase homolog 1 GN=NIT1 PE=1 SV=2 | 4.93 | 3 |
| 616 | P01762 | Ig heavy chain V-III region TRO PE=1 SV=1 | 4.92 | 13 |
| 617 | O15231 | Zinc finger protein 185 GN=ZNF185 PE=1 SV=3 | 4.89 | 3 |
| 618 | P68871 | Hemoglobin subunit beta GN=HBB PE=1 SV=2 | 4.87 | 3 |
| 619 | O95372 | Acyl-protein thioesterase 2 GN=LYPLA2 PE=1 SV=1 | 4.75 | 3 |
| 620 | P23396 | 40S ribosomal protein S3 GN=RPS3 PE=1 SV=2 | 4.74 | 4 |
| 621 | Q9BT78 | COP9 signalosome complex subunit 4 GN=COPS4 PE=1 SV=1 | 4.73 | 3 |
| 622 | P61604 | 10 kDa heat shock protein, mitochondrial GN=HSPE1 PE=1 SV=2 | 4.7 | 3 |
| 623 | Q99584 | Protein S100-A13 GN=S100A13 PE=1 SV=1 | 4.68 | 3 |
| 624 | P51858 | Hepatoma-derived growth factor GN=HDGF PE=1 SV=1 | 4.67 | 3 |
| 625 | Q8TCD5 | 5'(3')-deoxyribonucleotidase, cytosolic type GN=NT5C PE=1 SV=2 | 4.64 | 3 |
| 626 | P52597 | Heterogeneous nuclear ribonucleoprotein F GN=HNRNPF PE=1 SV=3 | 4.61 | 3 |
| 627 | Q04323 | UBX domain-containing protein 1 GN=UBXN1 PE=1 SV=2 | 4.6 | 4 |
| 628 | O75608 | Acyl-protein thioesterase 1 GN=LYPLA1 PE=1 SV=1 | 4.59 | 3 |
| 629 | P06865 | Beta-hexosaminidase subunit alpha GN=HEXA PE=1 SV=2 | 4.55 | 3 |
| 630 | P47897 | Glutamine--tRNA ligase GN=QARS PE=1 SV=1 | 4.54 | 3 |
| 631 | P02743 | Serum amyloid P-component GN=APCS PE=1 SV=2 | 4.54 | 3 |

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|-----|--------|--|------|---|
| 632 | Q15907 | Ras-related protein Rab-11B GN=RAB11B PE=1 SV=4 | 4.53 | 3 |
| 633 | P14780 | Matrix metalloproteinase-9 GN=MMP9 PE=1 SV=3 | 4.53 | 3 |
| 634 | O95361 | Tripartite motif-containing protein 16 GN=TRIM16 PE=1 SV=3 | 4.49 | 3 |
| 635 | P41250 | Glycine--tRNA ligase GN=GARS PE=1 SV=3 | 4.47 | 3 |
| 636 | Q8TE77 | Protein phosphatase Slingshot homolog 3 GN=SSH3 PE=1 SV=2 | 4.45 | 3 |
| 637 | Q16651 | Prostasin GN=PRSS8 PE=1 SV=1 | 4.42 | 4 |
| 638 | P30040 | Endoplasmic reticulum resident protein 29 GN=ERP29 PE=1 SV=4 | 4.42 | 2 |
| 639 | Q13838 | Spliceosome RNA helicase DDX39B GN=DDX39B PE=1 SV=1 | 4.39 | 3 |
| 640 | P62495 | Eukaryotic peptide chain release factor subunit 1 GN=ETF1 PE=1 SV=3 | 4.36 | 3 |
| 641 | P12081 | Histidine--tRNA ligase, cytoplasmic GN=HARS PE=1 SV=2 | 4.35 | 2 |
| 642 | P35998 | 26S protease regulatory subunit 7 GN=PSMC2 PE=1 SV=3 | 4.34 | 3 |
| 643 | O95394 | Phosphoacetylglucosamine mutase GN=PGM3 PE=1 SV=1 | 4.34 | 3 |
| 644 | P06316 | Ig lambda chain V-I region BL2 PE=2 SV=1 | 4.3 | 3 |
| 645 | Q16222 | UDP-N-acetylhexosamine pyrophosphorylase GN=UAP1 PE=1 SV=3 | 4.29 | 2 |
| 646 | O76003 | Glutaredoxin-3 GN=GLRX3 PE=1 SV=2 | 4.29 | 2 |
| 647 | Q08257 | Quinone oxidoreductase GN=CRYZ PE=1 SV=1 | 4.27 | 3 |
| 648 | P01611 | Ig kappa chain V-I region Wes PE=1 SV=1 | 4.27 | 8 |
| 649 | Q16772 | Glutathione S-transferase A3 GN=GSTA3 PE=1 SV=3 | 4.25 | 4 |
| 650 | P04066 | Tissue alpha-L-fucosidase GN=FUCA1 PE=1 SV=4 | 4.24 | 3 |

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|-----|--------|--|------|---|
| 651 | Q96HE7 | ERO1-like protein alpha GN=ERO1L PE=1 SV=2 | 4.23 | 3 |
| 652 | Q9UGI8 | Testin GN=TES PE=1 SV=1 | 4.21 | 2 |
| 653 | P14868 | Aspartate--tRNA ligase, cytoplasmic GN=DARS PE=1 SV=2 | 4.2 | 2 |
| 654 | P08697 | Alpha-2-antiplasmin GN=SERPINF2 PE=1 SV=3 | 4.18 | 2 |
| 655 | O75436 | Vacuolar protein sorting-associated protein 26A GN=VPS26A PE=1 SV=2 | 4.18 | 4 |
| 656 | Q9UQ80 | Proliferation-associated protein 2G4 GN=PA2G4 PE=1 SV=3 | 4.16 | 3 |
| 657 | P29218 | Inositol monophosphatase 1 GN=IMPA1 PE=1 SV=1 | 4.14 | 2 |
| 658 | P04207 | Ig kappa chain V-III region CLL PE=1 SV=2 | 4.13 | 7 |
| 659 | P13987 | CD59 glycoprotein GN=CD59 PE=1 SV=1 | 4.13 | 3 |
| 660 | P50238 | Cysteine-rich protein 1 GN=CRIP1 PE=1 SV=3 | 4.13 | 3 |
| 661 | Q9H361 | Polyadenylate-binding protein 3 GN=PABPC3 PE=1 SV=2 | 4.12 | 2 |
| 662 | P30047 | GTP cyclohydrolase 1 feedback regulatory protein GN=GCHFR PE=1 SV=3 | 4.11 | 3 |
| 663 | Q15257 | Serine/threonine-protein phosphatase 2A activator GN=PPP2R4 PE=1 SV=3 | 4.08 | 3 |
| 664 | P48594 | Serpin B4 GN=SERPINB4 PE=1 SV=2 | 4.07 | 4 |
| 665 | Q9NYL9 | Tropomodulin-3 GN=TMOD3 PE=1 SV=1 | 4.07 | 2 |
| 666 | P53367 | Arfaptin-1 GN=ARFIP1 PE=1 SV=2 | 4.07 | 2 |
| 667 | P01605 | Ig kappa chain V-I region Lay PE=1 SV=1 | 4.07 | 5 |
| 668 | Q9HAB8 | Phosphopantothenate--cysteine ligase GN=PPCS PE=1 SV=2 | 4.06 | 3 |
| 669 | Q7Z4W1 | L-xylulose reductase GN=DCXR PE=1 SV=2 | 4.06 | 3 |
| 670 | E9PAV3 | Nascent polypeptide-associated complex subunit alpha, muscle-specific form | 4.05 | 3 |

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|-----|--------|--|------|----|
| | | GN=NACA PE=1 SV=1 | | |
| 671 | P51884 | Lumican GN=LUM PE=1 SV=2 | 4.04 | 2 |
| 672 | P60763 | Ras-related C3 botulinum toxin substrate 3 GN=RAC3 PE=1 SV=1 | 4.04 | 2 |
| 673 | P05386 | 60S acidic ribosomal protein P1 GN=RPLP1 PE=1 SV=1 | 4.03 | 5 |
| 674 | O15145 | Actin-related protein 2/3 complex subunit 3 GN=ARPC3 PE=1 SV=3 | 4.03 | 3 |
| 675 | P39687 | Acidic leucine-rich nuclear phosphoprotein 32 family member A GN=ANP32A PE=1 SV=1 | 4.03 | 2 |
| 676 | P81605 | Dermcidin GN=DCD PE=1 SV=2 | 4.02 | 2 |
| 677 | P29466 | Caspase-1 GN=CASP1 PE=1 SV=1 | 4.02 | 3 |
| 678 | P84085 | ADP-ribosylation factor 5 GN=ARF5 PE=1 SV=2 | 4.02 | 2 |
| 679 | P06311 | Ig kappa chain V-III region IARC/BL41 PE=1 SV=1 | 4.02 | 13 |
| 680 | Q9BWS9 | Chitinase domain-containing protein 1 GN=CHID1 PE=1 SV=1 | 4.02 | 2 |
| 681 | O60610 | Protein diaphanous homolog 1 GN=DIAPH1 PE=1 SV=2 | 4.02 | 2 |
| 682 | P42224 | Signal transducer and activator of transcription 1-alpha/beta GN=STAT1 PE=1 SV=2 | 4.02 | 2 |
| 683 | Q13200 | 26S proteasome non-ATPase regulatory subunit 2 GN=PSMD2 PE=1 SV=3 | 4.01 | 2 |
| 684 | Q9NP97 | Dynein light chain roadblock-type 1 GN=DYNLRB1 PE=1 SV=3 | 4.01 | 2 |
| 685 | P01699 | Ig lambda chain V-I region VOR PE=1 SV=1 | 4.01 | 3 |
| 686 | A0M8Q6 | Ig lambda-7 chain C region GN=IGLC7 PE=1 SV=2 | 4.01 | 34 |
| 687 | Q9NT62 | Ubiquitin-like-conjugating enzyme ATG3 GN=ATG3 PE=1 SV=1 | 4.01 | 2 |
| 688 | P12830 | Cadherin-1 GN=CDH1 PE=1 SV=3 | 4.01 | 2 |

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|-----|--------|---|------|---|
| 689 | P07477 | Trypsin-1 GN=PRSS1 PE=1 SV=1 | 4.01 | 6 |
| 690 | O75348 | V-type proton ATPase subunit G 1 GN=ATP6V1G1 PE=1 SV=3 | 4.01 | 2 |
| 691 | O60506 | Heterogeneous nuclear ribonucleoprotein Q GN=SYNCRIP PE=1 SV=2 | 4 | 2 |
| 692 | Q15847 | Adipogenesis regulatory factor GN=ADIRF PE=1 SV=1 | 4 | 5 |
| 693 | Q96FQ6 | Protein S100-A16 GN=S100A16 PE=1 SV=1 | 4 | 2 |
| 694 | Q92882 | Osteoclast-stimulating factor 1 GN=OSTF1 PE=1 SV=2 | 4 | 2 |
| 695 | O60936 | Nucleolar protein 3 GN=NOL3 PE=1 SV=1 | 4 | 2 |
| 696 | Q15819 | Ubiquitin-conjugating enzyme E2 variant 2 GN=UBE2V2 PE=1 SV=4 | 4 | 2 |
| 697 | Q15121 | Astrocytic phosphoprotein PEA-15 GN=PEA15 PE=1 SV=2 | 4 | 3 |
| 698 | P55209 | Nucleosome assembly protein 1-like 1 GN=NAP1L1 PE=1 SV=1 | 4 | 2 |
| 699 | P25325 | 3-mercaptopyruvate sulfurtransferase GN=MPST PE=1 SV=3 | 4 | 2 |
| 700 | P06319 | Ig lambda chain V-VI region EB4 PE=2 SV=1 | 4 | 5 |
| 701 | P61457 | Pterin-4-alpha-carbinolamine dehydratase GN=PCBD1 PE=1 SV=2 | 4 | 3 |
| 702 | Q8N1G4 | Leucine-rich repeat-containing protein 47 GN=LRRC47 PE=1 SV=1 | 4 | 2 |
| 703 | Q9BUT1 | 3-hydroxybutyrate dehydrogenase type 2 GN=BDH2 PE=1 SV=2 | 4 | 3 |
| 704 | P25398 | 40S ribosomal protein S12 GN=RPS12 PE=1 SV=3 | 4 | 4 |
| 705 | O95782 | AP-2 complex subunit alpha-1 GN=AP2A1 PE=1 SV=3 | 4 | 2 |
| 706 | P35321 | Cornifin-A GN=SPRR1A PE=1 SV=2 | 4 | 2 |
| 707 | Q9H2G2 | STE20-like serine/threonine-protein kinase GN=SLK PE=1 SV=1 | 4 | 2 |

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| 708 | O75347 | Tubulin-specific chaperone A GN=TBCA PE=1 SV=3 | 4 | 2 |
| 709 | P52272 | Heterogeneous nuclear ribonucleoprotein M GN=HNRNPM PE=1 SV=3 | 4 | 2 |
| 710 | Q99471 | Prefoldin subunit 5 GN=PFDN5 PE=1 SV=2 | 4 | 2 |
| 711 | Q9UK22 | F-box only protein 2 GN=FBXO2 PE=1 SV=2 | 4 | 2 |
| 712 | P01767 | Ig heavy chain V-III region BUT PE=1 SV=1 | 4 | 9 |
| 713 | P01613 | Ig kappa chain V-I region Ni PE=1 SV=1 | 4 | 10 |
| 714 | Q96QK1 | Vacuolar protein sorting-associated protein 35 GN=VPS35 PE=1 SV=2 | 4 | 2 |
| 715 | Q9BW30 | Tubulin polymerization-promoting protein family member 3 GN=TPPP3 PE=1 SV=1 | 4 | 2 |
| 716 | P54725 | UV excision repair protein RAD23 homolog A GN=RAD23A PE=1 SV=1 | 4 | 2 |
| 717 | Q13740 | CD166 antigen GN=ALCAM PE=1 SV=2 | 4 | 3 |
| 718 | Q02878 | 60S ribosomal protein L6 GN=RPL6 PE=1 SV=3 | 4 | 2 |
| 719 | Q5VW32 | BRO1 domain-containing protein BROX GN=BROX PE=1 SV=1 | 4 | 2 |
| 720 | Q9GZT8 | Putative GTP cyclohydrolase 1 type 2 NIF3L1 GN=NIF3L1 PE=1 SV=2 | 4 | 2 |
| 721 | Q9HBR0 | Putative sodium-coupled neutral amino acid transporter 10 GN=SLC38A10 PE=1 SV=2 | 4 | 2 |
| 722 | Q14677 | Clathrin interactor 1 GN=CLINT1 PE=1 SV=1 | 4 | 2 |
| 723 | Q15046 | Lysine--tRNA ligase GN=KARS PE=1 SV=3 | 4 | 2 |
| 724 | P17980 | 26S protease regulatory subunit 6A GN=PSMC3 PE=1 SV=3 | 4 | 2 |
| 725 | Q99460 | 26S proteasome non-ATPase regulatory subunit 1 GN=PSMD1 PE=1 SV=2 | 4 | 2 |
| 726 | Q14118 | Dystroglycan GN=DAG1 PE=1 SV=2 | 4 | 2 |
| 727 | P09417 | Dihydropteridine reductase GN=QDPR PE=1 SV=2 | 4 | 2 |

