Supplementary Table S1. Proteins profile of 3D hiPSCs cultured in mTeSR medium

| Accession | Peptide count | Unique peptides | Confidence score | Anova (p) | q Value | Max fold change | Power | Highest mean condition | Lowest mean condition | Mass | Description |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Q99795 | 35 | 27 | 196.0983 | 1.608E-09 | 6.464E-11 | 1.591041 | 1 | P-mT-Susp | mT blank | 36259.29 | Cell surface A33 antigen OS=Homo sapiens OX=9606 GN=GPA33 PE=1 SV=1 |
| P02768;A0A0( | 35 | 24 | 279.9827 | 1.863E-07 | 4.053E-09 | 1.922179 | 1 | P-mT-Susp | mT blank | 71362.71 | Albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2 |
| O75326 | 35 | 22 | 234.0038 | 5.814E-12 | 7.714E-13 | 2.235417 | 1 | P-mT-Susp | P-0.5PG-mT | 75907.39 | Semaphorin-7A OS=Homo sapiens OX=9606 GN=SEMA7A PE=1 SV=1 |
| P02787;C9JVG | 22 | 19 | 247.1295 | 1.529E-09 | 6.243E-11 | 2.869405 | 1 | P-mT-Susp | mT blank | 79345.08 | Serotransferrin OS=Homo sapiens OX=9606 GN=TF PE=1 SV=3 |
| P18065 | 23 | 17 | 116.3566 | 5.701E-06 | 9.927E-08 | 1.409829 | 1 | F-0.5PG-mT | F-mT-2D | 35897.68 | Insulin-like growth factor-binding protein 2 OS=Homo sapiens OX=9606 GN=IGFBP2 PE=1 SV=2 |
| A0A0C4DFM7 | 18 | 17 | 106.7504 | 3.035E-10 | 1.611E-11 | 2.387918 | 1 | P-mT-Susp | mT blank | 188218.4 | Terminal uridylyltransferase 4 OS=Homo sapiens OX=9606 GN=TUT4 PE=1 SV=1 |
| A0A2U3TZM0 | 26 | 17 | 175.1846 | 5.807E-11 | 4.320E-12 | 3.232572 | 1 | P-mT-Susp | mT blank | 218420.6 | DNA helicase OS=Homo sapiens OX=9606 GN=CHD4 PE=1 SV=1 |
| P04264;A0A1\ | 20 | 15 | 169.012 | 3.247E-04 | 4.386E-06 | 1.808992 | 0.99939 | P-0.5PG-mT | F-0.5PG-mT | 66209.9 | Keratin_ type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6 |
| Q86UP2;G3V4 | 19 | 14 | 115.0122 | 3.668E-10 | 1.814E-11 | 2.583584 | 1 | P-mT-Susp | mT blank | 156560.6 | Kinectin OS=Homo sapiens OX=9606 GN=KTN1 PE=1 SV=1 |
| Q8NDI1;B5MC | 16 | 14 | 86.038 | 2.033E-11 | 2.048E-12 | 3.315162 | 1 | P-mT-Susp | mT blank | 140644.8 | EH domain-binding protein 1 OS=Homo sapiens OX=9606 GN=EHBP1 PE=1 SV=3 |
| A0A669KB77;( | 19 | 11 | 148.2589 | 6.019E-02 | 6.637E-04 | 1.149354 | 0.61749 | F-mT-2D | F-0.5PG-mT | 217419.6 | Microtubule-associated protein OS=Homo sapiens OX=9606 GN=MAP2 PE=1 SV=1 |
| P38398;A0A2I | 15 | 11 | 98.9662 | 3.223E-09 | 1.182E-10 | 1.564146 | 1 | P-0.5PG-mT | mT blank | 210230.3 | Breast cancer type 1 susceptibility protein OS=Homo sapiens OX=9606 GN=BRCA1 PE=1 SV=2 |
| O76093 | 15 | 10 | 102.5651 | 2.599E-08 | 7.118E-10 | 2.090961 | 1 | P-mT-Susp | mT blank | 24330.89 | Fibroblast growth factor 18 OS=Homo sapiens OX=9606 GN=FGF18 PE=1 SV=1 |
| A0A087WY61 | 13 | 10 | 84.3613 | 1.601E-01 | 1.711E-03 | 1.633045 | 0.41944 | mT blank | F-mT-2D | 237531.4 | Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=1 |
| Q9H9B1;A0A1 | 13 | 10 | 79.8177 | 3.571E-10 | 1.777E-11 | 3.067795 | 1 | P-mT-Susp | mT blank | 144089.8 | Histone-lysine N-methyltransferase EHMT1 OS=Homo sapiens OX=9606 GN=EHMT1 PE=1 SV=4 |
| Q9H1A4 | 10 | 10 | 52.5067 | 2.308E-07 | 4.939E-09 | 1.766734 | 1 | P-mT-Susp | mT blank | 218667.5 | Anaphase-promoting complex subunit 1 OS=Homo sapiens OX=9606 GN=ANAPC1 PE=1 SV=1 |
| O43320 | 11 | 10 | 62.9362 | 3.148E-10 | 1.638E-11 | 11.05664 | 1 | P-mT-Susp | P-0.5PG-mT | 23872.9 | Fibroblast growth factor 16 OS=Homo sapiens OX=9606 GN=FGF16 PE=1 SV=1 |
| P31946 | 12 | 10 | 70.8095 | 4.037E-11 | 3.348E-12 | 2.73753 | 1 | F-mT-2D | mT blank | 28196.51 | 14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=3 |
| Q8TEU7;E9PC | 12 | 9 | 81.3449 | 3.272E-03 | 3.941E-05 | 2.192957 | 0.96654 | mT blank | P-mT-Susp | 180962.9 | Rap guanine nucleotide exchange factor 6 OS=Homo sapiens OX=9606 GN=RAPGEF6 PE=1 SV=2 |
| Q9NZM3;A0A( | 10 | 9 | 51.0109 | 3.920E-09 | 1.369E-10 | 1.692759 | 1 | P-mT-Susp | F-0.5PG-mT | 194545.3 | Intersectin-2 OS=Homo sapiens OX=9606 GN=ITSN2 PE=1 SV=3 |
| Q9UIF8 | 10 | 9 | 46.0891 | 1.712E-04 | 2.387E-06 | 2.953753 | 0.99988 | P-0.5PG-mT | P-mT-Susp | 242227.4 | Bromodomain adjacent to zinc finger domain protein 2B OS=Homo sapiens OX=9606 GN=BAZ2B PE=1 |
| Q5TCS8;J3KP8 | 12 | 8 | 79.8553 | 1.791E-04 | 2.484E-06 | 1.640973 | 0.99986 | P-mT-Susp | mT blank | 222838.6 | Adenylate kinase 9 OS=Homo sapiens OX=9606 GN=AK9 PE=1 SV=2 |
| Q96N67 | 8 | 8 | 33.193 | 2.314E-03 | 2.825E-05 | 1.230843 | 0.97878 | P-mT-Susp | P-0.5PG-mT | 244443 | Dedicator of cytokinesis protein 7 OS=Homo sapiens OX=9606 GN=DOCK7 PE=1 SV=4 |
| Q12789;I3L1Z | 9 | 8 | 54.2936 | 3.890E-07 | 8.023E-09 | 2.990492 | 1 | P-0.5PG-mT | P-mT-Susp | 241213.3 | General transcription factor 3C polypeptide 1 OS=Homo sapiens OX=9606 GN=GTF3C1 PE=1 SV=4 |
| Q5THK1;C9J9\ | 16 | 8 | 105.0807 | 1.888E-03 | 2.323E-05 | 1.434947 | 0.98409 | P-0.5PG-mT | F-0.5PG-mT | 241291.9 | Protein PRR14L OS=Homo sapiens OX=9606 GN=PRR14L PE=1 SV=1 |
| A0A7I2V4I5;Q | 12 | 8 | 78.1045 | 3.580E-08 | 9.282E-10 | 1.891177 | 1 | P-mT-Susp | F-mT-2D | 197391 | Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens OX=9606 GN=ZC3H13 PE=1 SV=1 |
| Q8TBY8;F5GX\ | 10 | 8 | 48.4183 | 1.161E-09 | 4.889E-11 | 1.740061 | 1 | P-mT-Susp | P-0.5PG-mT | 119033.8 | Polyamine-modulated factor 1-binding protein 1 OS=Homo sapiens OX=9606 GN=PMFBP1 PE=2 SV=3 |
| Q9GZV9 | 10 | 8 | 59.6855 | 2.763E-10 | 1.496E-11 | 2.053379 | 1 | P-0.5PG-mT | P-mT-Susp | 28353.09 | Fibroblast growth factor 23 OS=Homo sapiens OX=9606 GN=FGF23 PE=1 SV=1 |
| O14647;A0A1 | 8 | 8 | 51.2974 | 6.851E-12 | 8.390E-13 | 2.482952 | 1 | P-mT-Susp | mT blank | 212313.2 | Chromodomain-helicase-DNA-binding protein 2 OS=Homo sapiens OX=9606 GN=CHD2 PE=1 SV=2 |
| A0A6E1W127 | 11 | 8 | 67.0913 | 5.407E-14 | 3.913E-14 | 4.992645 | 1 | P-mT-Susp | mT blank | 222529.5 | Myosin-7B OS=Homo sapiens OX=9606 GN=MYH7B PE=1 SV=1 |
| Q9NWH9;H7B | 10 | 8 | 53.984 | 1.945E-02 | 2.212E-04 | 1.474332 | 0.80926 | mT blank | F-mT-2D | 117433.7 | SAFB-like transcription modulator OS=Homo sapiens OX=9606 GN=SLTM PE=1 SV=2 |
| Q562F6 | 7 | 7 | 34.1557 | 1.366E-06 | 2.571E-08 | 1.720525 | 1 | P-mT-Susp | F-0.5PG-mT | 145879.9 | Shugoshin 2 OS=Homo sapiens OX=9606 GN=SGO2 PE=1 SV=2 |
| Q13136;E9PJZ | 13 | 7 | 76.8224 | 4.470E-11 | 3.554E-12 | 3.021142 | 1 | P-mT-Susp | mT blank | 136349.3 | Liprin-alpha-1 OS=Homo sapiens OX=9606 GN=PPFIA1 PE=1 SV=1 |
| P78423 | 8 | 7 | 67.2726 | 2.934E-12 | 5.431E-13 | 5.384873 | 1 | P-mT-Susp | P-0.5PG-mT | 42658.95 | Fractalkine OS=Homo sapiens OX=9606 GN=CX3CL1 PE=1 SV=1 |
| Q86U86;E7EV | 11 | 7 | 65.5957 | 4.768E-05 | 7.176E-07 | 2.656155 | 1 | F-0.5PG-mT | P-mT-Susp | 194202.8 | Protein polybromo-1 OS=Homo sapiens OX=9606 GN=PBRM1 PE=1 SV=1 |
| Q9BQE3 | 8 | 7 | 45.1049 | 7.726E-05 | 1.120E-06 | 1.247145 | 0.99999 | P-0.5PG-mT | mT blank | 50579.74 | Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1 |
| A0A2R8YF72;A | 8 | 7 | 57.0691 | 4.194E-03 | 5.006E-05 | 1.41699 | 0.95483 | F-0.5PG-mT | F-mT-2D | 137410 | Myelin transcription factor 1-like protein OS=Homo sapiens OX=9606 GN=MYT1L PE=1 SV=1 |
| P48723 | 8 | 7 | 56.5224 | 3.741E-11 | 3.168E-12 | 2.825657 | 1 | P-mT-Susp | mT blank | 51984.57 | Heat shock 70 kDa protein 13 OS=Homo sapiens OX=9606 GN=HSPA13 PE=1 SV=1 |
| P19174 | 7 | 6 | 32.9172 | 5.704E-07 | 1.141E-08 | 1.68233 | 1 | P-mT-Susp | mT blank | 149844 | 1-phosphatidylinositol 4_5-bisphosphate phosphodiesterase gamma-1 OS=Homo sapiens OX=9606 GN |
| Q8NHU2;A0A( | 7 | 6 | 39.0619 | 6.168E-06 | 1.066E-07 | 2.187184 | 1 | P-0.5PG-mT | P-mT-Susp | 143173.6 | Cilia- and flagella-associated protein 61 OS=Homo sapiens OX=9606 GN=CFAP61 PE=2 SV=3 |
| E7ESP2;J3KS3 | 6 | 6 | 37.4242 | 2.234E-02 | 2.526E-04 | 1.441847 | 0.78925 | P-mT-Susp | F-mT-2D | 50469.26 | Cyclin-dependent kinase 11A OS=Homo sapiens OX=9606 GN=CDK11A PE=1 SV=1 |
| J3QQJ5;Q9Y2L | 7 | 6 | 61.006 | 1.519E-08 | 4.396E-10 | 2.569997 | 1 | P-0.5PG-mT | F-0.5PG-mT | 156467.2 | Trafficking protein particle complex subunit 8 OS=Homo sapiens OX=9606 GN=TRAPPC8 PE=1 SV=1 |
| Q14515 | 7 | 6 | 47.0333 | 4.245E-10 | 2.048E-11 | 2.757934 | 1 | F-mT-2D | F-0.5PG-mT | 76063.26 | SPARC-like protein 1 OS=Homo sapiens OX=9606 GN=SPARCL1 PE=1 SV=2 |
| O95248;H0Y5 | 8 | 6 | 54.3841 | 5.829E-09 | 1.925E-10 | 2.432403 | 1 | P-mT-Susp | mT blank | 210553.6 | Myotubularin-related protein 5 OS=Homo sapiens OX=9606 GN=SBF1 PE=1 SV=4 |
| Q07890;C9K0 | 9 | 6 | 56.2226 | 1.486E-09 | 6.096E-11 | 2.842994 | 1 | P-0.5PG-mT | mT blank | 154348.1 | Son of sevenless homolog 2 OS=Homo sapiens OX=9606 GN=SOS2 PE=1 SV=2 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| O00160 | 10 | 6 | 62.3842 | 8.481E-06 | 1.418E-07 | 1.363425 | 1 | P-0.5PG-mT | P-mT-Susp | 125585.8 | Unconventional myosin-If OS=Homo sapiens OX=9606 GN=MYO1F PE=1 SV=3 |
| P49756;H0YE4 | 9 | 6 | 59.0699 | 1.237E-01 | 1.333E-03 | 1.117833 | 0.47249 | mT blank | P-mT-Susp | 100527.8 | RNA-binding protein 25 OS=Homo sapiens OX=9606 GN=RBM25 PE=1 SV=3 |
| Q9UQD0;A0A5 | 6 | 5 | 32.5516 | 3.143E-11 | 2.858E-12 | 2.056325 | 1 | P-0.5PG-mT | mT blank | 227504.7 | Sodium channel protein type 8 subunit alpha OS=Homo sapiens OX=9606 GN=SCN8A PE=1 SV=1 |
| D6W5U7;Q9U | 6 | 5 | 34.3658 | 2.516E-05 | 3.920E-07 | 1.33424 | 1 | P-mT-Susp | mT blank | 140432.5 | Cohesin subunit SA-3 OS=Homo sapiens OX=9606 GN=STAG3 PE=1 SV=1 |
| P10827;J3KTF | 5 | 5 | 25.2558 | 3.145E-10 | 1.638E-11 | 2.970759 | 1 | P-mT-Susp | mT blank | 55899.15 | Thyroid hormone receptor alpha OS=Homo sapiens OX=9606 GN=THRA PE=1 SV=1 |
| Q9NSY1;H0Y9 | 5 | 5 | 27.7673 | 1.177E-10 | 7.439E-12 | 3.211304 | 1 | F-mT-2D | F-0.5PG-mT | 130027.1 | BMP-2-inducible protein kinase OS=Homo sapiens OX=9606 GN=BMP2K PE=1 SV=2 |
| A0A0D9SG04; | 6 | 5 | 40.6413 | 2.217E-09 | 8.609E-11 | 2.0004 | 1 | P-mT-Susp | mT blank | 135659.9 | Cordon-bleu protein-like 1 OS=Homo sapiens OX=9606 GN=COBLL1 PE=1 SV=2 |
| Q86VW0;C9J4 | 6 | 5 | 28.843 | 1.371E-10 | 8.398E-12 | 2.39835 | 1 | P-mT-Susp | mT blank | 80089.78 | SEC14 domain and spectrin repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=SESTD1 PE=1 |
| Q9H792;H0YN | 5 | 5 | 39.1516 | 1.551E-13 | 6.498E-14 | 4.570707 | 1 | P-mT-Susp | mT blank | 195159.7 | Inactive tyrosine-protein kinase PEAK1 OS=Homo sapiens OX=9606 GN=PEAK1 PE=1 SV=4 |
| Q9HBG6;D6RA | 6 | 5 | 26.3454 | 1.304E-01 | 1.397E-03 | 1.090156 | 0.46168 | F-0.5PG-mT | mT blank | 143878.4 | Intraflagellar transport protein 122 homolog OS=Homo sapiens OX=9606 GN=IFT122 PE=1 SV=2 |
| Q9H9Y6 | 5 | 5 | 26.4362 | 4.999E-10 | 2.341E-11 | 2.445365 | 1 | P-mT-Susp | mT blank | 129883.6 | DNA-directed RNA polymerase I subunit RPA2 OS=Homo sapiens OX=9606 GN=POLR1B PE=1 SV=2 |
| Q5TB80 | 6 | 5 | 30.7505 | 4.986E-09 | 1.682E-10 | 2.21011 | 1 | P-mT-Susp | mT blank | 162456.5 | Centrosomal protein of 162 kDa OS=Homo sapiens OX=9606 GN=CEP162 PE=1 SV=2 |
| P31371 | 6 | 5 | 30.8225 | 9.408E-05 | 1.347E-06 | 2.312509 | 0.99998 | mT blank | P-mT-Susp | 23554.61 | Fibroblast growth factor 9 OS=Homo sapiens OX=9606 GN=FGF9 PE=1 SV=3 |
| O15067 | 5 | 5 | 33.8933 | 1.322E-03 | 1.654E-05 | 2.4264 | 0.99078 | P-mT-Susp | mT blank | 146388.4 | Phosphoribosylformylglycinamidine synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1 SV=4 |
| O14795 | 5 | 5 | 28.4423 | 2.697E-11 | 2.562E-12 | 3.665899 | 1 | P-mT-Susp | P-0.5PG-mT | 182789 | Protein unc-13 homolog B OS=Homo sapiens OX=9606 GN=UNC13B PE=1 SV=2 |
| A0A494C0R8; | 5 | 5 | 28.4962 | 9.916E-07 | 1.912E-08 | 1.927131 | 1 | P-mT-Susp | mT blank | 151892 | Clustered mitochondria protein homolog OS=Homo sapiens OX=9606 GN=CLUH PE=1 SV=1 |
| P55198;Q6P2 | 5 | 5 | 32.9597 | 2.854E-08 | 7.702E-10 | 1.988718 | 1 | P-mT-Susp | mT blank | 113530.8 | Protein AF-17 OS=Homo sapiens OX=9606 GN=MLLT6 PE=1 SV=3 |
| A0A0C4DH07; | 6 | 5 | 33.2988 | 4.878E-09 | 1.652E-10 | 2.600665 | 1 | P-mT-Susp | mT blank | 178352.8 | Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens OX=9606 GN=LTBP4 PE=1 |
| Q92608;E5RFJ | 7 | 5 | 43.0395 | 1.867E-04 | 2.580E-06 | 1.223702 | 0.99985 | P-mT-Susp | mT blank | 213260.4 | Dedicator of cytokinesis protein 2 OS=Homo sapiens OX=9606 GN=DOCK2 PE=1 SV=2 |
| P02647 | 10 | 5 | 62.9429 | 4.017E-08 | 1.028E-09 | 2.514365 | 1 | P-mT-Susp | mT blank | 30777.87 | Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1 |
| Q13751 | 7 | 5 | 52.6095 | 1.167E-09 | 4.889E-11 | 2.212769 | 1 | P-mT-Susp | mT blank | 133450.6 | Laminin subunit beta-3 OS=Homo sapiens OX=9606 GN=LAMB3 PE=1 SV=1 |
| Q12873 | 7 | 5 | 32.4451 | 3.447E-04 | 4.612E-06 | 2.327643 | 0.9993 | P-mT-Susp | F-mT-2D | 228131.8 | Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens OX=9606 GN=CHD3 PE=1 SV=3 |
| Q7Z6G8;H0YJ2 | 8 | 5 | 52.4612 | 1.151E-10 | 7.329E-12 | 2.197737 | 1 | F-mT-2D | mT blank | 139321 | Ankyrin repeat and sterile alpha motif domain-containing protein 1B OS=Homo sapiens OX=9606 GN=A |
| F8WD26;J3KP | 7 | 5 | 45.4662 | 2.001E-07 | 4.341E-09 | 2.370023 | 1 | P-mT-Susp | F-0.5PG-mT | 187376.4 | LIM domain only protein 7 OS=Homo sapiens OX=9606 GN=LMO7 PE=1 SV=2 |
| Q9P2R6;A0A5 | 8 | 5 | 50.4691 | 4.850E-05 | 7.285E-07 | 2.029078 | 1 | P-mT-Susp | mT blank | 173564.4 | Arginine-glutamic acid dipeptide repeats protein OS=Homo sapiens OX=9606 GN=RERE PE=1 SV=2 |
| Q9Y2P4;D6RA | 7 | 5 | 52.5075 | 1.487E-08 | 4.319E-10 | 1.92185 | 1 | P-mT-Susp | mT blank | 70910.09 | Long-chain fatty acid transport protein 6 OS=Homo sapiens OX=9606 GN=SLC27A6 PE=1 SV=1 |
| G8JLD3;Q8IUD | 4 | 4 | 27.2376 | 1.164E-05 | 1.911E-07 | 1.337228 | 1 | F-0.5PG-mT | F-mT-2D | 124991.5 | ELKS/Rab6-interacting/CAST family member 1 OS=Homo sapiens OX=9606 GN=ERC1 PE=1 SV=1 |
| Q8TE60 | 4 | 4 | 18.3873 | 2.520E-02 | 2.838E-04 | 1.258499 | 0.77088 | P-0.5PG-mT | F-mT-2D | 139558.4 | A disintegrin and metalloproteinase with thrombospondin motifs 18 OS=Homo sapiens OX=9606 GN=A |
| Q96MT7 | 5 | 4 | 26.1391 | 4.851E-08 | 1.211E-09 | 3.113624 | 1 | P-0.5PG-mT | F-mT-2D | 215120.3 | Cilia- and flagella-associated protein 44 OS=Homo sapiens OX=9606 GN=CFAP44 PE=1 SV=2 |
| Q49AJ0 | 5 | 4 | 26.0243 | 2.162E-04 | 2.978E-06 | 1.366471 | 0.99977 | P-mT-Susp | P-0.5PG-mT | 157138.6 | Protein FAM135B OS=Homo sapiens OX=9606 GN=FAM135B PE=1 SV=2 |
| G3V419;Q9UH | 5 | 4 | 31.0409 | 4.214E-06 | 7.488E-08 | 2.17655 | 1 | P-mT-Susp | F-0.5PG-mT | 145826.8 | DNA mismatch repair protein Mlh3 OS=Homo sapiens OX=9606 GN=MLH3 PE=1 SV=1 |
| A2RUS2;E9PF3 | 5 | 4 | 20.7992 | 4.674E-07 | 9.515E-09 | 2.028531 | 1 | P-0.5PG-mT | P-mT-Susp | 137829.3 | DENN domain-containing protein 3 OS=Homo sapiens OX=9606 GN=DENND3 PE=1 SV=2 |
| O00308;H3BP | 5 | 4 | 25.3138 | 1.733E-02 | 1.977E-04 | 1.287212 | 0.82503 | P-mT-Susp | F-mT-2D | 99482.48 | NEDD4-like E3 ubiquitin-protein ligase WWP2 OS=Homo sapiens OX=9606 GN=WWP2 PE=1 SV=2 |
| A0A0C4DFQ3; | 5 | 4 | 23.3195 | 4.713E-08 | 1.187E-09 | 2.123548 | 1 | P-0.5PG-mT | mT blank | 71227.38 | Zinc finger and SCAN domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ZSCAN2 PE=1 SV=1 |
| Q02410 | 4 | 4 | 30.018 | 5.495E-11 | 4.127E-12 | 8.270616 | 1 | P-mT-Susp | P-0.5PG-mT | 93321.34 | Amyloid-beta A4 precursor protein-binding family A member 1 OS=Homo sapiens OX=9606 GN=APBA1 |
| G3V200;O753 | 4 | 4 | 23.1875 | 2.702E-08 | 7.366E-10 | 3.732787 | 1 | P-mT-Susp | mT blank | 142564.7 | Liprin-alpha-2 OS=Homo sapiens OX=9606 GN=PPFIA2 PE=1 SV=2 |
| A0A2R8Y855; | 5 | 4 | 29.4 | 3.659E-11 | 3.132E-12 | 8.738727 | 1 | P-mT-Susp | P-0.5PG-mT | 41988.16 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS= |
| Q58EX7;H3BM | 5 | 4 | 36.597 | 1.737E-05 | 2.776E-07 | 1.574066 | 1 | P-0.5PG-mT | P-mT-Susp | 132513.6 | Puratrophin-1 OS=Homo sapiens OX=9606 GN=PLEKHG4 PE=1 SV=1 |
| Q92620 | 4 | 4 | 22.9054 | 2.111E-03 | 2.589E-05 | 3.757159 | 0.98133 | mT blank | P-mT-Susp | 141358.4 | Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 OS=Homo sapiens OX=9606 GN=DHX38 |
| O15523;C9J8C | 4 | 4 | 20.729 | 5.410E-11 | 4.102E-12 | 4.377966 | 1 | P-mT-Susp | P-0.5PG-mT | 73609.96 | ATP-dependent RNA helicase DDX3Y OS=Homo sapiens OX=9606 GN=DDX3Y PE=1 SV=2 |
| B7ZAX5;Q014 | 4 | 4 | 26.0577 | 8.040E-06 | 1.356E-07 | 1.758448 | 1 | P-mT-Susp | mT blank | 48547.6 | N-acetylgalactosamine kinase OS=Homo sapiens OX=9606 GN=GALK2 PE=1 SV=1 |
| A0A0G2JPU2;A | 4 | 4 | 24.4319 | 1.641E-09 | 6.543E-11 | 2.119935 | 1 | P-mT-Susp | P-0.5PG-mT | 99612.2 | Alpha-helical coiled-coil rod protein OS=Homo sapiens OX=9606 GN=CCHCR1 PE=1 SV=1 |
| O60765 | 4 | 4 | 29.5068 | 2.329E-11 | 2.289E-12 | 2.541249 | 1 | P-mT-Susp | mT blank | 71061.74 | Zinc finger protein 354A OS=Homo sapiens OX=9606 GN=ZNF354A PE=1 SV=2 |
| C9J066;E9PN6 | 5 | 4 | 33.018 | 1.787E-07 | 3.929E-09 | 2.047777 | 1 | P-mT-Susp | F-mT-2D | 240189.4 | Ninein OS=Homo sapiens OX=9606 GN=NIN PE=1 SV=1 |
| Q92613 | 4 | 4 | 29.2702 | 2.746E-09 | 1.031E-10 | 2.160855 | 1 | P-mT-Susp | mT blank | 95462.1 | Protein Jade-3 OS=Homo sapiens OX=9606 GN=JADE3 PE=1 SV=1 |
| A8MQ14;A0A0 | 4 | 4 | 35.0575 | 6.031E-05 | 8.973E-07 | 1.46618 | 1 | F-0.5PG-mT | F-mT-2D | 129651.2 | Zinc finger protein 850 OS=Homo sapiens OX=9606 GN=ZNF850 PE=3 SV=2 |
| A0A0A0MS30 | 4 | 4 | 23.2785 | 4.235E-11 | 3.448E-12 | 2.936724 | 1 | P-mT-Susp | P-0.5PG-mT | 34654.11 | Protein PRRC2C OS=Homo sapiens OX=9606 GN=PRRC2C PE=1 SV=1 |
| Q96KG7;A0A5 | 4 | 4 | 29.4899 | 2.153E-07 | 4.645E-09 | 1.650594 | 1 | F-mT-2D | mT blank | 130645.5 | Multiple epidermal growth factor-like domains protein 10 OS=Homo sapiens OX=9606 GN=MEGF10 PE |
| A0A087WTJ9; | 4 | 4 | 32.0976 | 8.895E-09 | 2.788E-10 | 1.815108 | 1 | P-mT-Susp | F-mT-2D | 125780.9 | E3 ubiquitin-protein ligase OS=Homo sapiens OX=9606 GN=UBR1 PE=1 SV=1 |
| Q9Y5Q9;A0A4 | 4 | 4 | 36.003 | 1.470E-06 | 2.753E-08 | 2.170982 | 1 | P-mT-Susp | mT blank | 102070.8 | General transcription factor 3C polypeptide 3 OS=Homo sapiens OX=9606 GN=GTF3C3 PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| A0A2R8YFV2;A | 4 | 4 | 27.3037 | 5.246E-03 | 6.224E-05 | 1.651034 | 0.94183 | P-0.5PG-mT | mT blank | 185512.9 | Protein Wiz OS=Homo sapiens OX=9606 GN=WIZ PE=1 SV=1 |
| B7WNT5;P364 | 4 | 4 | 33.126 | 5.778E-02 | 6.379E-04 | 2.103588 | 0.62539 | P-0.5PG-mT | mT blank | 52447.75 | Transcription factor 7 OS=Homo sapiens OX=9606 GN=TCF7 PE=1 SV=1 |
| F5H619;Q86X | 4 | 4 | 18.9836 | 2.649E-04 | 3.598E-06 | 1.333549 | 0.99962 | P-0.5PG-mT | F-mT-2D | 226068.7 | HEAT repeat-containing protein 5A OS=Homo sapiens OX=9606 GN=HEATR5A PE=1 SV=1 |
| O75717;H3BS | 4 | 4 | 26.6567 | 5.888E-11 | 4.340E-12 | 2.603615 | 1 | P-mT-Susp | mT blank | 127450.2 | WD repeat and HMG-box DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=WDHD1 PE=1 SV=1 |
| Q14678;Q5W | 5 | 4 | 23.9872 | 5.639E-08 | 1.373E-09 | 2.097207 | 1 | P-0.5PG-mT | mT blank | 149114.3 | KN motif and ankyrin repeat domain-containing protein 1 OS=Homo sapiens OX=9606 GN=KANK1 PE= |
| F5H538;J3KNE | 5 | 4 | 34.2814 | 1.930E-12 | 4.151E-13 | 3.13144 | 1 | P-mT-Susp | mT blank | 182949.4 | Mitogen-activated protein kinase kinase kinase 4 OS=Homo sapiens OX=9606 GN=MAP3K4 PE=1 SV=1 |
| Q6UXG2;H0YD | 6 | 4 | 37.7519 | 2.443E-12 | 4.862E-13 | 2.805056 | 1 | P-mT-Susp | mT blank | 114518.2 | Endosome/lysosome-associated apoptosis and autophagy regulator 1 OS=Homo sapiens OX=9606 GN= |
| Q9BY89 | 4 | 4 | 19.6354 | 2.507E-06 | 4.557E-08 | 1.82226 | 1 | P-mT-Susp | F-mT-2D | 197737.6 | Uncharacterized protein KIAA1671 OS=Homo sapiens OX=9606 GN=KIAA1671 PE=1 SV=2 |
| P06239 | 7 | 4 | 49.7097 | 2.487E-09 | 9.472E-11 | 3.000732 | 1 | P-0.5PG-mT | F-mT-2D | 58513.95 | Tyrosine-protein kinase Lck OS=Homo sapiens OX=9606 GN=LCK PE=1 SV=6 |
