|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table S4-1. KEGG enrichment analysis of PAH-related genes. | | | | |  |  |  |  |
| ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue | geneID | Count |
| hsa03013 | Nucleocytoplasmic transport | 35/1143 | 108/8644 | 1.87E-07 | 6.09E-05 | 5.31E-05 | 7514/11260/25909/1434/9775/51194/3843/10527/10526/3836/3838/3839/3840/3837/4686/22916/51068/57122/55746/9972/9631/23165/4927/55916/51808/5411/5903/9984/57187/3842/7175/26019/65109/64328/57510 | 35 |
| hsa04110 | Cell cycle | 43/1143 | 157/8644 | 1.52E-06 | 0.000247552 | 0.000215819 | 699/701/890/9133/990/983/1111/157570/26271/3066/4085/4172/4175/27085/10403/90381/7272/64682/472/545/546/9134/902/996/8454/10926/114799/4193/25836/23595/5000/23244/23047/5515/5591/5885/5925/5934/8243/9126/10274/10735/7529 | 43 |
| hsa04621 | NOD-like receptor signaling pathway | 45/1143 | 186/8644 | 2.99E-05 | 0.003246404 | 0.002830252 | 9447/329/330/79184/834/837/838/1147/1536/10059/2633/2634/2635/115362/3320/3326/3428/3454/3606/51135/3708/3709/3716/6885/5602/55669/4671/58484/114548/24145/5586/23236/5332/8737/8767/6041/6772/23118/257397/10010/29110/7099/7158/7188/54822 | 45 |
| hsa04141 | Protein processing in endoplasmic reticulum | 41/1143 | 170/8644 | 7.19E-05 | 0.005861737 | 0.005110329 | 6745/7993/22926/821/8454/3301/54431/5611/80267/9451/1965/3320/3326/7184/22824/3309/3312/10808/3998/10905/5602/4780/2923/10130/9373/6185/51128/10484/10483/9871/22872/7095/11231/6400/6747/201595/23190/56886/55757/7415/55432 | 41 |
| hsa05134 | Legionellosis | 18/1143 | 56/8644 | 0.000199081 | 0.012948069 | 0.011288275 | 718/834/836/57396/1378/1379/54205/10767/3312/3329/3606/4671/58484/5861/51128/7097/7099/7415 | 18 |
| hsa05132 | Salmonella infection | 53/1143 | 249/8644 | 0.000238308 | 0.012948069 | 0.011288275 | 64746/10097/10096/329/330/834/836/837/838/1147/1434/1499/54205/51164/1778/79659/55770/60412/10640/9648/3320/3326/7184/3606/51135/3799/3836/3839/3840/6885/5602/4646/4671/10787/3071/58484/114548/5286/5289/5290/5291/5294/5788/8737/8767/9475/51429/23118/257397/7097/7099/10333/27072 | 53 |
| hsa01524 | Platinum drug resistance | 21/1143 | 73/8644 | 0.000346194 | 0.016122754 | 0.014056001 | 672/4436/7153/472/538/329/330/836/54205/355/4193/4292/4437/2956/5290/5291/5295/8503/5980/1317/7155 | 21 |
| hsa05169 | Epstein-Barr virus infection | 44/1143 | 202/8644 | 0.000468463 | 0.018210724 | 0.015876318 | 890/3066/695/836/9134/1147/9541/54205/5610/953/355/3454/51135/3716/4067/6885/5602/4193/4734/2923/5290/5291/5295/8503/51426/5700/5701/5706/5707/5718/10213/5708/9861/5713/5925/3516/8737/22938/6772/23118/29110/7097/7188/7874 | 44 |
| hsa03440 | Homologous recombination | 14/1143 | 41/8644 | 0.00050275 | 0.018210724 | 0.015876318 | 641/672/675/83990/25788/7516/472/79184/4683/79728/10714/10111/5932/11073 | 14 |
| hsa05417 | Lipid and atherosclerosis | 45/1143 | 215/8644 | 0.000993889 | 0.032400785 | 0.028247375 | 19/22926/834/836/948/1147/1536/54205/9451/1965/355/3320/3326/7184/3308/3309/3312/3329/3606/51135/3708/3717/3845/4067/6885/5602/4312/4780/114548/5290/5291/5295/8503/23236/5332/5468/9475/23118/10010/29110/7097/7099/10333/7412/7436 | 45 |
| hsa03460 | Fanconi anemia pathway | 16/1143 | 54/8644 | 0.001205802 | 0.035735592 | 0.031154697 | 641/672/675/83990/2177/55215/545/2072/57697/4292/79728/51426/51455/5980/7398/57599 | 16 |
| hsa05017 | Spinocerebellar ataxia | 32/1143 | 143/8644 | 0.001673984 | 0.043065942 | 0.037545381 | 5685/488/8678/54205/3708/3709/5602/10528/4976/5289/5290/5291/5295/8503/30849/23236/5332/5684/5700/5701/5706/5707/5718/10213/5708/9861/5713/23369/9821/3516/6095/7436 | 32 |
| hsa03430 | Mismatch repair | 9/1143 | 23/8644 | 0.001717354 | 0.043065942 | 0.037545381 | 4436/5983/5984/4292/27030/4437/2956/10714/5981 | 9 |
| hsa01212 | Fatty acid metabolism | 16/1143 | 57/8644 | 0.002253063 | 0.052464187 | 0.045738878 | 79071/31/33/34/36/38/39/2180/2181/2182/54898/79993/3030/3295/5538/6342 | 16 |
| hsa04140 | Autophagy - animal | 35/1143 | 165/8644 | 0.002742901 | 0.059612378 | 0.051970753 | 55255/64422/115201/8678/57448/203228/1514/9451/440275/1965/3091/3146/3708/3845/6885/5602/9110/5289/5290/5291/5295/8503/30849/5515/5567/5861/9821/51100/55014/55578/10010/8887/29110/27072/23001 | 35 |
| hsa05222 | Small cell lung cancer | 22/1143 | 92/8644 | 0.00361532 | 0.07366214 | 0.064219496 | 329/330/836/9134/1147/54205/3673/3655/3685/3688/3908/3910/3912/3915/5290/5291/5295/8503/51426/5743/5925/7188 | 22 |
| hsa05205 | Proteoglycans in cancer | 41/1143 | 205/8644 | 0.003912415 | 0.075026306 | 0.065408792 | 287/288/23365/836/1499/1514/1655/1975/2066/7430/355/10818/3082/3091/3479/8826/3673/3685/3688/3690/3708/3709/3845/4193/4233/27250/5290/5291/5295/8503/4659/4660/5567/5781/5962/6093/9475/6654/6655/7097/7099 | 41 |
| hsa04510 | Focal adhesion | 40/1143 | 203/8644 | 0.00566234 | 0.091598593 | 0.0798567 | 329/330/1293/1499/1950/2321/3082/3479/3673/3676/3655/3685/3688/3690/3694/3696/3908/3910/3912/3915/5602/4233/56034/80310/5156/5290/5291/5295/8503/8395/4659/4660/6093/9475/6654/6655/6696/7058/3371/7414 | 40 |
| hsa05412 | Arrhythmogenic right ventricular cardiomyopathy | 20/1143 | 84/8644 | 0.005669811 | 0.091598593 | 0.0798567 | 488/781/1000/1495/1499/1756/1824/1829/1832/3673/3676/3655/3685/3688/3690/3694/3696/3908/5318/6262 | 20 |
| hsa00562 | Inositol phosphate metabolism | 18/1143 | 73/8644 | 0.005748706 | 0.091598593 | 0.0798567 | 9896/3612/8821/4534/8898/9110/9107/5286/5289/5290/5291/5294/200576/8395/23236/5332/23007/22908 | 18 |
| hsa05165 | Human papillomavirus infection | 60/1143 | 331/8644 | 0.006028215 | 0.091598593 | 0.0798567 | 890/3066/324/472/523/526/528/51382/545/836/9134/1108/1147/1293/1499/1739/1740/1950/5610/355/3454/3673/3676/3655/3685/3688/3690/3694/3696/3716/3845/3908/3910/3912/3915/4193/4799/5290/5291/5295/8503/5515/5523/55012/5567/5584/5700/5743/5925/5934/3516/6654/6655/6696/6772/29110/7058/7098/3371/23352 | 60 |
| hsa05130 | Pathogenic Escherichia coli infection | 39/1143 | 198/8644 | 0.006285211 | 0.091598593 | 0.0798567 | 10061/10097/10096/23365/834/836/837/1147/9076/54205/7430/355/3606/3554/51135/3688/6885/5602/4430/4643/4644/55930/4646/4671/4690/10787/3071/4691/114548/5781/5861/8737/6093/9475/9871/23118/257397/7082/7099 | 39 |
| hsa00640 | Propanoate metabolism | 10/1143 | 32/8644 | 0.006462477 | 0.091598593 | 0.0798567 | 31/79611/1629/1738/55862/3030/26275/3945/8803/8801 | 10 |
| hsa00280 | Valine, leucine and isoleucine degradation | 13/1143 | 48/8644 | 0.007826049 | 0.106303831 | 0.092676895 | 34/36/38/39/316/586/1629/1738/3030/26275/3157/56922/5019 | 13 |
| hsa05145 | Toxoplasmosis | 24/1143 | 111/8644 | 0.009343082 | 0.12183379 | 0.106216091 | 329/330/836/1147/54205/2773/3312/3459/51135/3655/3688/3716/3717/3908/3910/3912/3915/6885/5602/5294/6772/23118/7097/7099 | 24 |
| hsa04810 | Regulation of actin cytoskeleton | 43/1143 | 229/8644 | 0.010093109 | 0.126552062 | 0.110329534 | 81624/10097/10096/324/23365/727/729/730/1730/1950/7430/2252/8826/10788/3673/3676/3655/3685/3688/3690/3694/3696/3845/10787/3071/56034/80310/5156/5290/5291/5295/8503/200576/8395/4659/4660/5962/6093/9475/85477/6654/6655/7414 | 43 |
| hsa05144 | Malaria | 13/1143 | 50/8644 | 0.011201273 | 0.130915944 | 0.114134017 | 948/1378/1379/2993/3040/3043/3082/3606/4233/7058/7097/7099/7412 | 13 |
| hsa00670 | One carbon pool by folate | 7/1143 | 20/8644 | 0.011244314 | 0.130915944 | 0.114134017 | 160428/471/2618/4522/25902/10797/4548 | 7 |
| hsa05161 | Hepatitis B | 32/1143 | 162/8644 | 0.012008979 | 0.134997491 | 0.117692356 | 890/836/9134/1147/54205/1654/355/64135/3454/51135/3716/3717/3845/4214/6885/5602/5290/5291/5295/8503/5925/6654/6655/6772/6775/23118/29110/7046/7097/7098/7099/7529 | 32 |
| hsa04620 | Toll-like receptor signaling pathway | 23/1143 | 108/8644 | 0.0129285 | 0.136402822 | 0.11891754 | 942/1147/1513/3454/51135/3716/6885/5602/5290/5291/5295/8503/8737/6696/6772/23118/29110/7096/7097/7098/7099/10333/51311 | 23 |
| hsa03050 | Proteasome | 12/1143 | 46/8644 | 0.014143225 | 0.136402822 | 0.11891754 | 5685/5684/5700/5701/5706/5707/5718/10213/5708/9861/5713/23198 | 12 |
| hsa03015 | mRNA surveillance pathway | 21/1143 | 97/8644 | 0.014226061 | 0.136402822 | 0.11891754 | 53981/51692/1479/9775/2107/2935/10767/4686/22916/11051/55916/10914/64895/51585/5411/5515/5523/55012/8731/26019/65109 | 21 |
| hsa04070 | Phosphatidylinositol signaling system | 21/1143 | 97/8644 | 0.014226061 | 0.136402822 | 0.11891754 | 160851/3612/8821/3708/3709/4534/8898/9110/9107/5286/5289/5290/5291/5295/8503/200576/8395/23236/5332/23262/22908 | 21 |
| hsa05215 | Prostate cancer | 21/1143 | 97/8644 | 0.014226061 | 0.136402822 | 0.11891754 | 9134/1147/1499/1950/3320/3326/7184/3479/3845/4193/56034/80310/5156/5290/5291/5295/8503/5925/6654/6655/6935 | 21 |
| hsa00310 | Lysine degradation | 15/1143 | 63/8644 | 0.015397977 | 0.137236631 | 0.119644463 | 2146/10157/38/39/55870/1738/3030/58508/55904/2122/5352/80854/83852/6419/79723 | 15 |
| hsa05210 | Colorectal cancer | 19/1143 | 86/8644 | 0.015523886 | 0.137236631 | 0.119644463 | 4436/324/836/1499/54205/1950/3845/5602/4292/4437/2956/5290/5291/5295/8503/51426/6654/6655/7046 | 19 |
| hsa00500 | Starch and sucrose metabolism | 10/1143 | 36/8644 | 0.015575937 | 0.137236631 | 0.119644463 | 280/178/5167/2632/3099/8972/55276/283209/5836/7360 | 10 |
| hsa04210 | Apoptosis | 27/1143 | 136/8644 | 0.018689338 | 0.160334846 | 0.139781751 | 9131/472/329/330/836/1147/1513/1514/1520/54205/9451/1965/355/3708/3709/3845/4001/5602/142/143/5290/5291/5295/8503/5783/8737/6709 | 27 |
| hsa03450 | Non-homologous end-joining | 5/1143 | 13/8644 | 0.02062208 | 0.172379441 | 0.150282367 | 3981/5591/10111/7518/7520 | 5 |
| hsa05140 | Leishmaniasis | 17/1143 | 77/8644 | 0.021471676 | 0.174609714 | 0.152226745 | 718/1378/1379/1536/2214/3459/51135/3676/3688/3716/3717/6885/5743/6772/23118/7097/7099 | 17 |
| hsa04512 | ECM-receptor interaction | 19/1143 | 89/8644 | 0.021960117 | 0.174609714 | 0.152226745 | 3161/948/1293/341640/3673/3676/3655/3685/3688/3690/3694/3696/3908/3910/3912/3915/6696/7058/3371 | 19 |
| hsa05131 | Shigellosis | 44/1143 | 247/8644 | 0.022532489 | 0.174895037 | 0.152475492 | 10097/10096/472/8678/718/834/837/831/1147/8454/54205/54874/3099/3606/3554/3688/3708/3709/10892/6885/5602/4193/4671/58484/114548/5289/5290/5291/5295/8503/30849/23236/5332/8737/8767/6093/9475/9252/23118/257397/29110/7099/7188/7414 | 44 |
| hsa05218 | Melanoma | 16/1143 | 72/8644 | 0.023792189 | 0.178161161 | 0.155322936 | 1950/2252/3082/3479/3845/4193/4233/56034/80310/5156/5290/5291/5295/8503/51426/5925 | 16 |
| hsa04914 | Progesterone-mediated oocyte maturation | 21/1143 | 102/8644 | 0.024351672 | 0.178161161 | 0.155322936 | 699/890/9133/983/4085/64682/996/2773/3320/3326/3479/3845/5602/5140/5290/5291/5295/8503/5567/6197/27330 | 21 |
| hsa05160 | Hepatitis C | 30/1143 | 158/8644 | 0.024592798 | 0.178161161 | 0.155322936 | 836/1147/9076/1499/54205/1950/5610/9451/440275/1965/3646/355/439996/3454/3716/3845/5290/5291/5295/8503/5515/5925/8737/6041/6654/6655/6772/29110/7098/7529 | 30 |
| hsa04145 | Phagosome | 29/1143 | 152/8644 | 0.02523595 | 0.178846081 | 0.155920058 | 523/526/528/51382/718/821/948/81035/1514/1520/1536/1778/79659/8411/2214/3673/3685/3688/3690/4360/4481/5289/200576/22925/7037/7058/7097/7099/10333 | 29 |
| hsa04919 | Thyroid hormone signaling pathway | 24/1143 | 121/8644 | 0.025820137 | 0.179092862 | 0.156135204 | 3066/481/488/1499/3091/3685/3690/3845/4193/9969/8648/10499/8202/9611/5208/5290/5291/5295/8503/23236/5332/5567/6772/9882 | 24 |
| hsa01521 | EGFR tyrosine kinase inhibitor resistance | 17/1143 | 79/8644 | 0.02715977 | 0.184460104 | 0.160814427 | 1950/3082/3479/3716/3717/3845/4233/4763/56034/80310/5156/5290/5291/5295/8503/6654/6655 | 17 |