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|-----|--------|---|---|---|
| 728 | Q9NUQ9 | Protein FAM49B GN=FAM49B PE=1 SV=1 | 4 | 2 |
| 729 | Q11201 | CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 1 GN=ST3GAL1 PE=2 SV=1 | 4 | 2 |
| 730 | P62081 | 40S ribosomal protein S7 GN=RPS7 PE=1 SV=1 | 4 | 2 |
| 731 | P31944 | Caspase-14 GN=CASP14 PE=1 SV=2 | 4 | 3 |
| 732 | P02747 | Complement C1q subcomponent subunit C GN=C1QC PE=1 SV=3 | 4 | 2 |
| 733 | NA | Biognosys Retention time kit peptide | 4 | 4 |
| 734 | P62857 | 40S ribosomal protein S28 GN=RPS28 PE=1 SV=1 | 4 | 2 |
| 735 | P01714 | Ig lambda chain V-III region SH PE=1 SV=1 | 4 | 4 |
| 736 | NA | Biognosys Retention time kit peptide | 4 | 3 |
| 737 | NA | Biognosys Retention time kit peptide | 4 | 2 |
| 738 | P22528 | Cornifin-B GN=SPRR1B PE=1 SV=2 | 4 | 3 |
| 739 | P24534 | Elongation factor 1-beta GN=EEF1B2 PE=1 SV=3 | 4 | 2 |
| 740 | P41226 | Ubiquitin-like modifier-activating enzyme 7 GN=UBA7 PE=1 SV=2 | 4 | 2 |
| 741 | P16402 | Histone H1.3 GN=HIST1H1D PE=1 SV=2 | 4 | 2 |
| 742 | P09758 | Tumor-associated calcium signal transducer 2 GN=TACSTD2 PE=1 SV=3 | 4 | 2 |
| 743 | P01763 | Ig heavy chain V-III region WEA PE=1 SV=1 | 4 | 7 |
| 744 | P26639 | Threonine--tRNA ligase, cytoplasmic GN=TARS PE=1 SV=3 | 4 | 2 |
| 745 | Q9H788 | SH2 domain-containing protein 4A GN=SH2D4A PE=1 SV=1 | 4 | 2 |
| 746 | O60749 | Sorting nexin-2 GN=SNX2 PE=1 SV=2 | 4 | 3 |
| 747 | Q8N1Q1 | Carbonic anhydrase 13 GN=CA13 PE=1 SV=1 | 4 | 3 |
| 748 | P54819 | Adenylate kinase 2, mitochondrial GN=AK2 | 4 | 3 |

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| | | PE=1 SV=2 | | |
| 749 | Q92896 | Golgi apparatus protein 1 GN=GLG1 PE=1 SV=2 | 4 | 2 |
| 750 | Q53EL6 | Programmed cell death protein 4 GN=PDCD4 PE=1 SV=2 | 4 | 2 |
| 751 | P55735 | Protein SEC13 homolog GN=SEC13 PE=1 SV=3 | 4 | 2 |
| 752 | P22059 | Oxysterol-binding protein 1 GN=OSBP PE=1 SV=1 | 4 | 2 |
| 753 | Q15019 | Septin-2 GN=SEPT2 PE=1 SV=1 | 4 | 2 |
| 754 | P35813 | Protein phosphatase 1A GN=PPM1A PE=1 SV=1 | 4 | 2 |
| 755 | P63220 | 40S ribosomal protein S21 GN=RPS21 PE=1 SV=1 | 4 | 3 |
| 756 | Q16531 | DNA damage-binding protein 1 GN=DDB1 PE=1 SV=1 | 4 | 2 |
| 757 | Q02790 | Peptidyl-prolyl cis-trans isomerase FKBP4 GN=FKBP4 PE=1 SV=3 | 4 | 2 |
| 758 | P30626 | Sorcin GN=SRI PE=1 SV=1 | 4 | 3 |
| 759 | Q8TE68 | Epidermal growth factor receptor kinase substrate 8-like protein 1 GN=EPS8L1 PE=1 SV=3 | 4 | 2 |
| 760 | Q8NBS9 | Thioredoxin domain-containing protein 5 GN=TXNDC5 PE=1 SV=2 | 4 | 2 |
| 761 | Q15631 | Translin GN=TSN PE=1 SV=1 | 4 | 2 |
| 762 | P61077 | Ubiquitin-conjugating enzyme E2 D3 GN=UBE2D3 PE=1 SV=1 | 4 | 2 |
| 763 | Q9NZ08 | Endoplasmic reticulum aminopeptidase 1 GN=ERAP1 PE=1 SV=3 | 4 | 2 |
| 764 | P02794 | Ferritin heavy chain GN=FTH1 PE=1 SV=2 | 4 | 2 |
| 765 | Q13404 | Ubiquitin-conjugating enzyme E2 variant 1 GN=UBE2V1 PE=1 SV=2 | 4 | 2 |
| 766 | B0FP48 | Uroplakin-3b-like protein GN=UPK3BL PE=2 | 4 | 2 |

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|-----|--------|--|---|----|
| | | SV=1 | | |
| 767 | P08246 | Neutrophil elastase GN=ELANE PE=1 SV=1 | 4 | 2 |
| 768 | Q15185 | Prostaglandin E synthase 3 GN=PTGES3 PE=1 SV=1 | 4 | 3 |
| 769 | P01619 | Ig kappa chain V-III region B6 PE=1 SV=1 | 4 | 14 |
| 770 | Q8NCL4 | Polypeptide N-acetylgalactosaminyltransferase 6 GN=GALNT6 PE=2 SV=2 | 4 | 2 |
| 771 | P54136 | Arginine--tRNA ligase, cytoplasmic GN=RARS PE=1 SV=2 | 4 | 2 |
| 772 | Q14002 | Carcinoembryonic antigen-related cell adhesion molecule 7 GN=CEACAM7 PE=1 SV=1 | 4 | 2 |
| 773 | P43487 | Ran-specific GTPase-activating protein GN=RANBP1 PE=1 SV=1 | 4 | 2 |
| 774 | Q14203 | Dynactin subunit 1 GN=DCTN1 PE=1 SV=3 | 4 | 2 |
| 775 | P02545 | Prelamin-A/C GN=LMNA PE=1 SV=1 | 4 | 2 |
| 776 | P25705 | ATP synthase subunit alpha, mitochondrial GN=ATP5A1 PE=1 SV=1 | 4 | 2 |
| 777 | P14854 | Cytochrome c oxidase subunit 6B1 GN=COX6B1 PE=1 SV=2 | 4 | 2 |
| 778 | P53634 | Dipeptidyl peptidase 1 GN=CTSC PE=1 SV=2 | 4 | 2 |
| 779 | P80419 | Ig heavy chain V-III region GAR PE=1 SV=1 | 4 | 6 |
| 780 | P53621 | Coatomer subunit alpha GN=COPA PE=1 SV=2 | 4 | 3 |
| 781 | P54577 | Tyrosine--tRNA ligase, cytoplasmic GN=YARS PE=1 SV=4 | 4 | 2 |
| 782 | P60983 | Glia maturation factor beta GN=GMFB PE=1 SV=2 | 4 | 2 |
| 783 | P55795 | Heterogeneous nuclear ribonucleoprotein H2 GN=HNRNPH2 PE=1 SV=1 | 4 | 2 |
| 784 | P41222 | Prostaglandin-H2 D-isomerase GN=PTGDS PE=1 SV=1 | 4 | 2 |

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|-----|--------|---|---|----|
| 785 | Q9BTM1 | Histone H2A.J GN=H2AFJ PE=1 SV=1 | 4 | 2 |
| 786 | P06681 | Complement C2 GN=C2 PE=1 SV=2 | 4 | 2 |
| 787 | P26599 | Polypyrimidine tract-binding protein 1 GN=PTBP1 PE=1 SV=1 | 4 | 2 |
| 788 | P55064 | Aquaporin-5 GN=AQP5 PE=1 SV=1 | 4 | 2 |
| 789 | P19957 | Elafin GN=PI3 PE=1 SV=3 | 4 | 2 |
| 790 | O75131 | Copine-3 GN=CPNE3 PE=1 SV=1 | 4 | 2 |
| 791 | P50914 | 60S ribosomal protein L14 GN=RPL14 PE=1 SV=4 | 4 | 2 |
| 792 | P33176 | Kinesin-1 heavy chain GN=KIF5B PE=1 SV=1 | 4 | 2 |
| 793 | P02144 | Myoglobin GN=MB PE=1 SV=2 | 4 | 2 |
| 794 | P11586 | C-1-tetrahydrofolate synthase, cytoplasmic GN=MTHFD1 PE=1 SV=3 | 4 | 2 |
| 795 | Q99798 | Aconitate hydratase, mitochondrial GN=ACO2 PE=1 SV=2 | 4 | 2 |
| 796 | P68032 | Actin, alpha cardiac muscle 1 GN=ACTC1 PE=1 SV=1 | 4 | 32 |
| 797 | P05198 | Eukaryotic translation initiation factor 2 subunit 1 GN=EIF2S1 PE=1 SV=3 | 4 | 2 |
| 798 | Q16204 | Coiled-coil domain-containing protein 6 GN=CCDC6 PE=1 SV=2 | 4 | 2 |
| 799 | P67809 | Nuclease-sensitive element-binding protein 1 GN=YBX1 PE=1 SV=3 | 4 | 2 |
| 800 | P20339 | Ras-related protein Rab-5A GN=RAB5A PE=1 SV=2 | 4 | 2 |
| 801 | P15941 | Mucin-1 GN=MUC1 PE=1 SV=3 | 4 | 2 |
| 802 | Q99733 | Nucleosome assembly protein 1-like 4 GN=NAP1L4 PE=1 SV=1 | 4 | 2 |
| 803 | Q2VIR3 | Putative eukaryotic translation initiation factor 2 subunit 3-like protein GN=EIF2S3L PE=5 SV=2 | 4 | 2 |
| 804 | Q9UNM6 | 26S proteasome non-ATPase regulatory | 4 | 2 |

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|-----|--------|--|------|---|
| | | subunit 13 GN=PSMD13 PE=1 SV=2 | | |
| 805 | P08118 | Beta-microseminoprotein GN=MSMB PE=1 SV=1 | 4 | 2 |
| 806 | P32456 | Interferon-induced guanylate-binding protein 2 GN=GBP2 PE=1 SV=3 | 4 | 2 |
| 807 | Q9HCY8 | Protein S100-A14 GN=S100A14 PE=1 SV=1 | 4 | 2 |
| 808 | P35326 | Small proline-rich protein 2A GN=SPRR2A PE=1 SV=1 | 3.96 | 2 |
| 809 | P05156 | Complement factor I GN=CFI PE=1 SV=2 | 3.96 | 2 |
| 810 | O75882 | Attractin GN=ATRN PE=1 SV=2 | 3.96 | 2 |
| 811 | Q9NRV9 | Heme-binding protein 1 GN=HEBP1 PE=1 SV=1 | 3.92 | 2 |
| 812 | P46781 | 40S ribosomal protein S9 GN=RPS9 PE=1 SV=3 | 3.92 | 2 |
| 813 | P28482 | Mitogen-activated protein kinase 1 GN=MAPK1 PE=1 SV=3 | 3.91 | 5 |
| 814 | Q9H2U2 | Inorganic pyrophosphatase 2, mitochondrial GN=PPA2 PE=1 SV=2 | 3.89 | 3 |
| 815 | P00492 | Hypoxanthine-guanine phosphoribosyltransferase GN=HPRT1 PE=1 SV=2 | 3.89 | 2 |
| 816 | P07954 | Fumarate hydratase, mitochondrial GN=FH PE=1 SV=3 | 3.89 | 2 |
| 817 | Q9Y2S2 | Lambda-crystallin homolog GN=CRYL1 PE=1 SV=3 | 3.85 | 2 |
| 818 | P10412 | Histone H1.4 GN=HIST1H1E PE=1 SV=2 | 3.85 | 3 |
| 819 | P31153 | S-adenosylmethionine synthase isoform type-2 GN=MAT2A PE=1 SV=1 | 3.82 | 2 |
| 820 | Q9H008 | Phospholysine phosphohistidine inorganic pyrophosphate phosphatase GN=LHPP PE=1 SV=2 | 3.8 | 2 |
| 821 | P48444 | Coatomer subunit delta GN=ARCN1 PE=1 SV=1 | 3.78 | 2 |

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|-----|--------|---|------|---|
| 822 | P59666 | Neutrophil defensin 3 GN=DEFA3 PE=1 SV=1 | 3.74 | 3 |
| 823 | P01814 | Ig heavy chain V-II region OU PE=1 SV=1 | 3.74 | 2 |
| 824 | Q96DR8 | Mucin-like protein 1 GN=MUCL1 PE=1 SV=1 | 3.74 | 3 |
| 825 | Q92530 | Proteasome inhibitor PI31 subunit GN=PSMF1 PE=1 SV=2 | 3.7 | 3 |
| 826 | P01703 | Ig lambda chain V-I region NEWM PE=1 SV=1 | 3.68 | 3 |
| 827 | P27361 | Mitogen-activated protein kinase 3 GN=MAPK3 PE=1 SV=4 | 3.64 | 2 |
| 828 | Q7Z4S6 | Kinesin-like protein KIF21A GN=KIF21A PE=1 SV=2 | 3.62 | 2 |
| 829 | Q99877 | Histone H2B type 1-N GN=HIST1H2BN PE=1 SV=3 | 3.62 | 2 |
| 830 | P13861 | cAMP-dependent protein kinase type II-alpha regulatory subunit GN=PRKAR2A PE=1 SV=2 | 3.6 | 3 |
| 831 | O43399 | Tumor protein D54 GN=TPD52L2 PE=1 SV=2 | 3.59 | 2 |
| 832 | P28065 | Proteasome subunit beta type-9 GN=PSMB9 PE=1 SV=2 | 3.58 | 2 |
| 833 | P15374 | Ubiquitin carboxyl-terminal hydrolase isozyme L3 GN=UCHL3 PE=1 SV=1 | 3.57 | 2 |
| 834 | P41091 | Eukaryotic translation initiation factor 2 subunit 3 GN=EIF2S3 PE=1 SV=3 | 3.52 | 2 |
| 835 | P13671 | Complement component C6 GN=C6 PE=1 SV=3 | 3.51 | 2 |
| 836 | P30084 | Enoyl-CoA hydratase, mitochondrial GN=ECHS1 PE=1 SV=4 | 3.51 | 2 |
| 837 | O00592 | Podocalyxin GN=PODXL PE=1 SV=2 | 3.42 | 2 |
| 838 | P08185 | Corticosteroid-binding globulin GN=SERPINA6 PE=1 SV=1 | 3.41 | 2 |
| 839 | Q15691 | Microtubule-associated protein RP/EB family member 1 GN=MAPRE1 PE=1 SV=3 | 3.38 | 2 |
| 840 | Q6PCB0 | von Willebrand factor A domain-containing protein 1 GN=VWA1 PE=2 SV=1 | 3.37 | 2 |