| E9PHY5;O434 | 7 | 4 | 35.2358 | 4.376E-08 | 1.106E-09 | 3.122011 | 1 | P-0.5PG-mT | P-mT-Susp | 104873.2 | Band 4.1-like protein 2 OS=Homo sapiens OX=9606 GN=EPB41L2 PE=1 SV=1 |
| P05787 | 5 | 4 | 48.3781 | 2.736E-05 | 4.221E-07 | 1.846893 | 1 | F-0.5PG-mT | P-mT-Susp | 53704.36 | Keratin_ type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7 |
| A0A3B3ISG5;A | 5 | 4 | 28.4836 | 1.038E-09 | 4.465E-11 | 3.229183 | 1 | P-mT-Susp | mT blank | 118741.2 | Insulin-degrading enzyme OS=Homo sapiens OX=9606 GN=IDE PE=1 SV=1 |
| Q6B0I6;K7ES2 | 5 | 4 | 22.7227 | 1.172E-08 | 3.533E-10 | 2.786705 | 1 | P-mT-Susp | mT blank | 59230.15 | Lysine-specific demethylase 4D OS=Homo sapiens OX=9606 GN=KDM4D PE=1 SV=3 |
| Q13009 | 5 | 4 | 27.3478 | 2.922E-08 | 7.857E-10 | 1.465494 | 1 | P-mT-Susp | F-mT-2D | 178820 | Rho guanine nucleotide exchange factor TIAM1 OS=Homo sapiens OX=9606 GN=TIAM1 PE=1 SV=2 |
| G3V0I5;P4982 | 5 | 4 | 35.2835 | 6.291E-12 | 7.858E-13 | 2.85053 | 1 | P-mT-Susp | mT blank | 50738.67 | NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial OS=Homo sapiens OX=9606 GN=ND |
| G3XAE9;Q9Y4 | 8 | 4 | 47.2194 | 3.057E-02 | 3.418E-04 | 1.347047 | 0.73993 | P-0.5PG-mT | P-mT-Susp | 196689.1 | KIAA0423_ isoform CRA_a OS=Homo sapiens OX=9606 GN=TOGARAM1 PE=1 SV=1 |
| A0A286YEW9;I | 6 | 4 | 41.093 | 2.286E-09 | 8.790E-11 | 2.297286 | 1 | P-mT-Susp | F-mT-2D | 63770.86 | Mitogen-activated protein kinase OS=Homo sapiens OX=9606 GN=MAPK10 PE=1 SV=1 |
| E2QRF0;Q70E | 5 | 4 | 30.4862 | 6.821E-04 | 8.815E-06 | 1.48041 | 0.99711 | P-0.5PG-mT | mT blank | 87540.69 | Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens OX=9606 GN=USP45 PE=1 SV=1 |
| A6NNK5;Q128 | 5 | 4 | 31.1197 | 1.891E-12 | 4.151E-13 | 3.398461 | 1 | P-mT-Susp | P-0.5PG-mT | 211015.6 | TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2 |
| A0A0U1RQK4 | 5 | 4 | 23.6334 | 6.477E-07 | 1.283E-08 | 2.077454 | 1 | P-mT-Susp | mT blank | 213471.2 | [Protein ADP-ribosylarginine] hydrolase-like protein 1 OS=Homo sapiens OX=9606 GN=ADPRHL1 PE=1 |
| H0YJB5;Q6GY | 8 | 4 | 58.5444 | 3.041E-08 | 8.151E-10 | 2.065534 | 1 | P-mT-Susp | F-0.5PG-mT | 241791.7 | Ral GTPase-activating protein subunit alpha-1 OS=Homo sapiens OX=9606 GN=RALGAPA1 PE=1 SV=2 |
| H0Y6E7;P3815 | 7 | 4 | 30.4336 | 8.980E-06 | 1.492E-07 | 1.348031 | 1 | F-0.5PG-mT | F-mT-2D | 31745.77 | RNA-binding motif protein_ X chromosome (Fragment) OS=Homo sapiens OX=9606 GN=RBMX PE=1 S |
| P13497;B7ZKF | 3 | 3 | 16.6957 | 6.506E-05 | 9.645E-07 | 2.331128 | 0.99999 | mT blank | F-mT-2D | 113586.9 | Bone morphogenetic protein 1 OS=Homo sapiens OX=9606 GN=BMP1 PE=1 SV=2 |
| E9PKG2 | 4 | 3 | 19.272 | 1.268E-08 | 3.779E-10 | 3.623045 | 1 | P-0.5PG-mT | P-mT-Susp | 67707.93 | Low-density lipoprotein receptor-related protein 8 OS=Homo sapiens OX=9606 GN=LRP8 PE=1 SV=2 |
| A0A1W2PR94 | 3 | 3 | 16.9118 | 8.409E-02 | 9.157E-04 | 1.670498 | 0.55134 | P-mT-Susp | F-0.5PG-mT | 103457.7 | Death domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DTHD1 PE=1 SV=1 |
| A0A1B0GW10 | 4 | 3 | 22.7012 | 9.635E-04 | 1.229E-05 | 2.142609 | 0.99457 | P-mT-Susp | F-mT-2D | 162898 | Methyl-CpG-binding domain protein 5 OS=Homo sapiens OX=9606 GN=MBD5 PE=4 SV=2 |
| Q9HC52;C9J6I | 4 | 3 | 25.2879 | 2.594E-05 | 4.025E-07 | 1.467485 | 1 | F-mT-2D | mT blank | 43509.83 | Chromobox protein homolog 8 OS=Homo sapiens OX=9606 GN=CBX8 PE=1 SV=3 |
| O14640;A0A0 | 3 | 3 | 24.7716 | 2.758E-11 | 2.583E-12 | 7.299549 | 1 | F-0.5PG-mT | P-0.5PG-mT | 75586.07 | Segment polarity protein dishevelled homolog DVL-1 OS=Homo sapiens OX=9606 GN=DVL1 PE=1 SV=2 |
| A0A7P0T8Y0;( | 3 | 3 | 6.967 | 8.983E-11 | 6.062E-12 | 6.492913 | 1 | P-mT-Susp | mT blank | 196337.4 | Probable ATP-dependent RNA helicase DDX60 OS=Homo sapiens OX=9606 GN=DDX60 PE=4 SV=1 |
| A0A494C1F2;F | 4 | 3 | 17.3408 | 2.053E-06 | 3.774E-08 | 2.367838 | 1 | P-mT-Susp | mT blank | 213226 | Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=1 |
| Q9Y4F5;J3KQF | 3 | 3 | 9.4007 | 6.560E-05 | 9.688E-07 | 1.680852 | 0.99999 | P-mT-Susp | mT blank | 172258.5 | Centrosomal protein of 170 kDa protein B OS=Homo sapiens OX=9606 GN=CEP170B PE=1 SV=4 |
| Q9BZF1;F8VQ | 4 | 3 | 28.5559 | 2.647E-01 | 2.814E-03 | 1.652167 | 0.31749 | mT blank | F-mT-2D | 101823 | Oxysterol-binding protein-related protein 8 OS=Homo sapiens OX=9606 GN=OSBPL8 PE=1 SV=3 |
| P49765 | 4 | 3 | 27.7866 | 3.358E-09 | 1.221E-10 | 3.8403 | 1 | P-0.5PG-mT | P-mT-Susp | 22058.03 | Vascular endothelial growth factor B OS=Homo sapiens OX=9606 GN=VEGFB PE=1 SV=2 |
| Q7Z6I6;A0A0A | 4 | 3 | 20.9513 | 9.126E-08 | 2.162E-09 | 1.682656 | 1 | F-mT-2D | mT blank | 119722.8 | Rho GTPase-activating protein 30 OS=Homo sapiens OX=9606 GN=ARHGAP30 PE=1 SV=3 |
| Q8TDR0 | 4 | 3 | 19.9836 | 1.738E-06 | 3.225E-08 | 2.233626 | 1 | P-mT-Susp | mT blank | 78974.04 | TRAF3-interacting protein 1 OS=Homo sapiens OX=9606 GN=TRAF3IP1 PE=1 SV=1 |
| A0A3B3IRJ9;A | 3 | 3 | 15.8157 | 3.821E-10 | 1.877E-11 | 2.65718 | 1 | F-0.5PG-mT | P-mT-Susp | 122106.2 | Phosphatidylinositide phosphatase SAC2 OS=Homo sapiens OX=9606 GN=INPP5F PE=1 SV=1 |
| Q5JWF2;A0A0 | 3 | 3 | 16.1634 | 7.526E-02 | 8.218E-04 | 1.218922 | 0.57358 | P-mT-Susp | F-0.5PG-mT | 111766 | Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens OX=9606 GN= |
| D6RJB7;Q8N7 | 3 | 3 | 16.1182 | 9.694E-09 | 2.991E-10 | 2.494468 | 1 | P-mT-Susp | P-0.5PG-mT | 219731.4 | Ankyrin repeat domain-containing protein 31 OS=Homo sapiens OX=9606 GN=ANKRD31 PE=4 SV=2 |
| Q6NUP7 | 3 | 3 | 14.9981 | 4.812E-01 | 5.080E-03 | 1.453069 | 0.20279 | P-0.5PG-mT | F-mT-2D | 100535.7 | Serine/threonine-protein phosphatase 4 regulatory subunit 4 OS=Homo sapiens OX=9606 GN=PPP4R4 |
| P56199 | 3 | 3 | 15.0191 | 1.231E-02 | 1.419E-04 | 1.966558 | 0.86718 | P-mT-Susp | mT blank | 132387.7 | Integrin alpha-1 OS=Homo sapiens OX=9606 GN=ITGA1 PE=1 SV=2 |
| A0A087X2D8;I | 4 | 3 | 32.607 | 2.993E-07 | 6.302E-09 | 2.131124 | 1 | P-mT-Susp | F-mT-2D | 145967.9 | C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens OX=9606 GN=SPAG9 PE=1 SV=1 |
| Q8TAQ5;K7EL | 3 | 3 | 13.9763 | 1.619E-03 | 2.007E-05 | 4.251231 | 0.98735 | mT blank | P-mT-Susp | 82756.16 | Zinc finger protein 420 OS=Homo sapiens OX=9606 GN=ZNF420 PE=1 SV=1 |
| Q8WXA9 | 3 | 3 | 14.3705 | 3.839E-08 | 9.890E-10 | 3.617452 | 1 | P-mT-Susp | P-0.5PG-mT | 59437.39 | Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens OX=9606 GN=SREK1 PE=1 SV=1 |
| Q6SA08;H7C3 | 3 | 3 | 29.268 | 3.057E-09 | 1.127E-10 | 2.117769 | 1 | P-mT-Susp | mT blank | 37853.61 | Testis-specific serine/threonine-protein kinase 4 OS=Homo sapiens OX=9606 GN=TSSK4 PE=1 SV=1 |
| A8MQ02 | 3 | 3 | 16.4656 | 7.163E-06 | 1.216E-07 | 2.08845 | 1 | F-0.5PG-mT | F-mT-2D | 202832.5 | Afadin OS=Homo sapiens OX=9606 GN=AFDN PE=1 SV=2 |
| A0A3B3IRX3;F | 3 | 3 | 15.6789 | 5.286E-09 | 1.768E-10 | 12.63155 | 1 | P-0.5PG-mT | P-mT-Susp | 246927.1 | Mediator of RNA polymerase II transcription subunit 13 OS=Homo sapiens OX=9606 GN=MED13L PE=1 |
| A0A286YFC2;A | 3 | 3 | 14.582 | 1.057E-01 | 1.143E-03 | 1.395836 | 0.5048 | P-0.5PG-mT | F-0.5PG-mT | 88036.76 | Tubulin polyglutamylase TTLL13P OS=Homo sapiens OX=9606 GN=TTLL13P PE=4 SV=1 |
| P45844;E9PGV | 3 | 3 | 21.346 | 2.247E-07 | 4.821E-09 | 2.408303 | 1 | P-mT-Susp | mT blank | 76561.7 | ATP-binding cassette sub-family G member 1 OS=Homo sapiens OX=9606 GN=ABCG1 PE=1 SV=3 |
| M0R0P8;M0R | 3 | 3 | 21.7684 | 1.717E-07 | 3.786E-09 | 3.932092 | 1 | P-0.5PG-mT | mT blank | 244997 | Unconventional myosin-IXb OS=Homo sapiens OX=9606 GN=MYO9B PE=1 SV=1 |
| A0A087X0R2;A | 3 | 3 | 21.7779 | 2.315E-05 | 3.628E-07 | 1.389674 | 1 | F-0.5PG-mT | mT blank | 15532.1 | Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens OX=9606 GN=MDC1 PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Q9Y5I2;A0A5F | 3 | 3 | 16.6045 | 5.516E-08 | 1.347E-09 | 1.850957 | 1 | F-mT-2D | mT blank | 103673.7 | Protocadherin alpha-10 OS=Homo sapiens OX=9606 GN=PCDHA10 PE=2 SV=1 |
| Q9HCE5;A0A0 | 3 | 3 | 20.4985 | 1.809E-05 | 2.880E-07 | 1.641066 | 1 | P-mT-Susp | F-mT-2D | 52720.79 | N6-adenosine-methyltransferase non-catalytic subunit OS=Homo sapiens OX=9606 GN=METTL14 PE=1 |
| F5GXT3;Q9NC | 3 | 3 | 20.5649 | 1.607E-04 | 2.245E-06 | 2.743197 | 0.9999 | P-mT-Susp | mT blank | 114684.9 | Anoctamin OS=Homo sapiens OX=9606 GN=ANO2 PE=1 SV=2 |
| C9J4K5;C9JSP( | 3 | 3 | 21.2306 | 9.051E-11 | 6.062E-12 | 5.813746 | 1 | P-mT-Susp | mT blank | 55210.98 | Protein downstream neighbor of Son OS=Homo sapiens OX=9606 GN=DONSON PE=1 SV=1 |
| F8WA39;Q136 | 3 | 3 | 17.8428 | 3.030E-05 | 4.639E-07 | 2.364059 | 1 | mT blank | F-mT-2D | 76459.46 | Phosphatidylinositol-3_5-bisphosphate 3-phosphatase OS=Homo sapiens OX=9606 GN=MTMR1 PE=1 S |
| Q9Y239;G3XA | 3 | 3 | 13.7579 | 8.870E-06 | 1.477E-07 | 4.670439 | 1 | P-0.5PG-mT | P-mT-Susp | 109288.1 | Nucleotide-binding oligomerization domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NOD |
| B1AM31;Q5T1 | 3 | 3 | 26.5784 | 1.124E-10 | 7.282E-12 | 2.710276 | 1 | P-mT-Susp | mT blank | 102348.9 | Axonemal dynein light chain domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN= |
| Q96R06 | 3 | 3 | 16.2308 | 5.127E-10 | 2.387E-11 | 3.209396 | 1 | P-mT-Susp | mT blank | 135790.7 | Sperm-associated antigen 5 OS=Homo sapiens OX=9606 GN=SPAG5 PE=1 SV=2 |
| Q8IX18;J3KTK( | 3 | 3 | 23.6222 | 1.456E-05 | 2.361E-07 | 1.857836 | 1 | P-0.5PG-mT | F-mT-2D | 89871.86 | Probable ATP-dependent RNA helicase DHX40 OS=Homo sapiens OX=9606 GN=DHX40 PE=1 SV=2 |
| E2QRD4;Q6ZR | 3 | 3 | 21.2892 | 5.379E-09 | 1.791E-10 | 2.854248 | 1 | P-mT-Susp | mT blank | 139214.9 | Methyl methanesulfonate-sensitivity protein 22-like OS=Homo sapiens OX=9606 GN=MMS22L PE=1 S |
| Q6IV72 | 3 | 3 | 18.7251 | 7.609E-11 | 5.507E-12 | 2.068856 | 1 | P-mT-Susp | mT blank | 90686.35 | Zinc finger protein 425 OS=Homo sapiens OX=9606 GN=ZNF425 PE=1 SV=1 |
| Q53TQ3 | 3 | 3 | 27.4095 | 1.158E-06 | 2.205E-08 | 2.520024 | 1 | F-mT-2D | P-mT-Susp | 114399.8 | INO80 complex subunit D OS=Homo sapiens OX=9606 GN=INO80D PE=1 SV=3 |
| P49321 | 3 | 3 | 14.3682 | 5.513E-05 | 8.234E-07 | 2.445764 | 1 | mT blank | P-mT-Susp | 85522.96 | Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=2 |
| Q96JB5;J3QQY | 3 | 3 | 15.9285 | 1.168E-11 | 1.328E-12 | 2.715016 | 1 | F-mT-2D | F-0.5PG-mT | 57262.93 | CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3 PE=1 SV=2 |
| Q6ZMS4;A0A3 | 3 | 3 | 22.7062 | 2.465E-10 | 1.382E-11 | 7.846731 | 1 | P-mT-Susp | P-0.5PG-mT | 63680.76 | Zinc finger protein 852 OS=Homo sapiens OX=9606 GN=ZNF852 PE=1 SV=4 |
| G3V1R7;O149 | 4 | 3 | 28.809 | 1.883E-12 | 4.151E-13 | 17.18815 | 1 | P-mT-Susp | mT blank | 44343.85 | Solute carrier family 27 (Fatty acid transporter)_ member 2_ isoform CRA_b OS=Homo sapiens OX=96( |
| Q05516 | 3 | 3 | 10.951 | 8.745E-09 | 2.753E-10 | 2.11252 | 1 | F-mT-2D | P-0.5PG-mT | 75699.9 | Zinc finger and BTB domain-containing protein 16 OS=Homo sapiens OX=9606 GN=ZBTB16 PE=1 SV=2 |
| Q96RR1 | 3 | 3 | 18.7463 | 4.323E-04 | 5.726E-06 | 2.326532 | 0.99885 | P-0.5PG-mT | F-mT-2D | 77667.54 | Twinkle protein_ mitochondrial OS=Homo sapiens OX=9606 GN=TWNK PE=1 SV=1 |
| P21128 | 3 | 3 | 16.9917 | 1.078E-08 | 3.301E-10 | 2.044928 | 1 | P-mT-Susp | mT blank | 48126.94 | Poly(U)-specific endoribonuclease OS=Homo sapiens OX=9606 GN=ENDOU PE=1 SV=2 |
| H0Y3Q0;P291 | 3 | 3 | 19.678 | 3.346E-09 | 1.221E-10 | 3.096003 | 1 | P-mT-Susp | P-0.5PG-mT | 91635.2 | Proprotein convertase subtilisin/kexin type 6 (Fragment) OS=Homo sapiens OX=9606 GN=PCSK6 PE=1 |
| P11215 | 3 | 3 | 26.3586 | 3.080E-11 | 2.851E-12 | 2.459858 | 1 | F-mT-2D | F-0.5PG-mT | 128490.3 | Integrin alpha-M OS=Homo sapiens OX=9606 GN=ITGAM PE=1 SV=2 |
| A0A087X241;( | 3 | 3 | 20.2483 | 5.593E-03 | 6.626E-05 | 1.384823 | 0.93764 | P-mT-Susp | F-mT-2D | 123998.7 | Small G protein-signaling modulator 1 OS=Homo sapiens OX=9606 GN=SGSM1 PE=1 SV=1 |
| Q495T6 | 3 | 3 | 16.6049 | 2.793E-13 | 1.011E-13 | 11.45908 | 1 | P-mT-Susp | P-0.5PG-mT | 90051.34 | Membrane metallo-endopeptidase-like 1 OS=Homo sapiens OX=9606 GN=MMEL1 PE=2 SV=2 |
| Q86V71 | 4 | 3 | 21.1231 | 2.600E-04 | 3.538E-06 | 3.687063 | 0.99964 | mT blank | P-mT-Susp | 80547.58 | Zinc finger protein 429 OS=Homo sapiens OX=9606 GN=ZNF429 PE=2 SV=2 |
| G3V5P6;O954 | 3 | 3 | 17.2359 | 4.321E-09 | 1.476E-10 | 5.937691 | 1 | P-mT-Susp | mT blank | 103186.2 | Papilin OS=Homo sapiens OX=9606 GN=PAPLN PE=1 SV=1 |
| O15360;F5H8 | 4 | 3 | 26.8943 | 1.436E-02 | 1.647E-04 | 4.34875 | 0.84911 | mT blank | P-mT-Susp | 164942.5 | Fanconi anemia group A protein OS=Homo sapiens OX=9606 GN=FANCA PE=1 SV=2 |
| A0A494C1R4;A | 4 | 3 | 27.535 | 1.304E-08 | 3.874E-10 | 4.480283 | 1 | P-0.5PG-mT | F-mT-2D | 167972.3 | Protein-tyrosine-phosphatase OS=Homo sapiens OX=9606 GN=PTPRZ1 PE=1 SV=1 |
| Q8IW36;F6W2 | 5 | 3 | 19.7869 | 2.618E-07 | 5.542E-09 | 2.350717 | 1 | P-mT-Susp | mT blank | 62373.27 | Zinc finger protein 695 OS=Homo sapiens OX=9606 GN=ZNF695 PE=1 SV=4 |
| E7EVA0;P278 | 5 | 3 | 31.9842 | 1.027E-01 | 1.114E-03 | 1.571443 | 0.51068 | mT blank | P-mT-Susp | 246699.4 | Microtubule-associated protein OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=1 |
| Q7RTP6;J3QLA | 4 | 3 | 37.4912 | 2.350E-05 | 3.676E-07 | 1.648014 | 1 | P-mT-Susp | F-mT-2D | 225435.7 | [F-actin]-monooxygenase MICAL3 OS=Homo sapiens OX=9606 GN=MICAL3 PE=1 SV=2 |
| A0A0C4DG89;( | 4 | 3 | 20.6554 | 7.585E-05 | 1.106E-06 | 1.758266 | 0.99999 | P-mT-Susp | P-0.5PG-mT | 117974.7 | RNA helicase OS=Homo sapiens OX=9606 GN=DDX46 PE=1 SV=1 |
| Q6UB98;F5GY | 5 | 3 | 27.8818 | 2.767E-04 | 3.752E-06 | 2.241379 | 0.99958 | F-0.5PG-mT | F-mT-2D | 237191.6 | Ankyrin repeat domain-containing protein 12 OS=Homo sapiens OX=9606 GN=ANKRD12 PE=1 SV=3 |
| C9JFF0;Q9ULI | 4 | 3 | 26.6282 | 2.531E-12 | 4.913E-13 | 2.59438 | 1 | F-mT-2D | mT blank | 182318.3 | Kinesin-like protein KIF26A OS=Homo sapiens OX=9606 GN=KIF26A PE=1 SV=1 |
| Q9H3R0 | 4 | 3 | 29.8841 | 1.380E-01 | 1.476E-03 | 1.24134 | 0.45008 | P-mT-Susp | F-mT-2D | 122035 | Lysine-specific demethylase 4C OS=Homo sapiens OX=9606 GN=KDM4C PE=1 SV=2 |
| P16415;C9J2N | 4 | 3 | 32.166 | 9.656E-10 | 4.178E-11 | 4.040692 | 1 | P-mT-Susp | P-0.5PG-mT | 72836.72 | Zinc finger protein 823 OS=Homo sapiens OX=9606 GN=ZNF823 PE=2 SV=2 |
| A0A0B4J1T8;( | 4 | 3 | 23.3963 | 6.996E-05 | 1.028E-06 | 3.41636 | 0.99999 | F-mT-2D | F-0.5PG-mT | 128329.7 | Receptor protein-tyrosine kinase OS=Homo sapiens OX=9606 GN=EPHA6 PE=1 SV=1 |
| Q8NDV7 | 6 | 3 | 33.8208 | 4.518E-02 | 5.016E-04 | 4.200845 | 0.67163 | mT blank | F-mT-2D | 211095.9 | Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens OX=9606 GN=TNRC6A PE=1 SV=2 |
| Q9HCE3;K7EJI | 4 | 3 | 27.4336 | 1.591E-05 | 2.553E-07 | 2.17503 | 1 | P-0.5PG-mT | F-mT-2D | 144091.4 | Zinc finger protein 532 OS=Homo sapiens OX=9606 GN=ZNF532 PE=1 SV=2 |
| O96028 | 5 | 3 | 25.6458 | 6.109E-12 | 7.858E-13 | 5.648246 | 1 | P-mT-Susp | mT blank | 156307.4 | Histone-lysine N-methyltransferase NSD2 OS=Homo sapiens OX=9606 GN=NSD2 PE=1 SV=1 |
| A0A0A0MRA8 | 6 | 3 | 31.3948 | 6.724E-10 | 3.041E-11 | 3.15808 | 1 | P-mT-Susp | mT blank | 102744.3 | Band 4.1-like protein 3 OS=Homo sapiens OX=9606 GN=EPB41L3 PE=1 SV=1 |
| O75362;A2A3 | 5 | 3 | 46.9965 | 2.895E-03 | 3.507E-05 | 1.805762 | 0.97138 | F-0.5PG-mT | P-mT-Susp | 117154.1 | Zinc finger protein 217 OS=Homo sapiens OX=9606 GN=ZNF217 PE=1 SV=1 |
| A0A0C4DG98;( | 4 | 3 | 15.2044 | 5.258E-10 | 2.433E-11 | 2.172756 | 1 | P-mT-Susp | mT blank | 171235.7 | THO complex subunit 2 OS=Homo sapiens OX=9606 GN=THOC2 PE=1 SV=1 |
| O95782;A0A0 | 4 | 3 | 29.4295 | 8.206E-10 | 3.650E-11 | 6.374033 | 1 | mT blank | F-0.5PG-mT | 108629.6 | AP-2 complex subunit alpha-1 OS=Homo sapiens OX=9606 GN=AP2A1 PE=1 SV=3 |
| A0A2R8Y425 | 13 | 3 | 81.6517 | 1.046E-03 | 1.324E-05 | 2.062402 | 0.99374 | F-0.5PG-mT | P-mT-Susp | 216922.8 | DNA helicase (Fragment) OS=Homo sapiens OX=9606 GN=CHD4 PE=1 SV=1 |
| Q9H4G0;A0A0 | 8 | 3 | 52.277 | 1.111E-01 | 1.200E-03 | 1.203818 | 0.49466 | P-0.5PG-mT | F-mT-2D | 99073.28 | Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=EPB41L1 PE=1 SV=2 |
| Q10570 | 5 | 3 | 31.5577 | 1.046E-03 | 1.324E-05 | 1.699815 | 0.99374 | P-0.5PG-mT | F-mT-2D | 162138.7 | Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens OX=9606 GN=CPSF1 PE=1 |
| P23381;G3V2 | 3 | 3 | 16.967 | 6.745E-08 | 1.627E-09 | 2.349677 | 1 | P-0.5PG-mT | F-0.5PG-mT | 53507.68 | Tryptophan--tRNA ligase_ cytoplasmic OS=Homo sapiens OX=9606 GN=WARS1 PE=1 SV=2 |
| Q9UGU0 | 4 | 3 | 18.374 | 1.272E-10 | 7.909E-12 | 2.517189 | 1 | P-mT-Susp | mT blank | 213254.1 | Transcription factor 20 OS=Homo sapiens OX=9606 GN=TCF20 PE=1 SV=3 |
| H0YJG4 | 4 | 3 | 21.3014 | 2.804E-09 | 1.043E-10 | 2.308594 | 1 | P-mT-Susp | mT blank | 209392.2 | Chromodomain-helicase-DNA-binding protein 8 (Fragment) OS=Homo sapiens OX=9606 GN=CHD8 PE= |
| A0A7I2YBM0;( | 6 | 3 | 38.3124 | 4.805E-06 | 8.407E-08 | 2.373995 | 1 | P-0.5PG-mT | P-mT-Susp | 208006.9 | Endoribonuclease Dicer OS=Homo sapiens OX=9606 GN=DICER1 PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| P18615;A0A0A | 6 | 3 | 49.5791 | 5.161E-01 | 5.441E-03 | 1.332398 | 0.18989 | mT blank | P-mT-Susp | 43353.91 | Negative elongation factor E OS=Homo sapiens OX=9606 GN=NELFE PE=1 SV=3 |
| P35354;Q6ZYI | 4 | 3 | 25.9846 | 3.268E-11 | 2.923E-12 | 9.972472 | 1 | P-0.5PG-mT | F-0.5PG-mT | 69737.6 | Prostaglandin G/H synthase 2 OS=Homo sapiens OX=9606 GN=PTGS2 PE=1 SV=2 |
| Q9BZ29;A0A0 | 4 | 3 | 22.8118 | 5.713E-13 | 1.819E-13 | 5.540048 | 1 | P-mT-Susp | P-0.5PG-mT | 238670.1 | Dedicator of cytokinesis protein 9 OS=Homo sapiens OX=9606 GN=DOCK9 PE=1 SV=2 |
| O15015;C9J3L | 6 | 3 | 31.8276 | 1.879E-10 | 1.084E-11 | 2.448216 | 1 | P-mT-Susp | mT blank | 205444.5 | Zinc finger protein 646 OS=Homo sapiens OX=9606 GN=ZNF646 PE=1 SV=2 |
| J3KNI1;Q9H9E | 5 | 3 | 25.0937 | 1.310E-06 | 2.477E-08 | 3.32029 | 1 | P-0.5PG-mT | F-mT-2D | 90470.22 | Component of oligomeric Golgi complex 4 OS=Homo sapiens OX=9606 GN=COG4 PE=1 SV=1 |
| J3QR65;Q9NY | 2 | 2 | 16.0168 | 1.509E-07 | 3.374E-09 | 2.00115 | 1 | mT blank | P-0.5PG-mT | 129522.2 | Protein-tyrosine-phosphatase OS=Homo sapiens OX=9606 GN=MTMR4 PE=1 SV=1 |
| Q3SY46 | 2 | 2 | 20.8668 | 7.350E-14 | 4.501E-14 | 7.874845 | 1 | P-mT-Susp | P-0.5PG-mT | 20490.16 | Keratin-associated protein 13-3 OS=Homo sapiens OX=9606 GN=KRTAP13-3 PE=1 SV=1 |
| F8VZC3 | 2 | 2 | 10.9928 | 8.543E-03 | 1.003E-04 | 1.249747 | 0.90435 | F-0.5PG-mT | mT blank | 3761.25 | Calcyphosin-2 (Fragment) OS=Homo sapiens OX=9606 GN=CAPS2 PE=1 SV=8 |
| Q03181 | 2 | 2 | 11.5512 | 3.991E-12 | 6.484E-13 | 2.544149 | 1 | P-mT-Susp | mT blank | 50701.91 | Peroxisome proliferator-activated receptor delta OS=Homo sapiens OX=9606 GN=PPARD PE=1 SV=1 |
| H0Y650;Q86Y | 2 | 2 | 13.4827 | 3.313E-03 | 3.983E-05 | 2.749793 | 0.96602 | F-0.5PG-mT | F-mT-2D | 73442.21 | Dynein assembly factor 5_ axonemal (Fragment) OS=Homo sapiens OX=9606 GN=DNAAF5 PE=1 SV=1 |
| A0A7I2V554;C | 2 | 2 | 16.4961 | 1.528E-07 | 3.408E-09 | 2.992609 | 1 | F-mT-2D | P-mT-Susp | 94084.51 | UV-stimulated scaffold protein A OS=Homo sapiens OX=9606 GN=UVSSA PE=1 SV=1 |
| H0YL38;H0YLA | 2 | 2 | 16.1825 | 8.788E-03 | 1.030E-04 | 2.001887 | 0.90176 | F-0.5PG-mT | P-mT-Susp | 85753.8 | Zinc finger protein 280D OS=Homo sapiens OX=9606 GN=ZNF280D PE=1 SV=1 |
| M0QZ12;Q96( | 2 | 2 | 10.9372 | 9.006E-04 | 1.151E-05 | 1.956307 | 0.99518 | mT blank | F-mT-2D | 90419.63 | Protein Aster-A OS=Homo sapiens OX=9606 GN=GRAMD1A PE=1 SV=1 |
| A0A0A0MSI8;( | 2 | 2 | 15.698 | 1.393E-06 | 2.616E-08 | 2.02558 | 1 | mT blank | P-mT-Susp | 83145.8 | Exocyst complex component 5 OS=Homo sapiens OX=9606 GN=EXOC5 PE=1 SV=1 |