| hsa04151 | PI3K-Akt signaling pathway | 60/1143 | 359/8644 | 0.03058269 | 0.203468506 | 0.177386169 | 672/284/285/9134/1147/1293/1950/1975/2066/2252/2321/3082/3320/3326/7184/3454/3479/3559/3575/3673/3676/3655/3685/3688/3690/3694/3696/3716/3717/3845/3908/3910/3912/3915/4193/4233/9180/56034/80310/5156/118788/5290/5291/5294/5295/8503/5586/5515/5523/55012/5934/23678/6654/6655/6696/7058/7097/7099/3371/7529 | 60 |
| hsa03320 | PPAR signaling pathway | 16/1143 | 75/8644 | 0.033872152 | 0.220846429 | 0.192536441 | 4199/33/34/2180/2181/2182/948/2170/2710/3157/4023/4312/123/5468/6342/11001 | 16 |
| hsa05135 | Yersinia infection | 26/1143 | 137/8644 | 0.034788748 | 0.222375136 | 0.193869185 | 10097/10096/23365/834/1147/3606/51135/3676/3688/6885/5602/58484/114548/5290/5291/5295/8503/8395/5586/6093/9475/6197/27330/23118/29110/7099 | 26 |
| hsa05213 | Endometrial cancer | 13/1143 | 58/8644 | 0.036774653 | 0.230548784 | 0.200995065 | 324/1495/1499/1950/3845/4292/5290/5291/5295/8503/51426/6654/6655 | 13 |
| hsa05162 | Measles | 26/1143 | 138/8644 | 0.037681206 | 0.231774964 | 0.202064063 | 836/9134/1147/54205/5610/9451/440275/1965/355/3312/64135/3454/3559/51135/3716/6885/5602/5290/5291/5295/8503/6772/23118/29110/7097/7099 | 26 |
| hsa03030 | DNA replication | 9/1143 | 36/8644 | 0.040713825 | 0.243793973 | 0.212542372 | 4172/4175/5558/5983/5984/1763/5422/10714/5981 | 9 |
| hsa05203 | Viral carcinogenesis | 36/1143 | 204/8644 | 0.041130885 | 0.243793973 | 0.212542372 | 890/983/1111/2967/3066/718/836/9134/1108/1654/1739/5610/2965/3572/3716/3845/4067/4193/5290/5291/5295/8503/5567/5700/5922/5925/5934/3516/5966/85477/22938/6672/7188/23352/7874/7529 | 36 |
| hsa04217 | Necroptosis | 29/1143 | 159/8644 | 0.043001047 | 0.250327523 | 0.218238396 | 9131/329/330/834/25978/1536/1540/10059/5610/355/3146/3320/3326/3454/3459/3716/3717/5602/114548/142/5321/5836/8737/6772/6775/7098/7099/7188/54822 | 29 |

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| Table S4-2. GO enrichment analysis of PAH-related genes. | | | | | |  |  |  |  |
| ONTOLOGY | ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue | geneID | Count |
| BP | GO:0007059 | chromosome segregation | 123/2221 | 435/18614 | 9.07E-21 | 5.46E-17 | 4.61E-17 | ASPM/BRCA1/BRIP1/BUB1/BUB1B/CCNB2/CDC6/CDCA2/CENPE/CENPF/CENPK/DLGAP5/ECT2/ESCO2/FANCD2/FBXO5/KIF11/KIF14/KIF15/KIF18A/KIF23/KIF4A/KNTC1/MAD2L1/MKI67/MND1/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/NUSAP1/PRC1/RAD18/SASS6/SKA3/SPAG5/SPDL1/STIL/TOP2A/TPX2/TTK/ZWILCH/ACTR2/ACTR3/ANAPC1/APC/ARID2/ATM/ATRX/BAZ1B/BCCIP/BECN1/BRD7/CCNE2/CDC27/CDK5RAP2/CENPC/CENPJ/CENPN/CENPW/CEP192/CEP97/CHMP2B/CLASP2/CUL3/DDX3X/DYNC1H1/EML4/ERCC4/ESCO1/FANCM/GEM/GEN1/GPSM2/HAUS6/HNRNPU/KIF2A/KNSTRN/KPNB1/MAP9/MAPRE1/MIS12/MLH1/MLH3/NAA50/NCOR1/NIPBL/PBRM1/PDS5A/PDS5B/PIBF1/PUM2/RACGAP1/RAD21/RB1/RIOK2/RIOK3/RRS1/SENP6/SETDB2/SMARCA5/SMARCAD1/SMC1A/SMC2/SMC3/SMC4/SMC5/SMC6/SPICE1/SRPK1/STAG1/STAG2/SYCP2/TLK1/TOP1/TOP2B/TPR/TTN/USP44/USP9X/ZW10 | 123 |
| BP | GO:0000070 | mitotic sister chromatid segregation | 74/2221 | 199/18614 | 2.56E-20 | 7.71E-17 | 6.52E-17 | BUB1/BUB1B/CENPE/CENPF/CENPK/DLGAP5/ESCO2/FBXO5/KIF11/KIF14/KIF15/KIF18A/KIF23/KIF4A/KNTC1/MAD2L1/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/NUSAP1/PRC1/SPAG5/SPDL1/TPX2/TTK/ZWILCH/APC/ATM/ATRX/BAZ1B/BCCIP/BECN1/CDK5RAP2/CENPC/CEP192/CEP97/CHMP2B/CLASP2/CUL3/EML4/ESCO1/GEN1/HNRNPU/KIF2A/KNSTRN/KPNB1/MAP9/MAPRE1/MIS12/NAA50/NIPBL/PDS5A/PDS5B/PIBF1/RACGAP1/RAD21/RB1/RRS1/SMARCA5/SMC1A/SMC2/SMC3/SMC4/SMC5/SPICE1/STAG1/STAG2/TPR/TTN/USP44/ZW10 | 74 |
| BP | GO:0000819 | sister chromatid segregation | 83/2221 | 250/18614 | 5.08E-19 | 1.02E-15 | 8.61E-16 | BUB1/BUB1B/CDC6/CENPE/CENPF/CENPK/DLGAP5/ESCO2/FBXO5/KIF11/KIF14/KIF15/KIF18A/KIF23/KIF4A/KNTC1/MAD2L1/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/NUSAP1/PRC1/SPAG5/SPDL1/TOP2A/TPX2/TTK/ZWILCH/ANAPC1/APC/ARID2/ATM/ATRX/BAZ1B/BCCIP/BECN1/BRD7/CDC27/CDK5RAP2/CENPC/CEP192/CEP97/CHMP2B/CLASP2/CUL3/EML4/ESCO1/GEN1/HNRNPU/KIF2A/KNSTRN/KPNB1/MAP9/MAPRE1/MIS12/NAA50/NIPBL/PBRM1/PDS5A/PDS5B/PIBF1/RACGAP1/RAD21/RB1/RIOK2/RRS1/SMARCA5/SMC1A/SMC2/SMC3/SMC4/SMC5/SPICE1/STAG1/STAG2/TOP2B/TPR/TTN/USP44/ZW10 | 83 |
| BP | GO:0022613 | ribonucleoprotein complex biogenesis | 126/2221 | 475/18614 | 1.03E-18 | 1.55E-15 | 1.31E-15 | EIF3M/XPO1/AATF/ABCE1/ATM/ATR/BMS1/BRIX1/CHD7/COIL/CRNKL1/DDX1/DDX10/DDX18/DDX20/DDX21/DDX23/DDX3X/DDX46/DDX47/DDX52/DHX29/DHX9/DICER1/DIS3/DKC1/EBNA1BP2/EIF2A/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF4A3/EIF5/ERI1/ERI2/ESF1/EXOSC9/FASTKD2/GCFC2/GEMIN5/GNL2/GTPBP4/HEATR1/HSP90AA1/HSP90AB1/HTATSF1/KRR1/LSG1/LTV1/LUC7L3/LYAR/MAK16/MDN1/METTL15/METTL18/MPHOSPH10/MPHOSPH6/NCBP1/NGDN/NIFK/NIP7/NMD3/NOL10/NOL11/NOL8/NOLC1/NOP56/NOP58/NSA2/NUDT21/NUFIP1/NUP88/PAK1IP1/PRKDC/PRPF18/PRPF39/PSIP1/PTBP2/PWP1/RIOK1/RIOK2/RIOK3/RNASEL/RPF2/RPL7L1/RRP15/RRS1/RSL24D1/SCAF11/SDAD1/SDE2/SETX/SF3A3/SF3B1/SLU7/SNRNP200/SNRPA1/SPATA5/SRFBP1/SRPK1/SRPK2/SRSF10/TFB2M/TGS1/TSR1/UTP14A/UTP15/UTP18/UTP20/UTP23/UTP3/UTP6/WDR12/WDR3/WDR36/WDR43/WDR75/XRCC5/XRN2/YTHDC1/ZNF622/ZNF658/ZNHIT6 | 126 |
| BP | GO:0098813 | nuclear chromosome segregation | 99/2221 | 339/18614 | 5.36E-18 | 6.45E-15 | 5.45E-15 | ASPM/BRIP1/BUB1/BUB1B/CCNB2/CDC6/CENPE/CENPF/CENPK/DLGAP5/ECT2/ESCO2/FANCD2/FBXO5/KIF11/KIF14/KIF15/KIF18A/KIF23/KIF4A/KNTC1/MAD2L1/MND1/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/NUSAP1/PRC1/SPAG5/SPDL1/TOP2A/TPX2/TTK/ZWILCH/ACTR2/ACTR3/ANAPC1/APC/ARID2/ATM/ATRX/BAZ1B/BCCIP/BECN1/BRD7/CCNE2/CDC27/CDK5RAP2/CENPC/CEP192/CEP97/CHMP2B/CLASP2/CUL3/DYNC1H1/EML4/ERCC4/ESCO1/FANCM/GEM/GEN1/HNRNPU/KIF2A/KNSTRN/KPNB1/MAP9/MAPRE1/MIS12/MLH1/MLH3/NAA50/NIPBL/PBRM1/PDS5A/PDS5B/PIBF1/RACGAP1/RAD21/RB1/RIOK2/RRS1/SMARCA5/SMC1A/SMC2/SMC3/SMC4/SMC5/SPICE1/STAG1/STAG2/SYCP2/TOP2B/TPR/TTN/USP44/ZW10 | 99 |
| BP | GO:0140014 | mitotic nuclear division | 88/2221 | 286/18614 | 1.06E-17 | 1.07E-14 | 9.01E-15 | ANLN/BORA/BUB1/BUB1B/CDCA2/CENPE/CENPF/CENPK/CHEK1/DLGAP5/ESCO2/FBXO5/KIF11/KIF14/KIF15/KIF18A/KIF20B/KIF23/KIF4A/KNTC1/MAD2L1/MKI67/MTBP/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/NUSAP1/PRC1/SPAG5/SPDL1/TPX2/TTK/ZWILCH/APC/ATM/ATRX/BAZ1B/BCCIP/BECN1/CDK5RAP2/CENPC/CEP192/CEP97/CHMP2B/CLASP2/CUL3/EGF/EML4/EPS8/ESCO1/GEN1/HNRNPU/IGF1/KIF2A/KNSTRN/KPNB1/MAP9/MAPRE1/MIS12/NAA50/NIPBL/PDS5A/PDS5B/PHIP/PIBF1/RACGAP1/RAD21/RB1/RRS1/SMARCA5/SMC1A/SMC2/SMC3/SMC4/SMC5/SPICE1/STAG1/STAG2/TOM1L1/TPR/TTN/UBXN2B/USP16/USP44/ZW10 | 88 |
| BP | GO:0006260 | DNA replication | 86/2221 | 278/18614 | 1.73E-17 | 1.49E-14 | 1.26E-14 | ATAD5/BLM/BRCA1/BRCA2/CCNA2/CDC6/CDK1/CHEK1/DTL/ESCO2/FAM111B/FBXO5/GMNN/MCM3/MCM6/MCM8/MGME1/MMS22L/POLQ/PRIM2/RFC3/RFC4/TICRR/WDHD1/ACTR8/ANKRD17/ATR/ATRX/BAZ1A/BOD1L1/CCDC88A/CCNE2/DBF4/DHX9/DNA2/DNAJC2/EGF/ESCO1/ETAA1/FAM111A/FANCM/GEN1/GTPBP4/JADE1/LIG4/NAP1L1/NASP/NBN/NOC3L/NUCKS1/ORC3/ORC4/PARP1/PDS5A/POLA1/POLD3/POLK/PPP2CA/RAD17/RAD50/RBBP6/RBBP8/RECQL/REV1/REV3L/RFC1/RFWD3/RRM1/RRM2B/SAMHD1/SDE2/SETMAR/SLFN11/SMARCA5/SMC3/SUPT16H/THOC1/TOP1/TOPBP1/TSPYL2/UCHL5/USP37/WRN/ZBTB38/ZPR1/ZRANB3 | 86 |
| BP | GO:0000280 | nuclear division | 114/2221 | 450/18614 | 1.78E-15 | 1.34E-12 | 1.13E-12 | ANLN/ASPM/BORA/BRCA2/BRIP1/BUB1/BUB1B/CCNB2/CDCA2/CENPE/CENPF/CENPK/CHEK1/DLGAP5/ESCO2/FANCD2/FBXO5/KIF11/KIF14/KIF15/KIF18A/KIF20B/KIF23/KIF4A/KNTC1/MAD2L1/MKI67/MND1/MTBP/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/NUSAP1/PRC1/RAD51AP1/RAD54B/SPAG5/SPDL1/TOP2A/TPX2/TTK/ZWILCH/ACTR2/ACTR3/APC/ATM/ATRX/BAZ1B/BCCIP/BECN1/CCNE2/CDK5RAP2/CENPC/CEP192/CEP97/CHMP2B/CLASP2/CUL3/EGF/EML4/EPS8/ERCC4/ESCO1/FANCM/FIGNL1/GEN1/HNRNPU/IGF1/ING2/KIF2A/KNSTRN/KPNB1/MAP9/MAPRE1/MASTL/MIS12/MLH1/MLH3/NAA50/NIPBL/ORC4/PDS5A/PDS5B/PHIP/PIBF1/PLCB1/RACGAP1/RAD21/RAD50/RB1/RRS1/SMARCA5/SMC1A/SMC2/SMC3/SMC4/SMC5/SPICE1/SPIRE1/STAG1/STAG2/SYCP2/TOM1L1/TOP2B/TPR/TTN/UBR2/UBXN2B/USP16/USP44/ZW10 | 114 |
| BP | GO:0048285 | organelle fission | 122/2221 | 497/18614 | 2.26E-15 | 1.51E-12 | 1.28E-12 | ANLN/ASPM/BORA/BRCA2/BRIP1/BUB1/BUB1B/CCNB2/CDCA2/CENPE/CENPF/CENPK/CHEK1/DLGAP5/ESCO2/FANCD2/FBXO5/KIF11/KIF14/KIF15/KIF18A/KIF20B/KIF23/KIF4A/KNTC1/MAD2L1/MKI67/MND1/MTBP/MTFR2/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/NUSAP1/PRC1/RAD51AP1/RAD54B/SPAG5/SPDL1/TOP2A/TPX2/TTK/ZWILCH/ACTR2/ACTR3/AP3B1/APC/ATM/ATRX/BAZ1B/BCCIP/BECN1/CCNE2/CDK5RAP2/CENPC/CEP192/CEP97/CHMP2B/CLASP2/CORO1C/CUL3/DNM1L/EGF/EML4/EPS8/ERCC4/ESCO1/FANCM/FIGNL1/GEN1/HNRNPU/IGF1/ING2/KIF2A/KNSTRN/KPNB1/LRRK2/MAP9/MAPRE1/MASTL/MIS12/MLH1/MLH3/NAA50/NIPBL/OPA1/ORC4/PDS5A/PDS5B/PHIP/PIBF1/PLCB1/PPARG/RACGAP1/RAD21/RAD50/RB1/RRS1/SMARCA5/SMC1A/SMC2/SMC3/SMC4/SMC5/SPICE1/SPIRE1/STAG1/STAG2/SYCP2/TOM1L1/TOP2B/TPR/TTN/UBR2/UBXN2B/USP16/USP44/VPS35/ZW10 | 122 |
| BP | GO:0033044 | regulation of chromosome organization | 75/2221 | 250/18614 | 1.24E-14 | 7.45E-12 | 6.29E-12 | BUB1/BUB1B/CDC6/CENPE/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/SPDL1/TOP2A/TTK/ZWILCH/ACTR8/ANAPC1/APC/ARID2/ATF7IP/ATM/ATR/ATRX/BAZ1B/BECN1/BRD7/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CDC27/CDK5RAP2/CTNNB1/CUL3/DHX36/DKC1/ERCC4/GEN1/GNL3/HNRNPA1/HNRNPA2B1/HNRNPU/LIG4/MAP3K4/NBN/PARP1/PBRM1/POT1/RAD21/RAD50/RB1/RIOK2/SENP6/SETDB2/SETMAR/SMARCA5/SMC2/SMC4/SMC5/SMC6/TCP1/TNKS2/TPR/UCHL5/USP44/USP7/XRCC5/XRN1/ZW10 | 75 |
| BP | GO:0000075 | cell cycle checkpoint signaling | 62/2221 | 188/18614 | 2.10E-14 | 1.15E-11 | 9.71E-12 | BLM/BRCA1/BRCA2/BRIP1/BUB1/BUB1B/CDC6/CDK1/CENPF/CHEK1/DTL/FANCD2/KNTC1/MAD2L1/MSH2/NDC80/NUF2/SPDL1/TICRR/TTK/WDR76/ZWILCH/APC/ATM/ATR/BRCC3/CCNG1/CDC5L/CDK5RAP2/CLOCK/DNA2/DTX3L/EIF2AK4/ERCC6/ETAA1/GEN1/GIGYF2/INTS7/MDM2/NAE1/NBN/NEK11/NSUN2/PARP9/PRKDC/PTPN11/RAD17/RAD50/RBBP8/RFWD3/SDE2/SETMAR/STK33/SYF2/TAOK1/TAOK3/THOC1/TOPBP1/TP53BP1/TPR/USP44/ZW10 | 62 |
| BP | GO:0042254 | ribosome biogenesis | 83/2221 | 298/18614 | 5.05E-14 | 2.53E-11 | 2.14E-11 | XPO1/AATF/ABCE1/BMS1/BRIX1/CHD7/DDX10/DDX18/DDX21/DDX3X/DDX47/DDX52/DHX29/DIS3/DKC1/EBNA1BP2/EIF2A/EIF4A3/ERI1/ERI2/ESF1/EXOSC9/FASTKD2/GNL2/GTPBP4/HEATR1/KRR1/LSG1/LTV1/LYAR/MAK16/MDN1/METTL15/METTL18/MPHOSPH10/MPHOSPH6/NGDN/NIFK/NIP7/NMD3/NOL10/NOL11/NOL8/NOLC1/NOP56/NOP58/NSA2/NUP88/PAK1IP1/PRKDC/PWP1/RIOK1/RIOK2/RIOK3/RNASEL/RPF2/RPL7L1/RRP15/RRS1/RSL24D1/SDAD1/SDE2/SPATA5/SRFBP1/TFB2M/TSR1/UTP14A/UTP15/UTP18/UTP20/UTP23/UTP3/UTP6/WDR12/WDR3/WDR36/WDR43/WDR75/XRCC5/XRN2/ZNF622/ZNF658/ZNHIT6 | 83 |
| BP | GO:1901988 | negative regulation of cell cycle phase transition | 77/2221 | 274/18614 | 2.50E-13 | 1.16E-10 | 9.78E-11 | BLM/BRCA1/BRCA2/BRIP1/BUB1/BUB1B/CDC6/CDK1/CENPF/CHEK1/DTL/EZH2/FANCD2/FBXO5/KNTC1/MAD2L1/MSH2/NDC80/NUF2/SPDL1/TICRR/TTK/WDR76/ZWILCH/APC/ATM/ATR/BRCC3/BRD7/CCNG1/CDC5L/CDK5RAP2/CLOCK/DCUN1D3/DLG1/DNA2/DTX3L/EIF2AK4/ERCC6/ETAA1/GEN1/GIGYF2/GPNMB/INHBA/INTS7/JADE1/MDM2/MIR15B/MIR30C2/NAE1/NBN/NEK11/NSUN2/PARP9/PRKDC/PTPN11/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RFWD3/SDE2/SETMAR/SLFN11/STK33/SYF2/TAOK1/TAOK3/THOC1/TOPBP1/TP53BP1/TPR/USP44/USP47/ZW10 | 77 |
| BP | GO:0010948 | negative regulation of cell cycle process | 84/2221 | 317/18614 | 7.12E-13 | 3.06E-10 | 2.59E-10 | BLM/BRCA1/BRCA2/BRIP1/BUB1/BUB1B/CDC6/CDK1/CENPF/CHEK1/DTL/EZH2/FANCD2/FBXO5/KNTC1/MAD2L1/MSH2/MTBP/NDC80/NEK2/NUF2/SPDL1/TICRR/TTK/WDR76/ZWILCH/APC/ATM/ATR/ATRX/BAZ1B/BRCC3/BRD7/CCNG1/CCP110/CDC5L/CDK5RAP2/CLOCK/DCUN1D3/DLG1/DNA2/DTX3L/EIF2AK4/ERCC6/ETAA1/GEN1/GIGYF2/GPNMB/INHBA/INTS7/JADE1/MDM2/MIR15B/MIR30C2/NAE1/NBN/NEK11/NSUN2/PARP9/PRKDC/PTPN11/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RFWD3/SDE2/SETMAR/SLFN11/SMARCA5/STK33/SYF2/TAOK1/TAOK3/THOC1/TOM1L1/TOPBP1/TP53BP1/TPR/USP44/USP47/ZW10 | 84 |
| BP | GO:0006261 | DNA-templated DNA replication | 53/2221 | 160/18614 | 1.32E-12 | 5.31E-10 | 4.49E-10 | ATAD5/BLM/BRCA1/BRCA2/CDC6/FBXO5/GMNN/MCM3/MCM6/MCM8/MGME1/MMS22L/POLQ/PRIM2/RFC3/RFC4/TICRR/WDHD1/ATR/ATRX/BAZ1A/BOD1L1/CCNE2/DBF4/DNA2/ETAA1/FAM111A/FANCM/GEN1/NBN/NOC3L/NUCKS1/ORC3/ORC4/PARP1/POLA1/POLD3/RAD50/RBBP8/RECQL/REV3L/RFC1/RFWD3/RRM1/RRM2B/SAMHD1/SETMAR/SLFN11/THOC1/TOPBP1/WRN/ZPR1/ZRANB3 | 53 |