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|-----|--------|---|------|---|
| 841 | Q13296 | Mammaglobin-A GN=SCGB2A2 PE=1 SV=1 | 3.37 | 2 |
| 842 | P12259 | Coagulation factor V GN=F5 PE=1 SV=4 | 3.36 | 2 |
| 843 | P12277 | Creatine kinase B-type GN=CKB PE=1 SV=1 | 3.34 | 2 |
| 844 | Q9H773 | dCTP pyrophosphatase 1 GN=DCTPP1 PE=1 SV=1 | 3.34 | 2 |
| 845 | P53041 | Serine/threonine-protein phosphatase 5 GN=PPP5C PE=1 SV=1 | 3.34 | 2 |
| 846 | Q9Y4L1 | Hypoxia up-regulated protein 1 GN=HYOU1 PE=1 SV=1 | 3.34 | 2 |
| 847 | P15814 | Immunoglobulin lambda-like polypeptide 1 GN=IGLL1 PE=1 SV=1 | 3.33 | 6 |
| 848 | Q6DKJ4 | Nucleoredoxin GN=NXN PE=1 SV=2 | 3.33 | 3 |
| 849 | P27169 | Serum paraoxonase/arylesterase 1 GN=PON1 PE=1 SV=3 | 3.32 | 2 |
| 850 | Q9UHL4 | Dipeptidyl peptidase 2 GN=DPP7 PE=1 SV=3 | 3.31 | 2 |
| 851 | Q9H0R4 | Haloacid dehalogenase-like hydrolase domain-containing protein 2 GN=HDHD2 PE=1 SV=1 | 3.31 | 2 |
| 852 | P54578 | Ubiquitin carboxyl-terminal hydrolase 14 GN=USP14 PE=1 SV=3 | 3.28 | 2 |
| 853 | Q9Y6E0 | Serine/threonine-protein kinase 24 GN=STK24 PE=1 SV=1 | 3.25 | 2 |
| 854 | O95833 | Chloride intracellular channel protein 3 GN=CLIC3 PE=1 SV=2 | 3.24 | 2 |
| 855 | O95395 | Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 3 GN=GCNT3 PE=2 SV=1 | 3.23 | 2 |
| 856 | Q13442 | 28 kDa heat- and acid-stable phosphoprotein GN=PDAP1 PE=1 SV=1 | 3.23 | 2 |
| 857 | P06888 | Ig lambda chain V-I region EPS PE=1 SV=1 | 3.23 | 4 |
| 858 | Q99880 | Histone H2B type 1-L GN=HIST1H2BL PE=1 SV=3 | 3.21 | 2 |
| 859 | Q8NI22 | Multiple coagulation factor deficiency protein 2 | 3.19 | 2 |

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|-----|--------|---|------|----|
| | | GN=MCFD2 PE=1 SV=1 | | |
| 860 | P09871 | Complement C1s subcomponent GN=C1S PE=1 SV=1 | 3.19 | 2 |
| 861 | P01861 | Ig gamma-4 chain C region GN=IGHG4 PE=1 SV=1 | 3.19 | 48 |
| 862 | P13667 | Protein disulfide-isomerase A4 GN=PDIA4 PE=1 SV=2 | 3.15 | 3 |
| 863 | O14737 | Programmed cell death protein 5 GN=PDCD5 PE=1 SV=3 | 3.15 | 2 |
| 864 | Q9Y266 | Nuclear migration protein nudC GN=NUDC PE=1 SV=1 | 3.15 | 2 |
| 865 | Q9BS26 | Endoplasmic reticulum resident protein 44 GN=ERP44 PE=1 SV=1 | 3.09 | 2 |
| 866 | Q12805 | EGF-containing fibulin-like extracellular matrix protein 1 GN=EFEMP1 PE=1 SV=2 | 3.05 | 2 |
| 867 | Q6IBS0 | Twinfilin-2 GN=TWF2 PE=1 SV=2 | 2.99 | 2 |
| 868 | P55011 | Solute carrier family 12 member 2 GN=SLC12A2 PE=1 SV=1 | 2.96 | 2 |
| 869 | P04431 | Ig kappa chain V-I region Walker PE=1 SV=1 | 2.96 | 12 |
| 870 | P42574 | Caspase-3 GN=CASP3 PE=1 SV=2 | 2.94 | 2 |
| 871 | Q8TBC4 | NEDD8-activating enzyme E1 catalytic subunit GN=UBA3 PE=1 SV=2 | 2.92 | 2 |
| 872 | P54920 | Alpha-soluble NSF attachment protein GN=NAPA PE=1 SV=3 | 2.92 | 2 |
| 873 | P01880 | Ig delta chain C region GN=IGHD PE=1 SV=2 | 2.91 | 2 |
| 874 | Q03591 | Complement factor H-related protein 1 GN=CFHR1 PE=1 SV=2 | 2.9 | 4 |
| 875 | Q9BY32 | Inosine triphosphate pyrophosphatase GN=ITPA PE=1 SV=2 | 2.9 | 2 |
| 876 | P03950 | Angiogenin GN=ANG PE=1 SV=1 | 2.85 | 2 |
| 877 | Q00169 | Phosphatidylinositol transfer protein alpha isoform GN=PITPNA PE=1 SV=2 | 2.85 | 2 |

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|-----|--------|---|------|----|
| 878 | P52943 | Cysteine-rich protein 2 GN=CRIP2 PE=1 SV=1 | 2.83 | 2 |
| 879 | Q8N257 | Histone H2B type 3-B GN=HIST3H2BB PE=1 SV=3 | 2.83 | 2 |
| 880 | Q5VT79 | Annexin A8-like protein 2 GN=ANXA8L2 PE=2 SV=1 | 2.78 | 2 |
| 881 | P19021 | Peptidyl-glycine alpha-amidating monooxygenase GN=PAM PE=1 SV=2 | 2.77 | 2 |
| 882 | Q8WXI7 | Mucin-16 GN=MUC16 PE=1 SV=2 | 2.75 | 2 |
| 883 | Q9BV40 | Vesicle-associated membrane protein 8 GN=VAMP8 PE=1 SV=1 | 2.75 | 2 |
| 884 | Q15008 | 26S proteasome non-ATPase regulatory subunit 6 GN=PSMD6 PE=1 SV=1 | 2.7 | 2 |
| 885 | O95861 | 3'(2'),5'-bisphosphate nucleotidase 1 GN=BPNT1 PE=1 SV=1 | 2.7 | 3 |
| 886 | Q9Y2V2 | Calcium-regulated heat stable protein 1 GN=CARHSP1 PE=1 SV=2 | 2.68 | 2 |
| 887 | Q96GG9 | DCN1-like protein 1 GN=DCUN1D1 PE=1 SV=1 | 2.66 | 2 |
| 888 | P01597 | Ig kappa chain V-I region DEE PE=1 SV=1 | 2.65 | 14 |
| 889 | Q9UDY2 | Tight junction protein ZO-2 GN=TJP2 PE=1 SV=2 | 2.63 | 2 |
| 890 | Q12840 | Kinesin heavy chain isoform 5A GN=KIF5A PE=1 SV=2 | 2.59 | 2 |
| 891 | P52788 | Spermine synthase GN=SMS PE=1 SV=2 | 2.57 | 2 |
| 892 | O14908 | PDZ domain-containing protein GIPC1 GN=GIPC1 PE=1 SV=2 | 2.56 | 2 |
| 893 | Q99879 | Histone H2B type 1-M GN=HIST1H2BM PE=1 SV=3 | 2.53 | 2 |
| 894 | Q9Y315 | Putative deoxyribose-phosphate aldolase GN=DERA PE=1 SV=2 | 2.52 | 2 |
| 895 | O14773 | Tripeptidyl-peptidase 1 GN=TPP1 PE=1 SV=2 | 2.49 | 2 |
| 896 | Q15843 | NEDD8 GN=NEDD8 PE=1 SV=1 | 2.48 | 3 |

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|-----|--------|--|------|---|
| 897 | P05186 | Alkaline phosphatase, tissue-nonspecific isozyme GN=ALPL PE=1 SV=4 | 2.48 | 2 |
| 898 | Q9H3K6 | BolA-like protein 2 GN=BOLA2 PE=1 SV=1 | 2.46 | 2 |
| 899 | P22061 | Protein-L-isoaspartate(D-aspartate) O-methyltransferase GN=PCMT1 PE=1 SV=4 | 2.42 | 2 |
| 900 | P80217 | Interferon-induced 35 kDa protein GN=IFI35 PE=1 SV=5 | 2.37 | 2 |
| 901 | Q8WXG9 | G-protein coupled receptor 98 GN=GPR98 PE=1 SV=2 | 2.36 | 2 |
| 902 | P04433 | Ig kappa chain V-III region VG (Fragment) PE=1 SV=1 | 2.35 | 7 |
| 903 | O94760 | N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 GN=DDAH1 PE=1 SV=3 | 2.34 | 3 |
| 904 | P15559 | NAD(P)H dehydrogenase [quinone] 1 GN=NQO1 PE=1 SV=1 | 2.32 | 2 |
| 905 | Q9BV20 | Methylthioribose-1-phosphate isomerase GN=MRI1 PE=1 SV=1 | 2.32 | 2 |
| 906 | Q02487 | Desmocollin-2 GN=DSC2 PE=1 SV=1 | 2.31 | 2 |
| 907 | Q9Y3C8 | Ubiquitin-fold modifier-conjugating enzyme 1 GN=UFC1 PE=1 SV=3 | 2.31 | 2 |
| 908 | Q00341 | Vigilin GN=HDLBP PE=1 SV=2 | 2.31 | 2 |
| 909 | O43598 | 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 GN=DNPH1 PE=1 SV=1 | 2.3 | 1 |
| 910 | Q9Y3F4 | Serine-threonine kinase receptor-associated protein GN=STRAP PE=1 SV=1 | 2.28 | 2 |
| 911 | Q12882 | Dihydropyrimidine dehydrogenase [NADP(+)] GN=DPYD PE=1 SV=2 | 2.27 | 1 |
| 912 | Q14126 | Desmoglein-2 GN=DSG2 PE=1 SV=2 | 2.26 | 2 |
| 913 | P15880 | 40S ribosomal protein S2 GN=RPS2 PE=1 SV=2 | 2.25 | 2 |
| 914 | P23588 | Eukaryotic translation initiation factor 4B GN=EIF4B PE=1 SV=2 | 2.24 | 1 |

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|-----|--------|---|------|---|
| 915 | Q8IWE2 | Protein NOXP20 GN=FAM114A1 PE=1 SV=2 | 2.22 | 2 |
| 916 | P53618 | Coatomer subunit beta GN=COPB1 PE=1 SV=3 | 2.21 | 1 |
| 917 | Q9BWD1 | Acetyl-CoA acetyltransferase, cytosolic GN=ACAT2 PE=1 SV=2 | 2.2 | 2 |
| 918 | Q8NHP1 | Aflatoxin B1 aldehyde reductase member 4 GN=AKR7L PE=2 SV=6 | 2.2 | 1 |
| 919 | P55884 | Eukaryotic translation initiation factor 3 subunit B GN=EIF3B PE=1 SV=3 | 2.2 | 1 |
| 920 | O43768 | Alpha-endosulfine GN=ENSA PE=1 SV=1 | 2.19 | 1 |
| 921 | Q9Y3Z3 | Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 GN=SAMHD1 PE=1 SV=2 | 2.18 | 1 |
| 922 | O14907 | Tax1-binding protein 3 GN=TAX1BP3 PE=1 SV=2 | 2.15 | 2 |
| 923 | Q9UFH2 | Dynein heavy chain 17, axonemal GN=DNAH17 PE=1 SV=2 | 2.13 | 2 |
| 924 | Q15746 | Myosin light chain kinase, smooth muscle GN=MYLK PE=1 SV=4 | 2.11 | 2 |
| 925 | Q7L576 | Cytoplasmic FMR1-interacting protein 1 GN=CYFIP1 PE=1 SV=1 | 2.11 | 1 |
| 926 | P48556 | 26S proteasome non-ATPase regulatory subunit 8 GN=PSMD8 PE=1 SV=2 | 2.09 | 2 |
| 927 | Q8NC51 | Plasminogen activator inhibitor 1 RNA-binding protein GN=SERBP1 PE=1 SV=2 | 2.08 | 1 |
| 928 | P49588 | Alanine--tRNA ligase, cytoplasmic GN=AARS PE=1 SV=2 | 2.08 | 2 |
| 929 | P43686 | 26S protease regulatory subunit 6B GN=PSMC4 PE=1 SV=2 | 2.07 | 2 |
| 930 | O15212 | Prefoldin subunit 6 GN=PFDN6 PE=1 SV=1 | 2.07 | 1 |
| 931 | P08174 | Complement decay-accelerating factor GN=CD55 PE=1 SV=4 | 2.07 | 1 |
| 932 | Q32MZ4 | Leucine-rich repeat flightless-interacting protein 1 GN=LRRFIP1 PE=1 SV=2 | 2.06 | 1 |

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|-----|--------|--|------|---|
| 933 | Q13867 | Bleomycin hydrolase GN=BLMH PE=1 SV=1 | 2.06 | 1 |
| 934 | Q8NI27 | THO complex subunit 2 GN=THOC2 PE=1 SV=2 | 2.06 | 1 |
| 935 | P01612 | Ig kappa chain V-I region Mev PE=1 SV=1 | 2.06 | 4 |
| 936 | Q96CW1 | AP-2 complex subunit mu GN=AP2M1 PE=1 SV=2 | 2.06 | 1 |
| 937 | P46109 | Crk-like protein GN=CRKL PE=1 SV=1 | 2.06 | 1 |
| 938 | P53396 | ATP-citrate synthase GN=ACLY PE=1 SV=3 | 2.06 | 2 |
| 939 | Q9P2E9 | Ribosome-binding protein 1 GN=RRBP1 PE=1 SV=4 | 2.05 | 1 |
| 940 | P14923 | Junction plakoglobin GN=JUP PE=1 SV=3 | 2.04 | 1 |
| 941 | Q6UXB2 | VEGF coregulated chemokine 1 GN=CXCL17 PE=1 SV=1 | 2.04 | 1 |
| 942 | O14618 | Copper chaperone for superoxide dismutase GN=CCS PE=1 SV=1 | 2.04 | 1 |
| 943 | O60763 | General vesicular transport factor p115 GN=USO1 PE=1 SV=2 | 2.04 | 2 |
| 944 | Q14019 | Coactosin-like protein GN=COTL1 PE=1 SV=3 | 2.04 | 1 |
| 945 | O94973 | AP-2 complex subunit alpha-2 GN=AP2A2 PE=1 SV=2 | 2.04 | 1 |
| 946 | Q9UH65 | Switch-associated protein 70 GN=SWAP70 PE=1 SV=1 | 2.04 | 2 |
| 947 | P84103 | Serine/arginine-rich splicing factor 3 GN=SRSF3 PE=1 SV=1 | 2.04 | 1 |
| 948 | P12109 | Collagen alpha-1(VI) chain GN=COL6A1 PE=1 SV=3 | 2.03 | 2 |
| 949 | P35270 | Sepiapterin reductase GN=SPR PE=1 SV=1 | 2.03 | 1 |
| 950 | P27695 | DNA-(apurinic or apyrimidinic site) lyase GN=APEX1 PE=1 SV=2 | 2.03 | 3 |
| 951 | O94811 | Tubulin polymerization-promoting protein GN=TPPP PE=1 SV=1 | 2.03 | 2 |
| 952 | Q96FV2 | Secernin-2 GN=SCRN2 PE=1 SV=3 | 2.03 | 2 |