| P52736 | 2 | 2 | 9.5516 | 2.866E-01 | 3.042E-03 | 1.383824 | 0.30176 | F-mT-2D | mT blank | 75612.44 | Zinc finger protein 133 OS=Homo sapiens OX=9606 GN=ZNF133 PE=1 SV=2 |
| Q96P53;A0A0 | 2 | 2 | 17.2107 | 6.529E-05 | 9.661E-07 | 1.786584 | 0.99999 | P-mT-Susp | P-0.5PG-mT | 45952.8 | WD repeat and FYVE domain-containing protein 2 OS=Homo sapiens OX=9606 GN=WDFY2 PE=1 SV=2 |
| Q8WU20 | 2 | 2 | 10.8024 | 4.258E-06 | 7.532E-08 | 1.815706 | 1 | F-mT-2D | mT blank | 57428.33 | Fibroblast growth factor receptor substrate 2 OS=Homo sapiens OX=9606 GN=FRS2 PE=1 SV=4 |
| A0A669KAX4;A | 2 | 2 | 15.8092 | 7.109E-05 | 1.042E-06 | 3.87386 | 0.99999 | mT blank | P-mT-Susp | 103096.9 | Cullin-4B OS=Homo sapiens OX=9606 GN=CUL4B PE=1 SV=1 |
| A0A494BZY0;A | 2 | 2 | 16.7311 | 2.145E-08 | 6.014E-10 | 1.730701 | 1 | P-mT-Susp | mT blank | 63979.47 | Caspase recruitment domain-containing protein 14 OS=Homo sapiens OX=9606 GN=CARD14 PE=1 SV= |
| Q14585;E9PLT | 2 | 2 | 15.9397 | 2.469E-09 | 9.451E-11 | 2.754257 | 1 | P-mT-Susp | mT blank | 57265.22 | Zinc finger protein 345 OS=Homo sapiens OX=9606 GN=ZNF345 PE=1 SV=1 |
| A0A087WZT0;A | 2 | 2 | 22.005 | 2.600E-03 | 3.165E-05 | 2.142067 | 0.97514 | P-mT-Susp | mT blank | 72870.48 | Protein Smaug homolog 2 OS=Homo sapiens OX=9606 GN=SAMD4B PE=1 SV=1 |
| F6WQW2;P43 | 2 | 2 | 18.6023 | 3.390E-04 | 4.559E-06 | 2.990076 | 0.99933 | mT blank | P-mT-Susp | 32303.51 | Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1 |
| Q5R372 | 2 | 2 | 9.6234 | 1.549E-04 | 2.175E-06 | 2.624754 | 0.99991 | mT blank | F-0.5PG-mT | 93425.53 | Rab GTPase-activating protein 1-like OS=Homo sapiens OX=9606 GN=RABGAP1L PE=1 SV=1 |
| A0A2R8YG59;A | 2 | 2 | 10.0729 | 2.209E-05 | 3.483E-07 | 1.962513 | 1 | P-mT-Susp | P-0.5PG-mT | 42657.28 | Oxysterol-binding protein OS=Homo sapiens OX=9606 GN=OSBPL2 PE=1 SV=1 |
| P0C2Y1 | 2 | 2 | 18.1968 | 3.409E-10 | 1.731E-11 | 2.983148 | 1 | P-mT-Susp | mT blank | 48603.47 | Putative neuroblastoma breakpoint family member 7 OS=Homo sapiens OX=9606 GN=NBPF7 PE=5 SV= |
| Q9Y6D9 | 2 | 2 | 12.4643 | 7.459E-07 | 1.466E-08 | 3.819469 | 1 | F-mT-2D | mT blank | 83352.17 | Mitotic spindle assembly checkpoint protein MAD1 OS=Homo sapiens OX=9606 GN=MAD1L1 PE=1 SV= |
| P10072 | 2 | 2 | 9.6293 | 1.801E-05 | 2.873E-07 | 3.126691 | 1 | mT blank | P-mT-Susp | 77067.24 | Zinc finger protein 875 OS=Homo sapiens OX=9606 GN=ZNF875 PE=2 SV=4 |
| D6RCC7;Q9P2 | 2 | 2 | 14.9119 | 1.016E-05 | 1.677E-07 | 1.38149 | 1 | F-0.5PG-mT | F-mT-2D | 125104 | Protein FAM135A OS=Homo sapiens OX=9606 GN=FAM135A PE=1 SV=1 |
| Q9P2K8;H0YN | 2 | 2 | 11.2153 | 8.272E-11 | 5.813E-12 | 3.54518 | 1 | P-0.5PG-mT | F-0.5PG-mT | 188393.5 | eIF-2-alpha kinase GCN2 OS=Homo sapiens OX=9606 GN=EIF2AK4 PE=1 SV=3 |
| A0A7P0T8I1 | 2 | 2 | 15.6744 | 2.217E-09 | 8.609E-11 | 3.245463 | 1 | P-mT-Susp | mT blank | 62832.52 | Sodium-dependent neutral amino acid transporter B(0)AT2 OS=Homo sapiens OX=9606 GN=SLC6A15 |
| H0YFS2 | 3 | 2 | 35.062 | 1.271E-11 | 1.405E-12 | 5.555911 | 1 | P-mT-Susp | P-0.5PG-mT | 26161.72 | 4F2 cell-surface antigen heavy chain (Fragment) OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1 |
| H0YB24;Q8N1 | 2 | 2 | 8.6085 | 6.664E-02 | 7.297E-04 | 3.249324 | 0.59764 | P-0.5PG-mT | mT blank | 69382.98 | Cell cycle and apoptosis regulator protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CCAR2 PE=1 S |
| Q9ULG6 | 3 | 2 | 14.721 | 4.005E-07 | 8.238E-09 | 4.374824 | 1 | P-mT-Susp | P-0.5PG-mT | 88081.83 | Cell cycle progression protein 1 OS=Homo sapiens OX=9606 GN=CCPG1 PE=1 SV=3 |
| O43306;B3KW | 2 | 2 | 12.5894 | 1.278E-01 | 1.374E-03 | 3.314811 | 0.46588 | P-mT-Susp | F-0.5PG-mT | 132383.5 | Adenylate cyclase type 6 OS=Homo sapiens OX=9606 GN=ADCY6 PE=1 SV=2 |
| G8JLP4;Q9Y4F | 2 | 2 | 9.3983 | 1.333E-06 | 2.515E-08 | 46.53284 | 1 | F-mT-2D | P-mT-Susp | 177770.4 | Limkain-b1 OS=Homo sapiens OX=9606 GN=MARF1 PE=1 SV=1 |
| Q969K3;H7BY | 2 | 2 | 16.6321 | 9.432E-12 | 1.104E-12 | 3.587789 | 1 | P-mT-Susp | mT blank | 42952.41 | E3 ubiquitin-protein ligase RNF34 OS=Homo sapiens OX=9606 GN=RNF34 PE=1 SV=1 |
| H0YLK7;H0YK( | 2 | 2 | 10.9123 | 9.633E-05 | 1.374E-06 | 1.564948 | 0.99998 | P-mT-Susp | mT blank | 66515.95 | Spatacsin (Fragment) OS=Homo sapiens OX=9606 GN=SPG11 PE=1 SV=1 |
| Q7Z5M8 | 2 | 2 | 23.7684 | 4.702E-06 | 8.245E-08 | 1.643184 | 1 | P-mT-Susp | mT blank | 41346.68 | Protein ABHD12B OS=Homo sapiens OX=9606 GN=ABHD12B PE=1 SV=1 |
| A0A0A0MT64 | 2 | 2 | 12.2124 | 1.018E-02 | 1.180E-04 | 2.091247 | 0.8875 | mT blank | P-mT-Susp | 58788.01 | NADPH:adrenodoxin oxidoreductase_ mitochondrial OS=Homo sapiens OX=9606 GN=FDXR PE=1 SV=1 |
| Q32P51 | 2 | 2 | 19.0408 | 1.398E-08 | 4.107E-10 | 2.582081 | 1 | F-mT-2D | mT blank | 34396.47 | Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens OX=9606 GN=HNRNPA1L2 PE=2 |
| H3BM67;H3BU | 2 | 2 | 18.4614 | 1.794E-08 | 5.099E-10 | 5.805873 | 1 | P-0.5PG-mT | P-mT-Susp | 15152.77 | Nucleolar protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=NOL3 PE=1 SV=8 |
| E7EVK1 | 2 | 2 | 11.3332 | 1.802E-03 | 2.224E-05 | 42.04637 | 0.98514 | mT blank | F-0.5PG-mT | 116488.5 | Nuclear receptor corepressor 1 (Fragment) OS=Homo sapiens OX=9606 GN=NCOR1 PE=1 SV=2 |
| E5RFZ5;E5RI0 | 2 | 2 | 13.0526 | 1.068E-08 | 3.282E-10 | 2.893012 | 1 | P-mT-Susp | P-0.5PG-mT | 20173.66 | Double-strand-break repair protein rad21 homolog OS=Homo sapiens OX=9606 GN=RAD21 PE=1 SV=1 |
| Q96KR7;F6RP( | 2 | 2 | 14.8362 | 2.258E-06 | 4.141E-08 | 1.608271 | 1 | P-0.5PG-mT | F-mT-2D | 62723.35 | Phosphatase and actin regulator 3 OS=Homo sapiens OX=9606 GN=PHACTR3 PE=1 SV=1 |
| O00409 | 2 | 2 | 10.4737 | 7.041E-04 | 9.084E-06 | 2.001574 | 0.99693 | mT blank | P-mT-Susp | 54348.23 | Forkhead box protein N3 OS=Homo sapiens OX=9606 GN=FOXN3 PE=1 SV=1 |
| A6NDA9 | 2 | 2 | 10.5755 | 1.901E-05 | 3.014E-07 | 2.877558 | 1 | F-mT-2D | mT blank | 61365.67 | Leucine-rich repeat_ immunoglobulin-like domain and transmembrane domain-containing protein 2 O |
| Q13177 | 2 | 2 | 16.3584 | 2.504E-10 | 1.394E-11 | 2.655563 | 1 | P-mT-Susp | mT blank | 58327.86 | Serine/threonine-protein kinase PAK 2 OS=Homo sapiens OX=9606 GN=PAK2 PE=1 SV=3 |
| A0A590UJN0;( | 2 | 2 | 16.1094 | 3.729E-09 | 1.325E-10 | 1.659466 | 1 | P-0.5PG-mT | F-mT-2D | 67810.38 | Enhancer of polycomb homolog OS=Homo sapiens OX=9606 GN=EPC1 PE=1 SV=1 |
| A0A7P0T7Z8;A | 2 | 2 | 18.5514 | 8.795E-03 | 1.030E-04 | 1.71233 | 0.90168 | mT blank | F-mT-2D | 136809.4 | Jouberin OS=Homo sapiens OX=9606 GN=AHI1 PE=4 SV=1 |
| O60309 | 2 | 2 | 13.2129 | 1.185E-05 | 1.941E-07 | 2.130101 | 1 | F-0.5PG-mT | F-mT-2D | 181761.7 | Leucine-rich repeat-containing protein 37A3 OS=Homo sapiens OX=9606 GN=LRRC37A3 PE=2 SV=2 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Q86WZ6 | 2 | 2 | 8.7501 | 8.879E-11 | 6.062E-12 | 3.787073 | 1 | F-mT-2D | F-0.5PG-mT | 94656.23 | Zinc finger protein 227 OS=Homo sapiens OX=9606 GN=ZNF227 PE=1 SV=1 |
| Q9HCD6 | 2 | 2 | 8.1576 | 3.158E-08 | 8.325E-10 | 41.99076 | 1 | P-mT-Susp | mT blank | 221132.7 | Protein TANC2 OS=Homo sapiens OX=9606 GN=TANC2 PE=1 SV=3 |
| Q05397 | 2 | 2 | 16.0238 | 7.582E-13 | 2.110E-13 | 6.082905 | 1 | P-mT-Susp | P-0.5PG-mT | 120031.6 | Focal adhesion kinase 1 OS=Homo sapiens OX=9606 GN=PTK2 PE=1 SV=2 |
| O75976;J3QQ | 2 | 2 | 10.7389 | 7.170E-02 | 7.840E-04 | 1.322863 | 0.58321 | P-mT-Susp | F-mT-2D | 154014.8 | Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2 |
| A0A7P0T897;A | 2 | 2 | 10.1279 | 7.848E-06 | 1.329E-07 | 1.73651 | 1 | F-mT-2D | P-0.5PG-mT | 95069.38 | Very low-density lipoprotein receptor OS=Homo sapiens OX=9606 GN=VLDLR PE=4 SV=1 |
| F8VV64;Q63H | 2 | 2 | 16.3525 | 2.371E-06 | 4.328E-08 | 7.205759 | 1 | P-mT-Susp | P-0.5PG-mT | 147745.2 | Tensin-2 OS=Homo sapiens OX=9606 GN=TNS2 PE=1 SV=1 |
| Q13574;E9PK9 | 2 | 2 | 22.9742 | 3.906E-09 | 1.369E-10 | 1.780986 | 1 | P-0.5PG-mT | F-0.5PG-mT | 105463.8 | Diacylglycerol kinase zeta OS=Homo sapiens OX=9606 GN=DGKZ PE=1 SV=4 |
| Q96RE7;K7EL0 | 2 | 2 | 12.3589 | 1.475E-10 | 8.897E-12 | 2.924349 | 1 | P-mT-Susp | mT blank | 57942.7 | Nucleus accumbens-associated protein 1 OS=Homo sapiens OX=9606 GN=NACC1 PE=1 SV=1 |
| G3V236;G3V3 | 2 | 2 | 10.7432 | 2.559E-07 | 5.447E-09 | 1.650644 | 1 | P-mT-Susp | mT blank | 108375.2 | X-linked retinitis pigmentosa GTPase regulator-interacting protein 1 OS=Homo sapiens OX=9606 GN=R |
| Q14028 | 2 | 2 | 13.8427 | 2.703E-11 | 2.562E-12 | 2.956866 | 1 | P-mT-Susp | mT blank | 140590.4 | Cyclic nucleotide-gated cation channel beta-1 OS=Homo sapiens OX=9606 GN=CNGB1 PE=1 SV=2 |
| E5RIF2;Q9Y6D | 2 | 2 | 11.4695 | 1.834E-11 | 1.920E-12 | 4.144889 | 1 | P-mT-Susp | mT blank | 147092.4 | Brefeldin A-inhibited guanine nucleotide-exchange protein 1 (Fragment) OS=Homo sapiens OX=9606 G |
| A0A087X0M7 | 2 | 2 | 8.8952 | 2.285E-02 | 2.580E-04 | 1.72036 | 0.78586 | P-mT-Susp | P-0.5PG-mT | 68702.19 | Protein FAM13C OS=Homo sapiens OX=9606 GN=FAM13C PE=1 SV=1 |
| H3BPL3;A0A7 | 2 | 2 | 10.1524 | 1.156E-06 | 2.205E-08 | 1.717074 | 1 | P-mT-Susp | F-mT-2D | 19924.33 | Probable E3 ubiquitin-protein ligase makorin-3 OS=Homo sapiens OX=9606 GN=MKRN3 PE=1 SV=1 |
| O15031 | 2 | 2 | 12.7383 | 1.603E-04 | 2.242E-06 | 3.378223 | 0.9999 | mT blank | P-mT-Susp | 207864.8 | Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3 |
| F8VUX9;Q96K | 2 | 2 | 16.1444 | 3.321E-08 | 8.668E-10 | 2.194011 | 1 | P-mT-Susp | mT blank | 191045.1 | WD repeat-containing protein 90 OS=Homo sapiens OX=9606 GN=WDR90 PE=1 SV=1 |
| Q96L14 | 2 | 2 | 14.7242 | 1.906E-04 | 2.629E-06 | 10.36119 | 0.99984 | mT blank | P-mT-Susp | 32648.48 | Cep170-like protein OS=Homo sapiens OX=9606 GN=CEP170P1 PE=5 SV=2 |
| H0YBY1;E7EVI | 2 | 2 | 10.6621 | 1.497E-05 | 2.418E-07 | 1.736995 | 1 | P-mT-Susp | mT blank | 137082.2 | Thyroglobulin (Fragment) OS=Homo sapiens OX=9606 GN=TG PE=1 SV=1 |
| O00267 | 2 | 2 | 10.7901 | 1.828E-02 | 2.082E-04 | 1.418641 | 0.81781 | mT blank | F-mT-2D | 121399 | Transcription elongation factor SPT5 OS=Homo sapiens OX=9606 GN=SUPT5H PE=1 SV=1 |
| C9IZJ4;Q8N58 | 2 | 2 | 10.1878 | 6.863E-09 | 2.239E-10 | 2.339443 | 1 | P-mT-Susp | mT blank | 33286.45 | Zinc finger protein 561 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF561 PE=1 SV=1 |
| P50552 | 2 | 2 | 10.2018 | 8.687E-10 | 3.821E-11 | 2.729483 | 1 | P-mT-Susp | mT blank | 40000.87 | Vasodilator-stimulated phosphoprotein OS=Homo sapiens OX=9606 GN=VASP PE=1 SV=3 |
| Q2M218;A0A0 | 2 | 2 | 10.5762 | 1.552E-09 | 6.273E-11 | 3.397638 | 1 | F-0.5PG-mT | F-mT-2D | 78204.06 | Zinc finger protein 630 OS=Homo sapiens OX=9606 GN=ZNF630 PE=2 SV=1 |
| O95125 | 2 | 2 | 11.0335 | 2.546E-10 | 1.408E-11 | 6.206093 | 1 | P-mT-Susp | F-mT-2D | 76089.06 | Zinc finger protein 202 OS=Homo sapiens OX=9606 GN=ZNF202 PE=1 SV=4 |
| Q8NB42 | 2 | 2 | 10.2361 | 5.172E-08 | 1.275E-09 | 6.215668 | 1 | P-mT-Susp | P-0.5PG-mT | 72670.04 | Zinc finger protein 527 OS=Homo sapiens OX=9606 GN=ZNF527 PE=2 SV=2 |
| H0Y3U1 | 2 | 2 | 11.3027 | 3.121E-08 | 8.309E-10 | 3.478073 | 1 | F-0.5PG-mT | F-mT-2D | 20659.38 | Phosphatase and actin regulator (Fragment) OS=Homo sapiens OX=9606 GN=PHACTR1 PE=1 SV=9 |
| Q719I0 | 2 | 2 | 10.1671 | 3.614E-09 | 1.296E-10 | 4.191572 | 1 | F-mT-2D | F-0.5PG-mT | 34034.18 | Putative activator of 90 kDa heat shock protein ATPase homolog 2 OS=Homo sapiens OX=9606 GN=AH |
| A0A0G2JH68;A | 2 | 2 | 9.3344 | 3.026E-02 | 3.393E-04 | 1.587247 | 0.74159 | F-0.5PG-mT | F-mT-2D | 142043.1 | Protein diaphanous homolog 1 OS=Homo sapiens OX=9606 GN=DIAPH1 PE=1 SV=1 |
| A0A075B6P6;A | 2 | 2 | 11.7066 | 7.226E-09 | 2.338E-10 | 9.883194 | 1 | P-mT-Susp | P-0.5PG-mT | 30063.65 | Potassium voltage-gated channel subfamily G member 1 (Fragment) OS=Homo sapiens OX=9606 GN=K |
| Q58F21;A0A7 | 2 | 2 | 9.2987 | 2.511E-09 | 9.518E-11 | 3.596649 | 1 | P-mT-Susp | mT blank | 108582 | Bromodomain testis-specific protein OS=Homo sapiens OX=9606 GN=BRDT PE=1 SV=4 |
| P78524 | 2 | 2 | 9.4378 | 6.560E-09 | 2.149E-10 | 2.022682 | 1 | P-mT-Susp | F-0.5PG-mT | 127682.4 | DENN domain-containing protein 2B OS=Homo sapiens OX=9606 GN=DENND2B PE=1 SV=3 |
| Q9Y5B0;A0A0 | 2 | 2 | 9.5785 | 2.194E-02 | 2.488E-04 | 3.04928 | 0.79189 | mT blank | P-mT-Susp | 105368.8 | RNA polymerase II subunit A C-terminal domain phosphatase OS=Homo sapiens OX=9606 GN=CTDP1 P |
| E7ES84 | 2 | 2 | 9.1292 | 1.354E-08 | 3.993E-10 | 6.52252 | 1 | P-mT-Susp | mT blank | 130643.1 | Kinetochore-associated protein 1 OS=Homo sapiens OX=9606 GN=KNTC1 PE=1 SV=1 |
| A0A087WY96 | 2 | 2 | 10.4773 | 3.773E-05 | 5.709E-07 | 2.590362 | 1 | P-0.5PG-mT | P-mT-Susp | 82593.84 | Transporter OS=Homo sapiens OX=9606 GN=SLC6A6 PE=1 SV=1 |
| C9JID3 | 2 | 2 | 9.8448 | 1.301E-06 | 2.466E-08 | 2.347235 | 1 | P-0.5PG-mT | F-mT-2D | 15336.04 | Zinc finger protein 490 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF490 PE=1 SV=1 |
| P07550 | 2 | 2 | 17.0797 | 5.425E-07 | 1.088E-08 | 3.225889 | 1 | F-mT-2D | mT blank | 47200.11 | Beta-2 adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRB2 PE=1 SV=3 |
| B9A061;F8VW | 2 | 2 | 12.0092 | 1.660E-03 | 2.055E-05 | 2.266408 | 0.98685 | mT blank | P-mT-Susp | 54831.16 | Calcyphosin-2 OS=Homo sapiens OX=9606 GN=CAPS2 PE=1 SV=1 |
| H7BXR3 | 2 | 2 | 10.0404 | 1.170E-07 | 2.662E-09 | 3.954115 | 1 | P-0.5PG-mT | F-mT-2D | 70175.15 | Sorbin and SH3 domain-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=SORBS2 PE=1 |
| A0A7I2SVS4;P | 2 | 2 | 11.2454 | 2.211E-03 | 2.708E-05 | 1.74674 | 0.98008 | P-mT-Susp | mT blank | 120503 | Histone deacetylase OS=Homo sapiens OX=9606 GN=HDAC4 PE=1 SV=1 |
| A0A0U1RRL5; | 2 | 2 | 10.9988 | 4.046E-09 | 1.402E-10 | 2.619654 | 1 | F-mT-2D | mT blank | 67280.69 | ETS-related transcription factor Elf-1 (Fragment) OS=Homo sapiens OX=9606 GN=ELF1 PE=1 SV=1 |
| A0A0A0MQW | 2 | 2 | 10.6801 | 2.376E-08 | 6.590E-10 | 3.003117 | 1 | P-mT-Susp | mT blank | 45344.37 | Serpin B13 OS=Homo sapiens OX=9606 GN=SERPINB13 PE=1 SV=1 |
| Q9NZ94;E7EV | 2 | 2 | 11.116 | 6.417E-03 | 7.579E-05 | 2.046881 | 0.92794 | P-mT-Susp | mT blank | 94522.75 | Neuroligin-3 OS=Homo sapiens OX=9606 GN=NLGN3 PE=1 SV=2 |
| H7C2X8;H7C0 | 2 | 2 | 10.5745 | 2.291E-06 | 4.193E-08 | 1.916076 | 1 | P-0.5PG-mT | P-mT-Susp | 28164.47 | cAMP-regulated phosphoprotein 21 (Fragment) OS=Homo sapiens OX=9606 GN=ARPP21 PE=1 SV=1 |
| Q9P0L1 | 2 | 2 | 9.7343 | 2.966E-03 | 3.588E-05 | 4.678258 | 0.97046 | P-mT-Susp | F-mT-2D | 86972.13 | Zinc finger protein with KRAB and SCAN domains 7 OS=Homo sapiens OX=9606 GN=ZKSCAN7 PE=1 SV= |
| P78362 | 2 | 2 | 10.0522 | 2.246E-07 | 4.821E-09 | 1.606724 | 1 | P-mT-Susp | mT blank | 78268.13 | SRSF protein kinase 2 OS=Homo sapiens OX=9606 GN=SRPK2 PE=1 SV=3 |
| M0R2P6;Q8TE | 2 | 2 | 16.105 | 5.645E-05 | 8.415E-07 | 1.516601 | 1 | P-mT-Susp | P-0.5PG-mT | 74335.05 | SH3KBP1 binding protein 1_ isoform CRA_c OS=Homo sapiens OX=9606 GN=SHKBP1 PE=1 SV=1 |
| A0A2R8Y5S6;A | 2 | 2 | 16.13 | 4.419E-06 | 7.801E-08 | 2.572363 | 1 | P-mT-Susp | mT blank | 93434.19 | Connector enhancer of kinase suppressor of ras 2 OS=Homo sapiens OX=9606 GN=CNKSR2 PE=1 SV=1 |
| B4DNK4;H3BR | 2 | 2 | 11.49 | 2.521E-05 | 3.920E-07 | 1.46563 | 1 | P-0.5PG-mT | P-mT-Susp | 50468.13 | Pyruvate kinase OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=1 |
| B9EG95;O957 | 2 | 2 | 11.3104 | 4.853E-08 | 1.211E-09 | 2.175979 | 1 | P-0.5PG-mT | F-mT-2D | 61243.2 | ZNF682 protein OS=Homo sapiens OX=9606 GN=ZNF682 PE=1 SV=1 |
| O95153;J3KT6 | 2 | 2 | 15.3088 | 3.754E-09 | 1.328E-10 | 3.454389 | 1 | P-mT-Susp | mT blank | 202389.3 | Peripheral-type benzodiazepine receptor-associated protein 1 OS=Homo sapiens OX=9606 GN=TSPOA |
| Q92835 | 2 | 2 | 10.0672 | 1.010E-02 | 1.172E-04 | 4.015072 | 0.8883 | F-mT-2D | F-0.5PG-mT | 134205.1 | Phosphatidylinositol 3_4_5-trisphosphate 5-phosphatase 1 OS=Homo sapiens OX=9606 GN=INPP5D PE |
| Q7L2E3 | 2 | 2 | 9.713 | 3.512E-09 | 1.265E-10 | 2.369684 | 1 | P-mT-Susp | mT blank | 135021.9 | ATP-dependent RNA helicase DHX30 OS=Homo sapiens OX=9606 GN=DHX30 PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Q9H2S9 | 2 | 2 | 9.2373 | 3.307E-06 | 5.957E-08 | 4.214425 | 1 | P-0.5PG-mT | P-mT-Susp | 65303.65 | Zinc finger protein Eos OS=Homo sapiens OX=9606 GN=IKZF4 PE=1 SV=2 |
| A0A087WU35 | 2 | 2 | 16.2414 | 4.271E-10 | 2.048E-11 | 4.438378 | 1 | P-mT-Susp | mT blank | 65993.49 | Zinc finger protein 714 OS=Homo sapiens OX=9606 GN=ZNF714 PE=1 SV=1 |
| O15438 | 2 | 2 | 15.8885 | 1.891E-09 | 7.454E-11 | 2.579457 | 1 | P-0.5PG-mT | P-mT-Susp | 170768.8 | ATP-binding cassette sub-family C member 3 OS=Homo sapiens OX=9606 GN=ABCC3 PE=1 SV=3 |
| A0A087WVP9 | 2 | 2 | 10.688 | 8.430E-02 | 9.168E-04 | 1.785558 | 0.55082 | F-mT-2D | mT blank | 68108.01 | Zinc finger protein 461 OS=Homo sapiens OX=9606 GN=ZNF461 PE=1 SV=1 |
| Q14686 | 2 | 2 | 8.5714 | 9.151E-07 | 1.777E-08 | 8.657734 | 1 | F-0.5PG-mT | F-mT-2D | 219488.2 | Nuclear receptor coactivator 6 OS=Homo sapiens OX=9606 GN=NCOA6 PE=1 SV=3 |
| Q7Z6E9 | 2 | 2 | 11.8206 | 1.058E-09 | 4.529E-11 | 2.241156 | 1 | P-mT-Susp | mT blank | 202477 | E3 ubiquitin-protein ligase RBBP6 OS=Homo sapiens OX=9606 GN=RBBP6 PE=1 SV=1 |
| H0Y340 | 2 | 2 | 17.0509 | 5.077E-12 | 7.348E-13 | 7.811291 | 1 | F-0.5PG-mT | F-mT-2D | 12853.25 | E3 ubiquitin-protein ligase COP1 (Fragment) OS=Homo sapiens OX=9606 GN=COP1 PE=1 SV=1 |
| A0A1B0GV02; | 2 | 2 | 10.0204 | 3.726E-07 | 7.729E-09 | 1.960073 | 1 | P-0.5PG-mT | P-mT-Susp | 140620.5 | Zinc finger E-box-binding homeobox 2 OS=Homo sapiens OX=9606 GN=ZEB2 PE=1 SV=1 |
| O75145 | 2 | 2 | 12.9764 | 1.158E-07 | 2.642E-09 | 1.678334 | 1 | P-mT-Susp | F-0.5PG-mT | 134066.9 | Liprin-alpha-3 OS=Homo sapiens OX=9606 GN=PPFIA3 PE=1 SV=3 |
| Q8TF39;Q6P0 | 2 | 2 | 16.9011 | 3.174E-08 | 8.325E-10 | 2.198982 | 1 | P-mT-Susp | mT blank | 87037.1 | Zinc finger protein 483 OS=Homo sapiens OX=9606 GN=ZNF483 PE=1 SV=3 |
| Q9BWG4;U3K | 2 | 2 | 11.2448 | 1.224E-02 | 1.412E-04 | 2.232278 | 0.86783 | F-0.5PG-mT | F-mT-2D | 39559.61 | Single-stranded DNA-binding protein 4 OS=Homo sapiens OX=9606 GN=SSBP4 PE=1 SV=1 |
| A0A0G2JRB3;A | 2 | 2 | 10.1639 | 5.387E-08 | 1.323E-09 | 2.3157 | 1 | P-mT-Susp | mT blank | 181790.7 | Leucine-rich repeat-containing protein 37A OS=Homo sapiens OX=9606 GN=LRRC37A PE=4 SV=1 |
| Q8TAE7 | 2 | 2 | 12.0353 | 4.244E-11 | 3.448E-12 | 4.82283 | 1 | F-0.5PG-mT | F-mT-2D | 50391.09 | Potassium voltage-gated channel subfamily G member 3 OS=Homo sapiens OX=9606 GN=KCNG3 PE=1 |
| Q9H7Z3 | 2 | 2 | 16.337 | 4.102E-09 | 1.407E-10 | 2.896407 | 1 | P-mT-Susp | P-0.5PG-mT | 133927.7 | Nuclear exosome regulator NRDE2 OS=Homo sapiens OX=9606 GN=NRDE2 PE=1 SV=3 |
| Q96QB1 | 2 | 2 | 15.1713 | 1.065E-03 | 1.346E-05 | 1.561974 | 0.99354 | P-0.5PG-mT | F-mT-2D | 172302.5 | Rho GTPase-activating protein 7 OS=Homo sapiens OX=9606 GN=DLC1 PE=1 SV=4 |
| E9PFB9;J3KP9 | 2 | 2 | 9.6716 | 9.570E-05 | 1.368E-06 | 4.999131 | 0.99998 | P-0.5PG-mT | F-mT-2D | 152347.3 | Coiled-coil domain-containing protein 18 OS=Homo sapiens OX=9606 GN=CCDC18 PE=1 SV=2 |
| Q13275;C9IYS | 2 | 2 | 9.6359 | 2.671E-03 | 3.247E-05 | 1.268246 | 0.97423 | P-mT-Susp | P-0.5PG-mT | 89579.08 | Semaphorin-3F OS=Homo sapiens OX=9606 GN=SEMA3F PE=2 SV=2 |
| Q9GZX5 | 2 | 2 | 9.3971 | 1.551E-09 | 6.273E-11 | 2.050785 | 1 | P-mT-Susp | mT blank | 61323.05 | Zinc finger protein 350 OS=Homo sapiens OX=9606 GN=ZNF350 PE=1 SV=3 |
| A0A075B6F9;I | 2 | 2 | 14.5679 | 4.451E-10 | 2.121E-11 | 4.925482 | 1 | F-mT-2D | mT blank | 33944.48 | Nitric oxide synthase-interacting protein OS=Homo sapiens OX=9606 GN=NOSIP PE=1 SV=1 |