| BP | GO:0016072 | rRNA metabolic process | 71/2221 | 257/18614 | 5.18E-12 | 1.95E-09 | 1.64E-09 | GTF3C6/BMS1/BRIX1/CHD7/DDX10/DDX18/DDX21/DDX47/DDX52/DIS3/DIS3L/DKC1/EBNA1BP2/EIF4A3/ERCC6/ERI1/ERI2/ESF1/EXOSC9/GTF3C3/GTPBP4/HEATR1/KRR1/LYAR/MAK16/METTL15/METTL18/MPHOSPH10/MPHOSPH6/NCL/NGDN/NIFK/NOL10/NOL11/NOL8/NOLC1/NOP56/NOP58/NSA2/POLR1B/PRKDC/PWP1/RIOK1/RIOK2/RIOK3/RNASEL/RPF2/RPL7L1/RRP15/RRS1/SDE2/SLFN13/SRFBP1/TAF1B/TFB2M/TSR1/UTP14A/UTP15/UTP18/UTP20/UTP23/UTP3/UTP6/WDR12/WDR3/WDR36/WDR43/WDR75/XRN1/XRN2/ZNHIT6 | 71 |
| BP | GO:0051656 | establishment of organelle localization | 104/2221 | 445/18614 | 6.97E-12 | 2.39E-09 | 2.02E-09 | CENPE/CENPF/KIF14/KIF18A/MAD2L1/NDC80/NUF2/NUSAP1/SPAG5/SPDL1/XPO1/ABCE1/AP1AR/AP3B1/AP3M1/ARFGAP3/ARHGAP21/ATM/BECN1/BLOC1S6/BTK/C12orf4/CCDC186/CD84/CDK5RAP2/CENPC/CEP120/CEP83/CHMP2B/CLASP2/CTNNB1/CUL3/DLG1/DNM1L/DOCK7/DYNC1H1/EML4/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/EZR/FAM91A1/FER/FNBP1L/GEM/GPSM2/HIF1A/HNRNPU/HOOK3/ITGA4/ITGB1/KIF3A/KIF5B/KPNB1/LMNB1/LRPPRC/LRRK2/LSG1/LTV1/LYN/MAP1B/MAPRE1/MDN1/MIS12/MKKS/MLH1/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/NLGN1/NMD3/NUP88/OPA1/PCM1/PIBF1/PIK3CG/RAB1A/RAB27A/RABGEF1/RHOT1/RIOK2/RRS1/SAR1B/SDAD1/SDCBP/SPG11/SPICE1/SPIRE1/SYBU/SYNE2/TANC2/TBC1D23/TRAK2/TRAPPC11/TRAPPC13/TRAPPC8/TRIP11/UBXN2B/WDR11/ZW10 | 104 |
| BP | GO:1901987 | regulation of cell cycle phase transition | 106/2221 | 457/18614 | 7.14E-12 | 2.39E-09 | 2.02E-09 | ANLN/ATAD5/BLM/BRCA1/BRCA2/BRIP1/BUB1/BUB1B/CDC6/CDK1/CENPE/CENPF/CHEK1/DLGAP5/DTL/EZH2/FANCD2/FBXO5/KIF14/KNTC1/MAD2L1/MSH2/MTBP/NDC80/NUF2/SASS6/SPDL1/STIL/TICRR/TTK/WDR76/ZWILCH/ADAM17/ANKRD17/APC/ARID2/ATM/ATR/BRCC3/BRD7/CCNG1/CCNH/CDC5L/CDK5RAP2/CENPJ/CLOCK/CPSF3/CUL3/DBF4/DCUN1D3/DDX3X/DLG1/DNA2/DTX3L/ECD/EIF2AK4/ERCC6/ETAA1/GEN1/GIGYF2/GPNMB/INHBA/INTS7/JADE1/KMT2E/MDM2/MIR15B/MIR30C2/NAE1/NBN/NEK11/NSUN2/PARP9/PBRM1/PLCB1/PLRG1/PPP2CA/PRKDC/PTPN11/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RDX/RFWD3/RIOK2/RRM1/RRM2B/SDE2/SETMAR/SLFN11/STK33/STXBP4/SYF2/TAF1/TAOK1/TAOK3/THOC1/TOPBP1/TP53BP1/TPR/USP44/USP47/ZW10 | 106 |
| BP | GO:0006302 | double-strand break repair | 79/2221 | 303/18614 | 8.38E-12 | 2.65E-09 | 2.24E-09 | BLM/BRCA1/BRCA2/BRIP1/CHEK1/DEK/ESCO2/FANCD2/MCM3/MCM6/MCM8/MMS22L/MSH2/PARPBP/POLQ/RAD51AP1/RAD54B/XRCC2/ACTR2/ACTR8/ARID2/ATM/ATR/BRCC3/BRD7/CHD4/DCLRE1A/DDX1/DNA2/DTX3L/EPC2/ERCC4/ERCC5/ERCC6/FANCM/FIGNL1/GEN1/HMGB1/HMGB2/ING3/LIG4/MLH1/MORF4L2/NBN/NIPBL/NUCKS1/PALB2/PARP1/PARP9/PBRM1/POLA1/POT1/PPP4R2/PRKDC/PSMD14/RAD21/RAD50/RBBP8/RECQL/REV3L/RFWD3/RIF1/SAMHD1/SETMAR/SETX/SMARCAD1/SMC5/SMC6/SMCHD1/SPIRE1/TDP2/TP53BP1/TRIP12/UBR5/VCP/WDR48/WRN/XRCC4/XRCC5 | 79 |
| BP | GO:0140694 | non-membrane-bounded organelle assembly | 94/2221 | 390/18614 | 1.17E-11 | 3.52E-09 | 2.98E-09 | ANLN/ASPM/BRCA1/CCNB2/CENPE/CENPF/CENPK/CEP135/DLGAP5/FBXO5/KIF11/KIF15/KIF23/KIF4A/KNTC1/NDC80/NEK2/PLK4/PRC1/SASS6/SPAG5/STIL/TPX2/AKAP13/ALMS1/BCCIP/BIN2/BRIX1/C9orf72/CAPN3/CCP110/CDK5RAP2/CENPC/CENPJ/CENPN/CENPW/CEP120/CEP152/CEP192/CEP97/CHMP2B/CLASP2/CNOT1/CNOT6L/CSDE1/DDX3X/DHX29/DOCK5/DYNC1H1/EIF2A/EIF2S1/EZR/FASTKD2/G3BP1/G3BP2/GPSM2/HAUS6/HNRNPU/ITGB1/KIF2A/KPNB1/LCP1/MAP9/MAPRE1/MDN1/MIS12/MLH1/NCOR1/NEB/NIP7/OGFOD1/PDGFRA/PIBF1/PLS1/PRKDC/PRRC2C/PUM2/RACGAP1/RPF2/RRS1/SENP6/SH3PXD2B/SMC1A/SMC3/SPICE1/SQLE/STAG1/STAG2/TMOD2/TPM1/TPR/TTN/XRCC5/YTHDF3 | 94 |
| BP | GO:0006397 | mRNA processing | 112/2221 | 500/18614 | 1.87E-11 | 5.36E-09 | 4.53E-09 | AHCYL1/AQR/CDC40/CDC5L/CIR1/CNOT6L/COIL/CPSF2/CPSF3/CRNKL1/CSTF3/CWC22/CWC27/CWF19L2/DDX1/DDX20/DDX23/DDX46/DDX47/DDX5/DHX15/DHX36/DHX8/DHX9/ECD/EIF4A3/FMR1/FXR1/GCFC2/GEMIN5/HNRNPA1/HNRNPA2B1/HNRNPA3/HNRNPH3/HNRNPR/HNRNPU/HSPA8/HTATSF1/IWS1/LARP7/LEO1/LUC7L3/METTL14/MFAP1/NCBP1/NCBP2/NCL/NSRP1/NUDT21/PAPOLA/PAPOLG/PAXBP1/PCF11/PLRG1/PNN/PNPT1/PPP4R2/PPWD1/PRMT9/PRPF18/PRPF38B/PRPF39/PRPF4/PRPF40A/PRPF4B/PSIP1/PTBP2/PTCD2/PUS7/PUS7L/RBBP6/RBM25/RBM27/RBM39/RBM41/RNASEL/RNMT/RNPC3/RSRC1/SCAF11/SDE2/SETX/SF3A3/SF3B1/SLTM/SLU7/SMU1/SNRNP200/SNRPA1/SNW1/SON/SREK1/SREK1IP1/SRPK1/SRPK2/SRSF10/SRSF11/SYF2/SYNCRIP/TGS1/THOC1/THOC2/TTF2/WBP4/WTAP/XRN2/YTHDC1/ZC3H13/ZNF326/ZNF473/ZPR1/ZRANB2 | 112 |
| BP | GO:0044772 | mitotic cell cycle phase transition | 106/2221 | 467/18614 | 2.85E-11 | 7.81E-09 | 6.60E-09 | ANLN/ATAD5/BLM/BRCA1/BUB1/BUB1B/CCNA2/CCNB2/CDC6/CDK1/CDKN3/CENPE/CENPF/CHEK1/DLGAP5/DTL/EZH2/FBXO5/KIF14/KNTC1/MAD2L1/MELK/MTBP/NDC80/NUF2/SASS6/SPDL1/STIL/TICRR/TTK/ZWILCH/ABCB1/ADAM17/ANAPC1/ANKRD17/APC/ARID2/ATM/BACH1/BCAT1/BRCC3/BRD7/CCNE2/CCNG1/CCNH/CDC27/CDK5RAP2/CENPJ/CLASP2/CPSF3/CUL1/CUL2/CUL3/DBF4/DCUN1D3/DDX3X/DLG1/E2F6/ECD/EPS8/GEN1/GIGYF2/GPNMB/GSPT1/INHBA/ITGB1/JADE1/KMT2E/MASTL/MDM2/MIR15B/MIR30C2/NAE1/NBN/NEK11/NPAT/PBRM1/PLCB1/PLRG1/PPP2CA/PRKDC/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RDX/RFWD3/RIOK2/RRM1/RRM2B/SDE2/SLFN11/SMC5/SYF2/TAF2/TAOK1/TAOK3/TOPBP1/TPR/USP37/USP44/USP47/ZPR1/ZW10 | 106 |
| BP | GO:0006364 | rRNA processing | 62/2221 | 218/18614 | 3.04E-11 | 7.95E-09 | 6.72E-09 | BMS1/BRIX1/CHD7/DDX10/DDX18/DDX21/DDX47/DDX52/DIS3/DKC1/EBNA1BP2/EIF4A3/ERI1/ERI2/ESF1/EXOSC9/GTPBP4/HEATR1/KRR1/LYAR/MAK16/METTL15/METTL18/MPHOSPH10/MPHOSPH6/NGDN/NIFK/NOL10/NOL11/NOL8/NOLC1/NOP56/NOP58/NSA2/PRKDC/PWP1/RIOK1/RIOK2/RIOK3/RNASEL/RPF2/RPL7L1/RRP15/RRS1/SDE2/SRFBP1/TFB2M/TSR1/UTP14A/UTP15/UTP18/UTP20/UTP23/UTP3/UTP6/WDR12/WDR3/WDR36/WDR43/WDR75/XRN2/ZNHIT6 | 62 |
| BP | GO:0034470 | ncRNA processing | 99/2221 | 432/18614 | 7.33E-11 | 1.84E-08 | 1.55E-08 | ADAT1/ALKBH8/BMS1/BRIX1/CHD7/DDX1/DDX10/DDX18/DDX21/DDX3X/DDX47/DDX5/DDX52/DICER1/DIS3/DKC1/DPH3/EBNA1BP2/EIF4A3/ERI1/ERI2/ESF1/EXOSC9/FAM98A/GTPBP4/HEATR1/HNRNPA2B1/INTS12/INTS6/INTS7/KRR1/LARP7/LYAR/MAK16/METTL15/METTL18/MPHOSPH10/MPHOSPH6/NCBP1/NCBP2/NGDN/NIFK/NOL10/NOL11/NOL8/NOLC1/NOP56/NOP58/NSA2/NSUN2/NSUN6/NUP155/POP1/PRKDC/PUM2/PUS10/PUS3/PUS7/PWP1/RIOK1/RIOK2/RIOK3/RNASEL/RPF2/RPL7L1/RRP15/RRS1/RTCB/SDE2/SRFBP1/SSB/TFB2M/THADA/THUMPD1/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TRMT6/TRNT1/TSNAX/TSR1/TYW3/UTP14A/UTP15/UTP18/UTP20/UTP23/UTP3/UTP6/WDR12/WDR3/WDR36/WDR43/WDR75/XRN2/ZC3H7A/ZNHIT6 | 99 |
| BP | GO:0045786 | negative regulation of cell cycle | 94/2221 | 404/18614 | 9.31E-11 | 2.24E-08 | 1.89E-08 | BLM/BRCA1/BRCA2/BRIP1/BUB1/BUB1B/CDC6/CDK1/CENPF/CHEK1/DTL/EZH2/FANCD2/FBXO5/GMNN/KNTC1/MAD2L1/MSH2/MTBP/NDC80/NEK2/NUF2/SPDL1/TICRR/TTK/WDR76/ZWILCH/APC/ATM/ATR/ATRX/BAZ1B/BRCC3/BRD7/CASP3/CCNG1/CCP110/CDC5L/CDK5RAP2/CLOCK/CTNNB1/DCUN1D3/DLG1/DNA2/DTX3L/EIF2AK4/ERCC6/ETAA1/GEN1/GIGYF2/GPNMB/INHBA/INTS7/IPO5/IPO7/JADE1/MDM2/MIR15B/MIR30C2/NAE1/NBN/NEK11/NSUN2/PARP9/PRKDC/PTGS2/PTPN11/PTPN3/PTPRK/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RFWD3/SDE2/SETMAR/SLFN11/SMARCA5/STK33/SYF2/TAOK1/TAOK3/THOC1/TOM1L1/TOPBP1/TP53BP1/TP53BP2/TPR/TSPYL2/USP44/USP47/ZW10 | 94 |
| BP | GO:0007093 | mitotic cell cycle checkpoint signaling | 45/2221 | 140/18614 | 1.99E-10 | 4.61E-08 | 3.89E-08 | BLM/BRCA1/BUB1/BUB1B/CDC6/CDK1/CENPF/CHEK1/DTL/FANCD2/KNTC1/MAD2L1/MSH2/NDC80/NUF2/SPDL1/TICRR/TTK/ZWILCH/APC/ATM/BRCC3/CCNG1/CDK5RAP2/GEN1/GIGYF2/MDM2/NAE1/NBN/NEK11/PRKDC/RAD17/RAD50/RBBP8/RFWD3/SDE2/SETMAR/STK33/SYF2/TAOK1/TAOK3/TOPBP1/TPR/USP44/ZW10 | 45 |
| BP | GO:0051983 | regulation of chromosome segregation | 43/2221 | 131/18614 | 2.37E-10 | 5.27E-08 | 4.46E-08 | BUB1/BUB1B/CDC6/CDCA2/CENPE/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/MKI67/NCAPG/NCAPG2/NCAPH/NDC80/NUF2/RAD18/SPDL1/TTK/ZWILCH/ANAPC1/APC/ARID2/ATM/BECN1/BRD7/CDC27/CDK5RAP2/CUL3/GEN1/HNRNPU/PBRM1/PUM2/RAD21/RB1/RIOK2/SMC2/SMC4/SMC5/SMC6/TPR/USP44/ZW10 | 43 |
| BP | GO:0071103 | DNA conformation change | 34/2221 | 90/18614 | 2.59E-10 | 5.49E-08 | 4.64E-08 | BLM/BRIP1/MCM3/MCM6/MCM8/POLQ/RAD54B/RFC3/RFC4/TOP2A/ASCC3/CHD1L/CHD8/DDX1/DDX3X/DHX36/DHX9/DNA2/FANCM/G3BP1/HMGB1/HMGB2/HNRNPA2B1/MTERF1/NBN/POT1/RAD50/RECQL/SETX/TOP1/TOP2B/WRN/XRCC5/ZRANB3 | 34 |
| BP | GO:0008380 | RNA splicing | 103/2221 | 466/18614 | 2.72E-10 | 5.49E-08 | 4.64E-08 |  | 103 |
| BP | GO:0031297 | replication fork processing | 23/2221 | 46/18614 | 2.74E-10 | 5.49E-08 | 4.64E-08 | BLM/BRCA1/BRCA2/MMS22L/ATR/ATRX/BOD1L1/DNA2/ETAA1/FAM111A/FANCM/GEN1/NBN/NUCKS1/PARP1/RAD50/RBBP8/RFWD3/SAMHD1/SETMAR/THOC1/WRN/ZRANB3 | 23 |
| BP | GO:0031570 | DNA integrity checkpoint signaling | 43/2221 | 132/18614 | 3.11E-10 | 6.03E-08 | 5.10E-08 | BLM/BRCA1/BRCA2/BRIP1/CDC6/CDK1/CHEK1/DTL/FANCD2/MSH2/TICRR/WDR76/ATM/ATR/BRCC3/CCNG1/CDC5L/CLOCK/DNA2/DTX3L/EIF2AK4/ERCC6/ETAA1/GIGYF2/INTS7/MDM2/NAE1/NBN/NEK11/PARP9/PRKDC/PTPN11/RAD17/RFWD3/SDE2/SETMAR/STK33/SYF2/TAOK1/TAOK3/THOC1/TOPBP1/TP53BP1 | 43 |
| BP | GO:1901991 | negative regulation of mitotic cell cycle phase transition | 55/2221 | 194/18614 | 4.45E-10 | 8.37E-08 | 7.07E-08 | BLM/BRCA1/BUB1/BUB1B/CDC6/CDK1/CENPF/CHEK1/DTL/EZH2/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TICRR/TTK/ZWILCH/APC/ATM/BRCC3/BRD7/CCNG1/CDK5RAP2/DCUN1D3/DLG1/GEN1/GIGYF2/GPNMB/INHBA/JADE1/MDM2/MIR15B/MIR30C2/NAE1/NBN/PRKDC/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RFWD3/SDE2/SLFN11/SYF2/TAOK1/TAOK3/TOPBP1/TPR/USP44/USP47/ZW10 | 55 |
| BP | GO:0032392 | DNA geometric change | 32/2221 | 83/18614 | 4.71E-10 | 8.59E-08 | 7.26E-08 | BLM/BRIP1/MCM3/MCM6/MCM8/POLQ/RAD54B/RFC3/RFC4/TOP2A/ASCC3/CHD1L/CHD8/DDX1/DDX3X/DHX36/DHX9/DNA2/FANCM/G3BP1/HMGB1/HMGB2/HNRNPA2B1/MTERF1/NBN/POT1/RAD50/RECQL/SETX/WRN/XRCC5/ZRANB3 | 32 |
| BP | GO:0045930 | negative regulation of mitotic cell cycle | 64/2221 | 243/18614 | 5.06E-10 | 8.90E-08 | 7.52E-08 | BLM/BRCA1/BUB1/BUB1B/CDC6/CDK1/CENPF/CHEK1/DTL/EZH2/FANCD2/FBXO5/KNTC1/MAD2L1/MSH2/MTBP/NDC80/NUF2/SPDL1/TICRR/TTK/ZWILCH/APC/ATM/BRCC3/BRD7/CCNG1/CDK5RAP2/CTNNB1/DCUN1D3/DLG1/GEN1/GIGYF2/GPNMB/INHBA/JADE1/MDM2/MIR15B/MIR30C2/NAE1/NBN/NEK11/PRKDC/PTPN3/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RFWD3/SDE2/SETMAR/SLFN11/STK33/SYF2/TAOK1/TAOK3/TOM1L1/TOPBP1/TPR/USP44/USP47/ZW10 | 64 |
| BP | GO:0006913 | nucleocytoplasmic transport | 79/2221 | 328/18614 | 5.33E-10 | 8.90E-08 | 7.52E-08 | CDK1/ECT2/XPO1/XPOT/ABCE1/AHCTF1/AHCYL1/AKAP13/ANGPT1/CD36/CSE1L/CTDSPL2/DHX9/EFCAB7/EIF4A3/FYTTD1/HNRNPA1/HNRNPA2B1/HSP90AA1/HSPA9/IPO11/IPO5/IPO7/IPO8/IWS1/JAK2/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/LRRK2/LSG1/LTV1/MALT1/MDN1/NCBP1/NCBP2/NEDD4/NEMF/NF1/NMD3/NOLC1/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/PHAX/PIK3R1/PPP1R12A/PRKD1/PTGS2/PTPN11/RANBP2/RANBP6/RGPD1/RIOK2/RRS1/RSRC1/SDAD1/SP100/SPG11/SSB/THOC1/THOC2/TNPO1/TPR/UBR5/UFM1/UPF2/XPO4/XPO5/YTHDC1/ZC3H11A/ZPR1 | 79 |
| BP | GO:0051169 | nuclear transport | 79/2221 | 328/18614 | 5.33E-10 | 8.90E-08 | 7.52E-08 | CDK1/ECT2/XPO1/XPOT/ABCE1/AHCTF1/AHCYL1/AKAP13/ANGPT1/CD36/CSE1L/CTDSPL2/DHX9/EFCAB7/EIF4A3/FYTTD1/HNRNPA1/HNRNPA2B1/HSP90AA1/HSPA9/IPO11/IPO5/IPO7/IPO8/IWS1/JAK2/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/LRRK2/LSG1/LTV1/MALT1/MDN1/NCBP1/NCBP2/NEDD4/NEMF/NF1/NMD3/NOLC1/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/PHAX/PIK3R1/PPP1R12A/PRKD1/PTGS2/PTPN11/RANBP2/RANBP6/RGPD1/RIOK2/RRS1/RSRC1/SDAD1/SP100/SPG11/SSB/THOC1/THOC2/TNPO1/TPR/UBR5/UFM1/UPF2/XPO4/XPO5/YTHDC1/ZC3H11A/ZPR1 | 79 |
| BP | GO:0006310 | DNA recombination | 79/2221 | 332/18614 | 9.76E-10 | 1.56E-07 | 1.32E-07 | ATAD5/BLM/BRCA1/BRCA2/BRIP1/CHEK1/FANCD2/MCM3/MCM6/MCM8/MMS22L/MND1/MSH2/PARPBP/POLQ/RAD51AP1/RAD54B/TOP2A/XRCC2/ACTR2/ACTR8/ARID2/ATM/CHD4/EPC2/ERCC4/ERCC5/ERCC6/FANCM/FIGNL1/GEN1/HMGB1/HMGB2/HSPD1/IL7R/ING3/KPNA1/KPNA2/LIG4/MLH1/MLH3/MORF4L2/MSH3/MSH6/NBN/NIPBL/NUCKS1/PALB2/PARP1/PPP4R2/PRKDC/PSMD14/PTPRC/RAD21/RAD50/RBBP8/RECQL/REV3L/RFWD3/RIF1/SAMHD1/SETX/SMARCAD1/SMC5/SMC6/SMCHD1/SWAP70/TFRC/THOC1/TOP2B/TOPBP1/TP53BP1/UBR2/UCHL5/WDR48/WRN/XRCC4/XRCC5/ZRANB3 | 79 |
| BP | GO:0045005 | DNA-templated DNA replication maintenance of fidelity | 25/2221 | 56/18614 | 9.83E-10 | 1.56E-07 | 1.32E-07 | BLM/BRCA1/BRCA2/MCM8/MMS22L/ATR/ATRX/BOD1L1/DNA2/ETAA1/FAM111A/FANCM/GEN1/NBN/NUCKS1/PARP1/RAD50/RBBP8/RFWD3/SAMHD1/SETMAR/SLFN11/THOC1/WRN/ZRANB3 | 25 |