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|-----|--------|--|------|----|
| 953 | O00244 | Copper transport protein ATOX1 GN=ATOX1 PE=1 SV=1 | 2.03 | 2 |
| 954 | O00231 | 26S proteasome non-ATPase regulatory subunit 11 GN=PSMD11 PE=1 SV=3 | 2.03 | 2 |
| 955 | P63096 | Guanine nucleotide-binding protein G(i) subunit alpha-1 GN=GNAI1 PE=1 SV=2 | 2.03 | 1 |
| 956 | O43423 | Acidic leucine-rich nuclear phosphoprotein 32 family member C GN=ANP32C PE=2 SV=1 | 2.03 | 2 |
| 957 | Q09028 | Histone-binding protein RBBP4 GN=RBBP4 PE=1 SV=3 | 2.03 | 1 |
| 958 | P01616 | Ig kappa chain V-II region MIL PE=1 SV=1 | 2.02 | 12 |
| 959 | Q00534 | Cyclin-dependent kinase 6 GN=CDK6 PE=1 SV=1 | 2.02 | 1 |
| 960 | Q96F07 | Cytoplasmic FMR1-interacting protein 2 GN=CYFIP2 PE=1 SV=2 | 2.02 | 1 |
| 961 | O43813 | LanC-like protein 1 GN=LANCL1 PE=1 SV=1 | 2.01 | 1 |
| 962 | Q8WZA0 | Protein LZIC GN=LZIC PE=1 SV=1 | 2.01 | 1 |
| 963 | P62191 | 26S protease regulatory subunit 4 GN=PSMC1 PE=1 SV=1 | 2.01 | 1 |
| 964 | O60684 | Importin subunit alpha-7 GN=KPNA6 PE=1 SV=1 | 2.01 | 2 |
| 965 | P15170 | Eukaryotic peptide chain release factor GTP-binding subunit ERF3A GN=GSPT1 PE=1 SV=1 | 2.01 | 2 |
| 966 | P62906 | 60S ribosomal protein L10a GN=RPL10A PE=1 SV=2 | 2.01 | 1 |
| 967 | P62333 | 26S protease regulatory subunit 10B GN=PSMC6 PE=1 SV=1 | 2.01 | 2 |
| 968 | Q9Y6Q5 | AP-1 complex subunit mu-2 GN=AP1M2 PE=1 SV=4 | 2.01 | 1 |
| 969 | Q14116 | Interleukin-18 GN=IL18 PE=1 SV=1 | 2.01 | 1 |
| 970 | Q15404 | Ras suppressor protein 1 GN=RSU1 PE=1 SV=3 | 2.01 | 1 |

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|-----|--------|---|------|----|
| 971 | Q13162 | Peroxiredoxin-4 GN=PRDX4 PE=1 SV=1 | 2.01 | 9 |
| 972 | P09668 | Pro-cathepsin H GN=CTSH PE=1 SV=4 | 2.01 | 1 |
| 973 | P01040 | Cystatin-A GN=CSTA PE=1 SV=1 | 2.01 | 1 |
| 974 | Q8IU85 | Calcium/calmodulin-dependent protein kinase type 1D GN=CAMK1D PE=1 SV=1 | 2.01 | 1 |
| 975 | Q9UHD8 | Septin-9 GN=SEPT9 PE=1 SV=2 | 2.01 | 2 |
| 976 | A0AVT1 | Ubiquitin-like modifier-activating enzyme 6 GN=UBA6 PE=1 SV=1 | 2.01 | 2 |
| 977 | Q9Y263 | Phospholipase A-2-activating protein GN=PLAA PE=1 SV=2 | 2.01 | 1 |
| 978 | P36543 | V-type proton ATPase subunit E 1 GN=ATP6V1E1 PE=1 SV=1 | 2.01 | 1 |
| 979 | Q9NZL9 | Methionine adenosyltransferase 2 subunit beta GN=MAT2B PE=1 SV=1 | 2.01 | 2 |
| 980 | Q15327 | Ankyrin repeat domain-containing protein 1 GN=ANKRD1 PE=1 SV=2 | 2.01 | 1 |
| 981 | Q9UPS8 | Ankyrin repeat domain-containing protein 26 GN=ANKRD26 PE=1 SV=3 | 2.01 | 1 |
| 982 | P01860 | Ig gamma-3 chain C region GN=IGHG3 PE=1 SV=2 | 2 | 50 |
| 983 | P01770 | Ig heavy chain V-III region NIE PE=1 SV=1 | 2 | 9 |
| 984 | Q14152 | Eukaryotic translation initiation factor 3 subunit A GN=EIF3A PE=1 SV=1 | 2 | 1 |
| 985 | P19367 | Hexokinase-1 GN=HK1 PE=1 SV=3 | 2 | 1 |
| 986 | Q9UM54 | Unconventional myosin-VI GN=MYO6 PE=1 SV=4 | 2 | 1 |
| 987 | Q9UNH7 | Sorting nexin-6 GN=SNX6 PE=1 SV=1 | 2 | 1 |
| 988 | Q8IYJ1 | Copine-9 GN=CPNE9 PE=1 SV=3 | 2 | 1 |
| 989 | O00571 | ATP-dependent RNA helicase DDX3X GN=DDX3X PE=1 SV=3 | 2 | 1 |
| 990 | Q9BW04 | Specifically androgen-regulated gene protein GN=SARG PE=1 SV=2 | 2 | 1 |

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| 991 | P07358 | Complement component C8 beta chain GN=C8B PE=1 SV=3 | 2 | 1 |
| 992 | Q16629 | Serine/arginine-rich splicing factor 7 GN=SRSF7 PE=1 SV=1 | 2 | 1 |
| 993 | P62633 | Cellular nucleic acid-binding protein GN=CNBP PE=1 SV=1 | 2 | 1 |
| 994 | P35080 | Profilin-2 GN=PFN2 PE=1 SV=3 | 2 | 1 |
| 995 | P18827 | Syndecan-1 GN=SDC1 PE=1 SV=3 | 2 | 1 |
| 996 | P07476 | Involucrin GN=IVL PE=1 SV=2 | 2 | 2 |
| 997 | P02656 | Apolipoprotein C-III GN=APOC3 PE=1 SV=1 | 2 | 1 |
| 998 | O95969 | Secretoglobin family 1D member 2 GN=SCGB1D2 PE=2 SV=1 | 2 | 1 |
| 999 | O95274 | Ly6/PLAUR domain-containing protein 3 GN=LYPD3 PE=1 SV=2 | 2 | 1 |
| 1000 | O00625 | Pirin GN=PIR PE=1 SV=1 | 2 | 1 |
| 1001 | O00204 | Sulfotransferase family cytosolic 2B member 1 GN=SULT2B1 PE=1 SV=2 | 2 | 2 |
| 1002 | Q86UD1 | Out at first protein homolog GN=OAF PE=2 SV=1 | 2 | 1 |
| 1003 | Q6EEV6 | Small ubiquitin-related modifier 4 GN=SUMO4 PE=1 SV=2 | 2 | 2 |
| 1004 | Q15126 | Phosphomevalonate kinase GN=PMVK PE=1 SV=3 | 2 | 1 |
| 1005 | P69905 | Hemoglobin subunit alpha GN=HBA1 PE=1 SV=2 | 2 | 1 |
| 1006 | P61960 | Ubiquitin-fold modifier 1 GN=UFM1 PE=1 SV=1 | 2 | 2 |
| 1007 | P60866 | 40S ribosomal protein S20 GN=RPS20 PE=1 SV=1 | 2 | 1 |
| 1008 | P46782 | 40S ribosomal protein S5 GN=RPS5 PE=1 SV=4 | 2 | 1 |
| 1009 | P40855 | Peroxisomal biogenesis factor 19 GN=PEX19 PE=1 SV=1 | 2 | 1 |

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|------|--------|--|---|---|
| 1010 | P14317 | Hematopoietic lineage cell-specific protein GN=HCLS1 PE=1 SV=3 | 2 | 1 |
| 1011 | P07910 | Heterogeneous nuclear ribonucleoproteins C1/C2 GN=HNRNPC PE=1 SV=4 | 2 | 1 |
| 1012 | Q9NX46 | Poly(ADP-ribose) glycohydrolase ARH3 GN=ADPRHL2 PE=1 SV=1 | 2 | 1 |
| 1013 | Q6P996 | Pyridoxal-dependent decarboxylase domain- containing protein 1 GN=PDXDC1 PE=1 SV=2 | 2 | 1 |
| 1014 | Q5D862 | Filaggrin-2 GN=FLG2 PE=1 SV=1 | 2 | 1 |
| 1015 | Q9Y2T7 | Y-box-binding protein 2 GN=YBX2 PE=1 SV=2 | 2 | 1 |
| 1016 | P02746 | Complement C1q subcomponent subunit B GN=C1QB PE=1 SV=3 | 2 | 1 |
| 1017 | Q15714 | TSC22 domain family protein 1 GN=TSC22D1 PE=1 SV=3 | 2 | 1 |
| 1018 | P51452 | Dual specificity protein phosphatase 3 GN=DUSP3 PE=1 SV=1 | 2 | 1 |
| 1019 | P28072 | Proteasome subunit beta type-6 GN=PSMB6 PE=1 SV=4 | 2 | 1 |
| 1020 | P62263 | 40S ribosomal protein S14 GN=RPS14 PE=1 SV=3 | 2 | 1 |
| 1021 | Q07021 | Complement component 1 Q subcomponent- binding protein, mitochondrial GN=C1QBP PE=1 SV=1 | 2 | 1 |
| 1022 | P04211 | Ig lambda chain V region 4A PE=4 SV=1 | 2 | 3 |
| 1023 | P18124 | 60S ribosomal protein L7 GN=RPL7 PE=1 SV=1 | 2 | 1 |
| 1024 | P48163 | NADP-dependent malic enzyme GN=ME1 PE=1 SV=1 | 2 | 1 |
| 1025 | P21926 | CD9 antigen GN=CD9 PE=1 SV=4 | 2 | 1 |
| 1026 | P14735 | Insulin-degrading enzyme GN=IDE PE=1 SV=4 | 2 | 2 |
| 1027 | Q9ULC4 | Malignant T-cell-amplified sequence 1 GN=MCTS1 PE=1 SV=1 | 2 | 1 |

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| 1028 | O95793 | Double-stranded RNA-binding protein Staufens homolog 1 GN=STAU1 PE=1 SV=2 | 2 | 1 |
| 1029 | Q8TCB6 | Olfactory receptor 51E1 GN=OR51E1 PE=1 SV=1 | 2 | 1 |
| 1030 | P62879 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 GN=GNB2 PE=1 SV=3 | 2 | 1 |
| 1031 | O00560 | Syntenin-1 GN=SDCBP PE=1 SV=1 | 2 | 1 |
| 1032 | P17900 | Ganglioside GM2 activator GN=GM2A PE=1 SV=4 | 2 | 1 |
| 1033 | Q66K66 | Transmembrane protein 198 GN=TMEM198 PE=1 SV=1 | 2 | 2 |
| 1034 | P04155 | Trefoil factor 1 GN=TFF1 PE=1 SV=1 | 2 | 1 |
| 1035 | Q03113 | Guanine nucleotide-binding protein subunit alpha-12 GN=GNA12 PE=1 SV=4 | 2 | 1 |
| 1036 | Q99436 | Proteasome subunit beta type-7 GN=PSMB7 PE=1 SV=1 | 2 | 1 |
| 1037 | P60903 | Protein S100-A10 GN=S100A10 PE=1 SV=2 | 2 | 1 |
| 1038 | Q9Y6X4 | Soluble lamin-associated protein of 75 kDa GN=FAM169A PE=1 SV=2 | 2 | 2 |
| 1039 | P18085 | ADP-ribosylation factor 4 GN=ARF4 PE=1 SV=3 | 2 | 3 |
| 1040 | P26583 | High mobility group protein B2 GN=HMGB2 PE=1 SV=2 | 2 | 3 |
| 1041 | Q9UBL6 | Copine-7 GN=CPNE7 PE=2 SV=1 | 2 | 1 |
| 1042 | Q4VXU2 | Polyadenylate-binding protein 1-like GN=PABPC1L PE=2 SV=1 | 2 | 1 |
| 1043 | Q9NR46 | Endophilin-B2 GN=SH3GLB2 PE=1 SV=1 | 2 | 1 |
| 1044 | Q16864 | V-type proton ATPase subunit F GN=ATP6V1F PE=1 SV=2 | 2 | 1 |
| 1045 | P09622 | Dihydrolipoyl dehydrogenase, mitochondrial GN=DLD PE=1 SV=2 | 2 | 1 |
| 1046 | P09497 | Clathrin light chain B GN=CLTB PE=1 SV=1 | 2 | 1 |

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| 1047 | O60812 | Heterogeneous nuclear ribonucleoprotein C-like 1 GN=HNRNPCL1 PE=1 SV=1 | 2 | 1 |
| 1048 | O43286 | Beta-1,4-galactosyltransferase 5 GN=B4GALT5 PE=2 SV=1 | 2 | 1 |
| 1049 | P62195 | 26S protease regulatory subunit 8 GN=PSMC5 PE=1 SV=1 | 2 | 1 |
| 1050 | O60927 | Protein phosphatase 1 regulatory subunit 11 GN=PPP1R11 PE=1 SV=1 | 2 | 1 |
| 1051 | P61106 | Ras-related protein Rab-14 GN=RAB14 PE=1 SV=4 | 2 | 2 |
| 1052 | Q9H0E2 | Toll-interacting protein GN=TOLLIP PE=1 SV=1 | 2 | 1 |
| 1053 | P60891 | Ribose-phosphate pyrophosphokinase 1 GN=PRPS1 PE=1 SV=2 | 2 | 1 |
| 1054 | P55210 | Caspase-7 GN=CASP7 PE=1 SV=1 | 2 | 1 |
| 1055 | P04259 | Keratin, type II cytoskeletal 6B GN=KRT6B PE=1 SV=5 | 2 | 11 |
| 1056 | P62913 | 60S ribosomal protein L11 GN=RPL11 PE=1 SV=2 | 2 | 1 |
| 1057 | P47929 | Galectin-7 GN=LGALS7 PE=1 SV=2 | 2 | 1 |
| 1058 | Q07020 | 60S ribosomal protein L18 GN=RPL18 PE=1 SV=2 | 2 | 1 |
| 1059 | O75531 | Barrier-to-autointegration factor GN=BANF1 PE=1 SV=1 | 2 | 1 |
| 1060 | Q9NQ88 | Fructose-2,6-bisphosphatase TIGAR GN=TIGAR PE=1 SV=1 | 2 | 1 |
| 1061 | Q13283 | Ras GTPase-activating protein-binding protein 1 GN=G3BP1 PE=1 SV=1 | 2 | 1 |
| 1062 | Q9H910 | Hematological and neurological expressed 1-like protein GN=HN1L PE=1 SV=1 | 2 | 1 |
| 1063 | Q99963 | Endophilin-A3 GN=SH3GL3 PE=1 SV=1 | 2 | 3 |
| 1064 | P53999 | Activated RNA polymerase II transcriptional coactivator p15 GN=SUB1 PE=1 SV=3 | 2 | 1 |