| Q9NUT2;C9JY | 2 | 2 | 10.1126 | 3.152E-08 | 8.325E-10 | 2.357466 | 1 | P-mT-Susp | mT blank | 80844.4 | Mitochondrial potassium channel ATP-binding subunit OS=Homo sapiens OX=9606 GN=ABCB8 PE=1 SV |
| I3L3C6;Q9UQI | 2 | 2 | 18.0324 | 1.076E-09 | 4.579E-11 | 3.621867 | 1 | P-mT-Susp | mT blank | 23400.21 | Brain-specific angiogenesis inhibitor 1-associated protein 2 (Fragment) OS=Homo sapiens OX=9606 GN |
| E7EWN3;H0Y3 | 2 | 2 | 9.4427 | 5.072E-12 | 7.348E-13 | 13.79218 | 1 | P-mT-Susp | P-0.5PG-mT | 161032.8 | Histone-lysine N-methyltransferase SETD5 OS=Homo sapiens OX=9606 GN=SETD5 PE=1 SV=1 |
| A0A6Q8PGJ2; | 2 | 2 | 9.0743 | 1.093E-07 | 2.524E-09 | 2.504062 | 1 | P-mT-Susp | mT blank | 196607.9 | Intraflagellar transport protein 172 homolog OS=Homo sapiens OX=9606 GN=IFT172 PE=1 SV=1 |
| Q9NQ66 | 2 | 2 | 9.6187 | 3.406E-10 | 1.731E-11 | 2.944349 | 1 | P-mT-Susp | mT blank | 139422.5 | 1-phosphatidylinositol 4_5-bisphosphate phosphodiesterase beta-1 OS=Homo sapiens OX=9606 GN=P |
| Q6RI45 | 2 | 2 | 14.4405 | 3.897E-02 | 4.345E-04 | 1.589926 | 0.69828 | P-mT-Susp | P-0.5PG-mT | 205365.7 | Bromodomain and WD repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=BRWD3 PE=1 SV= |
| Q13200 | 2 | 2 | 11.8605 | 1.033E-05 | 1.698E-07 | 2.180885 | 1 | P-mT-Susp | mT blank | 100941.3 | 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PSMD2 PE=1 SV=3 |
| O75936 | 2 | 2 | 9.7799 | 2.602E-08 | 7.118E-10 | 6.485569 | 1 | P-mT-Susp | mT blank | 45228.25 | Gamma-butyrobetaine dioxygenase OS=Homo sapiens OX=9606 GN=BBOX1 PE=1 SV=1 |
| P59923 | 2 | 2 | 11.1298 | 5.601E-12 | 7.714E-13 | 4.923808 | 1 | P-mT-Susp | mT blank | 121358.1 | Zinc finger protein 445 OS=Homo sapiens OX=9606 GN=ZNF445 PE=1 SV=1 |
| Q9UJW2;Q5T4 | 3 | 2 | 17.2609 | 1.074E-04 | 1.527E-06 | 1.650964 | 0.99997 | F-mT-2D | F-0.5PG-mT | 55973.24 | Tubulointerstitial nephritis antigen OS=Homo sapiens OX=9606 GN=TINAG PE=2 SV=3 |
| Q8IWJ2 | 3 | 2 | 18.163 | 3.496E-06 | 6.268E-08 | 3.398644 | 1 | P-mT-Susp | mT blank | 196993.4 | GRIP and coiled-coil domain-containing protein 2 OS=Homo sapiens OX=9606 GN=GCC2 PE=1 SV=4 |
| H0Y2V6 | 5 | 2 | 26.8727 | 2.942E-14 | 2.342E-14 | 17.12667 | 1 | P-mT-Susp | mT blank | 172372.6 | Centrosomal protein of 170 kDa (Fragment) OS=Homo sapiens OX=9606 GN=CEP170 PE=1 SV=1 |
| A0A0U1RRB6; | 3 | 2 | 21.3754 | 1.306E-07 | 2.945E-09 | 2.291971 | 1 | P-mT-Susp | mT blank | 95427.84 | Exocyst complex component OS=Homo sapiens OX=9606 GN=EXOC6B PE=1 SV=1 |
| Q7Z4S6;A0A1 | 3 | 2 | 12.3913 | 4.477E-09 | 1.523E-10 | 3.13047 | 1 | mT blank | F-0.5PG-mT | 188491 | Kinesin-like protein KIF21A OS=Homo sapiens OX=9606 GN=KIF21A PE=1 SV=2 |
| A0A6Q8PF81; | 3 | 2 | 25.9885 | 9.789E-06 | 1.624E-07 | 2.473662 | 1 | P-mT-Susp | F-0.5PG-mT | 83283.32 | Dymeclin OS=Homo sapiens OX=9606 GN=DYM PE=1 SV=1 |
| J3KTM7;O145 | 3 | 2 | 16.3321 | 5.924E-07 | 1.182E-08 | 3.994872 | 1 | F-mT-2D | mT blank | 25225.29 | Suppressor of cytokine-signaling 6 (Fragment) OS=Homo sapiens OX=9606 GN=SOCS6 PE=1 SV=1 |
| A0A0C4DFX7; | 3 | 2 | 23.3345 | 2.273E-05 | 3.575E-07 | 1.707086 | 1 | P-mT-Susp | F-mT-2D | 63295.48 | WD repeat-containing protein 76 OS=Homo sapiens OX=9606 GN=WDR76 PE=1 SV=1 |
| E9PGT3;Q154 | 3 | 2 | 21.2556 | 3.388E-04 | 4.559E-06 | 3.208634 | 0.99933 | mT blank | P-mT-Susp | 81870.85 | Ribosomal protein S6 kinase OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1 SV=1 |
| A0A0A0MS79 | 3 | 2 | 21.0152 | 9.315E-09 | 2.896E-10 | 2.409557 | 1 | F-0.5PG-mT | P-mT-Susp | 210359.2 | Nck-associated protein 5 OS=Homo sapiens OX=9606 GN=NCKAP5 PE=1 SV=1 |
| P51161 | 3 | 2 | 17.0721 | 9.117E-03 | 1.063E-04 | 1.981926 | 0.89833 | mT blank | P-mT-Susp | 14371.28 | Gastrotropin OS=Homo sapiens OX=9606 GN=FABP6 PE=1 SV=2 |
| Q5SW79 | 5 | 2 | 28.5655 | 2.849E-03 | 3.457E-05 | 3.130037 | 0.97197 | P-0.5PG-mT | F-mT-2D | 175692.4 | Centrosomal protein of 170 kDa OS=Homo sapiens OX=9606 GN=CEP170 PE=1 SV=1 |
| Q08462;H0YA | 3 | 2 | 39.4208 | 2.779E-09 | 1.039E-10 | 2.310236 | 1 | P-0.5PG-mT | P-mT-Susp | 125257.4 | Adenylate cyclase type 2 OS=Homo sapiens OX=9606 GN=ADCY2 PE=1 SV=5 |
| A0A2R8Y6V7;( | 3 | 2 | 16.0522 | 1.589E-04 | 2.227E-06 | 1.341097 | 0.9999 | F-0.5PG-mT | P-mT-Susp | 127564.3 | Solute carrier family 12 member 1 OS=Homo sapiens OX=9606 GN=SLC12A1 PE=1 SV=1 |
| J3KPH8;Q8WU | 3 | 2 | 25.6785 | 3.160E-11 | 2.858E-12 | 2.345174 | 1 | P-mT-Susp | mT blank | 109993.7 | Histone deacetylase OS=Homo sapiens OX=9606 GN=HDAC7 PE=1 SV=1 |
| J3QQM1;J3QS | 3 | 2 | 21.6642 | 1.442E-05 | 2.342E-07 | 2.028791 | 1 | P-mT-Susp | mT blank | 29461.12 | 26S proteasome regulatory subunit 8 (Fragment) OS=Homo sapiens OX=9606 GN=PSMC5 PE=1 SV=1 |
| P41229 | 4 | 2 | 25.8222 | 3.728E-07 | 7.729E-09 | 2.812523 | 1 | P-mT-Susp | P-0.5PG-mT | 178400.9 | Lysine-specific demethylase 5C OS=Homo sapiens OX=9606 GN=KDM5C PE=1 SV=2 |
| P32780;E9PM | 4 | 2 | 36.0373 | 3.235E-07 | 6.741E-09 | 2.661271 | 1 | P-mT-Susp | mT blank | 62373.88 | General transcription factor IIH subunit 1 OS=Homo sapiens OX=9606 GN=GTF2H1 PE=1 SV=1 |
| H9KV53;Q5U5 | 4 | 2 | 26.7894 | 2.498E-03 | 3.045E-05 | 6.048969 | 0.97645 | P-mT-Susp | F-mT-2D | 105605 | Cytosolic carboxypeptidase 2 OS=Homo sapiens OX=9606 GN=AGBL2 PE=1 SV=1 |
| A0A087WW66 | 3 | 2 | 29.3953 | 9.863E-11 | 6.543E-12 | 2.631362 | 1 | P-mT-Susp | mT blank | 102523.9 | 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PSMD1 PE=1 SV=2 |
| O00410;H0Y8 | 5 | 2 | 31.2083 | 1.991E-02 | 2.261E-04 | 2.102044 | 0.80591 | P-mT-Susp | F-0.5PG-mT | 125113 | Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4 |
| Q7Z406;M0QY | 4 | 2 | 33.5937 | 4.607E-11 | 3.561E-12 | 2.297648 | 1 | F-mT-2D | mT blank | 228840.3 | Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=2 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| A8K2U0;H0YG | 3 | 2 | 13.3584 | 2.662E-07 | 5.621E-09 | 2.625301 | 1 | F-mT-2D | F-0.5PG-mT | 162532.5 | Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens OX=9606 GN=A2ML1 PE=1 SV=3 |
| A0A087WZ84; | 3 | 2 | 15.995 | 3.658E-12 | 6.196E-13 | 3.156643 | 1 | P-mT-Susp | mT blank | 76193.93 | Zinc finger protein 568 OS=Homo sapiens OX=9606 GN=ZNF568 PE=1 SV=1 |
| Q9P227 | 3 | 2 | 17.4584 | 5.370E-05 | 8.050E-07 | 1.836565 | 1 | mT blank | F-mT-2D | 163446.7 | Rho GTPase-activating protein 23 OS=Homo sapiens OX=9606 GN=ARHGAP23 PE=1 SV=2 |
| Q9UBW7;A0A | 5 | 2 | 32.4189 | 1.037E-03 | 1.316E-05 | 1.472386 | 0.99384 | mT blank | P-mT-Susp | 158503.8 | Zinc finger MYM-type protein 2 OS=Homo sapiens OX=9606 GN=ZMYM2 PE=1 SV=1 |
| A0A384DVL6;( | 3 | 2 | 16.951 | 7.856E-09 | 2.522E-10 | 4.281279 | 1 | P-mT-Susp | mT blank | 223348.5 | Nuclear receptor corepressor 2 OS=Homo sapiens OX=9606 GN=NCOR2 PE=1 SV=1 |
| Q96E39 | 6 | 2 | 28.033 | 5.451E-08 | 1.335E-09 | 3.602489 | 1 | F-mT-2D | mT blank | 42198.66 | RNA binding motif protein_ X-linked-like-1 OS=Homo sapiens OX=9606 GN=RBMXL1 PE=1 SV=1 |
| Q9NQI0;D6RC | 3 | 2 | 21.138 | 1.644E-09 | 6.543E-11 | 2.16717 | 1 | P-mT-Susp | mT blank | 80163.05 | Probable ATP-dependent RNA helicase DDX4 OS=Homo sapiens OX=9606 GN=DDX4 PE=1 SV=2 |
| Q9Y2J0;F8W1 | 5 | 2 | 38.0976 | 8.267E-06 | 1.388E-07 | 5.014024 | 1 | mT blank | P-mT-Susp | 77728.02 | Rabphilin-3A OS=Homo sapiens OX=9606 GN=RPH3A PE=1 SV=1 |
| H7C1F9;Q2PP | 6 | 2 | 42.6889 | 1.852E-07 | 4.039E-09 | 3.358802 | 1 | P-mT-Susp | mT blank | 197269.8 | Ral GTPase-activating protein subunit alpha-2 (Fragment) OS=Homo sapiens OX=9606 GN=RALGAPA2 |
| E7ERS3;Q86VI | 3 | 2 | 21.18 | 4.657E-07 | 9.506E-09 | 4.407742 | 1 | P-0.5PG-mT | P-mT-Susp | 109167.7 | Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18 PE=1 SV=1 |
| P82970 | 5 | 2 | 24.3742 | 7.978E-06 | 1.348E-07 | 3.374702 | 1 | P-0.5PG-mT | P-mT-Susp | 31524.64 | High mobility group nucleosome-binding domain-containing protein 5 OS=Homo sapiens OX=9606 GN= |
| A0A0A0MQS9 | 3 | 2 | 13.2914 | 3.864E-10 | 1.887E-11 | 3.046207 | 1 | P-mT-Susp | mT blank | 205191.8 | Laminin subunit alpha-4 OS=Homo sapiens OX=9606 GN=LAMA4 PE=1 SV=1 |
| A0A075B6E9;A | 3 | 2 | 18.5856 | 8.843E-05 | 1.275E-06 | 3.091022 | 0.99998 | mT blank | P-mT-Susp | 169302.4 | Leucine-rich repeat-containing protein 7 OS=Homo sapiens OX=9606 GN=LRRC7 PE=1 SV=1 |
| C9JL08 | 3 | 2 | 17.5681 | 1.173E-01 | 1.266E-03 | 3.414996 | 0.48342 | mT blank | F-0.5PG-mT | 27977.9 | 1-phosphatidylinositol 3-phosphate 5-kinase (Fragment) OS=Homo sapiens OX=9606 GN=PIKFYVE PE= |
| A0A0G2JPG6;I | 3 | 2 | 26.1567 | 3.215E-12 | 5.816E-13 | 7.066527 | 1 | P-mT-Susp | P-0.5PG-mT | 46005.58 | Killer cell immunoglobulin-like receptor 2DL4 OS=Homo sapiens OX=9606 GN=KIR2DL4 PE=1 SV=1 |
| A0A7I2PHE7;A | 5 | 2 | 21.8802 | 2.439E-08 | 6.742E-10 | 3.843783 | 1 | P-mT-Susp | mT blank | 144938.3 | Centrosome and spindle pole-associated protein 1 OS=Homo sapiens OX=9606 GN=CSPP1 PE=1 SV=1 |
| K7ENM7;Q9U | 3 | 2 | 20.5353 | 3.878E-09 | 1.366E-10 | 3.925647 | 1 | P-mT-Susp | mT blank | 70678.58 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |
| A0A0C4DG86; | 3 | 2 | 24.9062 | 5.112E-02 | 5.652E-04 | 1.216786 | 0.64868 | F-0.5PG-mT | F-mT-2D | 73795.45 | Syntabulin OS=Homo sapiens OX=9606 GN=SYBU PE=1 SV=1 |
| H0Y486;Q5TA | 3 | 2 | 22.9725 | 1.335E-09 | 5.534E-11 | 7.672899 | 1 | P-mT-Susp | P-0.5PG-mT | 19601.58 | Tetratricopeptide repeat protein 22 (Fragment) OS=Homo sapiens OX=9606 GN=TTC22 PE=1 SV=1 |
| C9JFJ0;D6REE | 3 | 2 | 16.5191 | 6.533E-04 | 8.470E-06 | 1.350161 | 0.99734 | F-0.5PG-mT | F-mT-2D | 23440.55 | Rho-associated protein kinase 2 (Fragment) OS=Homo sapiens OX=9606 GN=ROCK2 PE=1 SV=1 |
| Q9HCD5 | 3 | 2 | 28.8987 | 1.701E-07 | 3.771E-09 | 2.325792 | 1 | P-mT-Susp | mT blank | 65764.68 | Nuclear receptor coactivator 5 OS=Homo sapiens OX=9606 GN=NCOA5 PE=1 SV=2 |
| P23142;B1AH | 3 | 2 | 15.885 | 8.413E-11 | 5.824E-12 | 7.690768 | 1 | F-0.5PG-mT | F-mT-2D | 81320.11 | Fibulin-1 OS=Homo sapiens OX=9606 GN=FBLN1 PE=1 SV=4 |
| E7EVQ6;Q145 | 3 | 2 | 20.8069 | 2.712E-10 | 1.479E-11 | 4.036669 | 1 | P-mT-Susp | mT blank | 53352.77 | Squalene monooxygenase OS=Homo sapiens OX=9606 GN=SQLE PE=1 SV=1 |
| A0A494C0S0;( | 3 | 2 | 16.2927 | 2.261E-08 | 6.314E-10 | 2.759442 | 1 | P-mT-Susp | mT blank | 115065.2 | Sorting nexin-25 OS=Homo sapiens OX=9606 GN=SNX25 PE=1 SV=1 |
| A0A7I2YQ90;A | 3 | 2 | 30.4424 | 8.871E-10 | 3.880E-11 | 2.150588 | 1 | P-mT-Susp | mT blank | 67318.15 | Polyadenylate-binding protein 1 OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1 |
| Q6KB66 | 3 | 2 | 32.4368 | 8.418E-04 | 1.079E-05 | 2.335396 | 0.99573 | P-0.5PG-mT | F-mT-2D | 51038.63 | Keratin_ type II cytoskeletal 80 OS=Homo sapiens OX=9606 GN=KRT80 PE=1 SV=2 |
| A0A494C0Q6 | 4 | 2 | 30.5764 | 1.392E-13 | 6.498E-14 | 5.0582 | 1 | P-mT-Susp | mT blank | 67136.39 | Poly(A)-specific ribonuclease PARN OS=Homo sapiens OX=9606 GN=PARN PE=1 SV=1 |
| Q9NZQ3;C9JS( | 5 | 2 | 31.0377 | 3.053E-02 | 3.418E-04 | 1.353306 | 0.74014 | F-0.5PG-mT | P-mT-Susp | 79701.73 | NCK-interacting protein with SH3 domain OS=Homo sapiens OX=9606 GN=NCKIPSD PE=1 SV=1 |
| O75197 | 4 | 2 | 13.5387 | 4.055E-09 | 1.402E-10 | 2.60317 | 1 | P-mT-Susp | mT blank | 182395.4 | Low-density lipoprotein receptor-related protein 5 OS=Homo sapiens OX=9606 GN=LRP5 PE=1 SV=2 |
| A0A0U1RR27; | 3 | 2 | 15.4897 | 8.579E-10 | 3.794E-11 | 2.120215 | 1 | P-mT-Susp | mT blank | 217446.6 | C-myc promoter-binding protein OS=Homo sapiens OX=9606 GN=DENND4A PE=1 SV=2 |
| Q8N823;A0A1 | 3 | 2 | 17.1704 | 1.582E-06 | 2.956E-08 | 1.608426 | 1 | P-mT-Susp | F-0.5PG-mT | 84186.86 | Zinc finger protein 611 OS=Homo sapiens OX=9606 GN=ZNF611 PE=1 SV=2 |
| A6NHJ4 | 3 | 2 | 17.1209 | 1.014E-05 | 1.677E-07 | Infinity | 1 | P-0.5PG-mT | P-mT-Susp | 75638.66 | Zinc finger protein 860 OS=Homo sapiens OX=9606 GN=ZNF860 PE=1 SV=3 |
| P54753 | 3 | 2 | 15.043 | 1.540E-02 | 1.764E-04 | 1.181895 | 0.84043 | mT blank | F-0.5PG-mT | 111926.8 | Ephrin type-B receptor 3 OS=Homo sapiens OX=9606 GN=EPHB3 PE=1 SV=2 |
| J3QT46;Q9Y45 | 3 | 2 | 17.7933 | 8.251E-06 | 1.388E-07 | 1.902652 | 1 | P-mT-Susp | mT blank | 68748.99 | HBS1-like protein OS=Homo sapiens OX=9606 GN=HBS1L PE=1 SV=1 |
| A0A3B3ITH6;N | 3 | 2 | 15.5567 | 6.241E-07 | 1.242E-08 | 12.50759 | 1 | mT blank | P-mT-Susp | 33811.82 | Zinc finger imprinted 2 OS=Homo sapiens OX=9606 GN=ZIM2 PE=4 SV=1 |
| A0A087WUR8 | 3 | 2 | 29.6491 | 4.436E-04 | 5.866E-06 | 2.183235 | 0.99879 | F-0.5PG-mT | F-mT-2D | 47345.47 | Inactive serine protease PAMR1 OS=Homo sapiens OX=9606 GN=PAMR1 PE=1 SV=1 |
| A0A590UJQ1;/ | 4 | 2 | 27.8774 | 1.314E-03 | 1.648E-05 | 1.64458 | 0.99086 | P-mT-Susp | mT blank | 103749.5 | E3 ubiquitin-protein ligase OS=Homo sapiens OX=9606 GN=ITCH PE=1 SV=1 |
| A0A2R8YGD3; | 8 | 2 | 44.3865 | 2.915E-10 | 1.568E-11 | 6.521009 | 1 | P-0.5PG-mT | F-0.5PG-mT | 189394.2 | Cyclic nucleotide ras GEF OS=Homo sapiens OX=9606 GN=RAPGEF2 PE=1 SV=1 |
| Q9UBB9 | 3 | 2 | 23.0383 | 5.712E-06 | 9.927E-08 | 1.944462 | 1 | P-mT-Susp | mT blank | 97219.18 | Tuftelin-interacting protein 11 OS=Homo sapiens OX=9606 GN=TFIP11 PE=1 SV=1 |
| P18433;Q5JW | 3 | 2 | 21.4604 | 3.659E-05 | 5.548E-07 | 4.368115 | 1 | P-0.5PG-mT | F-mT-2D | 91631.64 | Receptor-type tyrosine-protein phosphatase alpha OS=Homo sapiens OX=9606 GN=PTPRA PE=1 SV=3 |
| Q8TDI0;K7EM | 4 | 2 | 20.0255 | 2.879E-05 | 4.416E-07 | 1.783679 | 1 | P-0.5PG-mT | mT blank | 224646.7 | Chromodomain-helicase-DNA-binding protein 5 OS=Homo sapiens OX=9606 GN=CHD5 PE=1 SV=1 |
| A0A2R8Y555;( | 3 | 2 | 14.388 | 1.264E-08 | 3.779E-10 | 2.231796 | 1 | P-mT-Susp | mT blank | 65624.68 | Calcium channel voltage-dependent subunit beta 2 (Fragment) OS=Homo sapiens OX=9606 GN=CACNB |
| F8WFA6 | 3 | 2 | 16.0901 | 3.026E-04 | 4.097E-06 | 2.792986 | 0.99948 | P-mT-Susp | F-mT-2D | 14952.92 | E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens OX=9606 GN=RAD18 PE=1 SV=1 |
| Q16825 | 4 | 2 | 18.1794 | 1.735E-10 | 1.016E-11 | 5.670719 | 1 | P-mT-Susp | P-0.5PG-mT | 134193.7 | Tyrosine-protein phosphatase non-receptor type 21 OS=Homo sapiens OX=9606 GN=PTPN21 PE=1 SV= |
| Q9Y263;E5RIN | 3 | 2 | 24.9959 | 6.294E-07 | 1.249E-08 | 3.100183 | 1 | P-mT-Susp | F-0.5PG-mT | 88696.94 | Phospholipase A-2-activating protein OS=Homo sapiens OX=9606 GN=PLAA PE=1 SV=2 |
| B1AKL4;Q9NR | 4 | 2 | 29.0128 | 4.262E-10 | 2.048E-11 | 2.790955 | 1 | P-mT-Susp | mT blank | 105892.1 | Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens OX=9606 GN=EIF4ENIF1 PE=1 |
| A0A384DVU0; | 4 | 2 | 21.0952 | 1.834E-07 | 4.010E-09 | 3.925898 | 1 | P-mT-Susp | mT blank | 151406.6 | Patatin-like phospholipase domain-containing protein 6 OS=Homo sapiens OX=9606 GN=PNPLA6 PE=1 |
| F5GWN5;O00 | 3 | 2 | 20.281 | 1.124E-03 | 1.419E-05 | 2.624994 | 0.99293 | P-0.5PG-mT | P-mT-Susp | 183796.5 | Phosphatidylinositol-4-phosphate 3-kinase OS=Homo sapiens OX=9606 GN=PIK3C2B PE=1 SV=1 |
| Q01118 | 4 | 2 | 26.1316 | 3.917E-06 | 6.975E-08 | 9.619152 | 1 | P-0.5PG-mT | P-mT-Susp | 195775 | Sodium channel protein type 7 subunit alpha OS=Homo sapiens OX=9606 GN=SCN7A PE=1 SV=2 |
| Q13591;D6RA | 4 | 2 | 33.3193 | 8.273E-11 | 5.813E-12 | 3.346832 | 1 | P-0.5PG-mT | F-0.5PG-mT | 124151.1 | Semaphorin-5A OS=Homo sapiens OX=9606 GN=SEMA5A PE=1 SV=3 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| F5H658;Q145 | 3 | 2 | 15.6861 | 6.839E-06 | 1.168E-07 | 3.803921 | 1 | P-mT-Susp | P-0.5PG-mT | 135028.3 | RNA helicase OS=Homo sapiens OX=9606 GN=DHX8 PE=1 SV=1 |
| E7EU96;A0A2 | 4 | 2 | 22.4696 | 2.109E-12 | 4.419E-13 | 9.980005 | 1 | P-mT-Susp | P-0.5PG-mT | 45482.08 | Casein kinase II subunit alpha OS=Homo sapiens OX=9606 GN=CSNK2A1 PE=1 SV=1 |
| Q16821;C9JZE | 3 | 2 | 21.0383 | 5.584E-04 | 7.303E-06 | 1.720395 | 0.99804 | P-0.5PG-mT | P-mT-Susp | 127078.5 | Protein phosphatase 1 regulatory subunit 3A OS=Homo sapiens OX=9606 GN=PPP1R3A PE=1 SV=3 |
| Q96LW9;C9JP | 3 | 2 | 22.7231 | 8.180E-09 | 2.615E-10 | 3.336398 | 1 | P-mT-Susp | P-0.5PG-mT | 48262.58 | Zinc finger and SCAN domain-containing protein 31 OS=Homo sapiens OX=9606 GN=ZSCAN31 PE=1 SV |
| J3KN75;Q0IIM | 3 | 2 | 15.5388 | 1.347E-03 | 1.683E-05 | 1.388116 | 0.9905 | F-0.5PG-mT | F-mT-2D | 129591.2 | TBC1 domain family member 8B OS=Homo sapiens OX=9606 GN=TBC1D8B PE=1 SV=1 |
| Q9H3C7 | 3 | 2 | 29.6815 | 2.226E-02 | 2.521E-04 | 1.390308 | 0.78972 | P-0.5PG-mT | F-mT-2D | 81367.64 | Gametogenetin-binding protein 2 OS=Homo sapiens OX=9606 GN=GGNBP2 PE=1 SV=1 |
| P05165;A0A2I | 3 | 2 | 21.4325 | 3.184E-05 | 4.865E-07 | 1.775318 | 1 | P-mT-Susp | mT blank | 80686.4 | Propionyl-CoA carboxylase alpha chain_ mitochondrial OS=Homo sapiens OX=9606 GN=PCCA PE=1 SV= |
| A0A140TA76;( | 3 | 2 | 24.5081 | 2.280E-04 | 3.124E-06 | 3.17403 | 0.99974 | mT blank | P-mT-Susp | 38247.05 | Protein LSM14 homolog A (Fragment) OS=Homo sapiens OX=9606 GN=LSM14A PE=1 SV=1 |
| D6REX3;H7BX | 3 | 2 | 19.7986 | 2.348E-04 | 3.211E-06 | 1.364007 | 0.99972 | P-mT-Susp | P-0.5PG-mT | 137196 | Protein transport protein Sec31A OS=Homo sapiens OX=9606 GN=SEC31A PE=1 SV=1 |
| Q96JM4 | 4 | 2 | 20.5344 | 1.664E-05 | 2.665E-07 | 2.138493 | 1 | mT blank | P-mT-Susp | 201410.6 | Leucine-rich repeat and IQ domain-containing protein 1 OS=Homo sapiens OX=9606 GN=LRRIQ1 PE=2 |
| Q5TYW1 | 3 | 2 | 14.9885 | 5.651E-10 | 2.600E-11 | 23.63215 | 1 | P-0.5PG-mT | P-mT-Susp | 125752.9 | Zinc finger protein 658 OS=Homo sapiens OX=9606 GN=ZNF658 PE=1 SV=2 |
| A0A087X0R0;A | 4 | 2 | 33.8565 | 3.103E-08 | 8.289E-10 | 3.952257 | 1 | P-0.5PG-mT | mT blank | 161727.1 | Lysine-specific demethylase 6A OS=Homo sapiens OX=9606 GN=KDM6A PE=1 SV=2 |
| Q96SB8;A0A0 | 3 | 2 | 23.9058 | 6.599E-13 | 1.946E-13 | 2.611938 | 1 | P-mT-Susp | mT blank | 127295.3 | Structural maintenance of chromosomes protein 6 OS=Homo sapiens OX=9606 GN=SMC6 PE=1 SV=2 |
| O15068 | 3 | 2 | 14.303 | 1.810E-06 | 3.351E-08 | 2.798997 | 1 | P-mT-Susp | P-0.5PG-mT | 129420.9 | Guanine nucleotide exchange factor DBS OS=Homo sapiens OX=9606 GN=MCF2L PE=1 SV=2 |
| X5D778 | 3 | 2 | 20.9132 | 2.006E-08 | 5.642E-10 | 3.923971 | 1 | F-mT-2D | P-0.5PG-mT | 47447.7 | Ankyrin repeat domain 11 isoform A (Fragment) OS=Homo sapiens OX=9606 GN=ANKRD11 PE=1 SV=1 |
| A0A2R8Y7T1;A | 4 | 2 | 22.6006 | 1.922E-06 | 3.550E-08 | 1.555376 | 1 | P-mT-Susp | mT blank | 17402.71 | Casein kinase II subunit alpha OS=Homo sapiens OX=9606 GN=CSNK2A1 PE=4 SV=1 |
| F5H7W8;Q960 | 3 | 2 | 23.5628 | 6.127E-04 | 7.969E-06 | 2.513253 | 0.99765 | F-mT-2D | F-0.5PG-mT | 31921.92 | Protein CUSTOS OS=Homo sapiens OX=9606 GN=C12orf43 PE=1 SV=2 |
| A0A087WVK0 | 3 | 2 | 24.9158 | 2.407E-06 | 4.385E-08 | Infinity | 1 | mT blank | P-mT-Susp | 54479.12 | Dual-specificity protein kinase CLK1 OS=Homo sapiens OX=9606 GN=CLK1 PE=1 SV=1 |
| Q5H9U9;D6RE | 3 | 2 | 15.3817 | 3.414E-10 | 1.731E-11 | 3.593144 | 1 | P-mT-Susp | mT blank | 199955 | Probable ATP-dependent RNA helicase DDX60-like OS=Homo sapiens OX=9606 GN=DDX60L PE=2 SV=2 |
| A0A7P0T9G4;I | 3 | 2 | 23.2345 | 1.976E-14 | 1.748E-14 | 32.99023 | 1 | P-mT-Susp | P-0.5PG-mT | 163532 | Chimeric ERCC6-PGBD3 protein OS=Homo sapiens OX=9606 GN=ERCC6 PE=4 SV=1 |
| Q9H7N4 | 4 | 2 | 23.8258 | 4.131E-05 | 6.228E-07 | 1.515728 | 1 | P-0.5PG-mT | P-mT-Susp | 139897.3 | Splicing factor_ arginine/serine-rich 19 OS=Homo sapiens OX=9606 GN=SCAF1 PE=1 SV=3 |
| D6RAM3;D6R( | 1 | 1 | 4.9938 | 1.155E-07 | 2.642E-09 | 2.566336 | 1 | P-mT-Susp | mT blank | 48286.3 | Docking protein 3 OS=Homo sapiens OX=9606 GN=DOK3 PE=1 SV=1 |
| A0A087WWR9 | 1 | 1 | 4.7133 | 2.871E-09 | 1.063E-10 | 7.4912 | 1 | P-mT-Susp | mT blank | 12978.98 | Kidney mitochondrial carrier protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=SLC25A30 PE=1 SV= |