| BP | GO:0010639 | negative regulation of organelle organization | 84/2221 | 362/18614 | 1.07E-09 | 1.65E-07 | 1.39E-07 | BRCA1/BUB1/BUB1B/CENPF/CHEK1/FBXO5/KNTC1/MAD2L1/MTBP/NDC80/NUF2/SPDL1/TOP2A/TPX2/TTK/ZWILCH/ADD3/APC/ARFGEF1/ARHGAP28/ATM/ATRX/BAZ1B/BECN1/CAMSAP2/CAPZA2/CCP110/CDK5RAP2/CEP97/CGNL1/CKAP2/CLASP2/EPS8/ERCC4/GCLC/GDI2/GEN1/HGF/HNRNPA1/HNRNPU/IGF1/LIMA1/LRRK2/MAP1B/MAPRE1/MET/MKKS/MPHOSPH9/MTM1/NAV3/NBN/ODF2L/OPA1/PARP1/PHLDB2/PIK3CA/PIK3R1/POT1/PPARG/PPFIA1/RAD21/RAD50/RDX/SCFD1/SCIN/SETMAR/SMARCA5/SPTAN1/SVIL/SWAP70/TAOK1/TBC1D30/TBC1D4/TFRC/TJP1/TMOD2/TNKS2/TOM1L1/TPR/TWF1/USP44/WDR47/XRN1/ZW10 | 84 |
| BP | GO:0034504 | protein localization to nucleus | 74/2221 | 304/18614 | 1.13E-09 | 1.70E-07 | 1.44E-07 | CDK1/ECT2/XPO1/ANGPT1/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CD2AP/CD36/CSE1L/CTNNA1/DCLK1/DKC1/DTX3L/EFCAB7/EIF2AK3/FERMT2/GBP2/HNRNPU/HSP90AA1/IPO11/IPO5/IPO7/IPO8/JAK2/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/LARP7/LMNB1/LRRK2/MDM2/NF1/NMD3/NOL8/NOLC1/NUP107/NUP133/NUP153/NUP155/NUP88/NXT2/OSBPL8/PARP1/PARP9/PIK3R1/PIKFYVE/PLRG1/PRKD1/PTGS2/RANBP2/RANBP6/RAP1GDS1/RGPD1/RPF2/RRS1/SP100/SPG11/SYNE1/TCP1/TFRC/TNPO1/TOPORS/TOR1AIP2/TPR/UBR5/UFM1/WRN/ZPR1 | 74 |
| BP | GO:1901990 | regulation of mitotic cell cycle phase transition | 82/2221 | 357/18614 | 2.80E-09 | 4.11E-07 | 3.47E-07 | ANLN/ATAD5/BLM/BRCA1/BUB1/BUB1B/CDC6/CDK1/CENPE/CENPF/CHEK1/DLGAP5/DTL/EZH2/FBXO5/KIF14/KNTC1/MAD2L1/MTBP/NDC80/NUF2/SASS6/SPDL1/STIL/TICRR/TTK/ZWILCH/ADAM17/ANKRD17/APC/ARID2/ATM/BRCC3/BRD7/CCNG1/CCNH/CDK5RAP2/CENPJ/CPSF3/CUL3/DCUN1D3/DDX3X/DLG1/ECD/GEN1/GIGYF2/GPNMB/INHBA/JADE1/KMT2E/MDM2/MIR15B/MIR30C2/NAE1/NBN/NEK11/PBRM1/PLCB1/PLRG1/PPP2CA/PRKDC/RAD17/RAD21/RAD50/RB1/RBBP8/RBL2/RDX/RFWD3/RIOK2/RRM1/RRM2B/SDE2/SLFN11/SYF2/TAOK1/TAOK3/TOPBP1/TPR/USP44/USP47/ZW10 | 82 |
| BP | GO:1902850 | microtubule cytoskeleton organization involved in mitosis | 47/2221 | 161/18614 | 2.87E-09 | 4.11E-07 | 3.47E-07 | BORA/CENPE/DLGAP5/KIF11/KIF15/KIF23/KIF4A/MAD2L1/NDC80/NEK2/NUF2/NUSAP1/PRC1/SASS6/SPDL1/STIL/TPX2/TTK/BCCIP/CDK5RAP2/CENPJ/CEP192/CEP97/CHMP2B/CKAP5/CLASP2/CLTC/DYNC1H1/GPSM2/HNRNPU/ITGB1/KIF2A/KPNB1/MAP9/MAPRE1/PIBF1/RACGAP1/SMC1A/SMC3/SPICE1/STAG1/STAG2/TACC1/TPR/UBXN2B/VCP/ZW10 | 47 |
| BP | GO:2001251 | negative regulation of chromosome organization | 33/2221 | 93/18614 | 3.09E-09 | 4.24E-07 | 3.58E-07 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TOP2A/TTK/ZWILCH/APC/ATM/ATRX/BAZ1B/CDK5RAP2/ERCC4/GEN1/HNRNPA1/HNRNPU/NBN/PARP1/POT1/RAD21/RAD50/SETMAR/SMARCA5/TNKS2/TPR/USP44/XRN1/ZW10 | 33 |
| BP | GO:0006275 | regulation of DNA replication | 42/2221 | 136/18614 | 3.10E-09 | 4.24E-07 | 3.58E-07 | ATAD5/BLM/BRCA2/CCNA2/CDC6/CDK1/ESCO2/FBXO5/GMNN/MCM3/MCM6/RFC3/RFC4/TICRR/ACTR8/ANKRD17/ATR/ATRX/BAZ1A/CCDC88A/DBF4/DHX9/DNA2/EGF/ESCO1/GTPBP4/JADE1/NBN/NUCKS1/ORC3/PDS5A/PPP2CA/RAD17/RBBP6/SLFN11/SMARCA5/SMC3/TSPYL2/UCHL5/USP37/ZBTB38/ZRANB3 | 42 |
| BP | GO:0000077 | DNA damage checkpoint signaling | 39/2221 | 123/18614 | 4.89E-09 | 6.53E-07 | 5.52E-07 | BLM/BRCA1/BRCA2/BRIP1/CDK1/CHEK1/DTL/FANCD2/MSH2/TICRR/WDR76/ATM/ATR/BRCC3/CCNG1/CDC5L/CLOCK/DTX3L/EIF2AK4/ERCC6/ETAA1/GIGYF2/INTS7/MDM2/NBN/NEK11/PARP9/PRKDC/PTPN11/RAD17/RFWD3/SDE2/STK33/SYF2/TAOK1/TAOK3/THOC1/TOPBP1/TP53BP1 | 39 |
| BP | GO:1904358 | positive regulation of telomere maintenance via telomere lengthening | 19/2221 | 37/18614 | 5.56E-09 | 7.27E-07 | 6.14E-07 | NEK2/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DHX36/DKC1/HNRNPA1/HNRNPA2B1/MAP3K4/POT1/TCP1/TNKS2/XRCC5 | 19 |
| BP | GO:0007051 | spindle organization | 53/2221 | 198/18614 | 8.35E-09 | 1.07E-06 | 9.03E-07 | ASPM/BORA/CCNB2/CENPE/DLGAP5/FBXO5/KIF11/KIF15/KIF23/KIF4A/NDC80/NEK2/NUF2/PRC1/SASS6/SPAG5/STIL/TPX2/TTK/ATRX/BCCIP/CENPJ/CEP120/CEP192/CEP97/CHMP2B/CKAP5/CLASP2/CLTC/DLG1/DYNC1H1/EZR/GPSM2/HAUS6/HNRNPU/KIF2A/KNSTRN/KPNB1/MAP9/MAPRE1/MLH1/NCOR1/PIBF1/RACGAP1/SENP6/SMC1A/SMC3/SPICE1/STAG1/STAG2/TACC1/TPR/VCP | 53 |
| BP | GO:2001252 | positive regulation of chromosome organization | 36/2221 | 111/18614 | 9.65E-09 | 1.21E-06 | 1.02E-06 | NCAPG/NCAPG2/NCAPH/NEK2/ACTR8/ATF7IP/ATM/ATR/ATRX/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DHX36/DKC1/GNL3/HNRNPA1/HNRNPA2B1/LIG4/MAP3K4/NBN/POT1/RAD21/RAD50/SETDB2/SMC2/SMC4/SMC5/TCP1/TNKS2/TPR/UCHL5/XRCC5 | 36 |
| BP | GO:0051383 | kinetochore organization | 14/2221 | 22/18614 | 1.43E-08 | 1.76E-06 | 1.49E-06 | CENPE/CENPF/CENPK/DLGAP5/KNTC1/NDC80/NUF2/CENPC/CENPN/CENPW/MIS12/SENP6/SMC2/SMC4 | 14 |
| BP | GO:0007264 | small GTPase mediated signal transduction | 100/2221 | 483/18614 | 1.86E-08 | 2.24E-06 | 1.89E-06 | ARHGAP11A/ARHGAP11B/CCNA2/ECT2/KIF14/ABCA1/ABL2/AKAP13/ARFGEF1/ARFGEF2/ARHGAP10/ARHGAP12/ARHGAP15/ARHGAP18/ARHGAP21/ARHGAP26/ARHGAP28/ARHGAP29/ARHGAP42/ARHGEF12/CCDC125/CCDC88A/CD2AP/CDON/CGNL1/CHM/CHML/COL3A1/CTNNAL1/CUL3/DENND4A/DENND4C/DOCK10/DOCK11/DOCK2/DOCK5/DOCK7/DOCK8/DOCK9/EPS8/FAM13A/FAM13B/FGD4/G3BP1/G3BP2/GDI2/GPSM2/IGF1/ITGAV/ITGB1/ITSN1/KPNB1/KRAS/KRIT1/MAP4K4/MET/MYO9A/NCKAP1/NET1/NF1/NUCB2/OGT/PIK3CB/PIK3CG/PLD1/PLEKHG1/PREX2/PSD3/RAB18/RABGEF1/RABL3/RACGAP1/RALGAPA1/RALGAPA2/RALGPS2/RAPGEF2/RAPGEF4/RAPGEF5/RAPGEF6/RASA2/RASGEF1B/RASGRF2/RASGRP3/RB1/RDX/RGL1/RHOT1/RIT1/ROCK1/ROCK2/SDCBP/SHOC2/SIPA1L1/SOS1/SOS2/SSX2IP/SWAP70/TRIO/USO1/USP8 | 100 |
| BP | GO:0006403 | RNA localization | 52/2221 | 197/18614 | 1.92E-08 | 2.26E-06 | 1.91E-06 | XPO1/XPOT/AHCTF1/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CKAP5/DHX36/DHX9/DKC1/EIF4A3/FMR1/FYTTD1/G3BP2/HNRNPA1/HNRNPA1L2/HNRNPA2B1/HNRNPA3/HNRNPU/IWS1/KPNB1/LRPPRC/NCBP1/NCBP2/NOP58/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/PHAX/PNPT1/RANBP2/SSB/TCP1/THOC1/THOC2/TPR/UPF2/UPF3B/XPO5/YTHDC1/ZC3H11A/ZNHIT6 | 52 |
| BP | GO:0007052 | mitotic spindle organization | 39/2221 | 130/18614 | 2.73E-08 | 3.16E-06 | 2.67E-06 | BORA/CENPE/DLGAP5/KIF11/KIF15/KIF23/KIF4A/NDC80/NEK2/NUF2/PRC1/SASS6/STIL/TPX2/TTK/BCCIP/CENPJ/CEP192/CEP97/CHMP2B/CKAP5/CLASP2/CLTC/DYNC1H1/GPSM2/HNRNPU/KIF2A/KPNB1/MAP9/PIBF1/RACGAP1/SMC1A/SMC3/SPICE1/STAG1/STAG2/TACC1/TPR/VCP | 39 |
| BP | GO:0000723 | telomere maintenance | 44/2221 | 156/18614 | 2.83E-08 | 3.22E-06 | 2.72E-06 | BLM/BRCA2/NEK2/ACTR8/ATM/ATR/ATRX/CCNE2/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DCLRE1A/DHX36/DKC1/DNA2/ERCC4/GNL3/HNRNPA1/HNRNPA2B1/HNRNPU/HSP90AA1/HSP90AB1/MAP3K4/NBN/PARP1/POT1/PRKDC/RAD50/RFC1/RIF1/SMC5/SMC6/SP100/TCP1/TNKS2/UCHL5/USP7/WRN/XRCC5/XRN1 | 44 |
| BP | GO:1905818 | regulation of chromosome separation | 27/2221 | 73/18614 | 3.00E-08 | 3.34E-06 | 2.82E-06 | BUB1/BUB1B/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NCAPG/NCAPG2/NCAPH/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/CUL3/GEN1/RAD21/RB1/SMC2/SMC4/TPR/USP44/ZW10 | 27 |
| BP | GO:0051054 | positive regulation of DNA metabolic process | 70/2221 | 303/18614 | 3.13E-08 | 3.42E-06 | 2.89E-06 | ATAD5/BRCA1/CDK1/MSH2/NEK2/PRIM2/RAD51AP1/RFC3/RFC4/ACTR2/ACTR8/ARID2/ATM/ATR/ATRX/BAZ1A/BRCC3/BRD7/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DBF4/DHX36/DHX9/DKC1/DNA2/EGF/EPC2/ERCC6/GNL3/GRHL2/HGF/HMGB1/HNRNPA1/HNRNPA2B1/HSP90AA1/HSP90AB1/ING3/MAP3K4/MLH1/MORF4L2/NBN/OTUD4/PARP1/PBRM1/POT1/PRKDC/PTPRC/RAD50/RBBP8/RIF1/SETMAR/SMARCA5/SMCHD1/SPIRE1/TCP1/TFRC/TNKS2/TP53BP1/UCHL5/USP1/USP7/USP9X/WDR48/WRN/XRCC5 | 70 |
| BP | GO:0007098 | centrosome cycle | 40/2221 | 136/18614 | 3.36E-08 | 3.61E-06 | 3.05E-06 | BRCA1/BRCA2/CDK1/CEP135/CHEK1/KIF11/NDC80/NEK2/PLK4/SASS6/STIL/XPO1/XRCC2/ALMS1/CCDC102B/CCNL1/CCP110/CDK5RAP2/CENPJ/CEP120/CEP152/CEP192/CHMP2B/CHORDC1/CKAP5/CNTLN/CTNNB1/GEN1/HAUS6/KIF3A/MAP9/NIN/PCM1/PPP1R12A/ROCK2/SDCCAG8/SLC16A1/SPICE1/SSX2IP/UBXN2B | 40 |
| BP | GO:0051225 | spindle assembly | 39/2221 | 131/18614 | 3.45E-08 | 3.64E-06 | 3.08E-06 | ASPM/CCNB2/FBXO5/KIF11/KIF15/KIF23/KIF4A/NDC80/NEK2/PRC1/SASS6/SPAG5/STIL/TPX2/BCCIP/CENPJ/CEP192/CEP97/CHMP2B/CLASP2/DYNC1H1/GPSM2/HAUS6/HNRNPU/KIF2A/KPNB1/MAP9/MAPRE1/MLH1/NCOR1/PIBF1/RACGAP1/SENP6/SMC1A/SMC3/SPICE1/STAG1/STAG2/TPR | 39 |
| BP | GO:0034502 | protein localization to chromosome | 36/2221 | 116/18614 | 3.52E-08 | 3.65E-06 | 3.08E-06 | BRCA2/BUB1B/CDK1/ESCO2/EZH2/KNTC1/MCM8/MSH2/MTBP/NDC80/SPDL1/TTK/VRK1/ZWILCH/ATR/ATRX/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/GNL3/MIS12/NIPBL/POT1/RAD21/RB1/SMC5/TCP1/TNKS2/VCP/XRCC4/XRCC5/ZW10 | 36 |
| BP | GO:0031023 | microtubule organizing center organization | 43/2221 | 152/18614 | 3.69E-08 | 3.76E-06 | 3.18E-06 | BRCA1/BRCA2/CDK1/CEP135/CHEK1/KIF11/NDC80/NEK2/PLK4/SASS6/STIL/XPO1/XRCC2/ALMS1/CCDC102B/CCNL1/CCP110/CDK5RAP2/CENPJ/CEP120/CEP152/CEP192/CHMP2B/CHORDC1/CKAP5/CLASP2/CNTLN/CTNNB1/GCC2/GEN1/HAUS6/KIF3A/MAP9/MPDZ/NIN/PCM1/PPP1R12A/ROCK2/SDCCAG8/SLC16A1/SPICE1/SSX2IP/UBXN2B | 43 |
| BP | GO:0048193 | Golgi vesicle transport | 68/2221 | 294/18614 | 4.67E-08 | 4.68E-06 | 3.96E-06 | ACSL3/ANK3/AP1AR/ARCN1/ARFGAP3/ARFGEF2/ATP2C1/BLZF1/CCDC93/CNST/COG5/COG6/COPA/COPB1/COPB2/CUL3/EPS15/ERGIC2/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/GCC2/GOLGA4/GOLGA5/GOLT1B/GOPC/KDELR3/KIF16B/LMAN1/LRRK2/MACF1/MIA3/MON2/MYO1B/MYO5A/NAPG/NBAS/NSF/PITPNB/PREPL/PRKCI/PRKD1/RAB1A/RAB8B/RABEP1/RP2/SAR1B/SCFD1/SEC23A/SEC23B/SEC24D/SEC31A/SNX2/SPIRE1/STEAP2/STX17/TRAPPC11/TRAPPC13/TRAPPC8/TRIP11/USO1/VCP/VPS13A/VPS13C/VPS54/ZW10 | 68 |
| BP | GO:0051304 | chromosome separation | 28/2221 | 79/18614 | 4.89E-08 | 4.82E-06 | 4.08E-06 | BUB1/BUB1B/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NCAPG/NCAPG2/NCAPH/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/CUL3/GEN1/RAD21/RB1/SMARCAD1/SMC2/SMC4/TPR/USP44/ZW10 | 28 |
| BP | GO:0000725 | recombinational repair | 47/2221 | 175/18614 | 5.12E-08 | 4.97E-06 | 4.20E-06 | BLM/BRCA1/BRCA2/CHEK1/MCM3/MCM6/MCM8/MMS22L/PARPBP/POLQ/RAD51AP1/RAD54B/XRCC2/ACTR2/ARID2/ATM/CHD4/EPC2/ERCC4/ERCC5/ERCC6/FANCM/FIGNL1/GEN1/ING3/MORF4L2/NBN/NIPBL/NUCKS1/PALB2/PARP1/PPP4R2/PSMD14/RAD21/RBBP8/RECQL/REV3L/RFWD3/RIF1/SAMHD1/SMC5/SMC6/SMCHD1/TP53BP1/WDR48/WRN/XRCC5 | 47 |
| BP | GO:0032212 | positive regulation of telomere maintenance via telomerase | 17/2221 | 34/18614 | 5.96E-08 | 5.69E-06 | 4.81E-06 | NEK2/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DKC1/HNRNPA1/MAP3K4/POT1/TCP1/TNKS2/XRCC5 | 17 |
| BP | GO:0000724 | double-strand break repair via homologous recombination | 46/2221 | 171/18614 | 6.72E-08 | 6.31E-06 | 5.34E-06 | BLM/BRCA1/BRCA2/CHEK1/MCM3/MCM6/MCM8/MMS22L/PARPBP/POLQ/RAD51AP1/RAD54B/XRCC2/ACTR2/ARID2/ATM/CHD4/EPC2/ERCC4/ERCC5/ERCC6/FANCM/FIGNL1/GEN1/ING3/MORF4L2/NBN/NIPBL/NUCKS1/PALB2/PARP1/PPP4R2/PSMD14/RAD21/RBBP8/RECQL/REV3L/RFWD3/RIF1/SAMHD1/SMC5/SMC6/SMCHD1/TP53BP1/WDR48/WRN | 46 |
| BP | GO:0051168 | nuclear export | 45/2221 | 166/18614 | 7.26E-08 | 6.72E-06 | 5.68E-06 | XPO1/XPOT/ABCE1/AHCYL1/AKAP13/CSE1L/CTDSPL2/DHX9/EIF4A3/FYTTD1/HNRNPA1/HNRNPA2B1/HSPA9/IWS1/LSG1/LTV1/MALT1/MDN1/NCBP1/NCBP2/NEMF/NMD3/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP88/NXT2/PHAX/PTPN11/RANBP2/RIOK2/RRS1/SDAD1/SP100/SSB/THOC1/THOC2/TPR/UPF2/XPO4/XPO5/YTHDC1/ZC3H11A | 45 |
| BP | GO:0090068 | positive regulation of cell cycle process | 62/2221 | 262/18614 | 7.52E-08 | 6.86E-06 | 5.80E-06 | ATAD5/CDC6/CDK1/DLGAP5/DTL/ECT2/EZH2/FBXO5/KIF14/KIF20B/KIF23/MAD2L1/MTBP/NCAPG/NCAPG2/NCAPH/NDC80/NUSAP1/PLK4/RAD18/RAD51AP1/SASS6/SPAG5/STIL/ADAM17/ANKRD17/ATRX/BECN1/CENPJ/CEP120/CPSF3/CUL3/DBF4/DDX3X/DYNC1H1/EGF/GEN1/GPSM2/HNRNPU/IGF1/KMT2E/MDM2/PHIP/PKN2/PLCB1/PLRG1/RACGAP1/RAD21/RB1/RDX/ROCK2/RRM1/RRM2B/SMC2/SMC4/SMC5/SMC6/STXBP4/SVIL/THOC1/TPR/UBXN2B | 62 |