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|------|--------|---|---|---|
| 1065 | Q9Y617 | Phosphoserine aminotransferase GN=PSAT1 PE=1 SV=2 | 2 | 1 |
| 1066 | P63165 | Small ubiquitin-related modifier 1 GN=SUMO1 PE=1 SV=1 | 2 | 1 |
| 1067 | P31942 | Heterogeneous nuclear ribonucleoprotein H3 GN=HNRNPH3 PE=1 SV=2 | 2 | 1 |
| 1068 | Q5JWF2 | Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas GN=GNAS PE=1 SV=2 | 2 | 1 |
| 1069 | Q9Y365 | PCTP-like protein GN=STARD10 PE=1 SV=2 | 2 | 1 |
| 1070 | P15289 | Arylsulfatase A GN=ARSA PE=1 SV=3 | 2 | 1 |
| 1071 | Q9UKA9 | Polypyrimidine tract-binding protein 2 GN=PTBP2 PE=1 SV=1 | 2 | 1 |
| 1072 | Q86V81 | THO complex subunit 4 GN=ALYREF PE=1 SV=3 | 2 | 1 |
| 1073 | Q6UXB3 | Ly6/PLAUR domain-containing protein 2 GN=LYPD2 PE=2 SV=1 | 2 | 1 |
| 1074 | P62314 | Small nuclear ribonucleoprotein Sm D1 GN=SNRPD1 PE=1 SV=1 | 2 | 1 |
| 1075 | O00757 | Fructose-1,6-bisphosphatase isozyme 2 GN=FBP2 PE=1 SV=2 | 2 | 2 |
| 1076 | Q9H9H4 | Vacuolar protein sorting-associated protein 37B GN=VPS37B PE=1 SV=1 | 2 | 1 |
| 1077 | Q76LX8 | A disintegrin and metalloproteinase with thrombospondin motifs 13 GN=ADAMTS13 PE=1 SV=1 | 2 | 1 |
| 1078 | Q86YQ8 | Copine-8 GN=CPNE8 PE=1 SV=2 | 2 | 1 |
| 1079 | P27105 | Erythrocyte band 7 integral membrane protein GN=STOM PE=1 SV=3 | 2 | 1 |
| 1080 | O43490 | Prominin-1 GN=PROM1 PE=1 SV=1 | 2 | 1 |
| 1081 | Q9Y5K8 | V-type proton ATPase subunit D GN=ATP6V1D PE=1 SV=1 | 2 | 2 |
| 1082 | Q96M27 | Protein PRRC1 GN=PRRC1 PE=1 SV=1 | 2 | 1 |

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|------|--------|---|---|---|
| 1083 | Q92688 | Acidic leucine-rich nuclear phosphoprotein 32 family member B GN=ANP32B PE=1 SV=1 | 2 | 1 |
| 1084 | Q92520 | Protein FAM3C GN=FAM3C PE=1 SV=1 | 2 | 1 |
| 1085 | Q15599 | Na(+)/H(+) exchange regulatory cofactor NHE-RF2 GN=SLC9A3R2 PE=1 SV=2 | 2 | 1 |
| 1086 | P67870 | Casein kinase II subunit beta GN=CSNK2B PE=1 SV=1 | 2 | 1 |
| 1087 | P17096 | High mobility group protein HMG-I/HMG-Y GN=HMGA1 PE=1 SV=3 | 2 | 1 |
| 1088 | P62269 | 40S ribosomal protein S18 GN=RPS18 PE=1 SV=3 | 2 | 1 |
| 1089 | Q15208 | Serine/threonine-protein kinase 38 GN=STK38 PE=1 SV=1 | 2 | 1 |
| 1090 | Q6DKI2 | Galectin-9C GN=LGALS9C PE=2 SV=2 | 2 | 1 |
| 1091 | Q96MN9 | Zinc finger protein 488 GN=ZNF488 PE=1 SV=1 | 2 | 1 |
| 1092 | P47712 | Cytosolic phospholipase A2 GN=PLA2G4A PE=1 SV=2 | 2 | 1 |
| 1093 | Q9NUU7 | ATP-dependent RNA helicase DDX19A GN=DDX19A PE=1 SV=1 | 2 | 1 |
| 1094 | P50452 | Serpin B8 GN=SERPINB8 PE=1 SV=2 | 2 | 4 |
| 1095 | Q99627 | COP9 signalosome complex subunit 8 GN=COPS8 PE=1 SV=1 | 2 | 1 |
| 1096 | O75828 | Carbonyl reductase [NADPH] 3 GN=CBR3 PE=1 SV=3 | 2 | 4 |
| 1097 | Q14166 | Tubulin--tyrosine ligase-like protein 12 GN=TTLL12 PE=1 SV=2 | 2 | 1 |
| 1098 | P01701 | Ig lambda chain V-I region NEW PE=1 SV=1 | 2 | 1 |
| 1099 | B2RXH8 | Heterogeneous nuclear ribonucleoprotein C-like 2 GN=HNRNPCL2 PE=2 SV=1 | 2 | 1 |
| 1100 | Q5TBC7 | Bcl-2-like protein 15 GN=BCL2L15 PE=2 SV=1 | 2 | 1 |
| 1101 | P12268 | Inosine-5'-monophosphate dehydrogenase 2 | 2 | 1 |

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|------|--------|--|---|---|
| | | GN=IMPDH2 PE=1 SV=2 | | |
| 1102 | Q9UBQ5 | Eukaryotic translation initiation factor 3 subunit K GN=EIF3K PE=1 SV=1 | 2 | 1 |
| 1103 | O00170 | AH receptor-interacting protein GN=AIP PE=1 SV=2 | 2 | 1 |
| 1104 | Q9NQP4 | Prefoldin subunit 4 GN=PFDN4 PE=1 SV=1 | 2 | 1 |
| 1105 | P01603 | Ig kappa chain V-I region Ka PE=1 SV=1 | 2 | 2 |
| 1106 | P61247 | 40S ribosomal protein S3a GN=RPS3A PE=1 SV=2 | 2 | 1 |
| 1107 | P36969 | Phospholipid hydroperoxide glutathione peroxidase, mitochondrial GN=GPX4 PE=1 SV=3 | 2 | 1 |
| 1108 | P07360 | Complement component C8 gamma chain GN=C8G PE=1 SV=3 | 2 | 1 |
| 1109 | P27487 | Dipeptidyl peptidase 4 GN=DPP4 PE=1 SV=2 | 2 | 1 |
| 1110 | P16989 | Y-box-binding protein 3 GN=YBX3 PE=1 SV=4 | 2 | 1 |
| 1111 | Q8TBX8 | Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma GN=PIP4K2C PE=1 SV=3 | 2 | 1 |
| 1112 | Q96AE4 | Far upstream element-binding protein 1 GN=FUBP1 PE=1 SV=3 | 2 | 1 |
| 1113 | Q6PIW4 | Fidgetin-like protein 1 GN=FIGNL1 PE=1 SV=2 | 2 | 2 |
| 1114 | Q7L1Q6 | Basic leucine zipper and W2 domain-containing protein 1 GN=BZW1 PE=1 SV=1 | 2 | 1 |
| 1115 | Q71UI9 | Histone H2A.V GN=H2AFV PE=1 SV=3 | 2 | 1 |
| 1116 | Q16774 | Guanylate kinase GN=GUK1 PE=1 SV=2 | 2 | 1 |
| 1117 | P61956 | Small ubiquitin-related modifier 2 GN=SUMO2 PE=1 SV=3 | 2 | 2 |
| 1118 | Q6IA69 | Glutamine-dependent NAD(+) synthetase GN=NADSYN1 PE=1 SV=3 | 2 | 1 |
| 1119 | Q03169 | Tumor necrosis factor alpha-induced protein 2 GN=TNFAIP2 PE=1 SV=2 | 2 | 1 |

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|------|--------|--|---|----|
| 1120 | P14866 | Heterogeneous nuclear ribonucleoprotein L GN=HNRNPL PE=1 SV=2 | 2 | 1 |
| 1121 | Q99829 | Copine-1 GN=CPNE1 PE=1 SV=1 | 2 | 2 |
| 1122 | Q92890 | Ubiquitin fusion degradation protein 1 homolog GN=UFD1L PE=1 SV=3 | 2 | 1 |
| 1123 | O75340 | Programmed cell death protein 6 GN=PDCD6 PE=1 SV=1 | 2 | 1 |
| 1124 | Q92499 | ATP-dependent RNA helicase DDX1 GN=DDX1 PE=1 SV=2 | 2 | 1 |
| 1125 | O60282 | Kinesin heavy chain isoform 5C GN=KIF5C PE=1 SV=1 | 2 | 1 |
| 1126 | Q9UN76 | Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+) GN=SLC6A14 PE=2 SV=1 | 2 | 1 |
| 1127 | Q8IYD1 | Eukaryotic peptide chain release factor GTP- binding subunit ERF3B GN=GSPT2 PE=1 SV=2 | 2 | 1 |
| 1128 | Q29963 | HLA class I histocompatibility antigen, Cw-6 alpha chain GN=HLA-C PE=2 SV=2 | 2 | 1 |
| 1129 | P49407 | Beta-arrestin-1 GN=ARRB1 PE=1 SV=2 | 2 | 1 |
| 1130 | Q9BY43 | Charged multivesicular body protein 4a GN=CHMP4A PE=1 SV=3 | 2 | 1 |
| 1131 | Q9UQ16 | Dynammin-3 GN=DNM3 PE=1 SV=4 | 2 | 1 |
| 1132 | Q9Y259 | Choline/ethanolamine kinase GN=CHKB PE=1 SV=3 | 2 | 1 |
| 1133 | O75822 | Eukaryotic translation initiation factor 3 subunit J GN=EIF3J PE=1 SV=2 | 2 | 1 |
| 1134 | Q96AT9 | Ribulose-phosphate 3-epimerase GN=RPE PE=1 SV=1 | 2 | 1 |
| 1135 | P41218 | Myeloid cell nuclear differentiation antigen GN=MNDA PE=1 SV=1 | 2 | 1 |
| 1136 | P01609 | Ig kappa chain V-I region Scw PE=1 SV=1 | 2 | 14 |
| 1137 | Q8IWP9 | Coiled-coil domain-containing protein 28A GN=CCDC28A PE=2 SV=1 | 2 | 1 |

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|------|--------|---|---|----|
| 1138 | P0CG04 | Ig lambda-1 chain C regions GN=IGLC1 PE=1 SV=1 | 2 | 58 |
| 1139 | Q9UHV9 | Prefoldin subunit 2 GN=PFDN2 PE=1 SV=1 | 2 | 1 |
| 1140 | Q9H7C9 | Mth938 domain-containing protein GN=AAMDC PE=1 SV=1 | 2 | 1 |
| 1141 | Q9H115 | Beta-soluble NSF attachment protein GN=NAPB PE=1 SV=2 | 2 | 1 |
| 1142 | Q9BUL8 | Programmed cell death protein 10 GN=PDCD10 PE=1 SV=1 | 2 | 1 |
| 1143 | P57764 | Gasdermin-D GN=GSDMD PE=1 SV=1 | 2 | 1 |
| 1144 | P10155 | 60 kDa SS-A/Ro ribonucleoprotein GN=TROVE2 PE=1 SV=2 | 2 | 1 |
| 1145 | Q13347 | Eukaryotic translation initiation factor 3 subunit I GN=EIF3I PE=1 SV=1 | 2 | 1 |
| 1146 | P49441 | Inositol polyphosphate 1-phosphatase GN=INPP1 PE=1 SV=1 | 2 | 1 |
| 1147 | Q6P1N9 | Putative deoxyribonuclease TATDN1 GN=TATDN1 PE=1 SV=2 | 2 | 1 |
| 1148 | Q15370 | Transcription elongation factor B polypeptide 2 GN=TCEB2 PE=1 SV=1 | 2 | 1 |
| 1149 | Q9UBW8 | COP9 signalosome complex subunit 7a GN=COPS7A PE=1 SV=1 | 2 | 1 |
| 1150 | Q8WUF5 | RelA-associated inhibitor GN=PPP1R13L PE=1 SV=4 | 2 | 1 |
| 1151 | Q16401 | 26S proteasome non-ATPase regulatory subunit 5 GN=PSMD5 PE=1 SV=3 | 2 | 1 |
| 1152 | Q8NDH3 | Probable aminopeptidase NPEPL1 GN=NPEPL1 PE=1 SV=3 | 2 | 1 |
| 1153 | P23141 | Liver carboxylesterase 1 GN=CES1 PE=1 SV=2 | 2 | 1 |
| 1154 | P15291 | Beta-1,4-galactosyltransferase 1 GN=B4GALT1 PE=1 SV=5 | 2 | 1 |
| 1155 | P02649 | Apolipoprotein E GN=APOE PE=1 SV=1 | 2 | 1 |

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|------|--------|---|---|---|
| 1156 | P54619 | 5'-AMP-activated protein kinase subunit gamma-1 GN=PRKAG1 PE=1 SV=1 | 2 | 1 |
| 1157 | P36507 | Dual specificity mitogen-activated protein kinase kinase 2 GN=MAP2K2 PE=1 SV=1 | 2 | 1 |
| 1158 | O60635 | Tetraspanin-1 GN=TSPAN1 PE=1 SV=2 | 2 | 1 |
| 1159 | P46783 | 40S ribosomal protein S10 GN=RPS10 PE=1 SV=1 | 2 | 1 |
| 1160 | P00748 | Coagulation factor XII GN=F12 PE=1 SV=3 | 2 | 1 |
| 1161 | P23246 | Splicing factor, proline- and glutamine-rich GN=SFPQ PE=1 SV=2 | 2 | 1 |
| 1162 | P20042 | Eukaryotic translation initiation factor 2 subunit 2 GN=EIF2S2 PE=1 SV=2 | 2 | 1 |
| 1163 | P16083 | Ribosylidihyronicotinamide dehydrogenase [quinone] GN=NQO2 PE=1 SV=5 | 2 | 1 |
| 1164 | O95379 | Tumor necrosis factor alpha-induced protein 8 GN=TNFAIP8 PE=1 SV=1 | 2 | 1 |
| 1165 | Q9NQX3 | Gephyrin GN=GPHN PE=1 SV=1 | 2 | 1 |
| 1166 | P08133 | Annexin A6 GN=ANXA6 PE=1 SV=3 | 2 | 2 |
| 1167 | Q9BXR6 | Complement factor H-related protein 5 GN=CFHR5 PE=1 SV=1 | 2 | 1 |
| 1168 | P30049 | ATP synthase subunit delta, mitochondrial GN=ATP5D PE=1 SV=2 | 2 | 1 |
| 1169 | Q6PCE3 | Glucose 1,6-bisphosphate synthase GN=PGM2L1 PE=1 SV=3 | 2 | 1 |
| 1170 | Q92804 | TATA-binding protein-associated factor 2N GN=TAF15 PE=1 SV=1 | 2 | 1 |
| 1171 | O00399 | Dynactin subunit 6 GN=DCTN6 PE=1 SV=1 | 2 | 1 |
| 1172 | P50552 | Vasodilator-stimulated phosphoprotein GN=VASP PE=1 SV=3 | 2 | 1 |
| 1173 | O14933 | Ubiquitin/ISG15-conjugating enzyme E2 L6 GN=UBE2L6 PE=1 SV=4 | 2 | 1 |
| 1174 | Q12904 | Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 GN=AIMP1 PE=1 | 2 | 1 |