| D6R905;D6RA | 1 | 1 | 5.4118 | 6.560E-02 | 7.193E-04 | 1.615141 | 0.60074 | P-mT-Susp | mT blank | 26228.23 | Exosome complex component RRP45 (Fragment) OS=Homo sapiens OX=9606 GN=EXOSC9 PE=1 SV=1 |
| Q14192 | 1 | 1 | 4.0838 | 3.251E-04 | 4.386E-06 | 3.304778 | 0.99939 | mT blank | P-mT-Susp | 34188.85 | Four and a half LIM domains protein 2 OS=Homo sapiens OX=9606 GN=FHL2 PE=1 SV=3 |
| F8VXK3;Q9NP | 1 | 1 | 6.1115 | 3.374E-10 | 1.731E-11 | 5.504427 | 1 | P-mT-Susp | mT blank | 18754.53 | Carbohydrate sulfotransferase (Fragment) OS=Homo sapiens OX=9606 GN=CHST11 PE=1 SV=1 |
| K7EJE5 | 1 | 1 | 4.9145 | 4.537E-06 | 7.973E-08 | 2.32586 | 1 | F-0.5PG-mT | F-mT-2D | 13227.25 | Zinc finger protein 233 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF233 PE=4 SV=1 |
| H3BR66;P082 | 1 | 1 | 4.2071 | 7.604E-05 | 1.107E-06 | 1.577548 | 0.99999 | F-mT-2D | mT blank | 23175.43 | PEX (Fragment) OS=Homo sapiens OX=9606 GN=MMP2 PE=1 SV=1 |
| Q5TA45;Q96H | 1 | 1 | 5.4282 | 1.986E-08 | 5.606E-10 | 3.240922 | 1 | P-mT-Susp | mT blank | 68404.09 | Integrator complex subunit 11 OS=Homo sapiens OX=9606 GN=INTS11 PE=1 SV=2 |
| Q9Y6N8 | 1 | 1 | 4.4631 | 6.562E-07 | 1.296E-08 | 2.347881 | 1 | P-0.5PG-mT | P-mT-Susp | 88850.63 | Cadherin-10 OS=Homo sapiens OX=9606 GN=CDH10 PE=1 SV=2 |
| A0A087WTR9 | 1 | 1 | 5.251 | 1.153E-07 | 2.642E-09 | 4.165818 | 1 | F-0.5PG-mT | F-mT-2D | 30833.28 | Protein Mdm4 OS=Homo sapiens OX=9606 GN=MDM4 PE=1 SV=1 |
| E7EWD6 | 1 | 1 | 4.2484 | 1.576E-08 | 4.529E-10 | 5.308744 | 1 | P-0.5PG-mT | P-mT-Susp | 151777.8 | Putative Polycomb group protein ASXL2 OS=Homo sapiens OX=9606 GN=ASXL2 PE=1 SV=1 |
| H7C0W8 | 1 | 1 | 14.4966 | 7.028E-14 | 4.501E-14 | 15.60326 | 1 | P-mT-Susp | P-0.5PG-mT | 11955.23 | Adipocyte enhancer-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=AEBP1 PE=1 SV=1 |
| A0A0B4J2A4;K | 1 | 1 | 5.7775 | 7.778E-13 | 2.110E-13 | 6.146567 | 1 | P-mT-Susp | mT blank | 42058.06 | 3-ketoacyl-CoA thiolase_ mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=1 |
| Q13099 | 1 | 1 | 4.4386 | 3.495E-10 | 1.761E-11 | 4.976847 | 1 | P-0.5PG-mT | F-mT-2D | 93761.95 | Intraflagellar transport protein 88 homolog OS=Homo sapiens OX=9606 GN=IFT88 PE=1 SV=3 |
| D6RB01;Q9Y6 | 1 | 1 | 5.2104 | 6.315E-03 | 7.470E-05 | 2.180956 | 0.92913 | F-0.5PG-mT | P-mT-Susp | 68340.1 | Soluble lamin-associated protein of 75 kDa OS=Homo sapiens OX=9606 GN=FAM169A PE=1 SV=1 |
| H0Y860;H7C5( | 1 | 1 | 5.0503 | 2.407E-12 | 4.862E-13 | 15.09355 | 1 | P-mT-Susp | mT blank | 85672.66 | Stromal interaction molecule 2 OS=Homo sapiens OX=9606 GN=STIM2 PE=1 SV=2 |
| A0A075B771;A | 1 | 1 | 5.6413 | 6.237E-12 | 7.858E-13 | 3.354335 | 1 | P-mT-Susp | mT blank | 21318.93 | Zinc finger protein 582 OS=Homo sapiens OX=9606 GN=ZNF582 PE=4 SV=1 |
| A0A7P0N7C4;I | 1 | 1 | 11.439 | 6.756E-04 | 8.745E-06 | 2.407202 | 0.99716 | F-0.5PG-mT | P-mT-Susp | 215996.8 | Zinc finger protein 142 OS=Homo sapiens OX=9606 GN=ZNF142 PE=4 SV=1 |
| Q15424 | 1 | 1 | 4.0321 | 1.011E-03 | 1.286E-05 | 2.498548 | 0.99409 | mT blank | P-mT-Susp | 103098 | Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB PE=1 SV=4 |
| A0A590UJ62;E | 1 | 1 | 5.5654 | 3.873E-08 | 9.945E-10 | 3.054946 | 1 | F-0.5PG-mT | F-mT-2D | 82509.89 | Potassium voltage-gated channel subfamily C member 3 OS=Homo sapiens OX=9606 GN=KCNC3 PE=1 |
| O94888 | 1 | 1 | 5.8316 | 3.856E-05 | 5.824E-07 | 1.540558 | 1 | F-0.5PG-mT | F-mT-2D | 55261.61 | UBX domain-containing protein 7 OS=Homo sapiens OX=9606 GN=UBXN7 PE=1 SV=2 |
| K7EJC2;Q9P10 | 1 | 1 | 5.0763 | 9.118E-09 | 2.846E-10 | 2.864647 | 1 | F-mT-2D | P-mT-Susp | 33709.49 | GEM-interacting protein (Fragment) OS=Homo sapiens OX=9606 GN=GMIP PE=1 SV=1 |
| O95377 | 1 | 1 | 5.0207 | 1.347E-10 | 8.311E-12 | 3.144201 | 1 | P-mT-Susp | mT blank | 31829.7 | Gap junction beta-5 protein OS=Homo sapiens OX=9606 GN=GJB5 PE=1 SV=2 |
| K7ERI5 | 1 | 1 | 5.4254 | 2.572E-09 | 9.705E-11 | 5.303257 | 1 | P-mT-Susp | mT blank | 18494.12 | KRAB domain-containing protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1 |
| Q9Y3Q7 | 1 | 1 | 5.1575 | 3.406E-04 | 4.564E-06 | 2.627728 | 0.99932 | mT blank | P-mT-Susp | 85365.8 | Disintegrin and metalloproteinase domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ADA |
| Q9H7X2 | 1 | 1 | 14.3584 | 8.462E-12 | 1.005E-12 | 3.215895 | 1 | P-0.5PG-mT | P-mT-Susp | 15573.66 | Uncharacterized protein C1orf115 OS=Homo sapiens OX=9606 GN=C1orf115 PE=2 SV=1 |
| A0A087WZG5 | 1 | 1 | 13.1678 | 7.672E-07 | 1.504E-08 | 2.258335 | 1 | P-mT-Susp | F-0.5PG-mT | 17368.96 | WW domain-containing oxidoreductase OS=Homo sapiens OX=9606 GN=WWOX PE=1 SV=1 |
| Q6NY19 | 1 | 1 | 4.9551 | 6.899E-06 | 1.176E-07 | 1.706809 | 1 | F-0.5PG-mT | P-mT-Susp | 89052.75 | KN motif and ankyrin repeat domain-containing protein 3 OS=Homo sapiens OX=9606 GN=KANK3 PE= |
| A0A0A0MRF9 | 1 | 1 | 4.2517 | 2.410E-01 | 2.565E-03 | 1.198975 | 0.33624 | F-0.5PG-mT | F-mT-2D | 147257.6 | 1-phosphatidylinositol 4_5-bisphosphate phosphodiesterase gamma OS=Homo sapiens OX=9606 GN= |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Q12965 | 1 | 1 | 5.1929 | 1.007E-07 | 2.344E-09 | 1.793572 | 1 | P-mT-Susp | mT blank | 127632.4 | Unconventional myosin-Ie OS=Homo sapiens OX=9606 GN=MYO1E PE=1 SV=2 |
| Q86WV1 | 1 | 1 | 5.0152 | 3.164E-08 | 8.325E-10 | 2.100201 | 1 | F-mT-2D | mT blank | 41717.65 | Src kinase-associated phosphoprotein 1 OS=Homo sapiens OX=9606 GN=SKAP1 PE=1 SV=3 |
| A0A0J9YWN0 | 1 | 1 | 9.1398 | 6.681E-03 | 7.879E-05 | 1.680622 | 0.9249 | F-mT-2D | F-0.5PG-mT | 21260.26 | Band 4.1-like protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=EPB41L3 PE=1 SV=3 |
| I3L3E0 | 1 | 1 | 6.522 | 3.465E-12 | 5.997E-13 | 9.294036 | 1 | P-mT-Susp | P-0.5PG-mT | 18077.55 | Uromodulin (Fragment) OS=Homo sapiens OX=9606 GN=UMOD PE=1 SV=1 |
| H0Y7V2 | 1 | 1 | 12.9978 | 2.586E-10 | 1.420E-11 | 2.696003 | 1 | P-mT-Susp | mT blank | 11742.43 | Small G protein-signaling modulator 3 (Fragment) OS=Homo sapiens OX=9606 GN=SGSM3 PE=1 SV=1 |
| J3KR97;Q9BTV | 1 | 1 | 9.9668 | 2.405E-11 | 2.335E-12 | 2.926923 | 1 | P-mT-Susp | mT blank | 138433.6 | Tubulin-specific chaperone D OS=Homo sapiens OX=9606 GN=TBCD PE=1 SV=1 |
| A0A0U1RQQ9 | 1 | 1 | 4.1252 | 1.493E-13 | 6.498E-14 | 6.850248 | 1 | P-mT-Susp | mT blank | 104796.7 | SCY1-like protein 2 OS=Homo sapiens OX=9606 GN=SCYL2 PE=1 SV=1 |
| Q8NGT0 | 1 | 1 | 12.1578 | 8.766E-06 | 1.463E-07 | 9.303802 | 1 | P-0.5PG-mT | F-mT-2D | 36310.2 | Olfactory receptor 13C9 OS=Homo sapiens OX=9606 GN=OR13C9 PE=3 SV=1 |
| P61978;Q5T6V | 1 | 1 | 6.265 | 6.898E-03 | 8.123E-05 | 1.924946 | 0.92242 | mT blank | P-mT-Susp | 51261.48 | Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1 |
| F5H5K1;J3QL1 | 1 | 1 | 13.2334 | 1.303E-04 | 1.840E-06 | 2.793216 | 0.99994 | P-mT-Susp | mT blank | 97345.63 | Leucine-rich repeat-containing protein 37B OS=Homo sapiens OX=9606 GN=LRRC37B PE=1 SV=1 |
| Q6UWB1 | 1 | 1 | 5.0668 | 3.179E-08 | 8.325E-10 | 3.96098 | 1 | P-mT-Susp | P-0.5PG-mT | 70386.31 | Interleukin-27 receptor subunit alpha OS=Homo sapiens OX=9606 GN=IL27RA PE=1 SV=2 |
| H0YBC9;Q141 | 1 | 1 | 4.4962 | 9.660E-08 | 2.275E-09 | 1.859671 | 1 | P-0.5PG-mT | F-mT-2D | 54994.97 | DNA repair-scaffolding protein (Fragment) OS=Homo sapiens OX=9606 GN=SPIDR PE=1 SV=1 |
| Q5VZT6;Q8IYX | 1 | 1 | 5.4742 | 1.208E-04 | 1.708E-06 | 2.811815 | 0.99995 | F-0.5PG-mT | P-mT-Susp | 8942.111 | Stabilizer of axonemal microtubules 1 OS=Homo sapiens OX=9606 GN=SAXO1 PE=1 SV=2 |
| P17036;Q86U | 1 | 1 | 8.724 | 2.113E-13 | 8.409E-14 | 12.06773 | 1 | F-mT-2D | mT blank | 51885.42 | Zinc finger protein 3 OS=Homo sapiens OX=9606 GN=ZNF3 PE=1 SV=3 |
| E9PJF3;E9PP5 | 1 | 1 | 12.9408 | 1.962E-09 | 7.692E-11 | 3.601636 | 1 | P-mT-Susp | mT blank | 32134.69 | Flavin-containing monooxygenase OS=Homo sapiens OX=9606 GN=FMO5 PE=1 SV=1 |
| Q8IVP9 | 1 | 1 | 10.1512 | 2.535E-06 | 4.597E-08 | 2.578831 | 1 | P-mT-Susp | mT blank | 47496.06 | Zinc finger protein 547 OS=Homo sapiens OX=9606 GN=ZNF547 PE=1 SV=2 |
| P26374 | 1 | 1 | 12.213 | 1.571E-08 | 4.529E-10 | 2.462015 | 1 | P-mT-Susp | F-0.5PG-mT | 75326.13 | Rab proteins geranylgeranyltransferase component A 2 OS=Homo sapiens OX=9606 GN=CHML PE=1 SV |
| A0A1W2PR36 | 1 | 1 | 6.6248 | 9.927E-04 | 1.264E-05 | 2.491162 | 0.99428 | P-mT-Susp | mT blank | 24032.41 | Guanidinoacetate N-methyltransferase OS=Homo sapiens OX=9606 GN=GAMT PE=1 SV=1 |
| P22460 | 1 | 1 | 5.6422 | 6.613E-08 | 1.600E-09 | 2.503939 | 1 | P-mT-Susp | mT blank | 67798.17 | Potassium voltage-gated channel subfamily A member 5 OS=Homo sapiens OX=9606 GN=KCNA5 PE=1 |
| A8MQD4 | 1 | 1 | 6.479 | 5.004E-11 | 3.830E-12 | 9.900773 | 1 | P-mT-Susp | P-0.5PG-mT | 16091.07 | Mesoderm induction early response protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=MIER3 PE=1 |
| P23229 | 1 | 1 | 5.606 | 2.363E-02 | 2.665E-04 | 1.393212 | 0.78078 | F-0.5PG-mT | F-mT-2D | 127803.2 | Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 PE=1 SV=5 |
| A0A7P0T8R2 | 1 | 1 | 12.7432 | 7.166E-08 | 1.718E-09 | 5.055366 | 1 | P-0.5PG-mT | P-mT-Susp | 5380.803 | Excitatory amino acid transporter 1 (Fragment) OS=Homo sapiens OX=9606 GN=SLC1A3 PE=4 SV=1 |
| A6NJL1;K7EJD | 1 | 1 | 4.8159 | 3.763E-06 | 6.716E-08 | 63.79619 | 1 | P-0.5PG-mT | P-mT-Susp | 56681.41 | Zinc finger and SCAN domain-containing protein 5B OS=Homo sapiens OX=9606 GN=ZSCAN5B PE=1 SV |
| J3QQY7 | 1 | 1 | 5.4616 | 1.386E-03 | 1.729E-05 | 1.483176 | 0.99005 | F-0.5PG-mT | mT blank | 11941.44 | Protein TANC2 (Fragment) OS=Homo sapiens OX=9606 GN=TANC2 PE=1 SV=1 |
| A0A0A0MSM0 | 1 | 1 | 4.5632 | 3.533E-10 | 1.769E-11 | 3.578696 | 1 | P-0.5PG-mT | P-mT-Susp | 89526.08 | Heat shock protein 105 kDa OS=Homo sapiens OX=9606 GN=HSPH1 PE=1 SV=1 |
| Q05707 | 1 | 1 | 4.475 | 1.643E-10 | 9.836E-12 | 4.328996 | 1 | P-mT-Susp | mT blank | 194599.3 | Collagen alpha-1(XIV) chain OS=Homo sapiens OX=9606 GN=COL14A1 PE=1 SV=3 |
| Q9BXU3 | 1 | 1 | 4.8741 | 2.271E-08 | 6.322E-10 | 2.079766 | 1 | P-mT-Susp | P-0.5PG-mT | 45924.91 | Testis-expressed protein 13A OS=Homo sapiens OX=9606 GN=TEX13A PE=1 SV=1 |
| I3L311 | 1 | 1 | 6.2879 | 4.610E-12 | 7.058E-13 | 6.576169 | 1 | mT blank | F-mT-2D | 7429.853 | Myb-binding protein 1A (Fragment) OS=Homo sapiens OX=9606 GN=MYBBP1A PE=1 SV=1 |
| A0A590UJA7;I | 1 | 1 | 5.6395 | 8.614E-09 | 2.732E-10 | 2.527523 | 1 | P-0.5PG-mT | mT blank | 19218.1 | Speckle-type POZ protein OS=Homo sapiens OX=9606 GN=SPOP PE=1 SV=1 |
| A0A2R8Y6Y9 | 1 | 1 | 5.5381 | 1.162E-09 | 4.889E-11 | 10.74946 | 1 | P-0.5PG-mT | F-mT-2D | 9424.005 | Breast cancer type 1 susceptibility protein OS=Homo sapiens OX=9606 GN=BRCA1 PE=1 SV=1 |
| H3BN49;H3BS | 1 | 1 | 11.2444 | 3.374E-12 | 5.969E-13 | 3.379093 | 1 | P-mT-Susp | mT blank | 12167.69 | Transforming growth factor beta-1-induced transcript 1 protein OS=Homo sapiens OX=9606 GN=TGFB |
| H0YIV4;P5520 | 1 | 1 | 5.2364 | 1.631E-11 | 1.755E-12 | 10.18271 | 1 | P-mT-Susp | mT blank | 44999.63 | Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1 |
| P30304 | 1 | 1 | 4.9314 | 9.338E-08 | 2.206E-09 | 2.255186 | 1 | P-mT-Susp | mT blank | 59771.23 | M-phase inducer phosphatase 1 OS=Homo sapiens OX=9606 GN=CDC25A PE=1 SV=2 |
| A0A286YF22;A | 1 | 1 | 6.08 | 4.319E-07 | 8.839E-09 | 2.15696 | 1 | P-mT-Susp | mT blank | 56680.14 | D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1 |
| A0A3B3ITD8;F | 1 | 1 | 5.0188 | 4.182E-08 | 1.060E-09 | 2.917687 | 1 | P-mT-Susp | mT blank | 144018 | Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens OX=9606 GN=NUP98 PE=1 SV=1 |
| P08172 | 1 | 1 | 11.6442 | 1.720E-10 | 1.014E-11 | 9.419725 | 1 | P-mT-Susp | P-0.5PG-mT | 52456.51 | Muscarinic acetylcholine receptor M2 OS=Homo sapiens OX=9606 GN=CHRM2 PE=1 SV=1 |
| A0A087WZX6 | 1 | 1 | 5.1636 | 9.774E-08 | 2.282E-09 | 9.265631 | 1 | P-0.5PG-mT | P-mT-Susp | 30318.19 | Phospholipid-transporting ATPase ABCA7 (Fragment) OS=Homo sapiens OX=9606 GN=ABCA7 PE=1 SV |
| Q9BRS2 | 1 | 1 | 5.4939 | 2.112E-07 | 4.570E-09 | 6.000947 | 1 | P-0.5PG-mT | mT blank | 65925.29 | Serine/threonine-protein kinase RIO1 OS=Homo sapiens OX=9606 GN=RIOK1 PE=1 SV=2 |
| D6R9P5;D6RC | 1 | 1 | 5.6437 | 1.865E-14 | 1.748E-14 | 24.78028 | 1 | P-mT-Susp | P-0.5PG-mT | 13917.67 | Prolactin receptor (Fragment) OS=Homo sapiens OX=9606 GN=PRLR PE=1 SV=1 |
| A0A0R4J2G7;A | 1 | 1 | 4.4432 | 3.606E-11 | 3.120E-12 | 9.86696 | 1 | P-mT-Susp | mT blank | 166535.9 | Neurexin-1-beta OS=Homo sapiens OX=9606 GN=NRXN1 PE=1 SV=1 |
| Q9UNQ0 | 1 | 1 | 4.4893 | 1.321E-12 | 3.186E-13 | 14.39779 | 1 | F-mT-2D | mT blank | 72998.66 | Broad substrate specificity ATP-binding cassette transporter ABCG2 OS=Homo sapiens OX=9606 GN=A |
| C9JH98 | 1 | 1 | 5.7143 | 1.814E-11 | 1.920E-12 | 3.31885 | 1 | P-mT-Susp | mT blank | 11893.21 | Neuropilin-2 (Fragment) OS=Homo sapiens OX=9606 GN=NRP2 PE=1 SV=8 |
| Q6Y2X3 | 1 | 1 | 6.1317 | 5.894E-04 | 7.692E-06 | 1.722191 | 0.99782 | P-0.5PG-mT | F-mT-2D | 79481.31 | DnaJ homolog subfamily C member 14 OS=Homo sapiens OX=9606 GN=DNAJC14 PE=2 SV=2 |
| A0A087X0B8;A | 1 | 1 | 11.8644 | 2.554E-15 | 6.776E-15 | 10.51402 | 1 | P-mT-Susp | F-0.5PG-mT | 8056.146 | Acyl-CoA-binding domain-containing protein 5 OS=Homo sapiens OX=9606 GN=ACBD5 PE=1 SV=1 |
| M0QZ20;M0R | 1 | 1 | 5.2986 | 3.463E-06 | 6.224E-08 | 3.89312 | 1 | P-0.5PG-mT | P-mT-Susp | 20406.18 | Calpain-12 (Fragment) OS=Homo sapiens OX=9606 GN=CAPN12 PE=3 SV=1 |
| M0QZS6 | 1 | 1 | 6.8642 | 2.550E-06 | 4.613E-08 | 4.912598 | 1 | mT blank | P-mT-Susp | 29650.71 | SUMO-activating enzyme subunit 1 OS=Homo sapiens OX=9606 GN=SAE1 PE=1 SV=1 |
| P09067 | 1 | 1 | 4.1672 | 9.244E-02 | 1.004E-03 | 2.95316 | 0.53216 | F-0.5PG-mT | F-mT-2D | 29605.6 | Homeobox protein Hox-B5 OS=Homo sapiens OX=9606 GN=HOXB5 PE=1 SV=3 |
| A0A087WUL9 | 1 | 1 | 5.54 | 7.255E-05 | 1.062E-06 | 1.685733 | 0.99999 | P-mT-Susp | F-0.5PG-mT | 43024.55 | 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens OX=9606 GN=PSMD13 PE=1 SV= |
| D6RA24;Q9NZ | 1 | 1 | 6.0311 | 2.235E-09 | 8.637E-11 | 6.762911 | 1 | mT blank | P-mT-Susp | 7170.202 | Placenta-specific 8_ isoform CRA_b OS=Homo sapiens OX=9606 GN=PLAC8 PE=1 SV=1 |
| P45983 | 1 | 1 | 5.2959 | 1.032E-02 | 1.194E-04 | 2.375598 | 0.88613 | mT blank | P-mT-Susp | 48865.95 | Mitogen-activated protein kinase 8 OS=Homo sapiens OX=9606 GN=MAPK8 PE=1 SV=2 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| E9PKT7;Q68D | 1 | 1 | 11.7516 | 1.221E-10 | 7.653E-12 | 4.822232 | 1 | P-mT-Susp | P-0.5PG-mT | 15097.24 | Schlafen family member 13 (Fragment) OS=Homo sapiens OX=9606 GN=SLFN13 PE=1 SV=8 |
| B4DY26;P368 | 1 | 1 | 5.3696 | 4.487E-10 | 2.126E-11 | 3.992761 | 1 | P-mT-Susp | mT blank | 49673.9 | Receptor protein serine/threonine kinase OS=Homo sapiens OX=9606 GN=TGFBR1 PE=1 SV=1 |
| E7ERK2;Q025 | 1 | 1 | 4.9587 | 1.698E-10 | 1.009E-11 | 11.69054 | 1 | P-mT-Susp | P-0.5PG-mT | 30377.61 | Paired box protein Pax-5 OS=Homo sapiens OX=9606 GN=PAX5 PE=1 SV=1 |
| Q8TAQ9 | 1 | 1 | 4.5385 | 4.536E-03 | 5.406E-05 | 2.323333 | 0.95055 | mT blank | P-mT-Susp | 40788.52 | SUN domain-containing protein 3 OS=Homo sapiens OX=9606 GN=SUN3 PE=1 SV=4 |
| Q9Y4D1;G3V2 | 3 | 1 | 16.2252 | 5.806E-12 | 7.714E-13 | 3.523516 | 1 | P-mT-Susp | F-0.5PG-mT | 124044 | Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens OX=9606 GN=DAAM1 PE=1 SV |
| J3QRC2 | 1 | 1 | 12.0124 | 3.147E-07 | 6.593E-09 | 2.99123 | 1 | P-mT-Susp | mT blank | 8204.119 | Rho GTPase-activating protein 28 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGAP28 PE=1 SV=1 |
| A0A087WTZ7 | 1 | 1 | 5.8624 | 2.480E-04 | 3.381E-06 | 8.147671 | 0.99968 | P-0.5PG-mT | P-mT-Susp | 22363.36 | Pleckstrin homology-like domain family B member 1 (Fragment) OS=Homo sapiens OX=9606 GN=PHLD |
| O00590;V9GY | 1 | 1 | 6.0434 | 9.919E-07 | 1.912E-08 | 41.65356 | 1 | P-mT-Susp | P-0.5PG-mT | 43956.18 | Atypical chemokine receptor 2 OS=Homo sapiens OX=9606 GN=ACKR2 PE=1 SV=2 |
| P51801 | 1 | 1 | 5.7969 | 1.136E-06 | 2.174E-08 | 7.591785 | 1 | P-mT-Susp | F-0.5PG-mT | 76073.45 | Chloride channel protein ClC-Kb OS=Homo sapiens OX=9606 GN=CLCNKB PE=1 SV=3 |
| M0R0A3;Q8IV | 1 | 1 | 5.2264 | 3.061E-10 | 1.614E-11 | 4.104789 | 1 | P-mT-Susp | mT blank | 44323.5 | Zinc finger protein 584 OS=Homo sapiens OX=9606 GN=ZNF584 PE=1 SV=1 |
| A8MSM7 | 1 | 1 | 5.1444 | 5.001E-03 | 5.951E-05 | 1.693581 | 0.94482 | F-mT-2D | mT blank | 21934.74 | Microtubule-associated protein 9 OS=Homo sapiens OX=9606 GN=MAP9 PE=1 SV=1 |
| Q7Z6W7 | 1 | 1 | 6.0625 | 7.922E-04 | 1.017E-05 | 57.19401 | 0.99617 | P-0.5PG-mT | P-mT-Susp | 35604.79 | DnaJ homolog subfamily B member 7 OS=Homo sapiens OX=9606 GN=DNAJB7 PE=2 SV=2 |
| K7EJ03;Q9279 | 1 | 1 | 11.8894 | 8.808E-03 | 1.030E-04 | 1.902175 | 0.90155 | P-mT-Susp | mT blank | 9655.899 | Endoplasmic reticulum protein SC65 (Fragment) OS=Homo sapiens OX=9606 GN=P3H4 PE=1 SV=1 |
| H7C2V2;Q9P2 | 1 | 1 | 4.5668 | 4.760E-07 | 9.665E-09 | 3.587159 | 1 | mT blank | P-mT-Susp | 18452.65 | Ankyrin repeat and IBR domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ANKI |
| F8VQT2;F8VY | 1 | 1 | 5.3232 | 9.012E-07 | 1.754E-08 | 11.08172 | 1 | P-mT-Susp | mT blank | 8319.967 | Zinc finger CCCH domain-containing protein 10 (Fragment) OS=Homo sapiens OX=9606 GN=ZC3H10 PE |
| A6XGL2;P013 | 1 | 1 | 6.3372 | 8.261E-07 | 1.612E-08 | 1.927379 | 1 | P-0.5PG-mT | P-mT-Susp | 11300.96 | Insulin OS=Homo sapiens OX=9606 GN=INS PE=1 SV=1 |
| Q8NC26 | 1 | 1 | 5.9984 | 8.353E-05 | 1.207E-06 | 7.878572 | 0.99999 | F-0.5PG-mT | F-mT-2D | 48830.2 | Zinc finger protein 114 OS=Homo sapiens OX=9606 GN=ZNF114 PE=1 SV=1 |
| Q6ZU80 | 1 | 1 | 4.2416 | 6.354E-09 | 2.090E-10 | 15.60631 | 1 | P-mT-Susp | mT blank | 128642.6 | Centrosomal protein of 128 kDa OS=Homo sapiens OX=9606 GN=CEP128 PE=1 SV=2 |
| A0A7P0T847;A | 1 | 1 | 5.7909 | 1.180E-08 | 3.546E-10 | Infinity | 1 | mT blank | P-mT-Susp | 43353.94 | A-kinase anchor protein 8-like OS=Homo sapiens OX=9606 GN=AKAP8L PE=4 SV=1 |
| O14986 | 1 | 1 | 6.1693 | 4.476E-06 | 7.882E-08 | 1.973203 | 1 | P-0.5PG-mT | mT blank | 61264.55 | Phosphatidylinositol 4-phosphate 5-kinase type-1 beta OS=Homo sapiens OX=9606 GN=PIP5K1B PE=1 |
| K7EL32 | 1 | 1 | 7.7996 | 3.009E-07 | 6.320E-09 | 4346.232 | 1 | P-mT-Susp | P-0.5PG-mT | 24423.42 | Thimet oligopeptidase (Fragment) OS=Homo sapiens OX=9606 GN=THOP1 PE=1 SV=1 |
| A0A024R3M2 | 1 | 1 | 4.2758 | 9.891E-03 | 1.151E-04 | 1.918764 | 0.89042 | P-mT-Susp | mT blank | 81199.1 | HCG39893_ isoform CRA_a OS=Homo sapiens OX=9606 GN=GRAMD1B PE=1 SV=1 |
| E9PJF0;E9PQV | 1 | 1 | 4.6204 | 5.857E-10 | 2.680E-11 | 7.85744 | 1 | P-mT-Susp | mT blank | 36193.53 | Mitogen-activated protein kinase OS=Homo sapiens OX=9606 GN=MAPK3 PE=1 SV=1 |
| Q7Z3V5 | 1 | 1 | 5.1902 | 3.956E-04 | 5.257E-06 | 5.611998 | 0.99905 | P-0.5PG-mT | mT blank | 73244.74 | Zinc finger protein 571 OS=Homo sapiens OX=9606 GN=ZNF571 PE=2 SV=3 |
| A0A0D9SGJ8;A | 1 | 1 | 5.3532 | 4.024E-07 | 8.256E-09 | 251.6246 | 1 | P-mT-Susp | P-0.5PG-mT | 82199.72 | PWWP domain-containing DNA repair factor 3A OS=Homo sapiens OX=9606 GN=PWWP3A PE=1 SV=1 |
| A0A2R8Y516;A | 1 | 1 | 5.0832 | 1.556E-05 | 2.507E-07 | 11.92576 | 1 | mT blank | P-0.5PG-mT | 17401.57 | Autism susceptibility gene 2 protein (Fragment) OS=Homo sapiens OX=9606 GN=AUTS2 PE=1 SV=1 |
| A6NK53 | 1 | 1 | 4.8557 | 3.536E-06 | 6.325E-08 | 3.628457 | 1 | F-mT-2D | F-0.5PG-mT | 78857.08 | Zinc finger protein 233 OS=Homo sapiens OX=9606 GN=ZNF233 PE=2 SV=3 |
| A0A140T947;Q | 1 | 1 | 4.6637 | 2.425E-07 | 5.176E-09 | 1.797335 | 1 | F-0.5PG-mT | P-mT-Susp | 77275.19 | Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 (Fragment) OS=Homo sapiens OX=9606 |