| BP | GO:0072594 | establishment of protein localization to organelle | 93/2221 | 453/18614 | 8.85E-08 | 7.95E-06 | 6.72E-06 | BRCA2/CDK1/ECT2/AIFM1/ANGPT1/AP3B1/AP3M1/BECN1/BNIP3L/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CD36/CSE1L/DKC1/DNAJA1/EFCAB7/GCC2/GNPTAB/GRPEL1/HK2/HSP90AA1/HSPA4/HSPA5/HSPA8/HSPD1/IPO11/IPO5/IPO7/IPO8/JAK2/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/LMAN1/LRRK2/NCOA4/NEDD4/NF1/NIPBL/NOLC1/NUP107/NUP133/NUP153/NUP155/NUP88/NXT2/PEX1/PIK3C3/PIK3R1/PIK3R4/PMPCB/POT1/PRKD1/PTGS2/RAB3GAP1/RAB3GAP2/RAB8B/RANBP2/RANBP6/RGPD1/RYR2/SEC62/SEC63/SH3GLB1/SNX16/SPG11/SRP54/SRP72/SRPRB/SSR3/STAM2/TCP1/TIMM21/TNPO1/TOMM34/TPR/UBR5/UFM1/USP9X/VPS13A/VPS13C/VPS13D/VPS41/VPS54/VPS8/ZFYVE16/ZPR1 | 93 |
| BP | GO:0000375 | RNA splicing, via transesterification reactions | 73/2221 | 329/18614 | 9.17E-08 | 8.11E-06 | 6.86E-06 | AQR/CDC40/CDC5L/COIL/CRNKL1/CWC22/CWC27/CWF19L2/DDX1/DDX20/DDX23/DDX46/DDX5/DHX8/DHX9/EIF4A3/FMR1/FXR1/GCFC2/GEMIN5/HNRNPA1/HNRNPA2B1/HNRNPA3/HNRNPH3/HNRNPR/HNRNPU/HSPA8/HTATSF1/LARP7/LUC7L3/METTL14/MFAP1/MPHOSPH10/NCBP1/NCBP2/NCL/NSRP1/PAXBP1/PLRG1/PNN/PPWD1/PRPF18/PRPF39/PRPF4/PRPF40A/PRPF4B/PSIP1/PTBP2/RBM25/RBM39/RBM41/RNPC3/RSRC1/SCAF11/SDE2/SETX/SF3A3/SF3B1/SLU7/SMU1/SNRNP200/SNRPA1/SNW1/SON/SRPK1/SRPK2/SRSF10/SYF2/SYNCRIP/TGS1/WBP4/WTAP/YTHDC1 | 73 |
| BP | GO:1900182 | positive regulation of protein localization to nucleus | 29/2221 | 86/18614 | 9.95E-08 | 8.68E-06 | 7.33E-06 | CDK1/ECT2/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CD2AP/DKC1/DTX3L/EFCAB7/EIF2AK3/FERMT2/HSP90AA1/IPO5/JAK2/LARP7/NMD3/PARP1/PARP9/PIK3R1/PRKD1/PTGS2/TCP1/TFRC/TPR/UBR5/ZPR1 | 29 |
| BP | GO:0032508 | DNA duplex unwinding | 27/2221 | 77/18614 | 1.09E-07 | 9.37E-06 | 7.92E-06 | BLM/BRIP1/MCM3/MCM6/MCM8/POLQ/RAD54B/RFC3/RFC4/TOP2A/ASCC3/CHD1L/CHD8/DDX1/DDX3X/DHX36/DHX9/DNA2/FANCM/G3BP1/NBN/POT1/RAD50/RECQL/SETX/WRN/XRCC5 | 27 |
| BP | GO:1902115 | regulation of organelle assembly | 52/2221 | 207/18614 | 1.11E-07 | 9.39E-06 | 7.94E-06 | BRCA1/CEP135/KIF15/PLK4/SASS6/SPAG5/STIL/ALMS1/ATG3/BECN1/C9orf72/CCDC88A/CCP110/CDK5RAP2/CDKL5/CENPJ/CEP120/CEP97/CHMP2B/CNOT1/CNOT6L/CYLD/DYNC1H1/EZR/G3BP1/G3BP2/GDI2/GPSM2/HNRNPU/IL1RAP/LCP1/LRRK2/LRRTM2/MNS1/MPHOSPH9/MTM1/ODF2L/PIKFYVE/PTPRD/RAB3GAP1/RAB3GAP2/RDX/SCFD1/SDCBP/SDCCAG8/SENP6/SH3GLB1/SNX30/SPICE1/SYNE2/TBC1D30/TPR | 52 |
| BP | GO:0000377 | RNA splicing, via transesterification reactions with bulged adenosine as nucleophile | 72/2221 | 325/18614 | 1.20E-07 | 9.86E-06 | 8.33E-06 | AQR/CDC40/CDC5L/COIL/CRNKL1/CWC22/CWC27/CWF19L2/DDX1/DDX20/DDX23/DDX46/DDX5/DHX8/DHX9/EIF4A3/FMR1/FXR1/GCFC2/GEMIN5/HNRNPA1/HNRNPA2B1/HNRNPA3/HNRNPH3/HNRNPR/HNRNPU/HSPA8/HTATSF1/LARP7/LUC7L3/METTL14/MFAP1/NCBP1/NCBP2/NCL/NSRP1/PAXBP1/PLRG1/PNN/PPWD1/PRPF18/PRPF39/PRPF4/PRPF40A/PRPF4B/PSIP1/PTBP2/RBM25/RBM39/RBM41/RNPC3/RSRC1/SCAF11/SDE2/SETX/SF3A3/SF3B1/SLU7/SMU1/SNRNP200/SNRPA1/SNW1/SON/SRPK1/SRPK2/SRSF10/SYF2/SYNCRIP/TGS1/WBP4/WTAP/YTHDC1 | 72 |
| BP | GO:0000398 | mRNA splicing, via spliceosome | 72/2221 | 325/18614 | 1.20E-07 | 9.86E-06 | 8.33E-06 | AQR/CDC40/CDC5L/COIL/CRNKL1/CWC22/CWC27/CWF19L2/DDX1/DDX20/DDX23/DDX46/DDX5/DHX8/DHX9/EIF4A3/FMR1/FXR1/GCFC2/GEMIN5/HNRNPA1/HNRNPA2B1/HNRNPA3/HNRNPH3/HNRNPR/HNRNPU/HSPA8/HTATSF1/LARP7/LUC7L3/METTL14/MFAP1/NCBP1/NCBP2/NCL/NSRP1/PAXBP1/PLRG1/PNN/PPWD1/PRPF18/PRPF39/PRPF4/PRPF40A/PRPF4B/PSIP1/PTBP2/RBM25/RBM39/RBM41/RNPC3/RSRC1/SCAF11/SDE2/SETX/SF3A3/SF3B1/SLU7/SMU1/SNRNP200/SNRPA1/SNW1/SON/SRPK1/SRPK2/SRSF10/SYF2/SYNCRIP/TGS1/WBP4/WTAP/YTHDC1 | 72 |
| BP | GO:0045839 | negative regulation of mitotic nuclear division | 22/2221 | 56/18614 | 1.63E-07 | 1.33E-05 | 1.12E-05 | BUB1/BUB1B/CENPF/CHEK1/FBXO5/KNTC1/MAD2L1/MTBP/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TOM1L1/TPR/USP44/ZW10 | 22 |
| BP | GO:1904356 | regulation of telomere maintenance via telomere lengthening | 23/2221 | 61/18614 | 2.08E-07 | 1.64E-05 | 1.39E-05 | NEK2/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DHX36/DKC1/ERCC4/HNRNPA1/HNRNPA2B1/HNRNPU/MAP3K4/PARP1/POT1/TCP1/TNKS2/XRCC5/XRN1 | 23 |
| BP | GO:1904869 | regulation of protein localization to Cajal body | 9/2221 | 11/18614 | 2.12E-07 | 1.64E-05 | 1.39E-05 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/LARP7/TCP1 | 9 |
| BP | GO:1904871 | positive regulation of protein localization to Cajal body | 9/2221 | 11/18614 | 2.12E-07 | 1.64E-05 | 1.39E-05 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/LARP7/TCP1 | 9 |
| BP | GO:0032206 | positive regulation of telomere maintenance | 25/2221 | 70/18614 | 2.13E-07 | 1.64E-05 | 1.39E-05 | NEK2/ACTR8/ATM/ATR/ATRX/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DHX36/DKC1/GNL3/HNRNPA1/HNRNPA2B1/MAP3K4/NBN/POT1/RAD50/TCP1/TNKS2/UCHL5/XRCC5 | 25 |
| BP | GO:1903829 | positive regulation of protein localization | 94/2221 | 468/18614 | 2.18E-07 | 1.66E-05 | 1.41E-05 | AGR2/CDK1/CEP135/ECT2/KIF20B/NDC80/VRK1/ACSL3/ACSL4/ADAM9/AKAP5/ANK3/APC/ATP2C1/C2CD5/CCDC88A/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CD2AP/CD38/CENPJ/CEP120/CEP290/CFTR/CNST/CTDSPL2/DKC1/DLG1/DNM1L/DTX3L/EFCAB7/EGF/EIF2AK3/EPB41/EPB41L2/EPHA3/ERBB4/EXOC1/EXPH5/EZR/FERMT2/GNL3/GPSM2/HIF1A/HSP90AA1/HSP90AB1/ICE1/IGF1/IPO5/ITGB1/ITPR1/JAK2/KIF5B/LARP7/MYOM1/NMD3/OSBP/OXCT1/PARP1/PARP9/PCM1/PCSK1/PFKFB2/PIK3R1/PLCB1/PLS1/PPARG/PRKCI/PRKD1/PTGS2/RAPGEF4/RDX/ROCK2/RUFY3/SAR1B/SH3GLB1/SLC5A3/TCP1/TFRC/TLR2/TLR4/TNFAIP6/TPR/TTN/UBR5/VPS35/WNK3/XPO4/ZFAND1/ZPR1 | 94 |
| BP | GO:0032204 | regulation of telomere maintenance | 32/2221 | 104/18614 | 2.48E-07 | 1.84E-05 | 1.56E-05 | NEK2/ACTR8/ATM/ATR/ATRX/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DHX36/DKC1/ERCC4/GNL3/HNRNPA1/HNRNPA2B1/HNRNPU/MAP3K4/NBN/PARP1/POT1/RAD50/SMC5/SMC6/TCP1/TNKS2/UCHL5/USP7/XRCC5/XRN1 | 32 |
| BP | GO:0033045 | regulation of sister chromatid segregation | 32/2221 | 104/18614 | 2.48E-07 | 1.84E-05 | 1.56E-05 | BUB1/BUB1B/CDC6/CENPE/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/ANAPC1/APC/ARID2/ATM/BECN1/BRD7/CDC27/CDK5RAP2/CUL3/GEN1/HNRNPU/PBRM1/RAD21/RB1/RIOK2/TPR/USP44/ZW10 | 32 |
| BP | GO:0033047 | regulation of mitotic sister chromatid segregation | 21/2221 | 53/18614 | 2.62E-07 | 1.92E-05 | 1.62E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/BECN1/CDK5RAP2/GEN1/HNRNPU/RAD21/TPR/USP44/ZW10 | 21 |
| BP | GO:0007091 | metaphase/anaphase transition of mitotic cell cycle | 30/2221 | 95/18614 | 3.11E-07 | 2.25E-05 | 1.91E-05 | BUB1/BUB1B/CDC6/CENPE/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/ANAPC1/APC/ARID2/ATM/BRD7/CDC27/CDK5RAP2/CUL3/GEN1/PBRM1/RAD21/RB1/RIOK2/TPR/USP44/ZW10 | 30 |
| BP | GO:0010965 | regulation of mitotic sister chromatid separation | 22/2221 | 58/18614 | 3.37E-07 | 2.42E-05 | 2.04E-05 | BUB1/BUB1B/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/CUL3/GEN1/RAD21/RB1/TPR/USP44/ZW10 | 22 |
| BP | GO:0010833 | telomere maintenance via telomere lengthening | 27/2221 | 81/18614 | 3.55E-07 | 2.51E-05 | 2.13E-05 | NEK2/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DHX36/DKC1/ERCC4/HNRNPA1/HNRNPA2B1/HNRNPU/HSP90AA1/HSP90AB1/MAP3K4/PARP1/POT1/RAD50/RFC1/TCP1/TNKS2/XRCC5/XRN1 | 27 |
| BP | GO:0070198 | protein localization to chromosome, telomeric region | 15/2221 | 30/18614 | 3.61E-07 | 2.53E-05 | 2.14E-05 | BRCA2/ATR/ATRX/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/GNL3/POT1/TCP1/TNKS2/XRCC5 | 15 |
| BP | GO:0071897 | DNA biosynthetic process | 49/2221 | 198/18614 | 4.14E-07 | 2.86E-05 | 2.42E-05 | CENPF/CHEK1/DTL/NEK2/POLQ/RFC3/RFC4/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DKC1/DNAJC2/GRHL2/HGF/HNRNPA1/HNRNPA2B1/HNRNPU/HSP90AA1/HSP90AB1/JADE1/LIG4/LOX/MAP3K4/PARP4/POLA1/POLD3/POLK/POT1/RAD50/REV1/REV3L/RFC1/RRM1/RRM2B/SPRTN/TCP1/TNKS2/USP1/VCP/WRN/XRCC5/XRN1/ZBTB1 | 49 |
| BP | GO:0071826 | ribonucleoprotein complex subunit organization | 56/2221 | 239/18614 | 4.46E-07 | 3.05E-05 | 2.58E-05 | EIF3M/ATM/ATR/BRIX1/COIL/CRNKL1/DDX1/DDX20/DDX23/DDX46/DHX29/DHX8/DHX9/DICER1/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF5/FASTKD2/GCFC2/GEMIN5/HSP90AA1/HSP90AB1/HTATSF1/KIF5B/LUC7L3/MDN1/NCBP1/NUDT21/NUFIP1/PRKDC/PRPF18/PRPF39/PSIP1/PTBP2/RPF2/RRS1/SCAF11/SETX/SF3A3/SF3B1/SLU7/SNRNP200/SNRPA1/SRPK1/SRPK2/SRSF10/TGS1/VCP/XRCC5/YTHDC1/ZFAND1/ZNHIT6 | 56 |
| BP | GO:0007088 | regulation of mitotic nuclear division | 34/2221 | 117/18614 | 4.80E-07 | 3.25E-05 | 2.74E-05 | BORA/BUB1/BUB1B/CDCA2/CENPF/CHEK1/DLGAP5/FBXO5/KIF20B/KNTC1/MAD2L1/MKI67/MTBP/NDC80/NEK2/NUF2/NUSAP1/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/CUL3/EGF/GEN1/IGF1/PHIP/RAD21/RB1/TOM1L1/TPR/USP44/ZW10 | 34 |
| BP | GO:0006413 | translational initiation | 35/2221 | 123/18614 | 5.71E-07 | 3.81E-05 | 3.22E-05 | EIF3M/ABCE1/BANK1/BZW1/BZW2/CSDE1/DDX1/DDX3X/DHX29/DNAJC3/EIF1AX/EIF2A/EIF2AK2/EIF2AK3/EIF2AK4/EIF2B3/EIF2S1/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF4B/EIF4G2/EIF5/EIF5B/FMR1/IMPACT/MTIF2/NCBP1/NCBP2/NCK1/TPR/YTHDF3 | 35 |
| BP | GO:0044784 | metaphase/anaphase transition of cell cycle | 30/2221 | 98/18614 | 6.59E-07 | 4.35E-05 | 3.68E-05 | BUB1/BUB1B/CDC6/CENPE/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/ANAPC1/APC/ARID2/ATM/BRD7/CDC27/CDK5RAP2/CUL3/GEN1/PBRM1/RAD21/RB1/RIOK2/TPR/USP44/ZW10 | 30 |
| BP | GO:0042770 | signal transduction in response to DNA damage | 46/2221 | 184/18614 | 6.79E-07 | 4.44E-05 | 3.76E-05 | ATAD5/BLM/BRCA1/BRCA2/BRIP1/CDK1/CHEK1/DTL/FANCD2/MSH2/TICRR/WDR76/ATM/ATR/ATRX/BRCC3/CCNG1/CDC5L/CLOCK/DDX5/DTX3L/EIF2AK4/ERCC6/ETAA1/GIGYF2/INTS7/MDM2/MYO6/NBN/NEK11/PARP9/PLA2R1/PRKDC/PTPN11/RAD17/RFWD3/RPS6KA6/SDE2/SP100/STK33/SYF2/TAOK1/TAOK3/THOC1/TOPBP1/TP53BP1 | 46 |
| BP | GO:1903405 | protein localization to nuclear body | 9/2221 | 12/18614 | 7.57E-07 | 4.80E-05 | 4.05E-05 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/LARP7/TCP1 | 9 |
| BP | GO:1904816 | positive regulation of protein localization to chromosome, telomeric region | 9/2221 | 12/18614 | 7.57E-07 | 4.80E-05 | 4.05E-05 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/GNL3/TCP1 | 9 |
| BP | GO:1904867 | protein localization to Cajal body | 9/2221 | 12/18614 | 7.57E-07 | 4.80E-05 | 4.05E-05 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/LARP7/TCP1 | 9 |
| BP | GO:0036092 | phosphatidylinositol-3-phosphate biosynthetic process | 12/2221 | 21/18614 | 8.41E-07 | 5.27E-05 | 4.46E-05 | ATM/BECN1/FIG4/INPP4B/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R3/PIK3R4/PIKFYVE | 12 |
| BP | GO:0051306 | mitotic sister chromatid separation | 22/2221 | 61/18614 | 9.30E-07 | 5.70E-05 | 4.82E-05 | BUB1/BUB1B/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/CUL3/GEN1/RAD21/RB1/TPR/USP44/ZW10 | 22 |
| BP | GO:0045945 | positive regulation of transcription by RNA polymerase III | 11/2221 | 18/18614 | 9.72E-07 | 5.70E-05 | 4.82E-05 | DEK/BAZ1B/CHD8/DDX21/ERCC6/ICE1/ICE2/INHBA/SF3B1/SMARCA5/ZNF143 | 11 |
| BP | GO:0000054 | ribosomal subunit export from nucleus | 10/2221 | 15/18614 | 9.75E-07 | 5.70E-05 | 4.82E-05 | XPO1/ABCE1/LSG1/LTV1/MDN1/NMD3/NUP88/RIOK2/RRS1/SDAD1 | 10 |
| BP | GO:0033750 | ribosome localization | 10/2221 | 15/18614 | 9.75E-07 | 5.70E-05 | 4.82E-05 | XPO1/ABCE1/LSG1/LTV1/MDN1/NMD3/NUP88/RIOK2/RRS1/SDAD1 | 10 |
| BP | GO:0033046 | negative regulation of sister chromatid segregation | 19/2221 | 48/18614 | 9.86E-07 | 5.70E-05 | 4.82E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TPR/USP44/ZW10 | 19 |
| BP | GO:0033048 | negative regulation of mitotic sister chromatid segregation | 19/2221 | 48/18614 | 9.86E-07 | 5.70E-05 | 4.82E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TPR/USP44/ZW10 | 19 |
| BP | GO:0045841 | negative regulation of mitotic metaphase/anaphase transition | 19/2221 | 48/18614 | 9.86E-07 | 5.70E-05 | 4.82E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TPR/USP44/ZW10 | 19 |
| BP | GO:2000816 | negative regulation of mitotic sister chromatid separation | 19/2221 | 48/18614 | 9.86E-07 | 5.70E-05 | 4.82E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TPR/USP44/ZW10 | 19 |