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|------|--------|---|---|---|
| | | SV=2 | | |
| 1175 | Q9UBX1 | Cathepsin F GN=CTSF PE=1 SV=1 | 2 | 1 |
| 1176 | Q9BUH6 | Uncharacterized protein C9orf142 GN=C9orf142 PE=1 SV=2 | 2 | 1 |
| 1177 | Q96A05 | V-type proton ATPase subunit E 2 GN=ATP6V1E2 PE=2 SV=1 | 2 | 1 |
| 1178 | Q96BW5 | Phosphotriesterase-related protein GN=PTER PE=1 SV=1 | 2 | 1 |
| 1179 | Q6P6B1 | Glutamate-rich protein 5 GN=ERICH5 PE=2 SV=1 | 2 | 1 |
| 1180 | Q9P218 | Collagen alpha-1(XX) chain GN=COL20A1 PE=1 SV=4 | 2 | 1 |
| 1181 | Q96QV6 | Histone H2A type 1-A GN=HIST1H2AA PE=1 SV=3 | 2 | 1 |
| 1182 | Q96P70 | Importin-9 GN=IPO9 PE=1 SV=3 | 2 | 1 |
| 1183 | P08582 | Melanotransferrin GN=MFI2 PE=1 SV=2 | 2 | 2 |
| 1184 | Q15942 | Zyxin GN=ZYX PE=1 SV=1 | 2 | 1 |
| 1185 | P62241 | 40S ribosomal protein S8 GN=RPS8 PE=1 SV=2 | 2 | 2 |
| 1186 | Q01459 | Di-N-acetylchitobiase GN=CTBS PE=1 SV=1 | 2 | 1 |
| 1187 | Q8NFJ5 | Retinoic acid-induced protein 3 GN=GPRC5A PE=1 SV=2 | 2 | 1 |
| 1188 | Q14195 | Dihydropyrimidinase-related protein 3 GN=DPYSL3 PE=1 SV=1 | 2 | 1 |
| 1189 | P98179 | Putative RNA-binding protein 3 GN=RBM3 PE=1 SV=1 | 2 | 1 |
| 1190 | O94903 | Proline synthase co-transcribed bacterial homolog protein GN=PROSC PE=1 SV=1 | 2 | 1 |
| 1191 | O00233 | 26S proteasome non-ATPase regulatory subunit 9 GN=PSMD9 PE=1 SV=3 | 2 | 1 |
| 1192 | Q01082 | Spectrin beta chain, non-erythrocytic 1 GN=SPTBN1 PE=1 SV=2 | 2 | 1 |

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|------|--------|--|---|---|
| 1193 | Q15437 | Protein transport protein Sec23B GN=SEC23B PE=1 SV=2 | 2 | 1 |
| 1194 | Q9UMX5 | Neudesin GN=NENF PE=1 SV=1 | 2 | 1 |
| 1195 | P36578 | 60S ribosomal protein L4 GN=RPL4 PE=1 SV=5 | 2 | 1 |
| 1196 | O43633 | Charged multivesicular body protein 2a GN=CHMP2A PE=1 SV=1 | 2 | 1 |
| 1197 | Q9H3U1 | Protein unc-45 homolog A GN=UNC45A PE=1 SV=1 | 2 | 1 |
| 1198 | P15498 | Proto-oncogene vav GN=VAV1 PE=1 SV=4 | 2 | 2 |
| 1199 | P07357 | Complement component C8 alpha chain GN=C8A PE=1 SV=2 | 2 | 1 |
| 1200 | Q9H3S4 | Thiamin pyrophosphokinase 1 GN=TPK1 PE=1 SV=1 | 2 | 1 |
| 1201 | Q08211 | ATP-dependent RNA helicase A GN=DHX9 PE=1 SV=4 | 2 | 1 |
| 1202 | P62993 | Growth factor receptor-bound protein 2 GN=GRB2 PE=1 SV=1 | 2 | 1 |
| 1203 | Q96CV9 | Optineurin GN=OPTN PE=1 SV=2 | 2 | 1 |
| 1204 | P01778 | Ig heavy chain V-III region ZAP PE=1 SV=1 | 2 | 4 |
| 1205 | O60701 | UDP-glucose 6-dehydrogenase GN=UGDH PE=1 SV=1 | 2 | 1 |
| 1206 | Q9Y5Y9 | Sodium channel protein type 10 subunit alpha GN=SCN10A PE=1 SV=2 | 2 | 1 |
| 1207 | Q9Y6W5 | Wiskott-Aldrich syndrome protein family member 2 GN=WASF2 PE=1 SV=3 | 2 | 1 |
| 1208 | P38646 | Stress-70 protein, mitochondrial GN=HSPA9 PE=1 SV=2 | 2 | 1 |
| 1209 | O75396 | Vesicle-trafficking protein SEC22b GN=SEC22B PE=1 SV=4 | 2 | 1 |
| 1210 | P35244 | Replication protein A 14 kDa subunit GN=RPA3 PE=1 SV=1 | 2 | 1 |
| 1211 | P30566 | Adenylosuccinate lyase GN=ADSL PE=1 | 2 | 1 |

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| | | SV=2 | | |
| 1212 | A5D8V6 | Vacuolar protein sorting-associated protein 37C GN=VPS37C PE=1 SV=2 | 2 | 1 |
| 1213 | O00232 | 26S proteasome non-ATPase regulatory subunit 12 GN=PSMD12 PE=1 SV=3 | 2 | 1 |
| 1214 | Q9BVA1 | Tubulin beta-2B chain GN=TUBB2B PE=1 SV=1 | 2 | 15 |
| 1215 | P01593 | Ig kappa chain V-I region AG PE=1 SV=1 | 2 | 13 |
| 1216 | Q7KZF4 | Staphylococcal nuclease domain-containing protein 1 GN=SND1 PE=1 SV=1 | 2 | 1 |
| 1217 | P55854 | Small ubiquitin-related modifier 3 GN=SUMO3 PE=1 SV=2 | 2 | 1 |
| 1218 | Q9C0C2 | 182 kDa tankyrase-1-binding protein GN=TNKS1BP1 PE=1 SV=4 | 2 | 1 |
| 1219 | Q9NZZ3 | Charged multivesicular body protein 5 GN=CHMP5 PE=1 SV=1 | 2 | 1 |
| 1220 | Q9Y6R7 | IgGFc-binding protein GN=FCGBP PE=1 SV=3 | 2 | 1 |
| 1221 | O43653 | Prostate stem cell antigen GN=PSCA PE=1 SV=1 | 2 | 1 |
| 1222 | Q8WXX0 | Dynein heavy chain 7, axonemal GN=DNAH7 PE=1 SV=2 | 2 | 1 |
| 1223 | O95886 | Disks large-associated protein 3 GN=DLGAP3 PE=1 SV=3 | 2 | 1 |
| 1224 | Q8N7X1 | RNA-binding motif protein, X-linked-like-3 GN=RBMXL3 PE=2 SV=2 | 2 | 1 |
| 1225 | Q9Y2W2 | WW domain-binding protein 11 GN=WBP11 PE=1 SV=1 | 2 | 1 |
| 1226 | P53990 | IST1 homolog GN=IST1 PE=1 SV=1 | 2 | 1 |
| 1227 | Q9Y376 | Calcium-binding protein 39 GN=CAB39 PE=1 SV=1 | 2 | 1 |
| 1228 | P01596 | Ig kappa chain V-I region CAR PE=1 SV=1 | 2 | 5 |
| 1229 | Q9Y3E7 | Charged multivesicular body protein 3 | 2 | 1 |

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|------|--------|---|---|---|
| | | GN=CHMP3 PE=1 SV=3 | | |
| 1230 | Q06033 | Inter-alpha-trypsin inhibitor heavy chain H3 GN=ITIH3 PE=1 SV=2 | 2 | 1 |
| 1231 | P02792 | Ferritin light chain GN=FTL PE=1 SV=2 | 2 | 1 |
| 1232 | Q04446 | 1,4-alpha-glucan-branching enzyme GN=GBE1 PE=1 SV=3 | 2 | 1 |
| 1233 | P61201 | COP9 signalosome complex subunit 2 GN=COPS2 PE=1 SV=1 | 2 | 1 |
| 1234 | P46777 | 60S ribosomal protein L5 GN=RPL5 PE=1 SV=3 | 2 | 1 |
| 1235 | Q5VWZ2 | Lysophospholipase-like protein 1 GN=LYPLAL1 PE=1 SV=3 | 2 | 1 |
| 1236 | P62249 | 40S ribosomal protein S16 GN=RPS16 PE=1 SV=2 | 2 | 1 |
| 1237 | Q9UJC5 | SH3 domain-binding glutamic acid-rich-like protein 2 GN=SH3BGRL2 PE=1 SV=2 | 2 | 1 |
| 1238 | Q9H8Y8 | Golgi reassembly-stacking protein 2 GN=GORASP2 PE=1 SV=3 | 2 | 1 |
| 1239 | Q16836 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial GN=HADH PE=1 SV=3 | 2 | 1 |
| 1240 | P50226 | Sulfotransferase 1A2 GN=SULT1A2 PE=1 SV=2 | 2 | 1 |
| 1241 | P01624 | Ig kappa chain V-III region POM PE=1 SV=1 | 2 | 3 |
| 1242 | Q92696 | Geranylgeranyl transferase type-2 subunit alpha GN=RABGGTA PE=1 SV=2 | 2 | 1 |
| 1243 | P62829 | 60S ribosomal protein L23 GN=RPL23 PE=1 SV=1 | 2 | 1 |
| 1244 | P61966 | AP-1 complex subunit sigma-1A GN=AP1S1 PE=1 SV=1 | 2 | 1 |
| 1245 | P12532 | Creatine kinase U-type, mitochondrial GN=CKMT1A PE=1 SV=1 | 2 | 1 |
| 1246 | P61923 | Coatomer subunit zeta-1 GN=COPZ1 PE=1 SV=1 | 2 | 2 |

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| 1247 | O75506 | Heat shock factor-binding protein 1 GN=HSBP1 PE=1 SV=1 | 2 | 1 |
| 1248 | Q8WXC6 | Myeloma-overexpressed gene 2 protein GN=MYEOV2 PE=2 SV=3 | 2 | 1 |
| 1249 | Q9UHB6 | LIM domain and actin-binding protein 1 GN=LIMA1 PE=1 SV=1 | 2 | 1 |
| 1250 | P04899 | Guanine nucleotide-binding protein G(i) subunit alpha-2 GN=GNAI2 PE=1 SV=3 | 2 | 1 |
| 1251 | Q9Y5K6 | CD2-associated protein GN=CD2AP PE=1 SV=1 | 2 | 1 |
| 1252 | Q96C90 | Protein phosphatase 1 regulatory subunit 14B GN=PPP1R14B PE=1 SV=3 | 2 | 1 |
| 1253 | Q9HCH3 | Copine-5 GN=CPNE5 PE=1 SV=2 | 2 | 1 |
| 1254 | Q9P0R6 | GSK3-beta interaction protein GN=GSKIP PE=1 SV=2 | 2 | 1 |
| 1255 | Q9H300 | Presenilins-associated rhomboid-like protein, mitochondrial GN=PARL PE=1 SV=2 | 2 | 1 |
| 1256 | Q8WTQ4 | Uncharacterized protein C16orf78 GN=C16orf78 PE=2 SV=1 | 2 | 1 |
| 1257 | Q8N0W5 | IQ domain-containing protein K GN=IQCK PE=2 SV=1 | 2 | 1 |
| 1258 | P57082 | T-box transcription factor TBX4 GN=TBX4 PE=1 SV=2 | 2 | 1 |
| 1259 | O95427 | GPI ethanolamine phosphate transferase 1 GN=PIGN PE=1 SV=1 | 2 | 1 |
| 1260 | P50570 | Dynamin-2 GN=DNM2 PE=1 SV=2 | 2 | 2 |
| 1261 | O00442 | RNA 3'-terminal phosphate cyclase GN=RTCA PE=1 SV=1 | 2 | 1 |
| 1262 | Q9BQE3 | Tubulin alpha-1C chain GN=TUBA1C PE=1 SV=1 | 2 | 13 |
| 1263 | P16401 | Histone H1.5 GN=HIST1H1B PE=1 SV=3 | 2 | 1 |
| 1264 | Q9UKS7 | Zinc finger protein Helios GN=IKZF2 PE=1 SV=2 | 2 | 1 |

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|------|--------|---|------|----|
| 1265 | O60925 | Prefoldin subunit 1 GN=PFDN1 PE=1 SV=2 | 2 | 1 |
| 1266 | P25685 | DnaJ homolog subfamily B member 1 GN=DNAJB1 PE=1 SV=4 | 1.89 | 1 |
| 1267 | Q9P289 | Serine/threonine-protein kinase MST4 GN=MST4 PE=1 SV=2 | 1.89 | 2 |
| 1268 | Q9Y2Z0 | Suppressor of G2 allele of SKP1 homolog GN=SUGT1 PE=1 SV=3 | 1.89 | 1 |
| 1269 | P57053 | Histone H2B type F-S GN=H2BFS PE=1 SV=2 | 1.89 | 2 |
| 1270 | P0DMN0 | Sulfotransferase 1A4 GN=SULT1A4 PE=1 SV=1 | 1.89 | 2 |
| 1271 | O00462 | Beta-mannosidase GN=MANBA PE=1 SV=3 | 1.89 | 1 |
| 1272 | Q92747 | Actin-related protein 2/3 complex subunit 1A GN=ARPC1A PE=1 SV=2 | 1.82 | 2 |
| 1273 | Q9Y2B0 | Protein canopy homolog 2 GN=CNPY2 PE=1 SV=1 | 1.8 | 1 |
| 1274 | P04438 | Ig heavy chain V-II region SESS PE=2 SV=1 | 1.8 | 1 |
| 1275 | P43251 | Biotinidase GN=BTD PE=1 SV=2 | 1.78 | 1 |
| 1276 | P08754 | Guanine nucleotide-binding protein G(k) subunit alpha GN=GNAI3 PE=1 SV=3 | 1.77 | 2 |
| 1277 | Q9C0G6 | Dynein heavy chain 6, axonemal GN=DNAH6 PE=1 SV=3 | 1.77 | 1 |
| 1278 | P35241 | Radixin GN=RDX PE=1 SV=1 | 1.72 | 11 |
| 1279 | Q8WZA6 | Olfactory receptor 1E3 GN=OR1E3 PE=3 SV=2 | 1.72 | 1 |
| 1280 | Q9UHA4 | Ragulator complex protein LAMTOR3 GN=LAMTOR3 PE=1 SV=1 | 1.72 | 1 |
| 1281 | O43390 | Heterogeneous nuclear ribonucleoprotein R GN=HNRNPR PE=1 SV=1 | 1.7 | 2 |
| 1282 | Q687X5 | Metalloreductase STEAP4 GN=STEAP4 PE=1 SV=1 | 1.7 | 1 |
| 1283 | Q9NP99 | Triggering receptor expressed on myeloid cells 1 GN=TREM1 PE=1 SV=1 | 1.7 | 1 |

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| 1284 | O95721 | Synaptosomal-associated protein 29 GN=SNAP29 PE=1 SV=1 | 1.68 | 1 |
| 1285 | P99999 | Cytochrome c GN=CYCS PE=1 SV=2 | 1.68 | 1 |
| 1286 | Q96BQ1 | Protein FAM3D GN=FAM3D PE=1 SV=1 | 1.68 | 1 |
| 1287 | P01824 | Ig heavy chain V-II region WAH PE=1 SV=1 | 1.68 | 2 |
| 1288 | Q04609 | Glutamate carboxypeptidase 2 GN=FOLH1 PE=1 SV=1 | 1.68 | 1 |
| 1289 | Q13409 | Cytoplasmic dynein 1 intermediate chain 2 GN=DYNC1I2 PE=1 SV=3 | 1.66 | 2 |
| 1290 | Q9Y333 | U6 snRNA-associated Sm-like protein LSm2 GN=LSM2 PE=1 SV=1 | 1.66 | 1 |
| 1291 | P62424 | 60S ribosomal protein L7a GN=RPL7A PE=1 SV=2 | 1.66 | 1 |
| 1292 | P11908 | Ribose-phosphate pyrophosphokinase 2 GN=PRPS2 PE=1 SV=2 | 1.66 | 1 |
| 1293 | Q00266 | S-adenosylmethionine synthase isoform type- 1 GN=MAT1A PE=1 SV=2 | 1.66 | 1 |
| 1294 | Q13287 | N-myc-interactor GN=NMI PE=1 SV=2 | 1.64 | 1 |
| 1295 | Q03013 | Glutathione S-transferase Mu 4 GN=GSTM4 PE=1 SV=3 | 1.64 | 1 |
| 1296 | O00629 | Importin subunit alpha-3 GN=KPNA4 PE=1 SV=1 | 1.62 | 1 |
| 1297 | P05067 | Amyloid beta A4 protein GN=APP PE=1 SV=3 | 1.62 | 1 |
| 1298 | Q5SGD2 | Protein phosphatase 1L GN=PPM1L PE=1 SV=1 | 1.62 | 1 |
| 1299 | P09237 | Matrilysin GN=MMP7 PE=1 SV=1 | 1.6 | 1 |
| 1300 | Q9BRG1 | Vacuolar protein-sorting-associated protein 25 GN=VPS25 PE=1 SV=1 | 1.6 | 1 |
| 1301 | Q03154 | Aminoacylase-1 GN=ACY1 PE=1 SV=1 | 1.59 | 1 |
| 1302 | Q9UI12 | V-type proton ATPase subunit H GN=ATP6V1H PE=1 SV=1 | 1.59 | 1 |
| 1303 | Q969R2 | Oxysterol-binding protein 2 GN=OSBP2 PE=1 | 1.59 | 1 |