| E9PM19;P295 | 1 | 1 | 5.1583 | 2.895E-12 | 5.431E-13 | 4.278654 | 1 | P-mT-Susp | mT blank | 114617.3 | Tyrosine-protein kinase OS=Homo sapiens OX=9606 GN=TYK2 PE=1 SV=1 |
| A0A6Q8PF27;A | 1 | 1 | 6.8024 | 3.753E-08 | 9.701E-10 | 13.06336 | 1 | P-mT-Susp | F-0.5PG-mT | 91342.17 | Polyphosphoinositide phosphatase OS=Homo sapiens OX=9606 GN=FIG4 PE=1 SV=1 |
| O95238 | 1 | 1 | 5.9387 | 1.327E-07 | 2.984E-09 | 13.07398 | 1 | P-mT-Susp | P-0.5PG-mT | 37802.8 | SAM pointed domain-containing Ets transcription factor OS=Homo sapiens OX=9606 GN=SPDEF PE=1 S |
| Q8N4M1 | 1 | 1 | 5.6884 | 7.719E-03 | 9.076E-05 | 2.876312 | 0.91325 | P-mT-Susp | F-mT-2D | 75152.19 | Choline transporter-like protein 3 OS=Homo sapiens OX=9606 GN=SLC44A3 PE=1 SV=4 |
| Q96MT3 | 1 | 1 | 5.0543 | 7.035E-09 | 2.286E-10 | 1001.509 | 1 | P-0.5PG-mT | P-mT-Susp | 96239.34 | Prickle-like protein 1 OS=Homo sapiens OX=9606 GN=PRICKLE1 PE=1 SV=2 |
| Q8IUC2 | 1 | 1 | 5.972 | 1.811E-04 | 2.507E-06 | 176.6085 | 0.99986 | F-0.5PG-mT | P-0.5PG-mT | 7053.731 | Keratin-associated protein 8-1 OS=Homo sapiens OX=9606 GN=KRTAP8-1 PE=1 SV=1 |
| E5RHS3;O602 | 1 | 1 | 4.7308 | 8.325E-11 | 5.813E-12 | Infinity | 1 | F-0.5PG-mT | P-mT-Susp | 69714.06 | Suppression of tumorigenicity 18 protein (Fragment) OS=Homo sapiens OX=9606 GN=ST18 PE=1 SV=1 |
| P46937 | 1 | 1 | 5.0444 | 2.229E-04 | 3.064E-06 | Infinity | 0.99976 | P-mT-Susp | F-0.5PG-mT | 54518.7 | Transcriptional coactivator YAP1 OS=Homo sapiens OX=9606 GN=YAP1 PE=1 SV=2 |
| A0A0A0MTT2 | 1 | 1 | 5.0197 | 4.889E-06 | 8.536E-08 | 27.23466 | 1 | P-mT-Susp | mT blank | 71794.24 | Zinc finger protein 559 OS=Homo sapiens OX=9606 GN=ZNF559 PE=1 SV=1 |
| P16070 | 1 | 1 | 5.3733 | 4.472E-11 | 3.554E-12 | Infinity | 1 | F-mT-2D | mT blank | 82050.98 | CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=3 |
| M0R2Q7 | 1 | 1 | 6.9073 | 3.216E-01 | 3.404E-03 | 4.510895 | 0.27924 | P-mT-Susp | mT blank | 20549.11 | Signal-induced proliferation-associated 1-like protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=SIF |
| V9GYG1 | 1 | 1 | 5.7496 | 5.757E-08 | 1.397E-09 | Infinity | 1 | mT blank | P-mT-Susp | 10391.07 | Histone-lysine N-methyltransferase SETD7 (Fragment) OS=Homo sapiens OX=9606 GN=SETD7 PE=1 SV |
| A0A0J9YX90 | 1 | 1 | 4.9599 | 2.572E-02 | 2.891E-04 | Infinity | 0.76776 | F-0.5PG-mT | P-mT-Susp | 31662.21 | Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1 |
| O60825 | 1 | 1 | 6.4902 | 1.951E-01 | 2.081E-03 | 3.212476 | 0.37902 | mT blank | P-0.5PG-mT | 58990.14 | 6-phosphofructo-2-kinase/fructose-2_6-bisphosphatase 2 OS=Homo sapiens OX=9606 GN=PFKFB2 PE= |
| A0A1B0GUB2;A | 1 | 1 | 4.8492 | 1.052E-02 | 1.215E-04 | 8.493974 | 0.8842 | F-mT-2D | P-mT-Susp | 51568.39 | Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1 |
| H7C1J8 | 1 | 1 | 5.6945 | 2.409E-01 | 2.565E-03 | 7.088612 | 0.33629 | mT blank | P-mT-Susp | 11354.88 | Heterogeneous nuclear ribonucleoprotein A3 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA3 P |
| A0A0B4J260 | 1 | 1 | 5.5237 | 4.128E-02 | 4.596E-04 | 3.385085 | 0.68801 | P-mT-Susp | P-0.5PG-mT | 6198.911 | PRKC apoptosis WT1 regulator protein (Fragment) OS=Homo sapiens OX=9606 GN=PAWR PE=1 SV=5 |
| F2Z3N3;Q68B | 1 | 1 | 5.1246 | 1.022E-07 | 2.372E-09 | Infinity | 1 | mT blank | P-mT-Susp | 84811.48 | Olfactomedin-like protein 2B OS=Homo sapiens OX=9606 GN=OLFML2B PE=1 SV=1 |
| A0A0G2JK11;A | 1 | 1 | 5.2003 | 7.604E-01 | 8.007E-03 | Infinity | 0.11923 | F-0.5PG-mT | P-mT-Susp | 33222.47 | MHC class I polypeptide-related sequence A OS=Homo sapiens OX=9606 GN=MICA PE=1 SV=1 |
| B1ANH2 | 1 | 1 | 5.5113 | 3.041E-03 | 3.668E-05 | 3.772485 | 0.9695 | P-mT-Susp | F-mT-2D | 27806.16 | Guanylate kinase (Fragment) OS=Homo sapiens OX=9606 GN=GUK1 PE=1 SV=1 |
| A0A7I2V3U5;A | 1 | 1 | 6.0073 | 1.134E-10 | 7.282E-12 | Infinity | 1 | F-mT-2D | F-0.5PG-mT | 44993.05 | Glycylpeptide N-tetradecanoyltransferase OS=Homo sapiens OX=9606 GN=NMT1 PE=1 SV=1 |
| P07686;Q5UR | 1 | 1 | 4.8553 | 1.018E-05 | 1.678E-07 | 154.0049 | 1 | P-0.5PG-mT | P-mT-Susp | 63567.64 | Beta-hexosaminidase subunit beta OS=Homo sapiens OX=9606 GN=HEXB PE=1 SV=3 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| A0A0A0MT39 | 1 | 1 | 4.8916 | 1.535E-04 | 2.159E-06 | 2.109344 | 0.99991 | F-0.5PG-mT | F-mT-2D | 223639.6 | Sodium channel protein OS=Homo sapiens OX=9606 GN=SCN5A PE=1 SV=1 |
| C9J3R7;C9J48 | 1 | 1 | 5.342 | 1.830E-05 | 2.907E-07 | 12.01888 | 1 | F-mT-2D | F-0.5PG-mT | 6888.897 | Zinc finger protein 789 OS=Homo sapiens OX=9606 GN=ZNF789 PE=4 SV=1 |
| A0A669KB17;A | 1 | 1 | 5.3211 | 7.837E-04 | 1.008E-05 | 187.996 | 0.99625 | F-0.5PG-mT | P-mT-Susp | 32521.54 | Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens OX=9606 GN=STAT1 P |
| J3KTM9;Q149 | 1 | 1 | 4.849 | 2.976E-03 | 3.595E-05 | 4.152831 | 0.97033 | F-0.5PG-mT | P-mT-Susp | 77648.34 | Importin subunit beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=1 |
| E9PIZ2 | 1 | 1 | 4.6039 | 6.430E-04 | 8.350E-06 | 7.346681 | 0.99742 | P-mT-Susp | F-0.5PG-mT | 79270.86 | LARGE xylosyl- and glucuronyltransferase 2 OS=Homo sapiens OX=9606 GN=LARGE2 PE=1 SV=1 |
| A0A087WVE9 | 1 | 1 | 4.7969 | 8.750E-09 | 2.753E-10 | Infinity | 1 | F-0.5PG-mT | F-mT-2D | 79638.2 | Aryl hydrocarbon receptor nuclear translocator 2 OS=Homo sapiens OX=9606 GN=ARNT2 PE=1 SV=1 |
| E7END6 | 1 | 1 | 4.169 | 1.271E-02 | 1.463E-04 | 6.078999 | 0.86353 | P-mT-Susp | F-0.5PG-mT | 56815.78 | Vitamin K-dependent protein C OS=Homo sapiens OX=9606 GN=PROC PE=1 SV=1 |
| H7BYF0 | 1 | 1 | 5.5256 | 2.646E-05 | 4.091E-07 | Infinity | 1 | P-0.5PG-mT | mT blank | 11352.37 | Leucine carboxyl methyltransferase 1 OS=Homo sapiens OX=9606 GN=LCMT1 PE=1 SV=1 |
| A0A7I2V5M7; | 1 | 1 | 5.2044 | 5.030E-09 | 1.689E-10 | 24.49225 | 1 | P-mT-Susp | mT blank | 53386.78 | Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=1 |
| C9JYY6;Q9282 | 1 | 1 | 4.3584 | 3.854E-07 | 7.969E-09 | 9.356371 | 1 | F-mT-2D | P-mT-Susp | 134669.2 | Neuronal cell adhesion molecule OS=Homo sapiens OX=9606 GN=NRCAM PE=1 SV=3 |
| I3L1N0;Q9BUL | 1 | 1 | 5.7771 | 1.716E-06 | 3.192E-08 | 17.53895 | 1 | P-mT-Susp | P-0.5PG-mT | 30073.67 | PHD finger protein 23 OS=Homo sapiens OX=9606 GN=PHF23 PE=1 SV=1 |
| Q12872 | 1 | 1 | 4.8031 | 1.754E-14 | 1.748E-14 | 18.03621 | 1 | P-mT-Susp | P-0.5PG-mT | 105220.8 | Splicing factor_ suppressor of white-apricot homolog OS=Homo sapiens OX=9606 GN=SFSWAP PE=1 S |
| Q9H0E9 | 1 | 1 | 4.0712 | 1.239E-06 | 2.354E-08 | 27.36017 | 1 | mT blank | F-mT-2D | 136134.5 | Bromodomain-containing protein 8 OS=Homo sapiens OX=9606 GN=BRD8 PE=1 SV=2 |
| C9J6P7;E9PH7 | 1 | 1 | 5.0711 | 3.421E-05 | 5.198E-07 | 3.342576 | 1 | P-mT-Susp | F-mT-2D | 20145.92 | Nuclear valosin-containing protein-like (Fragment) OS=Homo sapiens OX=9606 GN=NVL PE=1 SV=1 |
| Q9GZU1 | 1 | 1 | 5.4959 | 2.943E-10 | 1.573E-11 | 7.942213 | 1 | P-0.5PG-mT | F-0.5PG-mT | 66162.92 | Mucolipin-1 OS=Homo sapiens OX=9606 GN=MCOLN1 PE=1 SV=1 |
| P55287 | 1 | 1 | 4.6821 | 8.182E-08 | 1.956E-09 | 10.50172 | 1 | F-mT-2D | P-mT-Susp | 88421.65 | Cadherin-11 OS=Homo sapiens OX=9606 GN=CDH11 PE=2 SV=2 |
| K7EPR9 | 1 | 1 | 5.6138 | 2.443E-04 | 3.336E-06 | 2.353428 | 0.99969 | P-mT-Susp | mT blank | 3342.103 | Apolipoprotein C-I OS=Homo sapiens OX=9606 GN=APOC1 PE=4 SV=1 |
| Q9NRR3 | 1 | 1 | 5.5562 | 1.651E-02 | 1.886E-04 | 1.777633 | 0.83145 | P-mT-Susp | F-0.5PG-mT | 9394.614 | CDC42 small effector protein 2 OS=Homo sapiens OX=9606 GN=CDC42SE2 PE=1 SV=1 |
| Q6ZT52 | 1 | 1 | 5.3073 | 1.256E-05 | 2.049E-07 | 4.392747 | 1 | P-mT-Susp | mT blank | 37289.43 | Protein FAM43B OS=Homo sapiens OX=9606 GN=FAM43B PE=2 SV=1 |
| H3BRB6;Q8ND | 1 | 1 | 4.4114 | 5.035E-07 | 1.017E-08 | 39.9505 | 1 | mT blank | P-mT-Susp | 22163.67 | E3 ubiquitin-protein ligase ZNRF1 OS=Homo sapiens OX=9606 GN=ZNRF1 PE=1 SV=1 |
| O75052 | 1 | 1 | 9.3634 | 8.112E-05 | 1.174E-06 | 2.292252 | 0.99999 | F-0.5PG-mT | P-mT-Susp | 56492.02 | Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein OS=Homo sapiens OX=9606 GN |
| H0YMW5 | 1 | 1 | 5.0103 | 9.397E-09 | 2.911E-10 | 2.970569 | 1 | P-mT-Susp | mT blank | 14224.74 | Proprotein convertase subtilisin/kexin type 6 (Fragment) OS=Homo sapiens OX=9606 GN=PCSK6 PE=1 |
| A0A0B4J210;E | 1 | 1 | 5.3247 | 1.768E-10 | 1.027E-11 | 8.789312 | 1 | F-mT-2D | F-0.5PG-mT | 90993.69 | La-related protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=LARP1 PE=1 SV=5 |
| A0A494BZX2 | 1 | 1 | 5.8595 | 1.028E-10 | 6.763E-12 | 7.392984 | 1 | P-mT-Susp | P-0.5PG-mT | 12922.67 | Protein kinase C delta type (Fragment) OS=Homo sapiens OX=9606 GN=PRKCD PE=1 SV=1 |
| A0A7I2V3F8 | 1 | 1 | 5.0365 | 2.778E-08 | 7.523E-10 | 3.320443 | 1 | P-mT-Susp | mT blank | 21614.15 | DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens OX=9606 GN=DNMT1 PE=1 SV=1 |
| A0A494C0P1;I | 1 | 1 | 4.9 | 1.550E-13 | 6.498E-14 | 22.75082 | 1 | P-mT-Susp | P-0.5PG-mT | 83498.1 | Glucocorticoid receptor OS=Homo sapiens OX=9606 GN=NR3C1 PE=1 SV=1 |
| A0A087X043;( | 1 | 1 | 7.352 | 1.144E-07 | 2.633E-09 | 3.832467 | 1 | F-mT-2D | mT blank | 105007.5 | Glutamate receptor OS=Homo sapiens OX=9606 GN=GRID2 PE=1 SV=1 |
| Q9NQC3 | 1 | 1 | 4.7267 | 8.338E-13 | 2.141E-13 | 15.9863 | 1 | P-mT-Susp | mT blank | 130330.8 | Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 PE=1 SV=2 |
| A0A0R4J2E4;K | 1 | 1 | 12.2646 | 5.808E-06 | 1.007E-07 | 2.749013 | 1 | P-mT-Susp | mT blank | 121276.3 | Fas-binding factor 1 (Fragment) OS=Homo sapiens OX=9606 GN=FBF1 PE=1 SV=2 |
| Q9H6J7 | 1 | 1 | 4.7792 | 1.113E-04 | 1.579E-06 | 3.791319 | 0.99996 | F-0.5PG-mT | P-mT-Susp | 37923.79 | UPF0705 protein C11orf49 OS=Homo sapiens OX=9606 GN=C11orf49 PE=1 SV=2 |
| K7EIJ2;K7EIU8 | 1 | 1 | 5.5751 | 9.036E-05 | 1.301E-06 | 1.33521 | 0.99998 | P-0.5PG-mT | F-mT-2D | 16244.47 | Mothers against decapentaplegic homolog 4 (Fragment) OS=Homo sapiens OX=9606 GN=SMAD4 PE=1 |
| Q99581 | 1 | 1 | 6.2017 | 1.720E-03 | 2.126E-05 | 44.79794 | 0.98614 | F-0.5PG-mT | P-mT-Susp | 25144.59 | Protein FEV OS=Homo sapiens OX=9606 GN=FEV PE=1 SV=1 |
| P51617 | 1 | 1 | 9.1562 | 4.978E-08 | 1.238E-09 | 3.922923 | 1 | P-mT-Susp | F-mT-2D | 77506.24 | Interleukin-1 receptor-associated kinase 1 OS=Homo sapiens OX=9606 GN=IRAK1 PE=1 SV=2 |
| Q4KMG0 | 1 | 1 | 5.009 | 9.940E-03 | 1.155E-04 | 1.888854 | 0.88992 | P-mT-Susp | mT blank | 140743.9 | Cell adhesion molecule-related/down-regulated by oncogenes OS=Homo sapiens OX=9606 GN=CDON |
| P04746;P0DTE | 1 | 1 | 11.3818 | 4.516E-04 | 5.962E-06 | 3.887322 | 0.99874 | F-mT-2D | P-mT-Susp | 58391.27 | Pancreatic alpha-amylase OS=Homo sapiens OX=9606 GN=AMY2A PE=1 SV=2 |
| A0A087X254;I | 1 | 1 | 5.3551 | 3.730E-02 | 4.164E-04 | 1.884948 | 0.70601 | F-0.5PG-mT | mT blank | 87082.99 | Zinc finger protein 615 OS=Homo sapiens OX=9606 GN=ZNF615 PE=1 SV=1 |
| A0A0D9SFB9;A | 1 | 1 | 11.1942 | 8.883E-03 | 1.037E-04 | 4.502833 | 0.90076 | P-mT-Susp | F-0.5PG-mT | 19227.7 | Maternal embryonic leucine zipper kinase OS=Homo sapiens OX=9606 GN=MELK PE=1 SV=1 |
| E9PK59;E9PPN | 1 | 1 | 5.0778 | 1.461E-10 | 8.879E-12 | 6.015307 | 1 | P-mT-Susp | mT blank | 86810.79 | N-terminal kinase-like protein OS=Homo sapiens OX=9606 GN=SCYL1 PE=1 SV=1 |
| A0A3B3IS70 | 1 | 1 | 4.991 | 1.282E-01 | 1.375E-03 | 1.865502 | 0.46517 | mT blank | F-mT-2D | 30195.66 | Inositol 1_4_5-trisphosphate receptor type 1 (Fragment) OS=Homo sapiens OX=9606 GN=ITPR1 PE=1 S |
| H0YGI8 | 1 | 1 | 6.1293 | 3.433E-08 | 8.931E-10 | 2.817621 | 1 | F-mT-2D | mT blank | 16298.53 | Stress-induced-phosphoprotein 1 (Fragment) OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1 |
| F8VY42 | 1 | 1 | 5.5632 | 9.310E-05 | 1.335E-06 | 10.70552 | 0.99998 | P-0.5PG-mT | F-mT-2D | 10575.14 | Ceramide synthase 5 OS=Homo sapiens OX=9606 GN=CERS5 PE=1 SV=1 |
| A2RRD8;M0Q | 1 | 1 | 5.4436 | 9.771E-08 | 2.282E-09 | 2.136564 | 1 | P-mT-Susp | mT blank | 61151.35 | Zinc finger protein 320 OS=Homo sapiens OX=9606 GN=ZNF320 PE=1 SV=1 |
| A0A087WWN | 1 | 1 | 5.9575 | 2.764E-06 | 4.989E-08 | 3.451603 | 1 | P-mT-Susp | F-0.5PG-mT | 20030.9 | Cullin-4A OS=Homo sapiens OX=9606 GN=CUL4A PE=1 SV=1 |
| F5GYG7 | 1 | 1 | 5.0389 | 9.718E-08 | 2.282E-09 | 9.879343 | 1 | F-mT-2D | mT blank | 9160.554 | Alpha-2-macroglobulin-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=A2ML1 PE=1 SV=1 |
| P41227 | 1 | 1 | 5.0411 | 3.417E-05 | 5.198E-07 | 399.4092 | 1 | P-0.5PG-mT | P-mT-Susp | 26629.65 | N-alpha-acetyltransferase 10 OS=Homo sapiens OX=9606 GN=NAA10 PE=1 SV=1 |
| A0A087X0R9;I | 1 | 1 | 5.171 | 4.068E-09 | 1.402E-10 | 3.508063 | 1 | mT blank | P-mT-Susp | 63799.74 | Neutral and basic amino acid transport protein rBAT OS=Homo sapiens OX=9606 GN=SLC3A1 PE=1 SV= |
| K7ERR8;Q96N | 1 | 1 | 4.8191 | 2.632E-05 | 4.076E-07 | 12.60216 | 1 | F-0.5PG-mT | P-mT-Susp | 15383.11 | Zinc finger protein 396 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF396 PE=1 SV=1 |
| H3BND4;Q6P9 | 1 | 1 | 4.385 | 1.909E-05 | 3.021E-07 | 91.84344 | 1 | mT blank | P-mT-Susp | 89788.88 | Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PDX |
| Q5JNZ3 | 1 | 1 | 4.4383 | 1.094E-07 | 2.524E-09 | 3.306238 | 1 | P-mT-Susp | mT blank | 78545.69 | Zinc finger protein 311 OS=Homo sapiens OX=9606 GN=ZNF311 PE=2 SV=2 |
| C9JUF0;E7EMT | 1 | 1 | 5.7603 | 5.494E-05 | 8.221E-07 | 110.3776 | 1 | F-mT-2D | P-mT-Susp | 6325.851 | Eukaryotic initiation factor 4A-II (Fragment) OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| P51795 | 1 | 1 | 4.4128 | 1.214E-05 | 1.984E-07 | 2.26491 | 1 | P-mT-Susp | mT blank | 91754.85 | H(+)/Cl(-) exchange transporter 5 OS=Homo sapiens OX=9606 GN=CLCN5 PE=1 SV=2 |
| Q9UHJ3 | 1 | 1 | 4.42 | 2.280E-10 | 1.287E-11 | 8.086814 | 1 | F-mT-2D | mT blank | 99738.36 | Scm-like with four MBT domains protein 1 OS=Homo sapiens OX=9606 GN=SFMBT1 PE=1 SV=2 |
| O60500 | 1 | 1 | 4.8467 | 3.618E-04 | 4.832E-06 | 7.537257 | 0.99922 | P-mT-Susp | P-0.5PG-mT | 135882.9 | Nephrin OS=Homo sapiens OX=9606 GN=NPHS1 PE=1 SV=1 |
| Q5STZ8;Q8NE | 1 | 1 | 4.1743 | 6.806E-07 | 1.341E-08 | 3.9259 | 1 | mT blank | P-mT-Susp | 96510.23 | ATP-binding cassette sub-family F member 1 OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 SV=10 |
| A0A087X1U1; | 1 | 1 | 5.4795 | 1.217E-03 | 1.528E-05 | 113.5274 | 0.99193 | mT blank | P-mT-Susp | 83658.63 | Arf-GAP with GTPase_ ANK repeat and PH domain-containing protein 1 OS=Homo sapiens OX=9606 GI |
| E9PJU8 | 1 | 1 | 5.7379 | 4.928E-04 | 6.462E-06 | 2.423007 | 0.99849 | P-mT-Susp | mT blank | 21458.31 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| B0QYA5;B0QY | 1 | 1 | 5.2355 | 7.617E-05 | 1.107E-06 | 8.946289 | 0.99999 | mT blank | P-mT-Susp | 31957.2 | Eukaryotic translation initiation factor 3 subunit D (Fragment) OS=Homo sapiens OX=9606 GN=EIF3D P |
| Q969H0 | 1 | 1 | 4.4902 | 4.917E-02 | 5.451E-04 | 1.525291 | 0.65598 | P-mT-Susp | P-0.5PG-mT | 80632.55 | F-box/WD repeat-containing protein 7 OS=Homo sapiens OX=9606 GN=FBXW7 PE=1 SV=1 |
| Q6IMN6 | 1 | 1 | 4.2138 | 1.046E-04 | 1.490E-06 | 128.9892 | 0.99997 | P-0.5PG-mT | P-mT-Susp | 126552.3 | Caprin-2 OS=Homo sapiens OX=9606 GN=CAPRIN2 PE=1 SV=1 |
| H7C4F3 | 1 | 1 | 5.312 | 1.445E-08 | 4.229E-10 | 7.061301 | 1 | P-0.5PG-mT | P-mT-Susp | 13565.28 | Inactive histone-lysine N-methyltransferase 2E (Fragment) OS=Homo sapiens OX=9606 GN=KMT2E PE= |
| K7EL58;Q86YS | 1 | 1 | 5.2069 | 1.709E-07 | 3.780E-09 | 2.830988 | 1 | F-0.5PG-mT | mT blank | 14639.29 | Rab11 family-interacting protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=RAB11FIP4 PE=1 SV=1 |
| A6NHC0 | 1 | 1 | 5.3288 | 6.684E-06 | 1.144E-07 | 400.4926 | 1 | mT blank | P-mT-Susp | 80171.06 | Calpain-8 OS=Homo sapiens OX=9606 GN=CAPN8 PE=1 SV=3 |
| E9PJC9 | 1 | 1 | 5.6137 | 6.329E-02 | 6.950E-04 | 1.960117 | 0.60773 | P-0.5PG-mT | F-mT-2D | 18389.86 | Inactive pancreatic lipase-related protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PNLIPRP1 PE= |
| Q86YJ7 | 1 | 1 | 5.4052 | 2.313E-05 | 3.628E-07 | 2.784847 | 1 | P-mT-Susp | mT blank | 70661.7 | Ankyrin repeat domain-containing protein 13B OS=Homo sapiens OX=9606 GN=ANKRD13B PE=1 SV=4 |
| C9JP21;Q0182 | 1 | 1 | 4.6198 | 1.482E-03 | 1.841E-05 | 4.210702 | 0.98895 | mT blank | P-mT-Susp | 25004.55 | DNA-binding protein SATB1 (Fragment) OS=Homo sapiens OX=9606 GN=SATB1 PE=1 SV=1 |
| Q8IZ26 | 1 | 1 | 4.7052 | 1.390E-02 | 1.597E-04 | 1.659444 | 0.85304 | P-0.5PG-mT | F-mT-2D | 65578.24 | Zinc finger protein 34 OS=Homo sapiens OX=9606 GN=ZNF34 PE=1 SV=3 |
| O94875 | 1 | 1 | 5.0226 | 1.341E-08 | 3.970E-10 | 3.291275 | 1 | F-mT-2D | F-0.5PG-mT | 125248.2 | Sorbin and SH3 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=SORBS2 PE=1 SV=3 |
| G3V4I0;O7535 | 1 | 1 | 4.6538 | 2.761E-08 | 7.501E-10 | 3.233444 | 1 | P-0.5PG-mT | mT blank | 45735.04 | Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens OX=9606 GN=ENTPD5 PE=1 SV= |
| A0A7P0T8A6;A | 1 | 1 | 4.9772 | 1.498E-12 | 3.507E-13 | 17.95118 | 1 | P-mT-Susp | mT blank | 80491.59 | MICAL-like protein 1 OS=Homo sapiens OX=9606 GN=MICALL1 PE=4 SV=1 |
| U3KPZ6 | 1 | 1 | 19.5955 | 2.024E-11 | 2.048E-12 | 8.103277 | 1 | P-mT-Susp | P-0.5PG-mT | 4993.244 | E3 ubiquitin-protein ligase RNF220 OS=Homo sapiens OX=9606 GN=RNF220 PE=4 SV=1 |
| B4DJM9 | 1 | 1 | 9.4436 | 7.631E-09 | 2.459E-10 | 1.940873 | 1 | P-mT-Susp | mT blank | 26712.95 | Serine--tRNA ligase_ mitochondrial OS=Homo sapiens OX=9606 GN=SARS2 PE=1 SV=1 |
| P16284;A0A07 | 3 | 1 | 31.9964 | 3.954E-03 | 4.726E-05 | 2.124457 | 0.95786 | P-0.5PG-mT | F-mT-2D | 83434.77 | Platelet endothelial cell adhesion molecule OS=Homo sapiens OX=9606 GN=PECAM1 PE=1 SV=2 |
| A0A2R8Y549;( | 3 | 1 | 26.4168 | 5.360E-07 | 1.078E-08 | 2.765399 | 1 | P-mT-Susp | mT blank | 205496.3 | InaD-like protein OS=Homo sapiens OX=9606 GN=PATJ PE=1 SV=1 |
| A0A1X7SBR3;A | 3 | 1 | 31.6652 | 3.508E-03 | 4.206E-05 | 3.897773 | 0.96352 | P-0.5PG-mT | P-mT-Susp | 54301.36 | Glial fibrillary acidic protein OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1 |
| A0A087X0K9;( | 2 | 1 | 9.9879 | 3.422E-03 | 4.109E-05 | 12.17321 | 0.96462 | P-0.5PG-mT | F-mT-2D | 197801.5 | Tight junction protein 1 (Zona occludens 1)_ isoform CRA_a OS=Homo sapiens OX=9606 GN=TJP1 PE=1 |
| Q02156;C9JR2 | 2 | 1 | 17.9672 | 2.188E-05 | 3.456E-07 | 4.745537 | 1 | P-0.5PG-mT | P-mT-Susp | 85042.6 | Protein kinase C epsilon type OS=Homo sapiens OX=9606 GN=PRKCE PE=1 SV=1 |
| Q12901;K7ELA | 2 | 1 | 22.4444 | 1.422E-09 | 5.867E-11 | 4.01127 | 1 | P-mT-Susp | mT blank | 63963.27 | Zinc finger protein 155 OS=Homo sapiens OX=9606 GN=ZNF155 PE=1 SV=4 |
| Q9P2R3;I3L1Z | 2 | 1 | 10.9497 | 2.254E-03 | 2.756E-05 | 2.528927 | 0.97954 | P-mT-Susp | mT blank | 129996.2 | Rabankyrin-5 OS=Homo sapiens OX=9606 GN=ANKFY1 PE=1 SV=2 |
| Q8NEV1 | 3 | 1 | 17.4754 | 1.007E-06 | 1.937E-08 | 1.489815 | 1 | P-0.5PG-mT | mT blank | 45333.86 | Casein kinase II subunit alpha 3 OS=Homo sapiens OX=9606 GN=CSNK2A3 PE=1 SV=2 |
| A0A7I2V360;A | 1 | 1 | 5.6641 | 1.474E-08 | 4.299E-10 | Infinity | 1 | P-0.5PG-mT | P-mT-Susp | 11701.83 | Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA1 P |
| Q6YHU6 | 3 | 1 | 25.5509 | 4.831E-12 | 7.257E-13 | 5.686083 | 1 | F-mT-2D | mT blank | 223029.3 | Thyroid adenoma-associated protein OS=Homo sapiens OX=9606 GN=THADA PE=1 SV=1 |
| A0A6I8PRE0;A | 3 | 1 | 15.3452 | 4.712E-04 | 6.200E-06 | Infinity | 0.99862 | P-0.5PG-mT | mT blank | 56724.66 | NEDD4-binding protein 2-like 2 OS=Homo sapiens OX=9606 GN=N4BP2L2 PE=1 SV=1 |
| Q96PV7;H0Y9 | 2 | 1 | 17.4776 | 3.995E-11 | 3.348E-12 | 6.509887 | 1 | P-mT-Susp | P-0.5PG-mT | 98025.4 | Protein FAM193B OS=Homo sapiens OX=9606 GN=FAM193B PE=1 SV=3 |
| F2Z2W7;Q8IZ( | 2 | 1 | 13.7169 | 7.627E-02 | 8.317E-04 | 2.628204 | 0.57091 | F-mT-2D | F-0.5PG-mT | 71861.58 | tRNA (uracil-5-)-methyltransferase homolog A OS=Homo sapiens OX=9606 GN=TRMT2A PE=1 SV=1 |