| BP | GO:0044774 | mitotic DNA integrity checkpoint signaling | 27/2221 | 85/18614 | 1.05E-06 | 6.02E-05 | 5.09E-05 | BLM/BRCA1/CDC6/CDK1/CHEK1/DTL/FANCD2/MSH2/TICRR/ATM/BRCC3/CCNG1/GIGYF2/MDM2/NAE1/NBN/NEK11/PRKDC/RAD17/RFWD3/SDE2/SETMAR/STK33/SYF2/TAOK1/TAOK3/TOPBP1 | 27 |
| BP | GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process | 87/2221 | 439/18614 | 1.10E-06 | 6.23E-05 | 5.27E-05 | DTL/KIF14/PBK/PSMA4/UBXN8/XPO1/ANAPC1/ANKIB1/APC/ARIH1/ARMC8/ASCC3/BIRC2/CANX/CCDC47/CD2AP/CDC27/CLOCK/CTNNB1/CUL1/CUL2/CUL3/DNAJC10/EDEM3/ERLIN1/FBXL3/FBXL5/FBXO38/FBXO45/FEM1C/GCLC/HECTD1/HSP90AB1/HSP90B1/HSPA5/LRRK2/LTN1/MDM2/MTM1/NEMF/NFE2L2/NUB1/OGT/PHF20L1/PJA2/PLAA/PSMA3/PSMC1/PSMC2/PSMC6/PSMD1/PSMD12/PSMD14/PSMD2/PSMD6/PSMD7/RHOBTB3/RNF14/RNF19A/RNF217/RYBP/SDCBP/SEL1L/SOCS4/SPOPL/STT3B/TAF1/TBL1XR1/TOPORS/TRIM2/TRIM38/TRIP12/UBE4A/UBR1/UBR2/UBR3/UBXN2B/UBXN4/UCHL5/UFL1/USP14/USP44/USP7/USP9X/VCP/WWP1/YOD1 | 87 |
| BP | GO:0032200 | telomere organization | 46/2221 | 187/18614 | 1.11E-06 | 6.23E-05 | 5.27E-05 | BLM/BRCA2/EZH2/NEK2/ACTR8/ATM/ATR/ATRX/CCNE2/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DCLRE1A/DHX36/DKC1/DNA2/ERCC4/GNL3/HAT1/HNRNPA1/HNRNPA2B1/HNRNPU/HSP90AA1/HSP90AB1/MAP3K4/NBN/PARP1/POT1/PRKDC/RAD50/RFC1/RIF1/SMC5/SMC6/SP100/TCP1/TNKS2/UCHL5/USP7/WRN/XRCC5/XRN1 | 46 |
| BP | GO:0010212 | response to ionizing radiation | 38/2221 | 143/18614 | 1.25E-06 | 6.99E-05 | 5.91E-05 | BLM/BRCA1/BRCA2/ECT2/FANCD2/MSH2/RAD51AP1/RAD54B/TICRR/XRCC2/ATM/ATR/BRCC3/CASP3/CLOCK/DCUN1D3/ERCC6/FIGNL1/HSPA5/IFI16/INTS7/ITGB6/LIG4/MDM2/NET1/NIPBL/NUCKS1/PARP1/PRKDC/PTPRC/RFWD3/TANK/TOPBP1/TP53BP1/VCAM1/WRN/XRCC4/XRCC5 | 38 |
| BP | GO:0030071 | regulation of mitotic metaphase/anaphase transition | 28/2221 | 91/18614 | 1.37E-06 | 7.57E-05 | 6.40E-05 | BUB1/BUB1B/CDC6/CENPE/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ARID2/ATM/BRD7/CDK5RAP2/CUL3/GEN1/PBRM1/RAD21/RB1/RIOK2/TPR/USP44/ZW10 | 28 |
| BP | GO:1904851 | positive regulation of establishment of protein localization to telomere | 8/2221 | 10/18614 | 1.46E-06 | 8.00E-05 | 6.76E-05 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0051310 | metaphase plate congression | 24/2221 | 72/18614 | 1.57E-06 | 8.42E-05 | 7.11E-05 | CENPE/CENPF/KIF14/KIF18A/NDC80/NUF2/SPAG5/SPDL1/BECN1/CENPC/CHMP2B/CUL3/DYNC1H1/EML4/GEM/HNRNPU/KPNB1/MAPRE1/MIS12/MLH1/PIBF1/RRS1/SPICE1/ZW10 | 24 |
| BP | GO:0090307 | mitotic spindle assembly | 24/2221 | 72/18614 | 1.57E-06 | 8.42E-05 | 7.11E-05 | KIF11/KIF15/KIF23/KIF4A/NEK2/PRC1/TPX2/BCCIP/CEP192/CEP97/CHMP2B/CLASP2/HNRNPU/KIF2A/KPNB1/MAP9/PIBF1/RACGAP1/SMC1A/SMC3/SPICE1/STAG1/STAG2/TPR | 24 |
| BP | GO:0006623 | protein targeting to vacuole | 18/2221 | 45/18614 | 1.58E-06 | 8.43E-05 | 7.12E-05 | AP3B1/AP3M1/BECN1/GCC2/GNPTAB/HSPA8/NCOA4/NEDD4/PIK3C3/PIK3R4/SNX16/VPS13A/VPS13C/VPS13D/VPS41/VPS54/VPS8/ZFYVE16 | 18 |
| BP | GO:0006892 | post-Golgi vesicle-mediated transport | 30/2221 | 102/18614 | 1.68E-06 | 8.88E-05 | 7.51E-05 | ACSL3/ANK3/AP1AR/ARFGEF2/ATP2C1/BLZF1/CCDC93/CNST/EPS15/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/GOLGA4/GOPC/KIF16B/MACF1/MON2/MYO1B/MYO5A/NSF/PREPL/RABEP1/RP2/SCFD1/STEAP2/VPS13A/VPS13C/VPS54 | 30 |
| BP | GO:0051784 | negative regulation of nuclear division | 22/2221 | 63/18614 | 1.75E-06 | 9.07E-05 | 7.67E-05 | BUB1/BUB1B/CENPF/CHEK1/FBXO5/KNTC1/MAD2L1/MTBP/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TOM1L1/TPR/USP44/ZW10 | 22 |
| BP | GO:0050000 | chromosome localization | 28/2221 | 92/18614 | 1.75E-06 | 9.07E-05 | 7.67E-05 | CENPE/CENPF/DLGAP5/KIF14/KIF18A/NDC80/NUF2/SPAG5/SPDL1/ACTR2/ACTR3/ATM/BECN1/CENPC/CHMP2B/CUL3/DYNC1H1/EML4/GEM/HNRNPU/KPNB1/MAPRE1/MIS12/MLH1/PIBF1/RRS1/SPICE1/ZW10 | 28 |
| BP | GO:1900180 | regulation of protein localization to nucleus | 36/2221 | 134/18614 | 1.79E-06 | 9.20E-05 | 7.78E-05 | CDK1/ECT2/ANGPT1/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CD2AP/CD36/CTNNA1/DCLK1/DKC1/DTX3L/EFCAB7/EIF2AK3/FERMT2/HSP90AA1/IPO5/JAK2/LARP7/NF1/NMD3/NOLC1/PARP1/PARP9/PIK3R1/PRKD1/PTGS2/TCP1/TFRC/TPR/UBR5/UFM1/ZPR1 | 36 |
| BP | GO:0051056 | regulation of small GTPase mediated signal transduction | 64/2221 | 298/18614 | 1.83E-06 | 9.34E-05 | 7.90E-05 | ARHGAP11A/ARHGAP11B/ECT2/KIF14/ABCA1/ABL2/AKAP13/ARFGEF1/ARFGEF2/ARHGAP10/ARHGAP12/ARHGAP15/ARHGAP18/ARHGAP21/ARHGAP26/ARHGAP28/ARHGAP29/ARHGAP42/ARHGEF12/CCDC125/CD2AP/CDON/CGNL1/COL3A1/CUL3/DENND4A/DENND4C/DOCK2/DOCK8/EPS8/FAM13A/FAM13B/FGD4/IGF1/ITGAV/ITGB1/ITSN1/KRAS/MAP4K4/MET/MYO9A/NET1/NF1/OGT/PIK3CB/PIK3CG/PLEKHG1/PREX2/PSD3/RABGEF1/RABL3/RACGAP1/RALGAPA1/RALGAPA2/RASA2/RASGRF2/RDX/SHOC2/SIPA1L1/SOS1/SOS2/SSX2IP/SWAP70/TRIO | 64 |
| BP | GO:0000910 | cytokinesis | 45/2221 | 185/18614 | 2.00E-06 | 0.000101131 | 8.55E-05 | ANLN/BRCA2/CDC6/CEP55/ECT2/KIF14/KIF20A/KIF20B/KIF23/KIF4A/NUSAP1/PRC1/ACTR2/ACTR3/AHCTF1/ANK3/APC/BECN1/BIRC6/CCP110/CHMP2B/CKAP2/CUL3/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/KLHL13/MAP9/ORC4/PIK3C3/PIK3R4/PKN2/PRPF40A/RACGAP1/RASA1/ROCK1/ROCK2/SH3GLB1/SNX9/SON/SPIRE1/SVIL/USP8 | 45 |
| BP | GO:0051985 | negative regulation of chromosome segregation | 19/2221 | 50/18614 | 2.05E-06 | 0.000101131 | 8.55E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TPR/USP44/ZW10 | 19 |
| BP | GO:1902100 | negative regulation of metaphase/anaphase transition of cell cycle | 19/2221 | 50/18614 | 2.05E-06 | 0.000101131 | 8.55E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TPR/USP44/ZW10 | 19 |
| BP | GO:1905819 | negative regulation of chromosome separation | 19/2221 | 50/18614 | 2.05E-06 | 0.000101131 | 8.55E-05 | BUB1/BUB1B/CENPF/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/RAD21/TPR/USP44/ZW10 | 19 |
| BP | GO:0007064 | mitotic sister chromatid cohesion | 14/2221 | 30/18614 | 2.56E-06 | 0.000124813 | 0.000105482 | ESCO2/ATRX/ESCO1/NAA50/NIPBL/PDS5A/PDS5B/RAD21/RB1/SMC1A/SMC3/SMC5/STAG1/STAG2 | 14 |
| BP | GO:0007004 | telomere maintenance via telomerase | 23/2221 | 69/18614 | 2.57E-06 | 0.000124813 | 0.000105482 | NEK2/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DKC1/HNRNPA1/HNRNPU/HSP90AA1/HSP90AB1/MAP3K4/POT1/RAD50/RFC1/TCP1/TNKS2/XRCC5/XRN1 | 23 |
| BP | GO:2000573 | positive regulation of DNA biosynthetic process | 24/2221 | 74/18614 | 2.72E-06 | 0.000131041 | 0.000110745 | NEK2/RFC3/RFC4/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DKC1/GRHL2/HGF/HNRNPA1/HSP90AA1/HSP90AB1/MAP3K4/POT1/TCP1/TNKS2/USP1/XRCC5 | 24 |
| BP | GO:1902099 | regulation of metaphase/anaphase transition of cell cycle | 28/2221 | 94/18614 | 2.81E-06 | 0.000133935 | 0.00011319 | BUB1/BUB1B/CDC6/CENPE/CENPF/DLGAP5/FBXO5/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ARID2/ATM/BRD7/CDK5RAP2/CUL3/GEN1/PBRM1/RAD21/RB1/RIOK2/TPR/USP44/ZW10 | 28 |
| BP | GO:0044818 | mitotic G2/M transition checkpoint | 19/2221 | 51/18614 | 2.90E-06 | 0.000137591 | 0.000116281 | BLM/BRCA1/CDC6/CDK1/CHEK1/DTL/TICRR/ATM/BRCC3/CCNG1/NAE1/NBN/RAD17/RAD50/RBBP8/SYF2/TAOK1/TAOK3/TOPBP1 | 19 |
| BP | GO:0032727 | positive regulation of interferon-alpha production | 12/2221 | 23/18614 | 3.07E-06 | 0.000144437 | 0.000122066 | CHUK/DDX3X/DHX36/DHX9/HSPD1/IFIH1/RIPK2/STAT1/TBK1/TLR3/TLR4/TLR8 | 12 |
| BP | GO:0051053 | negative regulation of DNA metabolic process | 38/2221 | 148/18614 | 3.10E-06 | 0.000144609 | 0.000122211 | BLM/BRCA2/CDC6/CHEK1/FBXO5/GMNN/MSH2/PARPBP/POLQ/ATM/ATR/DNAJC2/ERCC4/ERCC6/GTPBP4/HNRNPA1/HNRNPU/MLH1/MSH3/MSH6/NBN/PARP1/PDS5A/POT1/RAD17/RAD50/RIF1/SLFN11/SMCHD1/THOC1/TNKS2/TP53BP1/TRIP12/TSPYL2/UBR5/XRCC5/XRN1/ZRANB3 | 38 |
| BP | GO:0046037 | GMP metabolic process | 13/2221 | 27/18614 | 3.79E-06 | 0.000175547 | 0.000148358 | ADK/ATIC/CASK/DLG1/DLG2/GART/GMPS/IMPDH2/MAGI3/MPP1/NT5C2/PAICS/PPAT | 13 |
| BP | GO:0022618 | ribonucleoprotein complex assembly | 52/2221 | 231/18614 | 4.00E-06 | 0.000183845 | 0.00015537 | EIF3M/ATM/ATR/BRIX1/COIL/CRNKL1/DDX1/DDX20/DDX23/DDX46/DHX29/DHX9/DICER1/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF5/FASTKD2/GCFC2/GEMIN5/HSP90AA1/HSP90AB1/HTATSF1/LUC7L3/MDN1/NCBP1/NUDT21/NUFIP1/PRKDC/PRPF18/PRPF39/PSIP1/PTBP2/RPF2/RRS1/SCAF11/SETX/SF3A3/SF3B1/SLU7/SNRNP200/SNRPA1/SRPK1/SRPK2/SRSF10/TGS1/XRCC5/YTHDC1/ZNHIT6 | 52 |
| BP | GO:0045943 | positive regulation of transcription by RNA polymerase I | 15/2221 | 35/18614 | 4.22E-06 | 0.000192286 | 0.000162504 | DEK/BAZ1B/DDX21/EIF2AK3/ERCC6/HEATR1/LYAR/NCL/NOL11/PWP1/SF3B1/SMARCA5/UTP15/WDR43/WDR75 | 15 |
| BP | GO:0030865 | cortical cytoskeleton organization | 18/2221 | 48/18614 | 4.74E-06 | 0.000214226 | 0.000181046 | ANLN/ECT2/AKAP11/DLG1/EPB41/EPB41L2/EPB41L3/EZR/FMNL2/LCP1/NCKAP1/NCKAP1L/NLGN1/PLS1/PPP2R3C/RACGAP1/ROCK1/ROCK2 | 18 |
| BP | GO:0070203 | regulation of establishment of protein localization to telomere | 8/2221 | 11/18614 | 4.80E-06 | 0.00021536 | 0.000182004 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0046822 | regulation of nucleocytoplasmic transport | 30/2221 | 107/18614 | 4.97E-06 | 0.000220951 | 0.000186729 | CDK1/ECT2/XPO1/ANGPT1/CD36/CTDSPL2/DHX9/EFCAB7/HSP90AA1/IPO5/IWS1/JAK2/NCBP2/NEDD4/NF1/NOLC1/NSUN2/NUP153/PIK3R1/PPP1R12A/PRKD1/PTGS2/PTPN11/RIOK2/SP100/TPR/UBR5/UFM1/XPO4/ZPR1 | 30 |
| BP | GO:0051382 | kinetochore assembly | 10/2221 | 17/18614 | 5.03E-06 | 0.000220951 | 0.000186729 | CENPE/CENPF/CENPK/DLGAP5/KNTC1/CENPC/CENPN/CENPW/MIS12/SENP6 | 10 |
| BP | GO:0070200 | establishment of protein localization to telomere | 10/2221 | 17/18614 | 5.03E-06 | 0.000220951 | 0.000186729 | BRCA2/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/POT1/TCP1 | 10 |
| BP | GO:1904814 | regulation of protein localization to chromosome, telomeric region | 9/2221 | 14/18614 | 5.50E-06 | 0.000238118 | 0.000201237 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/GNL3/TCP1 | 9 |
| BP | GO:1990173 | protein localization to nucleoplasm | 9/2221 | 14/18614 | 5.50E-06 | 0.000238118 | 0.000201237 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/LARP7/TCP1 | 9 |
| BP | GO:0032210 | regulation of telomere maintenance via telomerase | 19/2221 | 53/18614 | 5.64E-06 | 0.000242147 | 0.000204642 | NEK2/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DKC1/HNRNPA1/HNRNPU/MAP3K4/POT1/TCP1/TNKS2/XRCC5/XRN1 | 19 |
| BP | GO:0051236 | establishment of RNA localization | 40/2221 | 163/18614 | 5.77E-06 | 0.000245995 | 0.000207894 | XPO1/XPOT/AHCTF1/ATM/ATR/CKAP5/DHX9/EIF4A3/FMR1/FYTTD1/G3BP2/HNRNPA1/HNRNPA1L2/HNRNPA2B1/HNRNPA3/IWS1/KPNB1/LRPPRC/NCBP1/NCBP2/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/PHAX/PNPT1/RANBP2/SSB/THOC1/THOC2/TPR/UPF2/UPF3B/XPO5/YTHDC1/ZC3H11A | 40 |
| BP | GO:0006446 | regulation of translational initiation | 25/2221 | 82/18614 | 5.96E-06 | 0.000252429 | 0.000213331 | BANK1/BZW1/BZW2/CSDE1/DDX1/DDX3X/DHX29/DNAJC3/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/EIF3E/EIF4B/EIF4G2/EIF5/EIF5B/FMR1/IMPACT/MTIF2/NCBP1/NCBP2/NCK1/TPR/YTHDF3 | 25 |
| BP | GO:0030866 | cortical actin cytoskeleton organization | 16/2221 | 40/18614 | 6.00E-06 | 0.000252429 | 0.000213331 | ANLN/ECT2/AKAP11/DLG1/EPB41/EPB41L2/EPB41L3/EZR/FMNL2/LCP1/NCKAP1/NCKAP1L/PLS1/RACGAP1/ROCK1/ROCK2 | 16 |
| BP | GO:0010165 | response to X-ray | 14/2221 | 32/18614 | 6.59E-06 | 0.000271405 | 0.000229368 | BLM/BRCA2/MSH2/XRCC2/ATM/BRCC3/CASP3/ERCC6/LIG4/NIPBL/NUCKS1/TP53BP1/XRCC4/XRCC5 | 14 |
| BP | GO:0071539 | protein localization to centrosome | 14/2221 | 32/18614 | 6.59E-06 | 0.000271405 | 0.000229368 | SPAG5/STIL/APC/CCDC14/CEP192/CEP350/CEP83/GOLGB1/HOOK3/MAPRE1/PCM1/PIBF1/SNX10/UBXN2B | 14 |
| BP | GO:0045088 | regulation of innate immune response | 74/2221 | 373/18614 | 6.59E-06 | 0.000271405 | 0.000229368 | AIM2/ALPK1/ANKRD17/AP3B1/ARG1/BIRC2/BIRC3/BTK/CASP1/CD226/CD36/CD96/CFH/COLEC12/CR1/CTSS/CYLD/DDX3X/DDX60/DHX9/GBP5/HAVCR2/HMGB1/HMGB2/HSP90AA1/HSPD1/IFI16/IFIH1/IL18RAP/IRAK3/IRAK4/LACC1/LRP8/LYAR/LYN/MAP3K7/MATR3/MIR181B1/MNDA/NAIP/NFE2L2/NLRC4/NLRP3/OTUD4/PARP1/PARP14/PARP9/PIK3AP1/PJA2/POLR3B/POLR3C/PPARG/PRKDC/PTPN11/PTPN2/PUM2/RAB11FIP2/RIOK3/RIPK2/RPS6KA3/SAMHD1/TBK1/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/TRIM6/USP15/USP27X/XRCC5/YTHDF3/ZNFX1 | 74 |