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|------|--------|--|------|---|
| | | SV=2 | | |
| 1304 | P55010 | Eukaryotic translation initiation factor 5 GN=EIF5 PE=1 SV=2 | 1.57 | 1 |
| 1305 | Q76FK4 | Nucleolar protein 8 GN=NOL8 PE=1 SV=1 | 1.57 | 1 |
| 1306 | Q969T9 | WW domain-binding protein 2 GN=WBP2 PE=1 SV=1 | 1.55 | 1 |
| 1307 | Q92623 | Tetratricopeptide repeat protein 9A GN=TTC9 PE=2 SV=3 | 1.54 | 1 |
| 1308 | P47914 | 60S ribosomal protein L29 GN=RPL29 PE=1 SV=2 | 1.52 | 1 |
| 1309 | P34913 | Bifunctional epoxide hydrolase 2 GN=EPHX2 PE=1 SV=2 | 1.52 | 2 |
| 1310 | Q9UK41 | Vacuolar protein sorting-associated protein 28 homolog GN=VPS28 PE=1 SV=1 | 1.51 | 1 |
| 1311 | Q12906 | Interleukin enhancer-binding factor 3 GN=ILF3 PE=1 SV=3 | 1.49 | 1 |
| 1312 | Q9UBN7 | Histone deacetylase 6 GN=HDAC6 PE=1 SV=2 | 1.49 | 1 |
| 1313 | P48595 | Serpin B10 GN=SERPINB10 PE=1 SV=1 | 1.47 | 1 |
| 1314 | P35268 | 60S ribosomal protein L22 GN=RPL22 PE=1 SV=2 | 1.47 | 1 |
| 1315 | Q7Z478 | ATP-dependent RNA helicase DHX29 GN=DHX29 PE=1 SV=2 | 1.47 | 1 |
| 1316 | Q9UBR2 | Cathepsin Z GN=CTSZ PE=1 SV=1 | 1.46 | 1 |
| 1317 | Q8TED9 | Actin filament-associated protein 1-like 1 GN=AFAP1L1 PE=1 SV=2 | 1.44 | 1 |
| 1318 | Q8NBJ7 | Sulfatase-modifying factor 2 GN=SUMF2 PE=1 SV=2 | 1.43 | 1 |
| 1319 | O43237 | Cytoplasmic dynein 1 light intermediate chain 2 GN=DYNC1LI2 PE=1 SV=1 | 1.43 | 1 |
| 1320 | A0MZ66 | Shootin-1 GN=KIAA1598 PE=1 SV=4 | 1.42 | 1 |
| 1321 | Q9NR28 | Diablo homolog, mitochondrial GN=DIABLO PE=1 SV=1 | 1.41 | 1 |

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|------|--------|--|------|----|
| 1322 | Q99729 | Heterogeneous nuclear ribonucleoprotein A/B GN=HNRNPAB PE=1 SV=2 | 1.4 | 2 |
| 1323 | Q99519 | Sialidase-1 GN=NEU1 PE=1 SV=1 | 1.39 | 1 |
| 1324 | P01608 | Ig kappa chain V-I region Roy PE=1 SV=1 | 1.37 | 15 |
| 1325 | Q8WVQ1 | Soluble calcium-activated nucleotidase 1 GN=CANT1 PE=1 SV=1 | 1.36 | 1 |
| 1326 | P06731 | Carcinoembryonic antigen-related cell adhesion molecule 5 GN=CEACAM5 PE=1 SV=3 | 1.35 | 1 |
| 1327 | Q13596 | Sorting nexin-1 GN=SNX1 PE=1 SV=3 | 1.34 | 1 |
| 1328 | O95479 | GDH/6PGL endoplasmic bifunctional protein GN=H6PD PE=1 SV=2 | 1.34 | 1 |
| 1329 | O15247 | Chloride intracellular channel protein 2 GN=CLIC2 PE=1 SV=3 | 1.34 | 1 |
| 1330 | O95671 | N-acetylserotonin O-methyltransferase-like protein GN=ASMTL PE=1 SV=3 | 1.33 | 1 |
| 1331 | Q9Y5B9 | FACT complex subunit SPT16 GN=SUPT16H PE=1 SV=1 | 1.33 | 1 |
| 1332 | Q6MZZ7 | Calpain-13 GN=CAPN13 PE=1 SV=2 | 1.32 | 1 |
| 1333 | Q5VZK9 | Leucine-rich repeat-containing protein 16A GN=LRRRC16A PE=1 SV=1 | 1.31 | 1 |
| 1334 | P35542 | Serum amyloid A-4 protein GN=SAA4 PE=1 SV=2 | 1.3 | 1 |
| 1335 | Q00610 | Clathrin heavy chain 1 GN=CLTC PE=1 SV=5 | 1.28 | 1 |
| 1336 | P15328 | Folate receptor alpha GN=FOLR1 PE=1 SV=3 | 1.28 | 1 |
| 1337 | O00194 | Ras-related protein Rab-27B GN=RAB27B PE=1 SV=4 | 1.27 | 2 |
| 1338 | O00182 | Galectin-9 GN=LGALS9 PE=1 SV=2 | 1.27 | 1 |
| 1339 | Q11128 | Alpha-(1,3)-fucosyltransferase 5 GN=FUT5 PE=2 SV=1 | 1.27 | 1 |
| 1340 | P22894 | Neutrophil collagenase GN=MMP8 PE=1 SV=1 | 1.25 | 1 |

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|------|--------|---|------|----|
| 1341 | Q15582 | Transforming growth factor-beta-induced protein ig-h3 GN=TGFBI PE=1 SV=1 | 1.23 | 1 |
| 1342 | Q9UKE5 | TRAF2 and NCK-interacting protein kinase GN=TNIK PE=1 SV=1 | 1.23 | 1 |
| 1343 | P15531 | Nucleoside diphosphate kinase A GN=NME1 PE=1 SV=1 | 1.22 | 10 |
| 1344 | P16070 | CD44 antigen GN=CD44 PE=1 SV=3 | 1.22 | 1 |
| 1345 | Q15369 | Transcription elongation factor B polypeptide 1 GN=TCEB1 PE=1 SV=1 | 1.22 | 1 |
| 1346 | Q8NEY1 | Neuron navigator 1 GN=NAV1 PE=1 SV=2 | 1.22 | 1 |
| 1347 | P14324 | Farnesyl pyrophosphate synthase GN=FDPS PE=1 SV=4 | 1.19 | 1 |
| 1348 | Q15102 | Platelet-activating factor acetylhydrolase IB subunit gamma GN=PAFAH1B3 PE=1 SV=1 | 1.19 | 3 |
| 1349 | Q16186 | Proteasomal ubiquitin receptor ADRM1 GN=ADRM1 PE=1 SV=2 | 1.19 | 2 |
| 1350 | P10253 | Lysosomal alpha-glucosidase GN=GAA PE=1 SV=4 | 1.17 | 1 |
| 1351 | P57735 | Ras-related protein Rab-25 GN=RAB25 PE=1 SV=2 | 1.16 | 1 |
| 1352 | Q9BUP3 | Oxidoreductase HTATIP2 GN=HTATIP2 PE=1 SV=2 | 1.15 | 1 |
| 1353 | P58876 | Histone H2B type 1-D GN=HIST1H2BD PE=1 SV=2 | 1.14 | 1 |
| 1354 | P54802 | Alpha-N-acetylglucosaminidase GN=NAGLU PE=1 SV=2 | 1.13 | 1 |
| 1355 | P17050 | Alpha-N-acetylgalactosaminidase GN=NAGA PE=1 SV=2 | 1.12 | 1 |
| 1356 | Q16589 | Cyclin-G2 GN=CCNG2 PE=2 SV=1 | 1.11 | 2 |
| 1357 | Q86SF2 | N-acetylgalactosaminyltransferase 7 GN=GALNT7 PE=1 SV=1 | 1.1 | 1 |
| 1358 | O95741 | Copine-6 GN=CPNE6 PE=1 SV=3 | 1.09 | 1 |
| 1359 | P53680 | AP-2 complex subunit sigma GN=AP2S1 | 1.08 | 1 |

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|------|--------|--|------|---|
| | | PE=1 SV=2 | | |
| 1360 | Q14204 | Cytoplasmic dynein 1 heavy chain 1 GN=DYNC1H1 PE=1 SV=5 | 1.08 | 1 |
| 1361 | P48739 | Phosphatidylinositol transfer protein beta isoform GN=PITPNB PE=1 SV=2 | 1.08 | 1 |
| 1362 | Q12905 | Interleukin enhancer-binding factor 2 GN=ILF2 PE=1 SV=2 | 1.08 | 1 |
| 1363 | Q14134 | Tripartite motif-containing protein 29 GN=TRIM29 PE=1 SV=2 | 1.07 | 1 |
| 1364 | Q9C002 | Normal mucosa of esophagus-specific gene 1 protein GN=NMES1 PE=2 SV=1 | 1.04 | 1 |
| 1365 | Q9Y5X3 | Sorting nexin-5 GN=SNX5 PE=1 SV=1 | 1.04 | 1 |
| 1366 | Q9Y3I0 | tRNA-splicing ligase RtcB homolog GN=RTCB PE=1 SV=1 | 1.03 | 1 |
| 1367 | P10643 | Complement component C7 GN=C7 PE=1 SV=2 | 1.01 | 1 |
| 1368 | Q8IVS8 | Glycerate kinase GN=GLYCTK PE=1 SV=1 | 0.98 | 1 |
| 1369 | Q9BV57 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase GN=ADI1 PE=1 SV=1 | 0.97 | 1 |
| 1370 | P16930 | Fumarylacetoacetase GN=FAH PE=1 SV=2 | 0.97 | 1 |
| 1371 | Q8NH57 | Putative olfactory receptor 52P1 GN=OR52P1P PE=5 SV=2 | 0.97 | 1 |
| 1372 | Q9BY12 | S phase cyclin A-associated protein in the endoplasmic reticulum GN=SCAPER PE=1 SV=2 | 0.94 | 1 |
| 1373 | P62851 | 40S ribosomal protein S25 GN=RPS25 PE=1 SV=1 | 0.94 | 1 |
| 1374 | P42892 | Endothelin-converting enzyme 1 GN=ECE1 PE=1 SV=2 | 0.92 | 1 |
| 1375 | O43747 | AP-1 complex subunit gamma-1 GN=AP1G1 PE=1 SV=5 | 0.91 | 1 |
| 1376 | Q9H2H8 | Peptidyl-prolyl cis-trans isomerase-like 3 GN=PPIL3 PE=1 SV=1 | 0.91 | 1 |

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|------|--------|---|------|---|
| 1377 | Q16576 | Histone-binding protein RBBP7 GN=RBBP7 PE=1 SV=1 | 0.88 | 1 |
| 1378 | Q92597 | Protein NDRG1 GN=NDRG1 PE=1 SV=1 | 0.87 | 1 |
| 1379 | Q9NVS9 | Pyridoxine-5'-phosphate oxidase GN=PNPO PE=1 SV=1 | 0.86 | 1 |
| 1380 | Q13685 | Angio-associated migratory cell protein GN=AAMP PE=1 SV=2 | 0.86 | 1 |
| 1381 | Q14746 | Conserved oligomeric Golgi complex subunit 2 GN=COG2 PE=1 SV=1 | 0.86 | 1 |
| 1382 | Q99961 | Endophilin-A2 GN=SH3GL1 PE=1 SV=1 | 0.85 | 1 |
| 1383 | P10619 | Lysosomal protective protein GN=CTSA PE=1 SV=2 | 0.85 | 1 |
| 1384 | P01708 | Ig lambda chain V-II region BUR PE=1 SV=1 | 0.82 | 2 |
| 1385 | Q7Z6B7 | SLIT-ROBO Rho GTPase-activating protein 1 GN=SRGAP1 PE=1 SV=1 | 0.81 | 1 |
| 1386 | Q9BRT3 | Migration and invasion enhancer 1 GN=MIEN1 PE=1 SV=1 | 0.81 | 1 |
| 1387 | Q96RF0 | Sorting nexin-18 GN=SNX18 PE=1 SV=2 | 0.81 | 1 |
| 1388 | P58499 | Protein FAM3B GN=FAM3B PE=1 SV=2 | 0.81 | 1 |
| 1389 | P22692 | Insulin-like growth factor-binding protein 4 GN=IGFBP4 PE=1 SV=2 | 0.8 | 1 |
| 1390 | P16104 | Histone H2AX GN=H2AFX PE=1 SV=2 | 0.79 | 1 |
| 1391 | Q13438 | Protein OS-9 GN=OS9 PE=1 SV=1 | 0.79 | 1 |
| 1392 | P01615 | Ig kappa chain V-II region FR PE=1 SV=1 | 0.78 | 3 |
| 1393 | Q9UBS4 | DnaJ homolog subfamily B member 11 GN=DNAJB11 PE=1 SV=1 | 0.77 | 1 |
| 1394 | P09382 | Galectin-1 GN=LGALS1 PE=1 SV=2 | 0.76 | 1 |
| 1395 | Q8N9B5 | Junction-mediating and -regulatory protein GN=JMY PE=1 SV=2 | 0.76 | 1 |
| 1396 | P40429 | 60S ribosomal protein L13a GN=RPL13A PE=1 SV=2 | 0.75 | 1 |