| A0A2R8YDQ9; | 2 | 1 | 12.9349 | 4.246E-02 | 4.721E-04 | 8.574967 | 0.68294 | F-mT-2D | P-mT-Susp | 44184.19 | Succinate--CoA ligase [ADP-forming] subunit beta_ mitochondrial OS=Homo sapiens OX=9606 GN=SUC |
| Q8N2N9;A0A( | 3 | 1 | 19.578 | 5.994E-10 | 2.726E-11 | 2.075467 | 1 | P-mT-Susp | F-mT-2D | 155122.4 | Ankyrin repeat domain-containing protein 36B OS=Homo sapiens OX=9606 GN=ANKRD36B PE=1 SV=4 |
| Q96JN2;C9JE1 | 2 | 1 | 10.8329 | 9.586E-12 | 1.106E-12 | 79.4382 | 1 | F-mT-2D | P-mT-Susp | 135699.3 | Coiled-coil domain-containing protein 136 OS=Homo sapiens OX=9606 GN=CCDC136 PE=1 SV=3 |
| A0A5F9ZH29;( | 3 | 1 | 17.4981 | 6.318E-12 | 7.858E-13 | 10.00795 | 1 | P-mT-Susp | mT blank | 44133.64 | Cell division control protein 45 homolog OS=Homo sapiens OX=9606 GN=CDC45 PE=1 SV=1 |
| O75821 | 2 | 1 | 9.2684 | 9.318E-10 | 4.053E-11 | 5.983869 | 1 | P-mT-Susp | mT blank | 35896.2 | Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens OX=9606 GN=EIF3G PE=1 SV=2 |
| Q8NDW4;A0A | 3 | 1 | 20.9428 | 6.504E-06 | 1.118E-07 | 3.325623 | 1 | P-mT-Susp | mT blank | 68911.55 | Zinc finger protein 248 OS=Homo sapiens OX=9606 GN=ZNF248 PE=1 SV=1 |
| A0A1B0GTW1 | 2 | 1 | 9.2464 | 1.577E-05 | 2.536E-07 | 4.583066 | 1 | P-mT-Susp | F-0.5PG-mT | 141126.2 | Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=1 |
| B4DQX9 | 2 | 1 | 17.4303 | 6.806E-05 | 1.003E-06 | 4.810075 | 0.99999 | P-mT-Susp | mT blank | 14067.7 | Microtubule-actin cross-linking factor 1_ isoforms 1/2/3/5 OS=Homo sapiens OX=9606 GN=MACF1 PE= |
| Q9UBC5;C9JU | 2 | 1 | 15.5331 | 3.750E-04 | 5.001E-06 | 1.511058 | 0.99916 | mT blank | F-mT-2D | 119313.2 | Unconventional myosin-Ia OS=Homo sapiens OX=9606 GN=MYO1A PE=1 SV=1 |
| Q58FF8 | 2 | 1 | 15.6829 | 8.056E-07 | 1.576E-08 | 170.8564 | 1 | P-0.5PG-mT | P-mT-Susp | 44520.09 | Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens OX=9606 GN=HSP90AB2P PE=1 SV=2 |
| G3V5X9;Q9UN | 3 | 1 | 20.7485 | 1.395E-03 | 1.737E-05 | 56.25748 | 0.98996 | mT blank | P-mT-Susp | 25925.21 | Sorting nexin-6 (Fragment) OS=Homo sapiens OX=9606 GN=SNX6 PE=1 SV=2 |
| O43861 | 2 | 1 | 8.0108 | 6.787E-08 | 1.632E-09 | 2.970434 | 1 | P-0.5PG-mT | F-mT-2D | 130843.5 | Probable phospholipid-transporting ATPase IIB OS=Homo sapiens OX=9606 GN=ATP9B PE=2 SV=4 |
| Q05513;E9PB | 2 | 1 | 11.3187 | 4.984E-02 | 5.518E-04 | 2.258671 | 0.65345 | P-0.5PG-mT | mT blank | 68572.52 | Protein kinase C zeta type OS=Homo sapiens OX=9606 GN=PRKCZ PE=1 SV=4 |
| E7EU81 | 2 | 1 | 10.6295 | 1.322E-09 | 5.511E-11 | 2.647957 | 1 | P-mT-Susp | mT blank | 188742 | Golgin subfamily B member 1 (Fragment) OS=Homo sapiens OX=9606 GN=GOLGB1 PE=1 SV=1 |
| H7C4Q8 | 2 | 1 | 10.8048 | 1.053E-01 | 1.141E-03 | 5.064054 | 0.50554 | P-0.5PG-mT | F-mT-2D | 30937.4 | General transcription factor II-I repeat domain-containing protein 1 (Fragment) OS=Homo sapiens OX= |
| K7EPJ0 | 2 | 1 | 9.5377 | 7.620E-04 | 9.815E-06 | 75.56867 | 0.99644 | F-0.5PG-mT | P-mT-Susp | 26087.48 | Cysteine protease OS=Homo sapiens OX=9606 GN=ATG4D PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| A0A7I2V2J0;A | 2 | 1 | 9.249 | 3.614E-03 | 4.326E-05 | 50.07389 | 0.96218 | F-0.5PG-mT | P-mT-Susp | 131723 | Laminin subunit beta-1 OS=Homo sapiens OX=9606 GN=LAMB1 PE=1 SV=1 |
| A0A7P0TA23;( | 2 | 1 | 10.3214 | 7.252E-10 | 3.243E-11 | 2.618531 | 1 | P-mT-Susp | mT blank | 65720.33 | O-phosphoseryl-tRNA(Sec) selenium transferase OS=Homo sapiens OX=9606 GN=SEPSECS PE=4 SV=1 |
| F6SRV7;F8WB | 2 | 1 | 9.347 | 5.311E-07 | 1.070E-08 | 2.050926 | 1 | P-mT-Susp | F-mT-2D | 81941.93 | [Histone H3]-dimethyl-L-lysine(36) demethylase OS=Homo sapiens OX=9606 GN=KDM2B PE=1 SV=1 |
| F5GZ28;P1885 | 1 | 1 | 11.5942 | 2.069E-10 | 1.185E-11 | 3.580665 | 1 | P-mT-Susp | mT blank | 94575.02 | DNA ligase OS=Homo sapiens OX=9606 GN=LIG1 PE=1 SV=1 |
| F8VRS8;F8W1 | 2 | 1 | 10.4722 | 4.558E-11 | 3.557E-12 | 4.656235 | 1 | P-mT-Susp | mT blank | 29982.02 | CCR4-NOT transcription complex subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=CNOT2 PE=1 S |
| C9JDA4;Q9NR | 2 | 1 | 14.3319 | 1.496E-07 | 3.355E-09 | 4.912565 | 1 | mT blank | P-mT-Susp | 31684.73 | Serine/threonine-protein kinase 36 (Fragment) OS=Homo sapiens OX=9606 GN=STK36 PE=1 SV=8 |
| H0YMW2 | 2 | 1 | 11.3168 | 8.490E-08 | 2.017E-09 | 2.588069 | 1 | P-mT-Susp | mT blank | 188360.7 | A-kinase anchor protein 13 (Fragment) OS=Homo sapiens OX=9606 GN=AKAP13 PE=1 SV=1 |
| J3KMZ8;Q927 | 2 | 1 | 16.0061 | 4.509E-11 | 3.554E-12 | Infinity | 1 | F-mT-2D | P-mT-Susp | 46920.91 | Zinc finger protein ubi-d4 OS=Homo sapiens OX=9606 GN=DPF2 PE=1 SV=1 |
| A0A087WT21 | 2 | 1 | 8.4183 | 1.936E-11 | 2.002E-12 | 9.898209 | 1 | P-mT-Susp | F-0.5PG-mT | 160879.8 | Cat eye syndrome critical region protein 2 OS=Homo sapiens OX=9606 GN=CECR2 PE=1 SV=1 |
| Q15811;F8W7 | 2 | 1 | 11.9168 | 3.401E-04 | 4.564E-06 | 4.394476 | 0.99932 | F-0.5PG-mT | F-mT-2D | 196277.4 | Intersectin-1 OS=Homo sapiens OX=9606 GN=ITSN1 PE=1 SV=3 |
| A0A3F2YNW7 | 2 | 1 | 9.7001 | 3.940E-04 | 5.245E-06 | 92.75368 | 0.99906 | P-mT-Susp | mT blank | 246565 | AT-rich interactive domain-containing protein 1B OS=Homo sapiens OX=9606 GN=ARID1B PE=1 SV=1 |
| A0A1B0GVR6; | 2 | 1 | 15.1228 | 3.955E-12 | 6.484E-13 | Infinity | 1 | mT blank | P-mT-Susp | 73135.3 | Transcription factor 4 OS=Homo sapiens OX=9606 GN=TCF4 PE=1 SV=2 |
| H3BPJ7;A0A0 | 2 | 1 | 16.0252 | 3.643E-09 | 1.300E-10 | 340.1143 | 1 | P-mT-Susp | P-0.5PG-mT | 68711.24 | Transcription factor 4 OS=Homo sapiens OX=9606 GN=TCF4 PE=1 SV=1 |
| D6RIY9 | 2 | 1 | 16.1091 | 1.385E-11 | 1.510E-12 | 5.562319 | 1 | P-mT-Susp | mT blank | 12096.31 | Ankyrin-2 (Fragment) OS=Homo sapiens OX=9606 GN=ANK2 PE=1 SV=1 |
| H7C1N2;J3KR( | 3 | 1 | 15.6993 | 2.826E-05 | 4.343E-07 | 1.698622 | 1 | P-mT-Susp | mT blank | 119893.1 | Protein cordon-bleu (Fragment) OS=Homo sapiens OX=9606 GN=COBL PE=1 SV=1 |
| Q13464 | 2 | 1 | 9.2657 | 1.272E-05 | 2.070E-07 | 1.749927 | 1 | P-0.5PG-mT | mT blank | 159201.5 | Rho-associated protein kinase 1 OS=Homo sapiens OX=9606 GN=ROCK1 PE=1 SV=1 |
| F8VNV8;P542 | 2 | 1 | 11.5551 | 3.684E-13 | 1.222E-13 | 4.559459 | 1 | P-0.5PG-mT | mT blank | 51841.69 | Calcium channel voltage-dependent subunit beta 3 OS=Homo sapiens OX=9606 GN=CACNB3 PE=1 SV= |
| E7ENC7 | 2 | 1 | 15.6302 | 6.299E-06 | 1.085E-07 | 2.048496 | 1 | P-mT-Susp | P-0.5PG-mT | 4127.974 | Negative elongation factor E OS=Homo sapiens OX=9606 GN=NELFE PE=1 SV=1 |
| H3BPW9;Q96( | 3 | 1 | 19.5547 | 9.949E-13 | 2.475E-13 | 2.320839 | 1 | P-0.5PG-mT | P-mT-Susp | 28269.09 | Enhancer of mRNA-decapping protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=EDC3 PE=1 SV=1 |
| A0A087X0M8 | 2 | 1 | 8.7879 | 4.892E-04 | 6.426E-06 | 2.762564 | 0.99851 | F-0.5PG-mT | mT blank | 131878.3 | Neural cell adhesion molecule L1-like protein OS=Homo sapiens OX=9606 GN=CHL1 PE=1 SV=1 |
| O75808;A0A1 | 2 | 1 | 10.8168 | 4.516E-01 | 4.774E-03 | Infinity | 0.21458 | mT blank | F-0.5PG-mT | 119937.5 | Calpain-15 OS=Homo sapiens OX=9606 GN=CAPN15 PE=1 SV=1 |
| H3BSE5 | 2 | 1 | 23.306 | 1.829E-09 | 7.242E-11 | 4.113566 | 1 | P-mT-Susp | mT blank | 18811.23 | Alpha-mannosidase 2C1 (Fragment) OS=Homo sapiens OX=9606 GN=MAN2C1 PE=1 SV=2 |
| E9PL66 | 2 | 1 | 18.0717 | 8.255E-12 | 9.956E-13 | 2.831263 | 1 | P-mT-Susp | mT blank | 17637.26 | Syntabulin (Fragment) OS=Homo sapiens OX=9606 GN=SYBU PE=1 SV=1 |
| H0YJN0;Q9UI( | 2 | 1 | 14.2458 | 5.060E-08 | 1.253E-09 | 12.93177 | 1 | F-0.5PG-mT | F-mT-2D | 22056.61 | Ena/VASP-like protein (Fragment) OS=Homo sapiens OX=9606 GN=EVL PE=1 SV=1 |
| A0A1B0GVI3;F | 3 | 1 | 33.3316 | 3.577E-13 | 1.222E-13 | 5.231595 | 1 | F-mT-2D | mT blank | 63574.34 | Keratin_ type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=2 |
| A0A0C4DFL8;F | 2 | 1 | 9.2777 | 4.909E-07 | 9.944E-09 | 3.587621 | 1 | P-mT-Susp | mT blank | 123779.6 | [Histone H3]-trimethyl-L-lysine(9) demethylase OS=Homo sapiens OX=9606 GN=KDM4B PE=1 SV=1 |
| Q9UDV7 | 2 | 1 | 12.3478 | 7.772E-16 | 3.093E-15 | Infinity | 1 | P-0.5PG-mT | F-mT-2D | 75379.08 | Zinc finger protein 282 OS=Homo sapiens OX=9606 GN=ZNF282 PE=1 SV=3 |
| Q8TC05;F5H5 | 2 | 1 | 15.1583 | 2.823E-05 | 4.343E-07 | 22.53922 | 1 | mT blank | P-mT-Susp | 81020.43 | Nuclear protein MDM1 OS=Homo sapiens OX=9606 GN=MDM1 PE=1 SV=2 |
| A0A1W2PNT1 | 2 | 1 | 11.7037 | 1.000E+00 | 1.052E-02 | 1 | 1 | --- | --- | 26603.05 | Nck-associated protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=NCKAP5 PE=1 SV=1 |
| Q01085;E7ETJ | 2 | 1 | 19.8252 | 5.995E-15 | 9.545E-15 | 10.46226 | 1 | P-0.5PG-mT | P-mT-Susp | 41932.97 | Nucleolysin TIAR OS=Homo sapiens OX=9606 GN=TIAL1 PE=1 SV=1 |
| P03951;H0Y5 | 2 | 1 | 16.457 | 8.326E-06 | 1.395E-07 | 4.769669 | 1 | F-mT-2D | F-0.5PG-mT | 72162.18 | Coagulation factor XI OS=Homo sapiens OX=9606 GN=F11 PE=1 SV=1 |
| P17023 | 2 | 1 | 17.8801 | 4.651E-04 | 6.130E-06 | 2.421397 | 0.99866 | F-0.5PG-mT | F-mT-2D | 53703.71 | Zinc finger protein 19 OS=Homo sapiens OX=9606 GN=ZNF19 PE=1 SV=4 |
| E9PNL0;E9PP4 | 2 | 1 | 17.4831 | 5.302E-12 | 7.537E-13 | 2.391472 | 1 | P-0.5PG-mT | mT blank | 17921.72 | Leucine-rich repeat-containing protein 14 (Fragment) OS=Homo sapiens OX=9606 GN=LRRC14 PE=1 SV |
| Q6NSJ2;M0R0 | 2 | 1 | 21.6274 | 4.129E-08 | 1.053E-09 | 1.779751 | 1 | F-mT-2D | mT blank | 72653.22 | Pleckstrin homology-like domain family B member 3 OS=Homo sapiens OX=9606 GN=PHLDB3 PE=1 SV |
| Q9NS15 | 3 | 1 | 8.0888 | 2.022E-06 | 3.725E-08 | 25.24493 | 1 | mT blank | P-mT-Susp | 146545 | Latent-transforming growth factor beta-binding protein 3 OS=Homo sapiens OX=9606 GN=LTBP3 PE=1 |
| C9JIS1;C9JXA5 | 2 | 1 | 28.3208 | 9.830E-07 | 1.904E-08 | 9.136178 | 1 | P-0.5PG-mT | P-mT-Susp | 26051.15 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (Fragment) OS=Homo sapiens OX=9 |
| Q9H0W8 | 2 | 1 | 9.2941 | 1.709E-08 | 4.876E-10 | 2.625202 | 1 | F-mT-2D | F-0.5PG-mT | 57878.93 | Protein SMG9 OS=Homo sapiens OX=9606 GN=SMG9 PE=1 SV=1 |
| C9J9M8;Q86Y | 3 | 1 | 14.9929 | 5.983E-04 | 7.795E-06 | 2.960459 | 0.99776 | mT blank | P-mT-Susp | 76407.61 | RING-type E3 ubiquitin transferase (Fragment) OS=Homo sapiens OX=9606 GN=DZIP3 PE=1 SV=1 |
| Q9UHB7 | 2 | 1 | 14.9334 | 5.067E-08 | 1.253E-09 | 2.962196 | 1 | P-0.5PG-mT | mT blank | 127858.5 | AF4/FMR2 family member 4 OS=Homo sapiens OX=9606 GN=AFF4 PE=1 SV=1 |
| E9PG71;P547( | 2 | 1 | 11.8544 | 9.061E-11 | 6.062E-12 | 5.900621 | 1 | P-mT-Susp | mT blank | 107370 | Receptor protein-tyrosine kinase OS=Homo sapiens OX=9606 GN=EPHA4 PE=1 SV=1 |
| P98187 | 3 | 1 | 14.5491 | 4.811E-08 | 1.208E-09 | 3.139956 | 1 | P-mT-Susp | F-0.5PG-mT | 60679.06 | Cytochrome P450 4F8 OS=Homo sapiens OX=9606 GN=CYP4F8 PE=1 SV=1 |
| Q13123;A0A0 | 3 | 1 | 19.8225 | 4.232E-06 | 7.504E-08 | 4.546982 | 1 | P-mT-Susp | mT blank | 65716.43 | Protein Red OS=Homo sapiens OX=9606 GN=IK PE=1 SV=3 |
| Q9Y473 | 2 | 1 | 9.5618 | 1.206E-07 | 2.734E-09 | 2.66565 | 1 | mT blank | P-mT-Susp | 84061.75 | Zinc finger protein 175 OS=Homo sapiens OX=9606 GN=ZNF175 PE=1 SV=1 |
| Q9P2P5;A0A2 | 3 | 1 | 14.6319 | 1.719E-04 | 2.392E-06 | 7.115813 | 0.99988 | P-0.5PG-mT | P-mT-Susp | 176738.9 | E3 ubiquitin-protein ligase HECW2 OS=Homo sapiens OX=9606 GN=HECW2 PE=1 SV=2 |
| A0A0D9SFG5; | 3 | 1 | 17.1025 | 1.826E-07 | 4.004E-09 | Infinity | 1 | P-0.5PG-mT | P-mT-Susp | 56049.32 | Zinc finger protein 302 OS=Homo sapiens OX=9606 GN=ZNF302 PE=1 SV=1 |
| Q8N7H5 | 2 | 1 | 14.9698 | 1.447E-03 | 1.800E-05 | Infinity | 0.98935 | P-mT-Susp | P-0.5PG-mT | 60146.89 | RNA polymerase II-associated factor 1 homolog OS=Homo sapiens OX=9606 GN=PAF1 PE=1 SV=2 |
| P14410 | 2 | 1 | 15.1954 | 2.511E-05 | 3.919E-07 | 3.99235 | 1 | mT blank | P-mT-Susp | 210879 | Sucrase-isomaltase_ intestinal OS=Homo sapiens OX=9606 GN=SI PE=1 SV=6 |
| A0A087WT20 | 2 | 1 | 14.5393 | 4.170E-12 | 6.639E-13 | 5.21631 | 1 | P-mT-Susp | mT blank | 68406.7 | DDB1- and CUL4-associated factor 13 OS=Homo sapiens OX=9606 GN=DCAF13 PE=1 SV=1 |
| Q16630;F8WJ | 2 | 1 | 11.0279 | 5.587E-04 | 7.303E-06 | 9.684624 | 0.99804 | mT blank | P-mT-Susp | 59380.96 | Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens OX=9606 GN=CPSF6 PE=1 |
| A0A0D9SF53;A | 2 | 1 | 10.4368 | 1.151E-04 | 1.631E-06 | 2.253103 | 0.99996 | P-0.5PG-mT | P-mT-Susp | 82161.5 | RNA helicase OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Q5JVG8;F5H4 | 2 | 1 | 24.0966 | 4.387E-12 | 6.847E-13 | 3.364447 | 1 | F-mT-2D | P-mT-Susp | 53019.27 | Zinc finger protein 506 OS=Homo sapiens OX=9606 GN=ZNF506 PE=2 SV=2 |
| O75940 | 2 | 1 | 16.7286 | 1.686E-06 | 3.144E-08 | 3.898825 | 1 | P-mT-Susp | mT blank | 26882.23 | Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens OX=9606 GN=SMNDC1 PE=1 SV= |
| A0A2R8YEE0;F | 2 | 1 | 19.1412 | 1.134E-10 | 7.282E-12 | 4.549385 | 1 | P-mT-Susp | mT blank | 117025.3 | Rho family-interacting cell polarization regulator 2 OS=Homo sapiens OX=9606 GN=RIPOR2 PE=1 SV=1 |
| B4DWF2;E7EU | 2 | 1 | 16.0351 | 8.570E-09 | 2.729E-10 | 2.861571 | 1 | F-mT-2D | P-mT-Susp | 61458.48 | Zinc finger protein Helios OS=Homo sapiens OX=9606 GN=IKZF2 PE=1 SV=1 |
| F8WAE6;Q86Y | 2 | 1 | 10.1468 | 3.379E-09 | 1.223E-10 | 2.430294 | 1 | F-mT-2D | mT blank | 206233.1 | Mediator of RNA polymerase II transcription subunit 12-like protein OS=Homo sapiens OX=9606 GN=M |
| F5H0V4;Q9HA | 2 | 1 | 24.9194 | 8.659E-04 | 1.108E-05 | 4.007637 | 0.9955 | mT blank | P-mT-Susp | 33714.43 | MLX-interacting protein (Fragment) OS=Homo sapiens OX=9606 GN=MLXIP PE=1 SV=1 |
| E5RGK3 | 2 | 1 | 10.5767 | 1.199E-13 | 6.498E-14 | Infinity | 1 | F-mT-2D | mT blank | 15629.81 | Zinc finger homeobox protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=ZFHX4 PE=1 SV=1 |
| G5E9C8;Q078 | 2 | 1 | 11.0758 | 6.172E-06 | 1.066E-07 | 8.223192 | 1 | mT blank | P-mT-Susp | 151827 | Son of sevenless homolog 1 OS=Homo sapiens OX=9606 GN=SOS1 PE=1 SV=1 |
| O75298;Q7RT | 2 | 1 | 21.3968 | 3.426E-11 | 3.030E-12 | 2.861794 | 1 | F-mT-2D | F-0.5PG-mT | 59492 | Reticulon-2 OS=Homo sapiens OX=9606 GN=RTN2 PE=1 SV=1 |
| Q6P9F0;F5H0 | 2 | 1 | 23.259 | 1.633E-02 | 1.868E-04 | 4.44537 | 0.8329 | mT blank | P-mT-Susp | 78945.74 | Coiled-coil domain-containing protein 62 OS=Homo sapiens OX=9606 GN=CCDC62 PE=1 SV=2 |
| E5RIH3 | 2 | 1 | 18.9581 | 2.275E-04 | 3.122E-06 | 3.484119 | 0.99974 | F-0.5PG-mT | P-mT-Susp | 15731.65 | PH and SEC7 domain-containing protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=PSD3 PE=1 SV= |
| P17844;A0A7 | 2 | 1 | 16.8911 | 1.631E-07 | 3.627E-09 | 3.262371 | 1 | P-mT-Susp | mT blank | 69661.45 | Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1 |
| G3V2J8;P079 | 2 | 1 | 10.8158 | 4.060E-04 | 5.386E-06 | 3.477239 | 0.999 | P-0.5PG-mT | F-mT-2D | 20151.65 | Heat shock protein HSP 90-alpha (Fragment) OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=1 |
| E7ET87;E7EVI | 2 | 1 | 11.9898 | 5.692E-12 | 7.714E-13 | 2.809316 | 1 | P-mT-Susp | mT blank | 67613.11 | Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=1 |
| E5RFM9;A0AV | 2 | 1 | 19.3174 | 3.503E-11 | 3.065E-12 | 4.532627 | 1 | P-mT-Susp | mT blank | 59946.72 | Transforming acidic coiled-coil-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TACC |
| Q9NV72 | 2 | 1 | 11.2493 | 6.960E-06 | 1.184E-07 | 1.904315 | 1 | F-0.5PG-mT | F-mT-2D | 62271.81 | Zinc finger protein 701 OS=Homo sapiens OX=9606 GN=ZNF701 PE=1 SV=3 |
| P19013 | 2 | 1 | 25.8555 | 1.465E-05 | 2.371E-07 | 2.992272 | 1 | P-mT-Susp | mT blank | 56543.31 | Keratin_ type II cytoskeletal 4 OS=Homo sapiens OX=9606 GN=KRT4 PE=1 SV=5 |
| P08729 | 2 | 1 | 25.6374 | 7.417E-05 | 1.083E-06 | 2.008297 | 0.99999 | mT blank | P-mT-Susp | 51442.77 | Keratin_ type II cytoskeletal 7 OS=Homo sapiens OX=9606 GN=KRT7 PE=1 SV=5 |
| Q5RHP9 | 2 | 1 | 14.369 | 5.545E-09 | 1.839E-10 | 2.261958 | 1 | P-mT-Susp | F-mT-2D | 169150.5 | Glutamate-rich protein 3 OS=Homo sapiens OX=9606 GN=ERICH3 PE=1 SV=1 |
| P29074 | 2 | 1 | 10.2536 | 6.575E-06 | 1.128E-07 | 4.204008 | 1 | F-0.5PG-mT | F-mT-2D | 106994.7 | Tyrosine-protein phosphatase non-receptor type 4 OS=Homo sapiens OX=9606 GN=PTPN4 PE=1 SV=1 |
| O60341;R4GM | 2 | 1 | 11.2685 | 6.478E-05 | 9.621E-07 | Infinity | 0.99999 | P-mT-Susp | F-0.5PG-mT | 93416.01 | Lysine-specific histone demethylase 1A OS=Homo sapiens OX=9606 GN=KDM1A PE=1 SV=2 |
| E7ESJ3;Q9UPS | 2 | 1 | 9.4025 | 1.772E-04 | 2.461E-06 | 1.590261 | 0.99987 | P-0.5PG-mT | P-mT-Susp | 197521.5 | Ankyrin repeat domain-containing protein 26 OS=Homo sapiens OX=9606 GN=ANKRD26 PE=1 SV=2 |
| O15234 | 1 | 1 | 10.9942 | 1.116E-08 | 3.403E-10 | 3.028742 | 1 | P-mT-Susp | F-mT-2D | 76392.13 | Protein CASC3 OS=Homo sapiens OX=9606 GN=CASC3 PE=1 SV=2 |
| G3V287;G3V2 | 1 | 1 | 7.0506 | 1.174E-03 | 1.479E-05 | 1.499091 | 0.9924 | F-0.5PG-mT | P-mT-Susp | 9420.891 | Spermatogenesis-associated protein 7 OS=Homo sapiens OX=9606 GN=SPATA7 PE=1 SV=1 |
| O14494 | 1 | 1 | 12.1344 | 1.372E-13 | 6.498E-14 | 3.668895 | 1 | P-0.5PG-mT | P-mT-Susp | 32555.31 | Phospholipid phosphatase 1 OS=Homo sapiens OX=9606 GN=PLPP1 PE=1 SV=1 |
| A0A0A0MT47 | 1 | 1 | 6.2479 | 2.525E-13 | 9.570E-14 | 12.29514 | 1 | P-mT-Susp | P-0.5PG-mT | 36070.83 | M-phase phosphoprotein 8 (Fragment) OS=Homo sapiens OX=9606 GN=MPHOSPH8 PE=1 SV=1 |
| Q9UBZ4 | 1 | 1 | 13.5702 | 5.995E-15 | 9.545E-15 | 13.81745 | 1 | P-mT-Susp | P-0.5PG-mT | 58427.13 | DNA-(apurinic or apyrimidinic site) endonuclease 2 OS=Homo sapiens OX=9606 GN=APEX2 PE=1 SV=1 |
| H0YM42;O436 | 1 | 1 | 13.03 | 1.913E-03 | 2.350E-05 | 2.158788 | 0.98379 | mT blank | F-mT-2D | 18516.18 | Protein regulator of cytokinesis 1 (Fragment) OS=Homo sapiens OX=9606 GN=PRC1 PE=1 SV=1 |
| A6NMQ1 | 1 | 1 | 9.476 | 8.298E-08 | 1.978E-09 | 1.861087 | 1 | P-mT-Susp | F-0.5PG-mT | 168282.5 | DNA polymerase OS=Homo sapiens OX=9606 GN=POLA1 PE=1 SV=1 |
| E9PK01;E9PQ | 1 | 1 | 10.7796 | 3.174E-07 | 6.632E-09 | 1.576374 | 1 | P-0.5PG-mT | mT blank | 28935.33 | Elongation factor 1-delta (Fragment) OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=1 |
| A0A5F9ZHI2;F | 4 | 1 | 33.3302 | 1.124E-06 | 2.156E-08 | 9.344891 | 1 | P-mT-Susp | F-0.5PG-mT | 23568.24 | Adenine DNA glycosylase OS=Homo sapiens OX=9606 GN=MUTYH PE=1 SV=1 |
| A0A087WV57 | 1 | 1 | 10.56 | 2.489E-08 | 6.856E-10 | 1.846022 | 1 | P-mT-Susp | mT blank | 86827.4 | Protein kinase C-binding protein 1 OS=Homo sapiens OX=9606 GN=ZMYND8 PE=1 SV=1 |
| F8VS10;Q86X | 1 | 1 | 12.213 | 1.207E-11 | 1.354E-12 | 3.36726 | 1 | P-0.5PG-mT | F-0.5PG-mT | 32646.7 | Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens OX=9606 GN=SPATS2 PE=1 SV=1 |
| A0A5F9ZHJ9 | 1 | 1 | 9.933 | 6.545E-11 | 4.780E-12 | 2.308793 | 1 | F-mT-2D | F-0.5PG-mT | 23785.21 | Arf-GAP with coiled-coil_ ANK repeat and PH domain-containing protein 2 (Fragment) OS=Homo sapie |
| Q8ND76 | 1 | 1 | 8.9556 | 4.148E-08 | 1.055E-09 | 13.83207 | 1 | P-0.5PG-mT | P-mT-Susp | 39849.94 | Cyclin-Y OS=Homo sapiens OX=9606 GN=CCNY PE=1 SV=2 |
| A0A3B3ITE4 | 1 | 1 | 5.1852 | 1.805E-03 | 2.224E-05 | 3.035649 | 0.98511 | F-0.5PG-mT | P-mT-Susp | 80093.6 | Zinc finger protein 23 OS=Homo sapiens OX=9606 GN=ZNF23 PE=1 SV=1 |
| Q96DT6 | 1 | 1 | 0 | 1.254E-07 | 2.837E-09 | 2.022054 | 1 | P-mT-Susp | mT blank | 53067.77 | Cysteine protease ATG4C OS=Homo sapiens OX=9606 GN=ATG4C PE=1 SV=1 |
| H3BNV0;J3QS | 1 | 1 | 10.1632 | 1.144E-08 | 3.463E-10 | 2.392369 | 1 | P-0.5PG-mT | F-mT-2D | 14624.6 | Leucine-rich repeat-containing protein 36 OS=Homo sapiens OX=9606 GN=LRRC36 PE=1 SV=1 |
| P46977 | 1 | 1 | 5.1346 | 1.192E-03 | 1.500E-05 | 1.78881 | 0.9922 | P-mT-Susp | mT blank | 81157.09 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens OX= |