| BP | GO:0030490 | maturation of SSU-rRNA | 19/2221 | 54/18614 | 7.73E-06 | 0.000316237 | 0.000267257 | BMS1/DDX52/HEATR1/MPHOSPH10/NGDN/NOL10/NOL11/RIOK1/RIOK2/RIOK3/RRS1/SRFBP1/TSR1/UTP20/UTP23/UTP3/UTP6/WDR3/WDR43 | 19 |
| BP | GO:0062197 | cellular response to chemical stress | 70/2221 | 349/18614 | 7.87E-06 | 0.000319709 | 0.000270191 | CDK1/ECT2/EZH2/FANCD2/GSKIP/HDAC2/MELK/AIFM1/ARG1/ATM/ATP2A2/ATP7A/BECN1/BTK/CAB39/CAPN3/CASP1/CASP3/CD36/CHUK/CTNNB1/DDX3X/DNAJA1/EIF2AK3/EIF2S1/ERCC6L2/FAS/FER/FUT8/GPX8/HGF/HIF1A/IL18RAP/IMPACT/JAK2/LRRC8D/LRRK2/MET/NCOA7/NET1/NFAT5/NFE2L2/NLRP3/OSER1/OXR1/OXSR1/PARP1/PDGFD/PDGFRA/PIK3CA/PLA2R1/PNPLA8/PNPT1/PRKD1/PTGS2/PTPRK/PYROXD1/RIPK1/SETX/SLC7A11/TLR4/TLR6/TPM1/USP15/VNN1/VRK2/WNK3/XRCC5/ZNF277/ZNF622 | 70 |
| BP | GO:0070646 | protein modification by small protein removal | 42/2221 | 177/18614 | 8.41E-06 | 0.000339653 | 0.000287046 | BRCA1/CDK1/BRCC3/COPS2/COPS4/CYLD/MYSM1/OTUD4/OTUD6B/PSMD14/SENP1/SENP5/SENP6/SENP7/SUPT20H/TAF2/TAF7/TANK/UCHL3/UCHL5/USP1/USP13/USP14/USP15/USP16/USP24/USP25/USP27X/USP32/USP34/USP37/USP38/USP44/USP47/USP53/USP7/USP8/USP9X/USPL1/VCP/YOD1/ZRANB1 | 42 |
| BP | GO:0006338 | chromatin remodeling | 78/2221 | 402/18614 | 8.79E-06 | 0.000352546 | 0.000297942 | CHEK1/DEK/EZH2/HDAC2/HELLS/RAD54B/ACTR8/ARID2/ATF7IP/ATRX/BAZ1A/BAZ1B/BAZ2B/BRD7/BTAF1/CENPW/CHD1/CHD1L/CHD2/CHD4/CHD6/CHD7/CHD8/CHD9/CTR9/DDX21/DDX23/ERCC6/ERCC6L2/HAT1/HCFC2/HLTF/HMGB1/HMGB2/KAT6A/KDM4C/KDM5A/KDM5B/KDM6A/L3MBTL3/LMNB1/MECOM/MYSM1/NAP1L1/NASP/NFAT5/PBRM1/PIK3CA/RB1/RBBP5/RIF1/RSF1/RYBP/SETD7/SETDB2/SF3B1/SHPRH/SMARCA1/SMARCA5/SMARCAD1/SMCHD1/SPTY2D1/SRPK2/SUPT16H/SUV39H2/SUZ12/TOP1/TPR/TRIP12/TSPYL2/TTF2/UBR2/UBR5/UCHL5/ZBTB1/ZDBF2/ZNFX1/ZRANB3 | 78 |
| BP | GO:0000281 | mitotic cytokinesis | 25/2221 | 84/18614 | 9.57E-06 | 0.000378742 | 0.00032008 | ANLN/CEP55/ECT2/KIF20A/KIF20B/KIF23/KIF4A/NUSAP1/ANK3/APC/CHMP2B/CKAP2/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/MAP9/RACGAP1/RASA1/ROCK1/ROCK2/SNX9/SON/USP8 | 25 |
| BP | GO:0051303 | establishment of chromosome localization | 25/2221 | 84/18614 | 9.57E-06 | 0.000378742 | 0.00032008 | CENPE/CENPF/KIF14/KIF18A/NDC80/NUF2/SPAG5/SPDL1/ATM/BECN1/CENPC/CHMP2B/CUL3/DYNC1H1/EML4/GEM/HNRNPU/KPNB1/MAPRE1/MIS12/MLH1/PIBF1/RRS1/SPICE1/ZW10 | 25 |
| BP | GO:0043087 | regulation of GTPase activity | 72/2221 | 364/18614 | 9.72E-06 | 0.000382004 | 0.000322837 | ARHGAP11A/ECT2/EZH2/WDR41/ARAP2/ARFGEF1/ARHGAP12/ARHGAP15/ARHGAP29/ARHGAP42/C9orf72/CCDC125/CCPG1/CDKL5/CORO1C/DOCK10/DOCK11/DOCK7/DOCK8/DOCK9/EIF2S1/EPHA3/EPHA4/EVI5/FERMT2/FGD4/FGD6/GAPVD1/IQGAP1/IQGAP2/ITGA6/ITGB1/LRRK2/MAP4K4/MET/MKKS/MYO9A/NET1/NF1/PLXNC1/RAB11FIP2/RAB3GAP1/RAB3GAP2/RABGAP1/RALGAPA1/RALGAPA2/RALGPS2/RAP1GDS1/RAPGEF2/RAPGEF4/RAPGEF5/RAPGEF6/RASA1/RASA2/RASAL2/RASGEF1B/RASGRF2/RASGRP3/RDX/RGL1/RGS1/RICTOR/SIPA1L1/SNX13/SNX9/SOS1/SOS2/TBC1D15/TBC1D30/TBC1D4/TBC1D8B/ZC3H15 | 72 |
| BP | GO:0070507 | regulation of microtubule cytoskeleton organization | 38/2221 | 155/18614 | 1.00E-05 | 0.000390266 | 0.000329819 | BORA/KIF15/KIF18A/SASS6/SKA3/SPAG5/STIL/TPX2/AKAP9/APC/CAMSAP2/CDK5RAP2/CENPJ/CEP70/CEP97/CHMP2B/CKAP2/CKAP5/CLASP2/CLIP1/CLTC/CYLD/DYNC1H1/EPHA3/GPSM2/HNRNPU/MAP1B/MAP9/MAPRE1/MET/MPDZ/NAV3/PHLDB2/ROCK1/SENP6/TAOK1/TPR/WDR47 | 38 |
| BP | GO:0032607 | interferon-alpha production | 13/2221 | 29/18614 | 1.02E-05 | 0.000390266 | 0.000329819 | CHUK/DDX3X/DHX36/DHX9/HAVCR2/HSPD1/IFIH1/RIPK2/STAT1/TBK1/TLR3/TLR4/TLR8 | 13 |
| BP | GO:0032647 | regulation of interferon-alpha production | 13/2221 | 29/18614 | 1.02E-05 | 0.000390266 | 0.000329819 | CHUK/DDX3X/DHX36/DHX9/HAVCR2/HSPD1/IFIH1/RIPK2/STAT1/TBK1/TLR3/TLR4/TLR8 | 13 |
| BP | GO:0034508 | centromere complex assembly | 13/2221 | 29/18614 | 1.02E-05 | 0.000390266 | 0.000329819 | CENPE/CENPF/CENPK/DLGAP5/HELLS/KNTC1/CENPC/CENPN/CENPW/MIS12/NASP/RB1/SENP6 | 13 |
| BP | GO:0000082 | G1/S transition of mitotic cell cycle | 54/2221 | 251/18614 | 1.08E-05 | 0.00040698 | 0.000343945 | CDC6/CDKN3/EZH2/KIF14/MTBP/SASS6/STIL/ADAM17/ANKRD17/APC/ARID2/ATM/BACH1/BCAT1/BRD7/CCNE2/CCNH/CENPJ/CPSF3/CUL1/CUL2/CUL3/DBF4/DCUN1D3/DDX3X/DLG1/E2F6/ECD/GIGYF2/GPNMB/GSPT1/INHBA/ITGB1/JADE1/KMT2E/MDM2/MIR15B/MIR30C2/NPAT/PBRM1/PLCB1/PLRG1/PPP2CA/PRKDC/RB1/RBBP8/RBL2/RDX/RFWD3/RRM1/SDE2/SLFN11/USP37/ZPR1 | 54 |
| BP | GO:0007094 | mitotic spindle assembly checkpoint signaling | 17/2221 | 46/18614 | 1.09E-05 | 0.00040698 | 0.000343945 | BUB1/BUB1B/CENPF/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/TPR/USP44/ZW10 | 17 |
| BP | GO:0071173 | spindle assembly checkpoint signaling | 17/2221 | 46/18614 | 1.09E-05 | 0.00040698 | 0.000343945 | BUB1/BUB1B/CENPF/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/TPR/USP44/ZW10 | 17 |
| BP | GO:0071174 | mitotic spindle checkpoint signaling | 17/2221 | 46/18614 | 1.09E-05 | 0.00040698 | 0.000343945 | BUB1/BUB1B/CENPF/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/TPR/USP44/ZW10 | 17 |
| BP | GO:0010972 | negative regulation of G2/M transition of mitotic cell cycle | 21/2221 | 65/18614 | 1.21E-05 | 0.000447725 | 0.000378379 | BLM/BRCA1/CDC6/CDK1/CHEK1/DTL/TICRR/ATM/BRCC3/CCNG1/NAE1/NBN/RAD17/RAD21/RAD50/RBBP8/SYF2/TAOK1/TAOK3/TOPBP1/USP47 | 21 |
| BP | GO:0006278 | RNA-templated DNA biosynthetic process | 23/2221 | 75/18614 | 1.25E-05 | 0.00045761 | 0.000386733 | NEK2/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DKC1/HNRNPA1/HNRNPU/HSP90AA1/HSP90AB1/MAP3K4/POT1/RAD50/RFC1/TCP1/TNKS2/XRCC5/XRN1 | 23 |
| BP | GO:0071479 | cellular response to ionizing radiation | 23/2221 | 75/18614 | 1.25E-05 | 0.00045761 | 0.000386733 | BLM/BRCA1/BRCA2/ECT2/RAD51AP1/ATM/ATR/BRCC3/CLOCK/FIGNL1/HSPA5/IFI16/INTS7/ITGB6/LIG4/MDM2/NET1/NIPBL/NUCKS1/TANK/TP53BP1/WRN/XRCC5 | 23 |
| BP | GO:0051783 | regulation of nuclear division | 36/2221 | 145/18614 | 1.26E-05 | 0.000457868 | 0.000386951 | BORA/BUB1/BUB1B/CDCA2/CENPF/CHEK1/DLGAP5/FBXO5/KIF20B/KNTC1/MAD2L1/MKI67/MTBP/NDC80/NEK2/NUF2/NUSAP1/RAD51AP1/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/CUL3/EGF/GEN1/IGF1/PHIP/PLCB1/RAD21/RB1/TOM1L1/TPR/USP44/ZW10 | 36 |
| BP | GO:0070202 | regulation of establishment of protein localization to chromosome | 8/2221 | 12/18614 | 1.29E-05 | 0.000466637 | 0.000394362 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0032728 | positive regulation of interferon-beta production | 15/2221 | 38/18614 | 1.42E-05 | 0.000510383 | 0.000431332 | DDX3X/DHX9/HMGB2/HSP90AA1/IFIH1/POLR3B/POLR3C/PTPN11/RIOK3/RIPK2/TBK1/TLR2/TLR3/TLR4/TLR8 | 15 |
| BP | GO:0031577 | spindle checkpoint signaling | 17/2221 | 47/18614 | 1.52E-05 | 0.000543468 | 0.000459293 | BUB1/BUB1B/CENPF/KNTC1/MAD2L1/NDC80/NUF2/SPDL1/TTK/ZWILCH/APC/ATM/CDK5RAP2/GEN1/TPR/USP44/ZW10 | 17 |
| BP | GO:1905508 | protein localization to microtubule organizing center | 14/2221 | 34/18614 | 1.54E-05 | 0.000548905 | 0.000463888 | SPAG5/STIL/APC/CCDC14/CEP192/CEP350/CEP83/GOLGB1/HOOK3/MAPRE1/PCM1/PIBF1/SNX10/UBXN2B | 14 |
| BP | GO:0044773 | mitotic DNA damage checkpoint signaling | 24/2221 | 81/18614 | 1.56E-05 | 0.000551101 | 0.000465744 | BLM/BRCA1/CDK1/CHEK1/DTL/FANCD2/MSH2/TICRR/ATM/BRCC3/CCNG1/GIGYF2/MDM2/NBN/NEK11/PRKDC/RAD17/RFWD3/SDE2/STK33/SYF2/TAOK1/TAOK3/TOPBP1 | 24 |
| BP | GO:0006359 | regulation of transcription by RNA polymerase III | 13/2221 | 30/18614 | 1.60E-05 | 0.000563359 | 0.000476103 | DEK/BAZ1B/CHD8/DDX21/DHX36/ERCC6/ICE1/ICE2/INHBA/POLR3C/SF3B1/SMARCA5/ZNF143 | 13 |
| BP | GO:0008608 | attachment of spindle microtubules to kinetochore | 16/2221 | 43/18614 | 1.78E-05 | 0.000620895 | 0.000524728 | CENPE/ECT2/NDC80/NEK2/NUF2/SPAG5/APC/BECN1/CENPC/EML4/HNRNPU/KNSTRN/MAPRE1/MIS12/RACGAP1/RB1 | 16 |
| BP | GO:0002831 | regulation of response to biotic stimulus | 86/2221 | 463/18614 | 1.79E-05 | 0.000620895 | 0.000524728 | AIM2/ALPK1/ANKRD17/AP3B1/ARG1/BIRC2/BIRC3/BTK/CASP1/CD180/CD226/CD36/CD96/CFH/COLEC12/CR1/CTSS/CYLD/DDX3X/DDX60/DHX9/DTX3L/EIF2AK4/ELMOD2/FBXO38/FGL2/GBP5/HAVCR2/HMGB1/HMGB2/HSP90AA1/HSPD1/IFI16/IFIH1/IL18RAP/IRAK3/IRAK4/LACC1/LRP8/LYAR/LYN/MAP3K7/MATR3/MIR181B1/MNDA/NAIP/NFE2L2/NLRC4/NLRP3/OTUD4/PARP1/PARP14/PARP9/PIK3AP1/PJA2/POLR3B/POLR3C/PPARG/PPM1B/PPP2R3C/PRKDC/PTPN11/PTPN2/PUM2/RAB11FIP2/RIOK3/RIPK2/RPS6KA3/SAMHD1/SPINK5/STAT1/TBK1/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/TRIM38/TRIM44/TRIM6/USP15/USP27X/XRCC5/YTHDF3/ZNFX1 | 86 |
| BP | GO:0016482 | cytosolic transport | 41/2221 | 177/18614 | 1.98E-05 | 0.000681582 | 0.000576015 | ACTR2/AP1AR/BECN1/CLTC/DNAJC13/EEA1/EPS15/ERC1/EVI5/EZR/GCC2/GOLT1B/HEATR5A/HEATR5B/HOOK1/HOOK3/KIF16B/KIF5B/LRRK2/MON2/MTMR2/PIK3C3/PIK3R4/PIKFYVE/PREPL/RDX/RHOBTB3/SNX16/SNX2/SNX6/SPAG9/SRSF10/TANC2/TBC1D23/TMEM87A/USP7/VPS13A/VPS13C/VPS26A/VPS35/VPS54 | 41 |
| BP | GO:0032481 | positive regulation of type I interferon production | 20/2221 | 62/18614 | 1.98E-05 | 0.000681582 | 0.000576015 | CHUK/DDX3X/DHX36/DHX9/G3BP1/HMGB2/HSP90AA1/HSPD1/IFIH1/POLR3B/POLR3C/PTPN11/RIOK3/RIPK2/STAT1/TBK1/TLR2/TLR3/TLR4/TLR8 | 20 |
| BP | GO:1902750 | negative regulation of cell cycle G2/M phase transition | 21/2221 | 67/18614 | 2.03E-05 | 0.000694971 | 0.000587331 | BLM/BRCA1/CDC6/CDK1/CHEK1/DTL/TICRR/ATM/BRCC3/CCNG1/NAE1/NBN/RAD17/RAD21/RAD50/RBBP8/SYF2/TAOK1/TAOK3/TOPBP1/USP47 | 21 |
| BP | GO:0045132 | meiotic chromosome segregation | 29/2221 | 109/18614 | 2.14E-05 | 0.000725868 | 0.000613442 | ASPM/BRIP1/BUB1/BUB1B/CCNB2/FANCD2/FBXO5/MND1/NCAPH/NDC80/NUF2/TOP2A/TTK/ACTR2/ACTR3/ATM/CCNE2/CENPC/ERCC4/FANCM/MLH1/MLH3/RAD21/SMC1A/SMC2/SMC3/SMC4/SYCP2/TOP2B | 29 |
| BP | GO:0050657 | nucleic acid transport | 38/2221 | 160/18614 | 2.17E-05 | 0.000728685 | 0.000615823 | XPO1/XPOT/AHCTF1/CKAP5/DHX9/EIF4A3/FMR1/FYTTD1/G3BP2/HNRNPA1/HNRNPA1L2/HNRNPA2B1/HNRNPA3/IWS1/KPNB1/LRPPRC/NCBP1/NCBP2/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/PHAX/PNPT1/RANBP2/SSB/THOC1/THOC2/TPR/UPF2/UPF3B/XPO5/YTHDC1/ZC3H11A | 38 |
| BP | GO:0050658 | RNA transport | 38/2221 | 160/18614 | 2.17E-05 | 0.000728685 | 0.000615823 | XPO1/XPOT/AHCTF1/CKAP5/DHX9/EIF4A3/FMR1/FYTTD1/G3BP2/HNRNPA1/HNRNPA1L2/HNRNPA2B1/HNRNPA3/IWS1/KPNB1/LRPPRC/NCBP1/NCBP2/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/PHAX/PNPT1/RANBP2/SSB/THOC1/THOC2/TPR/UPF2/UPF3B/XPO5/YTHDC1/ZC3H11A | 38 |
| BP | GO:0007095 | mitotic G2 DNA damage checkpoint signaling | 14/2221 | 35/18614 | 2.29E-05 | 0.000764928 | 0.000646452 | BLM/BRCA1/CDK1/CHEK1/DTL/TICRR/ATM/BRCC3/CCNG1/NBN/SYF2/TAOK1/TAOK3/TOPBP1 | 14 |
| BP | GO:0045787 | positive regulation of cell cycle | 69/2221 | 354/18614 | 2.43E-05 | 0.000808873 | 0.00068359 | ATAD5/BRCA2/CDC6/CDK1/CHEK1/DLGAP5/DTL/ECT2/EZH2/FBXO5/KIF14/KIF20B/KIF23/MAD2L1/MTBP/NCAPG/NCAPG2/NCAPH/NDC80/NUSAP1/PLK4/RAD18/RAD51AP1/SASS6/SPAG5/STIL/ADAM17/ANKRD17/ATRX/BECN1/CCPG1/CENPJ/CEP120/CPSF3/CUL3/DBF4/DDX3X/DYNC1H1/EGF/GEN1/GPSM2/HNRNPU/IGF1/KMT2E/LRP6/MDM2/PHIP/PKN2/PLCB1/PLRG1/PTPN11/RACGAP1/RAD21/RB1/RDX/ROCK2/RRM1/RRM2B/SMC2/SMC4/SMC5/SMC6/SRPK2/STXBP4/SVIL/THOC1/TPR/UBXN2B/ZPR1 | 69 |
| BP | GO:0046777 | protein autophosphorylation | 49/2221 | 227/18614 | 2.46E-05 | 0.000813923 | 0.000687859 | MELK/NEK2/TTK/VRK1/ATM/ATR/BMX/BTK/CDKL5/CLK4/DDX3X/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/ENPP1/EPHA4/ERBB4/FER/FLT1/GPNMB/IMPACT/IRAK3/JAK2/LRRK2/LYN/MAP3K13/NBN/OXSR1/PDGFC/PDGFD/PDGFRA/PIKFYVE/PRKD1/PTPRC/RAD50/RB1CC1/RIOK2/RIPK1/SLK/STK33/TAF1/TAOK1/TAOK3/TNIK/TOM1L1/TRPM7/VRK2/WNK3 | 49 |
| BP | GO:0006893 | Golgi to plasma membrane transport | 19/2221 | 58/18614 | 2.49E-05 | 0.000818096 | 0.000691385 | ACSL3/ANK3/ARFGEF2/ATP2C1/BLZF1/CCDC93/CNST/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/GOLGA4/GOPC/MACF1/NSF/PREPL/RABEP1/STEAP2 | 19 |