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|------|--------|--|------|---|
| 1397 | P42704 | Leucine-rich PPR motif-containing protein, mitochondrial GN=LRPPRC PE=1 SV=3 | 0.75 | 1 |
| 1398 | O14841 | 5-oxoprolinase GN=OPLAH PE=1 SV=3 | 0.75 | 1 |
| 1399 | Q10570 | Cleavage and polyadenylation specificity factor subunit 1 GN=CPSF1 PE=1 SV=2 | 0.75 | 1 |
| 1400 | Q9Y2J4 | Angiotensin-like protein 2 GN=AMOTL2 PE=1 SV=3 | 0.74 | 1 |
| 1401 | O95352 | Ubiquitin-like modifier-activating enzyme ATG7 GN=ATG7 PE=1 SV=1 | 0.74 | 1 |
| 1402 | O95573 | Long-chain-fatty-acid--CoA ligase 3 GN=ACSL3 PE=1 SV=3 | 0.73 | 1 |
| 1403 | P38405 | Guanine nucleotide-binding protein G(olf) subunit alpha GN=GNAL PE=1 SV=1 | 0.72 | 1 |
| 1404 | Q8TDN4 | CDK5 and ABL1 enzyme substrate 1 GN=CABLES1 PE=1 SV=2 | 0.72 | 1 |
| 1405 | A6NCS6 | Uncharacterized protein C2orf72 GN=C2orf72 PE=2 SV=2 | 0.71 | 1 |
| 1406 | P30460 | HLA class I histocompatibility antigen, B-8 alpha chain GN=HLA-B PE=1 SV=1 | 0.7 | 1 |
| 1407 | O95819 | Mitogen-activated protein kinase kinase kinase kinase 4 GN=MAP4K4 PE=1 SV=2 | 0.7 | 1 |
| 1408 | Q96QB1 | Rho GTPase-activating protein 7 GN=DLC1 PE=1 SV=4 | 0.69 | 1 |
| 1409 | Q9BVJ7 | Dual specificity protein phosphatase 23 GN=DUSP23 PE=1 SV=1 | 0.68 | 1 |
| 1410 | Q9NZD2 | Glycolipid transfer protein GN=GLTP PE=1 SV=3 | 0.66 | 1 |
| 1411 | Q04637 | Eukaryotic translation initiation factor 4 gamma 1 GN=EIF4G1 PE=1 SV=4 | 0.66 | 1 |
| 1412 | Q9UMY4 | Sorting nexin-12 GN=SNX12 PE=1 SV=3 | 0.66 | 1 |
| 1413 | Q99613 | Eukaryotic translation initiation factor 3 subunit C GN=EIF3C PE=1 SV=1 | 0.66 | 1 |
| 1414 | P38432 | Coilin GN=COIL PE=1 SV=1 | 0.64 | 1 |

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|------|--------|---|------|---|
| 1415 | Q7L014 | Probable ATP-dependent RNA helicase DDX46 GN=DDX46 PE=1 SV=2 | 0.64 | 1 |
| 1416 | Q674X7 | Kazrin GN=KAZN PE=1 SV=2 | 0.64 | 1 |
| 1417 | P51991 | Heterogeneous nuclear ribonucleoprotein A3 GN=HNRNPA3 PE=1 SV=2 | 0.63 | 2 |
| 1418 | P01815 | Ig heavy chain V-II region COR PE=1 SV=1 | 0.62 | 1 |
| 1419 | P20336 | Ras-related protein Rab-3A GN=RAB3A PE=1 SV=1 | 0.61 | 2 |
| 1420 | Q14533 | Keratin, type II cuticular Hb1 GN=KRT81 PE=1 SV=3 | 0.61 | 1 |
| 1421 | Q15562 | Transcriptional enhancer factor TEF-4 GN=TEAD2 PE=1 SV=2 | 0.61 | 1 |
| 1422 | P62280 | 40S ribosomal protein S11 GN=RPS11 PE=1 SV=3 | 0.59 | 1 |
| 1423 | O00148 | ATP-dependent RNA helicase DDX39A GN=DDX39A PE=1 SV=2 | 0.58 | 1 |
| 1424 | P62995 | Transformer-2 protein homolog beta GN=TRA2B PE=1 SV=1 | 0.57 | 1 |
| 1425 | P56211 | cAMP-regulated phosphoprotein 19 GN=ARPP19 PE=1 SV=2 | 0.55 | 1 |
| 1426 | Q9UH36 | SRR1-like protein GN=SRRD PE=2 SV=1 | 0.54 | 1 |
| 1427 | Q92820 | Gamma-glutamyl hydrolase GN=GGH PE=1 SV=2 | 0.54 | 1 |
| 1428 | Q6NUQ4 | Transmembrane protein 214 GN=TMEM214 PE=1 SV=2 | 0.53 | 1 |
| 1429 | O43505 | N-acetyllactosaminide beta-1,3-N- acetylglucosaminyltransferase GN=B3GNT1 PE=1 SV=1 | 0.53 | 1 |
| 1430 | O43681 | ATPase ASNA1 GN=ASNA1 PE=1 SV=2 | 0.51 | 1 |
| 1431 | O60493 | Sorting nexin-3 GN=SNX3 PE=1 SV=3 | 0.5 | 1 |
| 1432 | Q96C86 | m7GpppX diphosphatase GN=DCPS PE=1 SV=2 | 0.5 | 1 |
| 1433 | Q29836 | HLA class I histocompatibility antigen, B-67 | 0.49 | 1 |

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|------|--------|--|------|----|
| | | alpha chain GN=HLA-B PE=1 SV=1 | | |
| 1434 | Q13045 | Protein flightless-1 homolog GN=FLII PE=1 SV=2 | 0.49 | 1 |
| 1435 | Q9NUP9 | Protein lin-7 homolog C GN=LIN7C PE=1 SV=1 | 0.49 | 1 |
| 1436 | Q14444 | Caprin-1 GN=CAPRIN1 PE=1 SV=2 | 0.48 | 1 |
| 1437 | Q9H074 | Polyadenylate-binding protein-interacting protein 1 GN=PAIP1 PE=1 SV=1 | 0.48 | 1 |
| 1438 | P55008 | Allograft inflammatory factor 1 GN=AIF1 PE=1 SV=1 | 0.47 | 1 |
| 1439 | Q8IZ07 | Ankyrin repeat domain-containing protein 13A GN=ANKRD13A PE=1 SV=3 | 0.47 | 1 |
| 1440 | P36915 | Guanine nucleotide-binding protein-like 1 GN=GNL1 PE=1 SV=2 | 0.46 | 1 |
| 1441 | P06310 | Ig kappa chain V-II region RPMI 6410 PE=4 SV=1 | 0.46 | 11 |
| 1442 | Q8WZA9 | Immunity-related GTPase family Q protein GN=IRGQ PE=1 SV=1 | 0.46 | 1 |
| 1443 | P62899 | 60S ribosomal protein L31 GN=RPL31 PE=1 SV=1 | 0.46 | 1 |
| 1444 | P46060 | Ran GTPase-activating protein 1 GN=RANGAP1 PE=1 SV=1 | 0.46 | 1 |
| 1445 | Q96GX5 | Serine/threonine-protein kinase greatwall GN=MASTL PE=1 SV=1 | 0.46 | 1 |
| 1446 | Q96FJ2 | Dynein light chain 2, cytoplasmic GN=DYNLL2 PE=1 SV=1 | 0.45 | 1 |
| 1447 | P62701 | 40S ribosomal protein S4, X isoform GN=RPS4X PE=1 SV=2 | 0.44 | 1 |
| 1448 | P29034 | Protein S100-A2 GN=S100A2 PE=1 SV=3 | 0.43 | 2 |
| 1449 | Q9NYB0 | Telomeric repeat-binding factor 2-interacting protein 1 GN=TERF2IP PE=1 SV=1 | 0.43 | 1 |
| 1450 | Q5SRE5 | Nucleoporin NUP188 homolog GN=NUP188 PE=1 SV=1 | 0.42 | 1 |

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|------|--------|--|------|----|
| 1451 | O43583 | Density-regulated protein GN=DENR PE=1 SV=2 | 0.41 | 1 |
| 1452 | Q9Y224 | UPF0568 protein C14orf166 GN=C14orf166 PE=1 SV=1 | 0.41 | 1 |
| 1453 | P01621 | Ig kappa chain V-III region NG9 (Fragment) PE=1 SV=1 | 0.4 | 18 |
| 1454 | Q3MJ13 | WD repeat-containing protein 72 GN=WDR72 PE=2 SV=2 | 0.39 | 1 |
| 1455 | Q9GZP4 | PITH domain-containing protein 1 GN=PITHD1 PE=1 SV=1 | 0.38 | 1 |
| 1456 | Q13177 | Serine/threonine-protein kinase PAK 2 GN=PAK2 PE=1 SV=3 | 0.38 | 1 |
| 1457 | P20783 | Neurotrophin-3 GN=NTF3 PE=1 SV=1 | 0.38 | 1 |
| 1458 | Q15785 | Mitochondrial import receptor subunit TOM34 GN=TOMM34 PE=1 SV=2 | 0.37 | 1 |
| 1459 | Q9UBQ0 | Vacuolar protein sorting-associated protein 29 GN=VPS29 PE=1 SV=1 | 0.37 | 1 |
| 1460 | Q16666 | Gamma-interferon-inducible protein 16 GN=IFI16 PE=1 SV=3 | 0.36 | 2 |
| 1461 | Q92734 | Protein TFG GN=TFG PE=1 SV=2 | 0.36 | 1 |
| 1462 | P39019 | 40S ribosomal protein S19 GN=RPS19 PE=1 SV=2 | 0.36 | 1 |
| 1463 | O94823 | Probable phospholipid-transporting ATPase VB GN=ATP10B PE=2 SV=2 | 0.36 | 1 |
| 1464 | Q9UNF0 | Protein kinase C and casein kinase substrate in neurons protein 2 GN=PACSIN2 PE=1 SV=2 | 0.35 | 1 |
| 1465 | Q8NAB2 | Kelch repeat and BTB domain-containing protein 3 GN=KBTBD3 PE=2 SV=2 | 0.35 | 1 |
| 1466 | P41240 | Tyrosine-protein kinase CSK GN=CSK PE=1 SV=1 | 0.34 | 1 |
| 1467 | Q17RC7 | Exocyst complex component 3-like protein 4 GN=EXOC3L4 PE=2 SV=2 | 0.34 | 1 |
| 1468 | P16885 | 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 GN=PLCG2 | 0.34 | 1 |

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|------|--------|---|------|---|
| | | PE=1 SV=4 | | |
| 1469 | P49207 | 60S ribosomal protein L34 GN=RPL34 PE=1 SV=3 | 0.34 | 1 |
| 1470 | P29350 | Tyrosine-protein phosphatase non-receptor type 6 GN=PTPN6 PE=1 SV=1 | 0.33 | 1 |
| 1471 | Q9UK76 | Hematological and neurological expressed 1 protein GN=HN1 PE=1 SV=3 | 0.33 | 1 |
| 1472 | P61328 | Fibroblast growth factor 12 GN=FGF12 PE=1 SV=1 | 0.32 | 1 |
| 1473 | Q96IV0 | Peptide-N(4)-(N-acetyl-beta-glucosaminy)asparagine amidase GN=NGLY1 PE=1 SV=1 | 0.32 | 1 |
| 1474 | Q9NYC9 | Dynein heavy chain 9, axonemal GN=DNAH9 PE=1 SV=3 | 0.32 | 1 |
| 1475 | O00273 | DNA fragmentation factor subunit alpha GN=DFFA PE=1 SV=1 | 0.32 | 1 |
| 1476 | P18621 | 60S ribosomal protein L17 GN=RPL17 PE=1 SV=3 | 0.31 | 1 |
| 1477 | O95758 | Polypyrimidine tract-binding protein 3 GN=PTBP3 PE=1 SV=2 | 0.31 | 1 |
| 1478 | Q00688 | Peptidyl-prolyl cis-trans isomerase FKBP3 GN=FKBP3 PE=1 SV=1 | 0.31 | 1 |
| 1479 | O00487 | 26S proteasome non-ATPase regulatory subunit 14 GN=PSMD14 PE=1 SV=1 | 0.3 | 1 |
| 1480 | O15085 | Rho guanine nucleotide exchange factor 11 GN=ARHGEF11 PE=1 SV=1 | 0.29 | 1 |
| 1481 | P07814 | Bifunctional glutamate/proline--tRNA ligase GN=EPRS PE=1 SV=5 | 0.29 | 1 |
| 1482 | Q7LG56 | Ribonucleoside-diphosphate reductase subunit M2 B GN=RRM2B PE=1 SV=1 | 0.28 | 1 |
| 1483 | Q9Y295 | Developmentally-regulated GTP-binding protein 1 GN=DRG1 PE=1 SV=1 | 0.28 | 1 |
| 1484 | P34949 | Mannose-6-phosphate isomerase GN=MPI PE=1 SV=2 | 0.27 | 1 |

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|------|--------|---|------|---|
| 1485 | Q6PJP8 | DNA cross-link repair 1A protein GN=DCLRE1A PE=1 SV=3 | 0.27 | 1 |
| 1486 | P36873 | Serine/threonine-protein phosphatase PP1- gamma catalytic subunit GN=PPP1CC PE=1 SV=1 | 0.27 | 4 |
| 1487 | Q04206 | Transcription factor p65 GN=RELA PE=1 SV=2 | 0.27 | 1 |
| 1488 | P06132 | Uroporphyrinogen decarboxylase GN=UROD PE=1 SV=2 | 0.27 | 1 |
| 1489 | Q96B23 | Uncharacterized protein C18orf25 GN=C18orf25 PE=1 SV=2 | 0.26 | 1 |
| 1490 | Q9UJX4 | Anaphase-promoting complex subunit 5 GN=ANAPC5 PE=1 SV=2 | 0.26 | 1 |
| 1491 | P29144 | Tripeptidyl-peptidase 2 GN=TPP2 PE=1 SV=4 | 0.26 | 1 |
| 1492 | A3KMH1 | von Willebrand factor A domain-containing protein 8 GN=VWA8 PE=1 SV=2 | 0.25 | 1 |
| 1493 | Q8ND23 | Leucine-rich repeat-containing protein 16B GN=LRRRC16B PE=2 SV=2 | 0.25 | 1 |
| 1494 | Q9H5H4 | Zinc finger protein 768 GN=ZNF768 PE=1 SV=2 | 0.25 | 1 |
| 1495 | Q8IYT4 | Katanin p60 ATPase-containing subunit A-like 2 GN=KATNAL2 PE=2 SV=3 | 0.25 | 2 |
| 1496 | O95359 | Transforming acidic coiled-coil-containing protein 2 GN=TACC2 PE=1 SV=3 | 0.24 | 1 |
| 1497 | Q8N3Y7 | Epidermal retinol dehydrogenase 2 GN=SDR16C5 PE=2 SV=2 | 0.24 | 1 |
| 1498 | Q8NBF2 | NHL repeat-containing protein 2 GN=NHLRC2 PE=1 SV=1 | 0.23 | 1 |
| 1499 | P11171 | Protein 4.1 GN=EPB41 PE=1 SV=4 | 0.23 | 1 |
| 1500 | Q9NP79 | Vacuolar protein sorting-associated protein VTA1 homolog GN=VTA1 PE=1 SV=1 | 0.2 | 1 |
| 1501 | Q99466 | Neurogenic locus notch homolog protein 4 GN=NOTCH4 PE=1 SV=2 | 0.19 | 1 |
| 1502 | P55061 | Bax inhibitor 1 GN=TMBIM6 PE=1 SV=2 | 0.19 | 0 |

| | | | | |
|------|--------|---|------|---|
| 1503 | P42025 | Beta-centractin GN=ACTR1B PE=1 SV=1 | 0.19 | 2 |
| 1504 | Q07075 | Glutamyl aminopeptidase GN=ENPEP PE=1 SV=3 | 0.19 | 1 |
| 1505 | Q9BRP8 | Partner of Y14 and mago GN=WIBG PE=1 SV=1 | 0.19 | 1 |
| 1506 | Q8N8A2 | Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B GN=ANKRD44 PE=1 SV=3 | 0.16 | 0 |
| 1507 | Q14153 | Protein FAM53B GN=FAM53B PE=1 SV=2 | 0.14 | 0 |
| 1508 | Q9C0D0 | Phosphatase and actin regulator 1 GN=PHACTR1 PE=2 SV=3 | 0.12 | 0 |

Supplemental Table S4. The list of unique proteins identified from DDA (FDR < 1%, 95% peptide confidence level) in the spectral library used to process SWATH data.