| A0A096LPK7;A | 1 | 1 | 10.2906 | 1.144E-08 | 3.463E-10 | 2.380112 | 1 | P-0.5PG-mT | F-mT-2D | 50570.65 | Thioredoxin-disulfide reductase OS=Homo sapiens OX=9606 GN=TXNRD2 PE=1 SV=1 |
| A0A2R8Y5K9;A | 1 | 1 | 6.046 | 2.103E-10 | 1.196E-11 | 2.090486 | 1 | P-mT-Susp | mT blank | 168641.8 | GATOR complex protein DEPDC5 (Fragment) OS=Homo sapiens OX=9606 GN=DEPDC5 PE=1 SV=1 |
| A6PVD3;P566 | 1 | 1 | 6.1114 | 2.255E-11 | 2.244E-12 | 3.172981 | 1 | P-mT-Susp | mT blank | 23472.27 | Transcription factor SOX-10 (Fragment) OS=Homo sapiens OX=9606 GN=SOX10 PE=1 SV=1 |
| Q8IXT1 | 1 | 1 | 4.6096 | 0.000E+00 | 0.000E+00 | 144.0393 | 1 | P-mT-Susp | P-0.5PG-mT | 113555.3 | DNA damage-induced apoptosis suppressor protein OS=Homo sapiens OX=9606 GN=DDIAS PE=2 SV=2 |
| Q9P2Y4 | 1 | 1 | 5.2941 | 4.986E-10 | 2.341E-11 | 2.779996 | 1 | P-mT-Susp | mT blank | 77960.86 | Zinc finger protein 219 OS=Homo sapiens OX=9606 GN=ZNF219 PE=1 SV=2 |
| H3BRF9 | 1 | 1 | 5.76 | 6.050E-13 | 1.852E-13 | 2.778769 | 1 | P-mT-Susp | mT blank | 50059.32 | Abscission/NoCut checkpoint regulator OS=Homo sapiens OX=9606 GN=ZFYVE19 PE=1 SV=1 |
| H0Y9P3;K7ELX | 1 | 1 | 10.0724 | 2.602E-07 | 5.524E-09 | 6.899096 | 1 | F-0.5PG-mT | F-mT-2D | 45631.84 | Centrosomal protein of 192 kDa (Fragment) OS=Homo sapiens OX=9606 GN=CEP192 PE=1 SV=1 |
| Q6P988 | 1 | 1 | 11.5868 | 7.080E-10 | 3.184E-11 | 2.354781 | 1 | P-mT-Susp | mT blank | 56668.96 | Palmitoleoyl-protein carboxylesterase NOTUM OS=Homo sapiens OX=9606 GN=NOTUM PE=1 SV=2 |
| I3L3L5 | 1 | 1 | 5.4466 | 1.855E-08 | 5.256E-10 | 2.493999 | 1 | P-mT-Susp | mT blank | 6142.723 | Zinc finger protein 771 OS=Homo sapiens OX=9606 GN=ZNF771 PE=1 SV=1 |
| Q5JX61 | 1 | 1 | 6.9052 | 7.954E-13 | 2.110E-13 | 6.901414 | 1 | P-mT-Susp | P-0.5PG-mT | 24049.01 | Copine-1 (Fragment) OS=Homo sapiens OX=9606 GN=CPNE1 PE=1 SV=1 |
| A0A0C3SFZ9;N | 1 | 1 | 13.6774 | 2.950E-01 | 3.127E-03 | 6.249704 | 0.29609 | P-0.5PG-mT | F-0.5PG-mT | 97646.46 | F-BAR domain only protein 1 OS=Homo sapiens OX=9606 GN=FCHO1 PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| G8JLA2 | 1 | 1 | 8.8532 | 5.079E-03 | 6.034E-05 | 2.571458 | 0.94387 | F-0.5PG-mT | P-mT-Susp | 17260.39 | Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=1 |
| Q6P047 | 1 | 1 | 4.9506 | 1.280E-01 | 1.375E-03 | Infinity | 0.46551 | mT blank | P-mT-Susp | 33963.07 | Uncharacterized protein C8orf74 OS=Homo sapiens OX=9606 GN=C8orf74 PE=1 SV=3 |
| Q96BW9;A0A( | 2 | 1 | 9.7152 | 2.963E-02 | 3.326E-04 | Infinity | 0.74507 | F-mT-2D | mT blank | 51979.36 | Phosphatidate cytidylyltransferase_ mitochondrial OS=Homo sapiens OX=9606 GN=TAMM41 PE=1 SV= |
| A0A2R8Y661 | 7 | 1 | 46.1772 | 1.481E-04 | 2.087E-06 | 3.465738 | 0.99992 | mT blank | P-mT-Susp | 175158 | Cyclic nucleotide ras GEF OS=Homo sapiens OX=9606 GN=RAPGEF2 PE=1 SV=1 |
| P11047 | 2 | 1 | 9.1099 | 6.089E-02 | 6.704E-04 | Infinity | 0.61528 | P-0.5PG-mT | P-mT-Susp | 183305.8 | Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3 |
| B4DXZ6;C9JY2 | 2 | 1 | 11.0917 | 6.322E-02 | 6.950E-04 | 1.570085 | 0.60795 | F-0.5PG-mT | P-mT-Susp | 68669.49 | Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens OX=9606 GN=FXR1 PE=1 S |
| J3KNE0;A6NK | 5 | 1 | 24.7361 | 1.589E-08 | 4.550E-10 | 4.364839 | 1 | P-mT-Susp | mT blank | 198991.2 | RanBP2-like and GRIP domain-containing protein 3 OS=Homo sapiens OX=9606 GN=RGPD3 PE=1 SV=2 |
| Q5H9F3 | 2 | 1 | 11.6482 | 1.343E-14 | 1.748E-14 | Infinity | 1 | F-0.5PG-mT | P-0.5PG-mT | 184351.4 | BCL-6 corepressor-like protein 1 OS=Homo sapiens OX=9606 GN=BCORL1 PE=1 SV=1 |
| Q7Z7K2;C9JAX | 2 | 1 | 11.9154 | 9.175E-05 | 1.318E-06 | 6.037782 | 0.99998 | F-mT-2D | P-mT-Susp | 67006.3 | Zinc finger protein 467 OS=Homo sapiens OX=9606 GN=ZNF467 PE=1 SV=1 |
| Q3KP31 | 2 | 1 | 10.6474 | 3.246E-05 | 4.951E-07 | 1.918599 | 1 | P-mT-Susp | mT blank | 69152.8 | Zinc finger protein 791 OS=Homo sapiens OX=9606 GN=ZNF791 PE=1 SV=1 |
| Q9P0K1 | 2 | 1 | 9.7795 | 6.817E-05 | 1.003E-06 | 12.10318 | 0.99999 | F-mT-2D | P-mT-Susp | 103056.1 | Disintegrin and metalloproteinase domain-containing protein 22 OS=Homo sapiens OX=9606 GN=ADA |
| A0A286YES2;F | 5 | 1 | 28.6723 | 8.026E-11 | 5.756E-12 | 3.364109 | 1 | P-mT-Susp | mT blank | 198801.5 | RANBP2-like and GRIP domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RGPD1 PE=4 SV=1 |
| E7EPB6;P1356 | 2 | 0 | 14.6486 | | | | | --- | --- | 164381 | Cystic fibrosis transmembrane conductance regulator (Fragment) OS=Homo sapiens OX=9606 GN=CFT |
| E7EVH7;F8W6 | 1 | 0 | 5.0761 | | | | | --- | --- | 83223.87 | Kinesin light chain OS=Homo sapiens OX=9606 PE=3 SV=2 |
| C9JTV7;Q8N5 | 1 | 0 | 6.9038 | | | | | --- | --- | 22261.67 | Ephexin-1 (Fragment) OS=Homo sapiens OX=9606 GN=NGEF PE=1 SV=1 |
| E9PRL4;Q141 | 1 | 0 | 11.094 | | | | | --- | --- | 37536.04 | Tripartite motif-containing protein 29 OS=Homo sapiens OX=9606 GN=TRIM29 PE=1 SV=1 |
| A0A3B3IRS5;A | 1 | 0 | 8.6998 | | | | | --- | --- | 75573.8 | Forkhead box P1_ isoform CRA_g OS=Homo sapiens OX=9606 GN=FOXP1 PE=1 SV=1 |
| A0A0G2JNE3;A | 1 | 0 | 11.4488 | | | | | --- | --- | 44383.03 | Killer cell immunoglobulin-like receptor 2DS4 OS=Homo sapiens OX=9606 GN=KIR2DS4 PE=4 SV=1 |
| E5RI93;E5RG7 | 3 | 0 | 15.1927 | | | | | --- | --- | 186175.5 | Zinc finger homeobox protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=ZFHX4 PE=1 SV=2 |
| Q13342 | 1 | 0 | 4.958 | | | | | --- | --- | 100333.3 | Nuclear body protein SP140 OS=Homo sapiens OX=9606 GN=SP140 PE=1 SV=2 |
| O60895 | 1 | 0 | 5.5968 | | | | | --- | --- | 19892.84 | Receptor activity-modifying protein 2 OS=Homo sapiens OX=9606 GN=RAMP2 PE=1 SV=2 |
| A0A590UJ53;( | 1 | 0 | 11.3612 | | | | | --- | --- | 96550.05 | KAT8 regulatory NSL complex subunit 3 OS=Homo sapiens OX=9606 GN=KANSL3 PE=1 SV=1 |
| A0A3B3ITF1 | 2 | 0 | 16.7964 | | | | | --- | --- | 114495.9 | Disks large homolog 2 OS=Homo sapiens OX=9606 GN=DLG2 PE=1 SV=1 |
| Q15583 | 1 | 0 | 12.3446 | | | | | --- | --- | 43525.98 | Homeobox protein TGIF1 OS=Homo sapiens OX=9606 GN=TGIF1 PE=1 SV=3 |
| Q9NX65 | 1 | 0 | 5.1995 | | | | | --- | --- | 80153.88 | Zinc finger and SCAN domain-containing protein 32 OS=Homo sapiens OX=9606 GN=ZSCAN32 PE=1 SV |
| H0Y306 | 1 | 0 | 6.3094 | | | | | --- | --- | 20522.87 | Histone-lysine N-methyltransferase SUV39H2 (Fragment) OS=Homo sapiens OX=9606 GN=SUV39H2 PE |
| B0QYR0;B0QY | 1 | 0 | 4.8636 | | | | | --- | --- | 11045.83 | BTB/POZ domain-containing protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=BTBD3 PE=1 SV=8 |
| A0A0A0MRU9 | 1 | 0 | 12.6788 | | | | | --- | --- | 82430.51 | Non-specific serine/threonine protein kinase OS=Homo sapiens OX=9606 GN=MARK2 PE=1 SV=1 |
| H7BZ66;Q037 | 1 | 0 | 9.993 | | | | | --- | --- | 69617.97 | Potassium voltage-gated channel subfamily C member 4 OS=Homo sapiens OX=9606 GN=KCNC4 PE=1 |
| G3V2R5;G3V5 | 1 | 0 | 6.2407 | | | | | --- | --- | 14549.91 | Myc-associated factor X OS=Homo sapiens OX=9606 GN=MAX PE=1 SV=1 |
| B5MCC0;Q8W | 1 | 0 | 5.1009 | | | | | --- | --- | 21717.93 | Peroxynitrite isomerase THAP4 OS=Homo sapiens OX=9606 GN=THAP4 PE=1 SV=1 |
| Q9NTI5 | 2 | 0 | 22.946 | | | | | --- | --- | 165922.1 | Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens OX=9606 GN=PDS5B PE=1 SV=1 |
| A0A0J9YWD6; | 1 | 0 | 11.6134 | | | | | --- | --- | 18043.38 | Deformed epidermal autoregulatory factor 1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=DE |
| E7EQT4;G3V3 | 1 | 0 | 5.375 | | | | | --- | --- | 147761.9 | Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 |
| A0A0A0MSA4 | 4 | 0 | 16.3247 | | | | | --- | --- | 116452.1 | Band 4.1-like protein 3 OS=Homo sapiens OX=9606 GN=EPB41L3 PE=1 SV=1 |
| B7Z6K7 | 1 | 0 | 4.9241 | | | | | --- | --- | 100645.1 | Zinc finger protein 814 OS=Homo sapiens OX=9606 GN=ZNF814 PE=1 SV=2 |
| K7EJ76 | 1 | 0 | 12.9092 | | | | | --- | --- | 35369.03 | Putative Polycomb group protein ASXL3 OS=Homo sapiens OX=9606 GN=ASXL3 PE=1 SV=1 |
| A0A5F9ZHX9;A | 1 | 0 | 14.315 | | | | | --- | --- | 44916.79 | DNA polymerase subunit gamma-2_ mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=POLG2 |
| Q9P1V8 | 1 | 0 | 5.2087 | | | | | --- | --- | 77378.9 | Sterile alpha motif domain-containing protein 15 OS=Homo sapiens OX=9606 GN=SAMD15 PE=2 SV=1 |
| Q6NX45 | 1 | 0 | 5.4344 | | | | | --- | --- | 56721.37 | Zinc finger protein 774 OS=Homo sapiens OX=9606 GN=ZNF774 PE=1 SV=2 |
| A0A0C4DGA7; | 1 | 0 | 10.0712 | | | | | --- | --- | 75878.59 | Actin-binding LIM protein 3 OS=Homo sapiens OX=9606 GN=ABLIM3 PE=1 SV=1 |
| E9PGI0;Q6UW | 1 | 0 | 6.4302 | | | | | --- | --- | 45244.2 | Arylsulfatase K OS=Homo sapiens OX=9606 GN=ARSK PE=1 SV=1 |
| A0A6Q8PFA6; | 1 | 0 | 5.3158 | | | | | --- | --- | 78726.87 | Kinesin-like protein OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=1 |
| A0A0D9SF71 | 1 | 0 | 10.463 | | | | | --- | --- | 4868.59 | Zinc finger E-box-binding homeobox 2 OS=Homo sapiens OX=9606 GN=ZEB2 PE=4 SV=1 |
| P36888 | 1 | 0 | 13.5716 | | | | | --- | --- | 114785.6 | Receptor-type tyrosine-protein kinase FLT3 OS=Homo sapiens OX=9606 GN=FLT3 PE=1 SV=2 |
| O15440 | 1 | 0 | 11.3194 | | | | | --- | --- | 161744.2 | Multidrug resistance-associated protein 5 OS=Homo sapiens OX=9606 GN=ABCC5 PE=1 SV=2 |
| Q02818 | 1 | 0 | 5.1311 | | | | | --- | --- | 53879.39 | Nucleobindin-1 OS=Homo sapiens OX=9606 GN=NUCB1 PE=1 SV=4 |
| A0A182DWI3; | 1 | 0 | 6.4518 | | | | | --- | --- | 62948.53 | Thioredoxin-disulfide reductase OS=Homo sapiens OX=9606 GN=TXNRD1 PE=1 SV=1 |
| O14576 | 1 | 0 | 10.3944 | | | | | --- | --- | 73468.73 | Cytoplasmic dynein 1 intermediate chain 1 OS=Homo sapiens OX=9606 GN=DYNC1I1 PE=1 SV=2 |
| A0A494C1C7;A | 1 | 0 | 5.8607 | | | | | --- | --- | 26528.27 | Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| F8W910 | 1 | 0 | 12.4108 | | | | | --- | --- | 16607.52 | RNA-binding protein 5 (Fragment) OS=Homo sapiens OX=9606 GN=RBM5 PE=1 SV=8 |
| F2Z2D4 | 1 | 0 | 11.8454 | | | | | --- | --- | 23587.68 | Patatin-like phospholipase domain-containing protein 7 OS=Homo sapiens OX=9606 GN=PNPLA7 PE=1 |
| H7C508 | 1 | 0 | 7.061 | | | | | --- | --- | 6792.365 | Short transient receptor potential channel 1 (Fragment) OS=Homo sapiens OX=9606 GN=TRPC1 PE=4 S |
| B5ME80;F8WA | 1 | 0 | 11.926 | | | | | --- | --- | 122223.6 | Semaphorin-5B (Fragment) OS=Homo sapiens OX=9606 GN=SEMA5B PE=1 SV=2 |
| A0A0G2JMX7; | 2 | 0 | 21.8002 | | | | | --- | --- | 81143.03 | Microtubule-associated protein OS=Homo sapiens OX=9606 GN=MAPT PE=1 SV=1 |
| P09769;Q5TG | 1 | 0 | 5.4961 | | | | | --- | --- | 60106.03 | Tyrosine-protein kinase Fgr OS=Homo sapiens OX=9606 GN=FGR PE=1 SV=2 |
| A0A0D9SFY2;F | 1 | 0 | 13.4076 | | | | | --- | --- | 28165.11 | Secretin receptor (Fragment) OS=Homo sapiens OX=9606 GN=SCTR PE=4 SV=1 |
| E9PLT4 | 4 | 0 | 27.884 | | | | | --- | --- | 6501.273 | Adenine DNA glycosylase OS=Homo sapiens OX=9606 GN=MUTYH PE=4 SV=1 |
| Q9NS91 | 1 | 0 | 9.7102 | | | | | --- | --- | 57078.15 | E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens OX=9606 GN=RAD18 PE=1 SV=2 |
| C9J6T3 | 1 | 0 | 12.4258 | | | | | --- | --- | 8511.772 | Zinc finger protein ZIC 4 (Fragment) OS=Homo sapiens OX=9606 GN=ZIC4 PE=4 SV=1 |
| H7BXL6 | 1 | 0 | 10.8518 | | | | | --- | --- | 89532.7 | Otogelin-like protein (Fragment) OS=Homo sapiens OX=9606 GN=OTOGL PE=1 SV=1 |
| Q5VYS8 | 1 | 0 | 3.6274 | | | | | --- | --- | 173396.5 | Terminal uridylyltransferase 7 OS=Homo sapiens OX=9606 GN=TUT7 PE=1 SV=1 |
| A0A2R8Y4P5 | 1 | 0 | 11.5638 | | | | | --- | --- | 14413.38 | Required for meiotic nuclear division protein 1 homolog (Fragment) OS=Homo sapiens OX=9606 GN=R |
| A0A3B3IRU6;A | 2 | 0 | 9.7836 | | | | | --- | --- | 164828.7 | Paternally-expressed gene 3 protein OS=Homo sapiens OX=9606 GN=PEG3 PE=1 SV=1 |
| Q9C0B2 | 1 | 0 | 4.7616 | | | | | --- | --- | 179957.7 | Cilia- and flagella-associated protein 74 OS=Homo sapiens OX=9606 GN=CFAP74 PE=2 SV=3 |
| H0YBJ5 | 1 | 0 | 23.2041 | | | | | --- | --- | 6289.843 | La-related protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=LARP1 PE=1 SV=1 |
| D6RCM2;D6R | 1 | 0 | 5.7524 | | | | | --- | --- | 12877.01 | 28S ribosomal protein S18c_ mitochondrial OS=Homo sapiens OX=9606 GN=MRPS18C PE=1 SV=1 |
| F8VWZ5 | 1 | 0 | 15.463 | | | | | --- | --- | 16980.93 | H2.0-like homeobox protein (Fragment) OS=Homo sapiens OX=9606 GN=HLX PE=1 SV=1 |
| A0A0A0MR47 | 1 | 0 | 5.9138 | | | | | --- | --- | 70434.5 | Neurotrophin receptor-interacting factor homolog OS=Homo sapiens OX=9606 GN=ZNF274 PE=1 SV=1 |
| O94830 | 1 | 0 | 10.2118 | | | | | --- | --- | 81716.26 | Phospholipase DDHD2 OS=Homo sapiens OX=9606 GN=DDHD2 PE=1 SV=2 |
| A0A3B3ITZ5 | 1 | 0 | 6.9506 | | | | | --- | --- | 161873.6 | DBF4-type zinc finger-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=ZDBF2 PE=1 SV |
| B1ANB7;Q8TD | 1 | 0 | 7.5441 | | | | | --- | --- | 37756.14 | Mucolipin 3_ isoform CRA_d OS=Homo sapiens OX=9606 GN=MCOLN3 PE=1 SV=1 |
| Q8TF46;E9PI2 | 3 | 0 | 25.479 | | | | | --- | --- | 122270.3 | DIS3-like exonuclease 1 OS=Homo sapiens OX=9606 GN=DIS3L PE=1 SV=2 |
| H7C224 | 1 | 0 | 12.5966 | | | | | --- | --- | 42738.85 | Interleukin-1 receptor-associated kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=IRAK1 PE=1 SV= |
| A0A0A0MQX1 | 1 | 0 | 10.1988 | | | | | --- | --- | 240513.4 | Unconventional myosin-X OS=Homo sapiens OX=9606 GN=MYO10 PE=1 SV=1 |
| H7C146 | 1 | 0 | 13.7904 | | | | | --- | --- | 7552.551 | Microtubule-associated serine/threonine-protein kinase 4 (Fragment) OS=Homo sapiens OX=9606 GN= |
| A1A519;A2VC | 1 | 0 | 10.8358 | | | | | --- | --- | 37728.29 | Protein FAM170A OS=Homo sapiens OX=9606 GN=FAM170A PE=2 SV=1 |
| Q6PDB4 | 1 | 0 | 11.0932 | | | | | --- | --- | 68701.03 | Zinc finger protein 880 OS=Homo sapiens OX=9606 GN=ZNF880 PE=2 SV=2 |
| F5H0Y6;F5H6V | 1 | 0 | 12.5724 | | | | | --- | --- | 13890.18 | NXPE family member 1 (Fragment) OS=Homo sapiens OX=9606 GN=NXPE1 PE=1 SV=8 |
| A0A0U1RRM8 | 1 | 0 | 10.6626 | | | | | --- | --- | 62367.34 | Fermitin family homolog 2 (Fragment) OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1 |
| F5H6S5;Q9NZ | 1 | 0 | 5.4768 | | | | | --- | --- | 21242.83 | Complement C1r subcomponent-like protein (Fragment) OS=Homo sapiens OX=9606 GN=C1RL PE=1 S |
| A0A1B0GTW6 | 7 | 0 | 43.7704 | | | | | --- | --- | 175840.1 | Band 4.1-like protein 1 OS=Homo sapiens OX=9606 GN=EPB41L1 PE=1 SV=2 |
| C9JZI2 | 1 | 0 | 7.4113 | | | | | --- | --- | 11637.39 | Septin-2 (Fragment) OS=Homo sapiens OX=9606 GN=SEPTIN2 PE=1 SV=1 |
| Q5JPF3 | 2 | 0 | 9.0724 | | | | | --- | --- | 201516.2 | Ankyrin repeat domain-containing protein 36C OS=Homo sapiens OX=9606 GN=ANKRD36C PE=1 SV=3 |
| Q969X5 | 2 | 0 | 11.2683 | | | | | --- | --- | 32991.54 | Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens OX=9606 GN=ER |
| C9K0V9;F8WD | 1 | 0 | 6.7501 | | | | | --- | --- | 78816.97 | Ataxin-7-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ATXN7L1 PE=1 SV=1 |
| P98082;D6RFF | 3 | 0 | 26.0682 | | | | | --- | --- | 82562.04 | Disabled homolog 2 OS=Homo sapiens OX=9606 GN=DAB2 PE=1 SV=3 |
| A0A0G2JLQ8;A | 2 | 0 | 7.8626 | | | | | --- | --- | 101545.3 | NACHT_ LRR and PYD domains-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=NLRP |
| A0A6Q8PGC2; | 3 | 0 | 20.7142 | | | | | --- | --- | 69410.4 | Phosphatase and actin regulator OS=Homo sapiens OX=9606 GN=PHACTR1 PE=1 SV=1 |
| A0A1B0GVP4 | 1 | 0 | 4.7772 | | | | | --- | --- | 214110.6 | Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens OX=9606 GN=LCORL PE |
| A0A087WZY0; | 1 | 0 | 4.6234 | | | | | --- | --- | 22060.09 | Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens OX=9606 GN=CLN5 PE=1 SV=3 |
| P35612 | 1 | 0 | 10.4874 | | | | | --- | --- | 81310.58 | Beta-adducin OS=Homo sapiens OX=9606 GN=ADD2 PE=1 SV=3 |
| A0A7I2V2X6;A | 1 | 0 | 13.314 | | | | | --- | --- | 57929.96 | 60 kDa chaperonin OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=1 |
| E5RGD1 | 1 | 0 | 11.555 | | | | | --- | --- | 25278.93 | Androglobin OS=Homo sapiens OX=9606 GN=ADGB PE=1 SV=1 |
| Q9GZU2 | 2 | 0 | 10.8183 | | | | | --- | --- | 183051.6 | Paternally-expressed gene 3 protein OS=Homo sapiens OX=9606 GN=PEG3 PE=1 SV=1 |
| B3KNX7;Q131 | 1 | 0 | 5.1283 | | | | | --- | --- | 58488.23 | Non-specific serine/threonine protein kinase OS=Homo sapiens OX=9606 GN=PAK1 PE=1 SV=1 |
| C9IZE3;C9JVX0 | 3 | 0 | 18.6038 | | | | | --- | --- | 20197.77 | Zinc finger protein 808 (Fragment) OS=Homo sapiens OX=9606 GN=ZNF808 PE=1 SV=1 |
| Q8IYE0 | 3 | 0 | 15.6666 | | | | | --- | --- | 113205.9 | Coiled-coil domain-containing protein 146 OS=Homo sapiens OX=9606 GN=CCDC146 PE=1 SV=2 |
| O15063 | 1 | 0 | 9.2082 | | | | | --- | --- | 117274.5 | Granule associated Rac and RHOG effector protein 1 OS=Homo sapiens OX=9606 GN=GARRE1 PE=1 SV |
| A0A3B3ITK0;A | 1 | 0 | 12.3456 | | | | | --- | --- | 134458.8 | Thrombospondin-2 OS=Homo sapiens OX=9606 GN=THBS2 PE=1 SV=1 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Q9Y6A1 | 1 | 0 | 6.1241 | | | | | --- | --- | 85736.22 | Protein O-mannosyl-transferase 1 OS=Homo sapiens OX=9606 GN=POMT1 PE=1 SV=3 |
| E9PE72;P2241 | 1 | 0 | 5.3894 | | | | | --- | --- | 43443.76 | Ectonucleotide pyrophosphatase/phosphodiesterase family member 1 OS=Homo sapiens OX=9606 GN |
| G3V5M4 | 1 | 0 | 5.5842 | | | | | --- | --- | 14095.27 | Alpha-actinin-1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1 |
| E5RGZ2;H0YK | 1 | 0 | 4.5444 | | | | | --- | --- | 43880.51 | Homeobox-containing protein 1 OS=Homo sapiens OX=9606 GN=HMBOX1 PE=1 SV=1 |
| D6R938;E9PB | 1 | 0 | 8.7774 | | | | | --- | --- | 56925.72 | Calcium/calmodulin-dependent protein kinase OS=Homo sapiens OX=9606 GN=CAMK2D PE=1 SV=1 |
| A0A4W8VX11 | 2 | 0 | 8.7388 | | | | | --- | --- | 211501.6 | Pericentriolar material 1 protein OS=Homo sapiens OX=9606 GN=PCM1 PE=4 SV=1 |
| Q96NG3;A0A0 | 2 | 0 | 9.5043 | | | | | --- | --- | 77054.62 | Outer dynein arm-docking complex subunit 4 OS=Homo sapiens OX=9606 GN=ODAD4 PE=1 SV=2 |
| D3DQV9;H0Y3 | 1 | 0 | 4.9958 | | | | | --- | --- | 102843.3 | Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G2 |
| C9JRQ0 | 1 | 0 | 6.4391 | | | | | --- | --- | 15922.68 | Suppressor of tumorigenicity 7 protein (Fragment) OS=Homo sapiens OX=9606 GN=ST7 PE=1 SV=1 |
| F5H3E8;P5779 | 1 | 0 | 12.8456 | | | | | --- | --- | 13408.82 | Calcium-binding protein 4 OS=Homo sapiens OX=9606 GN=CABP4 PE=1 SV=1 |
| Q96FN4 | 2 | 0 | 8.8732 | | | | | --- | --- | 61874.28 | Copine-2 OS=Homo sapiens OX=9606 GN=CPNE2 PE=1 SV=3 |
| E9PJ80;E9PKX | 1 | 0 | 6.7749 | | | | | --- | --- | 4724.853 | Oxysterol-binding protein-related protein 9 OS=Homo sapiens OX=9606 GN=OSBPL9 PE=1 SV=1 |
| A0A0G2JRY5;( | 1 | 0 | 5.0522 | | | | | --- | --- | 50465.44 | Transcription initiation factor TFIID subunit 4 (Fragment) OS=Homo sapiens OX=9606 GN=TAF4 PE=1 S |
| Q9NZV7 | 1 | 0 | 5.2598 | | | | | --- | --- | 62304.42 | Zinc finger imprinted 2 OS=Homo sapiens OX=9606 GN=ZIM2 PE=1 SV=1 |
| P24723 | 1 | 0 | 8.9822 | | | | | --- | --- | 79197.27 | Protein kinase C eta type OS=Homo sapiens OX=9606 GN=PRKCH PE=1 SV=4 |
| Q96SK3 | 1 | 0 | 9.784 | | | | | --- | --- | 83129.89 | Zinc finger protein 607 OS=Homo sapiens OX=9606 GN=ZNF607 PE=1 SV=3 |
| I3L2H4 | 1 | 0 | 12.1224 | | | | | --- | --- | 7836.641 | Hepatocyte growth factor-regulated tyrosine kinase substrate (Fragment) OS=Homo sapiens OX=9606 |
| E9PQS1;Q9H0 | 1 | 0 | 4.8474 | | | | | --- | --- | 26789.9 | Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1 |
| D7R525;E5RJ5 | 1 | 0 | 12.8912 | | | | | --- | --- | 24960.04 | Mitogen-activated protein kinase OS=Homo sapiens OX=9606 GN=MAPK9 PE=1 SV=1 |