| BP | GO:2000278 | regulation of DNA biosynthetic process | 31/2221 | 121/18614 | 2.54E-05 | 0.00083093 | 0.000702231 | CHEK1/NEK2/RFC3/RFC4/ATM/ATR/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CTNNB1/DKC1/DNAJC2/GRHL2/HGF/HNRNPA1/HNRNPA2B1/HNRNPU/HSP90AA1/HSP90AB1/JADE1/MAP3K4/PARP4/POT1/TCP1/TNKS2/USP1/XRCC5/XRN1 | 31 |
| BP | GO:0022411 | cellular component disassembly | 89/2221 | 488/18614 | 2.64E-05 | 0.000857904 | 0.000725027 | CDK1/KIF18A/TOP2A/TPX2/VRK1/ABCE1/ADAM10/ADAMTS5/ADD3/AIFM1/APC/ARID2/ASCC3/ASPH/ATG3/ATP2A2/BECN1/BNIP3L/C3/CAMSAP2/CAPZA2/CHMP2B/CKAP2/CKAP5/CLASP2/CTSK/CTSS/DHX8/DICER1/DNM1L/DPP4/EPHA4/EPS8/ETF1/FAP/FER/GFM2/GSPT1/HIF1A/HK2/HSPA8/IRAK3/ITGB1/KIF2A/KIF5B/LAMC1/LCP1/LIMA1/LRBA/MAP1B/MAP4K4/MMP1/MMP8/MTIF2/NAV3/NSF/OGFOD1/OGT/PIK3C3/PIK3CA/PIK3R1/PIK3R4/PLIN2/PLXNC1/RB1CC1/RDX/SCIN/SETX/SH3PXD2B/SNX30/SPTAN1/STX17/SUPT16H/SVIL/SWAP70/TAOK1/TGFBR1/TMOD2/TWF1/UBA5/UFL1/UFM1/VCP/VPS13C/VPS13D/VPS54/VTA1/WDR47/ZFAND1 | 89 |
| BP | GO:0051170 | import into nucleus | 39/2221 | 168/18614 | 2.96E-05 | 0.000957732 | 0.000809394 | CDK1/ECT2/ANGPT1/CD36/CSE1L/EFCAB7/HNRNPA1/HSP90AA1/IPO11/IPO5/IPO7/IPO8/JAK2/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/LRRK2/NF1/NOLC1/NUP107/NUP133/NUP153/NUP155/NUP88/NXT2/PIK3R1/PRKD1/PTGS2/RANBP2/RANBP6/RGPD1/SPG11/TNPO1/TPR/UBR5/UFM1/ZPR1 | 39 |
| BP | GO:0044839 | cell cycle G2/M phase transition | 36/2221 | 151/18614 | 3.23E-05 | 0.001039484 | 0.000878483 | ATAD5/BLM/BRCA1/CCNA2/CCNB2/CDC6/CDK1/CENPF/CHEK1/DTL/FBXO5/KIF14/MELK/NDC80/TICRR/ABCB1/ATM/BACH1/BRCC3/CCNG1/MASTL/NAE1/NBN/PLCB1/RAD17/RAD21/RAD50/RBBP8/RRM1/RRM2B/SYF2/TAF2/TAOK1/TAOK3/TOPBP1/USP47 | 36 |
| BP | GO:0006303 | double-strand break repair via nonhomologous end joining | 20/2221 | 64/18614 | 3.34E-05 | 0.001051609 | 0.00088873 | DEK/POLQ/ATM/DCLRE1A/ERCC4/ERCC6/HMGB1/HMGB2/LIG4/MLH1/POLA1/POT1/PRKDC/PSMD14/RIF1/SETMAR/SMCHD1/TP53BP1/XRCC4/XRCC5 | 20 |
| BP | GO:0006360 | transcription by RNA polymerase I | 20/2221 | 64/18614 | 3.34E-05 | 0.001051609 | 0.00088873 | DEK/BAZ1B/DDX21/EIF2AK3/ERCC6/GTF2H1/HEATR1/LYAR/NCL/NOL11/PWP1/SF3B1/SMARCA5/SPTY2D1/TAF1/TAF1A/TAF1B/UTP15/WDR43/WDR75 | 20 |
| BP | GO:0035825 | homologous recombination | 20/2221 | 64/18614 | 3.34E-05 | 0.001051609 | 0.00088873 | BRCA1/BRIP1/FANCD2/MND1/RAD51AP1/RAD54B/TOP2A/ATM/ERCC4/FANCM/MLH1/MLH3/NBN/NUCKS1/RAD21/RAD50/RBBP8/TOP2B/TOPBP1/UBR2 | 20 |
| BP | GO:0042273 | ribosomal large subunit biogenesis | 21/2221 | 69/18614 | 3.34E-05 | 0.001051609 | 0.00088873 | BRIX1/DDX18/EBNA1BP2/FASTKD2/GTPBP4/MAK16/MDN1/NIFK/NIP7/NSA2/PAK1IP1/RPF2/RPL7L1/RRP15/RRS1/RSL24D1/SDAD1/SPATA5/WDR12/ZNF622/ZNHIT6 | 21 |
| BP | GO:0006606 | protein import into nucleus | 38/2221 | 163/18614 | 3.37E-05 | 0.001055275 | 0.000891828 | CDK1/ECT2/ANGPT1/CD36/CSE1L/EFCAB7/HSP90AA1/IPO11/IPO5/IPO7/IPO8/JAK2/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/LRRK2/NF1/NOLC1/NUP107/NUP133/NUP153/NUP155/NUP88/NXT2/PIK3R1/PRKD1/PTGS2/RANBP2/RANBP6/RGPD1/SPG11/TNPO1/TPR/UBR5/UFM1/ZPR1 | 38 |
| BP | GO:0000018 | regulation of DNA recombination | 33/2221 | 134/18614 | 3.39E-05 | 0.001055275 | 0.000891828 | ATAD5/BLM/CHEK1/MSH2/PARPBP/POLQ/RAD51AP1/ACTR2/ARID2/EPC2/ERCC6/FIGNL1/IL7R/ING3/KPNA1/KPNA2/MLH1/MORF4L2/MSH3/MSH6/PARP1/PPP4R2/PTPRC/RAD50/RBBP8/RIF1/SMARCAD1/SMCHD1/TFRC/THOC1/TP53BP1/WDR48/ZRANB3 | 33 |
| BP | GO:0006405 | RNA export from nucleus | 25/2221 | 90/18614 | 3.53E-05 | 0.001095636 | 0.000925938 | XPOT/DHX9/EIF4A3/FYTTD1/HNRNPA1/HNRNPA2B1/IWS1/NCBP1/NCBP2/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP88/NXT2/PHAX/SSB/THOC1/THOC2/TPR/UPF2/XPO5/YTHDC1/ZC3H11A | 25 |
| BP | GO:0006622 | protein targeting to lysosome | 13/2221 | 32/18614 | 3.69E-05 | 0.001126211 | 0.000951778 | AP3B1/AP3M1/BECN1/GCC2/GNPTAB/HSPA8/NCOA4/NEDD4/PIK3C3/PIK3R4/SNX16/VPS54/ZFYVE16 | 13 |
| BP | GO:0051642 | centrosome localization | 13/2221 | 32/18614 | 3.69E-05 | 0.001126211 | 0.000951778 | ASPM/DLGAP5/MAD2L1/AKAP9/CCDC141/CEP83/DLG1/EZR/GPSM2/KIF5B/NIN/RANBP2/SYNE2 | 13 |
| BP | GO:0061842 | microtubule organizing center localization | 13/2221 | 32/18614 | 3.69E-05 | 0.001126211 | 0.000951778 | ASPM/DLGAP5/MAD2L1/AKAP9/CCDC141/CEP83/DLG1/EZR/GPSM2/KIF5B/NIN/RANBP2/SYNE2 | 13 |
| BP | GO:0030705 | cytoskeleton-dependent intracellular transport | 46/2221 | 212/18614 | 3.76E-05 | 0.001129906 | 0.000954901 | KIF4A/AP3B1/AP3M1/ARHGAP21/BLOC1S6/CCDC186/CCDC88A/DLG2/DST/DYNC1H1/DYNC2H1/FNBP1L/HIF1A/HNRNPU/HOOK1/HOOK3/HSPA8/IFT57/IFT74/IFT80/KIF3A/KIF5B/LCA5/LRPPRC/MAP1B/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/OPA1/PCM1/RAB1A/RAB27B/RABGEF1/RHOT1/RPGR/SPG11/SSX2IP/SYBU/SYNE2/TANC2/TRAK2/TTC21B/WDR19/WDR35 | 46 |
| BP | GO:0071214 | cellular response to abiotic stimulus | 66/2221 | 339/18614 | 3.76E-05 | 0.001129906 | 0.000954901 | BLM/BRCA1/BRCA2/CHEK1/ECT2/PBK/RAD51AP1/ATM/ATR/BRCC3/CAB39/CAPN3/CASP1/CASP3/CASP5/CASP8AP2/CLOCK/DDX3X/DHX36/EIF2AK4/EIF2S1/ERCC4/FAS/FIGNL1/GCLC/HSPA5/IFI16/IMPACT/INTS7/ITGA2/ITGB3/ITGB6/LIG4/LRRC8D/MAP3K1/MAP3K2/MDM2/MMP1/NEDD4/NET1/NFAT5/NIPBL/NLRP3/NUCKS1/OXSR1/PARP1/PIK3CA/PIK3R1/POLD3/POLK/PTGS2/PTPRK/SDE2/SLC38A2/TAF1/TANK/TLR3/TLR4/TLR8/TP53BP1/USP15/USP47/WNK3/WRN/XRCC5/ZBTB1 | 66 |
| BP | GO:0104004 | cellular response to environmental stimulus | 66/2221 | 339/18614 | 3.76E-05 | 0.001129906 | 0.000954901 | BLM/BRCA1/BRCA2/CHEK1/ECT2/PBK/RAD51AP1/ATM/ATR/BRCC3/CAB39/CAPN3/CASP1/CASP3/CASP5/CASP8AP2/CLOCK/DDX3X/DHX36/EIF2AK4/EIF2S1/ERCC4/FAS/FIGNL1/GCLC/HSPA5/IFI16/IMPACT/INTS7/ITGA2/ITGB3/ITGB6/LIG4/LRRC8D/MAP3K1/MAP3K2/MDM2/MMP1/NEDD4/NET1/NFAT5/NIPBL/NLRP3/NUCKS1/OXSR1/PARP1/PIK3CA/PIK3R1/POLD3/POLK/PTGS2/PTPRK/SDE2/SLC38A2/TAF1/TANK/TLR3/TLR4/TLR8/TP53BP1/USP15/USP47/WNK3/WRN/XRCC5/ZBTB1 | 66 |
| BP | GO:0044843 | cell cycle G1/S phase transition | 57/2221 | 281/18614 | 3.79E-05 | 0.001134642 | 0.000958903 | CCNA2/CDC6/CDKN3/EZH2/KIF14/MTBP/SASS6/STIL/ADAM17/ANKRD17/APC/ARID2/ATM/BACH1/BCAT1/BRD7/CCNE2/CCNH/CENPJ/CPSF3/CUL1/CUL2/CUL3/DBF4/DCUN1D3/DDX3X/DLG1/E2F6/ECD/GIGYF2/GPNMB/GSPT1/INHBA/ITGB1/JADE1/KMT2E/MDM2/MIR15B/MIR30C2/NPAT/PBRM1/PLCB1/PLRG1/PPP2CA/PRKDC/RB1/RBBP8/RBL2/RDX/RFWD3/RRM1/SDE2/SLFN11/STXBP4/TAF1/USP37/ZPR1 | 57 |
| BP | GO:0016032 | viral process | 79/2221 | 426/18614 | 4.09E-05 | 0.001216197 | 0.001027826 | CDK1/DEK/TOP2A/ACE2/BECN1/CANX/CCNT1/CCNT2/CD86/CHD1/CHMP2B/CLDN1/CR1/CSDE1/CTSL/CXADR/DDX3X/DHX9/DPP4/EIF2AK2/EIF2AK4/EIF3A/EIF3D/EIF3L/EPS15/FAM111A/FMR1/FUT8/GALNT1/GYPA/HCFC2/HMGB1/HSP90AB1/HSPA8/HTATSF1/HTR2A/IDE/IFI16/IFIH1/IFIT5/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/KPNA2/KPNA3/LARP7/LIG4/MGAT4A/MRC1/NEDD4/NPC1/NUCKS1/NUP153/PARP9/PIK3C3/PIKFYVE/PKN2/RAB1A/RNASEL/RSF1/SNW1/SRPK1/SRPK2/SSB/ST6GALNAC3/STAT1/TFRC/TOP2B/TRIM22/TRIM38/TRIM59/TRIM6/VCP/VTA1/WWP1/ZNF502/ZNFX1 | 79 |
| BP | GO:0097193 | intrinsic apoptotic signaling pathway | 60/2221 | 301/18614 | 4.10E-05 | 0.001216197 | 0.001027826 | ATAD5/BRCA1/BRCA2/DDIAS/GSKIP/HELLS/MELK/MSH2/AIFM1/ATM/BCLAF1/BECN1/CASP3/CASP4/CUL1/CUL2/CUL3/CYCS/CYLD/DDX3X/DDX5/DNAJA1/DNAJC10/DNM1L/EIF2AK3/ERCC6/FIGNL1/FNIP2/HIF1A/IFI16/ING2/ITPR1/IVNS1ABP/JAK2/JMY/LRRK2/MDM2/MIR186/MLH1/MSH6/NBN/NCK1/NFE2L2/OPA1/PARP1/PIK3CB/PIK3R1/PRKDC/PTGS2/PTPN2/RRM2B/SKIL/SNW1/TOPORS/TP53BP2/USP15/USP47/VNN1/ZNF385B/ZNF622 | 60 |
| BP | GO:1901880 | negative regulation of protein depolymerization | 21/2221 | 70/18614 | 4.24E-05 | 0.001249932 | 0.001056336 | TPX2/ADD3/APC/CAMSAP2/CAPZA2/CKAP2/CLASP2/EPS8/LIMA1/MAP1B/NAV3/PIK3CA/RDX/SCIN/SPTAN1/SVIL/SWAP70/TAOK1/TMOD2/TWF1/WDR47 | 21 |
| BP | GO:0061640 | cytoskeleton-dependent cytokinesis | 29/2221 | 113/18614 | 4.42E-05 | 0.001297101 | 0.001096199 | ANLN/CEP55/ECT2/KIF20A/KIF20B/KIF23/KIF4A/NUSAP1/ACTR2/ACTR3/ANK3/APC/CHMP2B/CKAP2/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/MAP9/ORC4/RACGAP1/RASA1/ROCK1/ROCK2/SNX9/SON/SPIRE1/USP8 | 29 |
| BP | GO:0031349 | positive regulation of defense response | 81/2221 | 441/18614 | 4.64E-05 | 0.001353076 | 0.001143505 | SUCNR1/AIM2/ALPK1/ANKRD17/AP3B1/ARG1/BIRC2/BIRC3/BTK/C3/CASP1/CASP4/CD226/CD36/CLOCK/CNR1/COLEC12/CTSS/CYLD/DDX3X/DDX60/DHX9/GBP5/HAVCR2/HMGB1/HMGB2/HSP90AA1/HSPD1/IFI16/IFIH1/IL18/IL18RAP/IL6ST/IRAK3/IRAK4/ITGA2/JAK2/LACC1/LPL/LRRK2/LYN/MAP3K7/MATR3/MEF2C/MIR142/MIR181B1/MMP8/MNDA/NAIP/NLRC4/NLRP3/OSMR/OTUD4/PARP9/PDCD4/PIK3AP1/PIK3CG/PJA2/POLR3B/POLR3C/PRKDC/PTGS2/PUM2/RAB11FIP2/RIOK3/RIPK1/RIPK2/RPS6KA3/STAP1/TBK1/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/TRIM6/USP15/USP27X/XRCC5/ZNFX1 | 81 |
| BP | GO:0000086 | G2/M transition of mitotic cell cycle | 33/2221 | 136/18614 | 4.66E-05 | 0.001353076 | 0.001143505 | BLM/BRCA1/CCNA2/CDC6/CDK1/CENPF/CHEK1/DTL/FBXO5/KIF14/MELK/TICRR/ABCB1/ATM/BACH1/BRCC3/CCNG1/MASTL/NAE1/NBN/PLCB1/RAD17/RAD21/RAD50/RBBP8/RRM1/RRM2B/SYF2/TAF2/TAOK1/TAOK3/TOPBP1/USP47 | 33 |
| BP | GO:0070536 | protein K63-linked deubiquitination | 14/2221 | 37/18614 | 4.78E-05 | 0.001382345 | 0.00116824 | BRCA1/BRCC3/CYLD/OTUD4/PSMD14/USP13/USP16/USP25/USP27X/USP8/USP9X/VCP/YOD1/ZRANB1 | 14 |
| BP | GO:1902117 | positive regulation of organelle assembly | 23/2221 | 81/18614 | 4.91E-05 | 0.001413689 | 0.001194729 | CEP135/PLK4/SASS6/SPAG5/STIL/BECN1/CCDC88A/CCP110/CENPJ/CEP120/CNOT1/CNOT6L/DYNC1H1/G3BP1/G3BP2/GPSM2/LCP1/MNS1/RAB3GAP1/RAB3GAP2/SDCBP/SH3GLB1/SNX30 | 23 |
| BP | GO:0002218 | activation of innate immune response | 49/2221 | 233/18614 | 5.00E-05 | 0.001433332 | 0.00121133 | AIM2/ALPK1/ANKRD17/AP3B1/BIRC2/BIRC3/BTK/CASP1/CD36/COLEC12/CTSS/CYLD/DDX3X/DDX60/HAVCR2/HMGB1/HSP90AA1/HSPD1/IFI16/IFIH1/IRAK3/IRAK4/LACC1/LYN/MAP3K7/MATR3/MNDA/NAIP/NLRC4/NLRP3/OTUD4/PIK3AP1/PJA2/PRKDC/PUM2/RAB11FIP2/RIOK3/RIPK2/RPS6KA3/TBK1/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/USP15/XRCC5/ZNFX1 | 49 |
| BP | GO:0001776 | leukocyte homeostasis | 27/2221 | 103/18614 | 5.37E-05 | 0.001518507 | 0.001283313 | CCNB2/ADAM17/BTK/CASP3/DOCK10/DOCK11/FAS/GAPT/HIF1A/HMGB1/IL2RA/IL7R/LIPA/LYN/MEF2C/MERTK/MTHFD1/NCKAP1L/NF1/PDE4B/PIK3CB/PPP2R3C/RC3H2/SKIL/SLC7A11/SOS1/SOS2 | 27 |
| BP | GO:0032608 | interferon-beta production | 18/2221 | 56/18614 | 5.38E-05 | 0.001518507 | 0.001283313 | DDX3X/DHX9/HMGB2/HSP90AA1/IFIH1/POLR3B/POLR3C/PPM1B/PTPN11/REL/RIOK3/RIPK2/TBK1/TLR2/TLR3/TLR4/TLR8/TRIM38 | 18 |
| BP | GO:0032648 | regulation of interferon-beta production | 18/2221 | 56/18614 | 5.38E-05 | 0.001518507 | 0.001283313 | DDX3X/DHX9/HMGB2/HSP90AA1/IFIH1/POLR3B/POLR3C/PPM1B/PTPN11/REL/RIOK3/RIPK2/TBK1/TLR2/TLR3/TLR4/TLR8/TRIM38 | 18 |
| BP | GO:0071478 | cellular response to radiation | 42/2221 | 191/18614 | 5.80E-05 | 0.001630599 | 0.001378044 | BLM/BRCA1/BRCA2/CHEK1/ECT2/PBK/RAD51AP1/ATM/ATR/BRCC3/CLOCK/DHX36/EIF2AK4/EIF2S1/ERCC4/FIGNL1/HSPA5/IFI16/IMPACT/INTS7/ITGB6/LIG4/MDM2/MMP1/NEDD4/NET1/NIPBL/NUCKS1/PARP1/PIK3R1/POLD3/POLK/PTGS2/PTPRK/SDE2/TAF1/TANK/TP53BP1/USP47/WRN/XRCC5/ZBTB1 | 42 |
| BP | GO:0090224 | regulation of spindle organization | 16/2221 | 47/18614 | 6.34E-05 | 0.001773669 | 0.001498954 | BORA/KIF15/SASS6/SPAG5/STIL/TPX2/CENPJ/CEP97/CHMP2B/CLTC/DYNC1H1/GPSM2/HNRNPU/MAP9/SENP6/TPR | 16 |
| BP | GO:1904951 | positive regulation of establishment of protein localization | 63/2221 | 325/18614 | 6.37E-05 | 0.001774611 | 0.00149975 | CDK1/CEP135/ECT2/KIF20B/ACSL3/ACSL4/ADAM9/AKAP5/ANK3/ATP2C1/C2CD5/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CD2AP/CD38/CENPJ/CEP120/CEP290/CFTR/CNST/CTDSPL2/DKC1/DNM1L/EFCAB7/EXOC1/EXPH5/EZR/HIF1A/HSP90AA1/ICE1/IGF1/IPO5/ITPR1/JAK2/MYOM1/OSBP/OXCT1/PCM1/PCSK1/PFKFB2/PIK3R1/PLCB1/PPARG/PRKD1/PTGS2/RAPGEF4/RUFY3/SAR1B/SH3GLB1/TCP1/TLR2/TLR4/TPR/TTN/UBR5/VPS35/XPO4/ZFAND1/ZPR1 | 63 |
| BP | GO:0007080 | mitotic metaphase plate congression | 18/2221 | 57/18614 | 6.99E-05 | 0.001937236 | 0.001637187 | CENPE/KIF14/KIF18A/NDC80/NUF2/SPDL1/BECN1/CENPC/CHMP2B/CUL3/EML4/HNRNPU/KPNB1/MAPRE1/MIS12/PIBF1/RRS1/ZW10 | 18 |
| BP | GO:0072666 | establishment of protein localization to vacuole | 19/2221 | 62/18614 | 7.03E-05 | 0.001937236 | 0.001637187 | AP3B1/AP3M1/BECN1/GCC2/GNPTAB/HSPA8/NCOA4/NEDD4/PIK3C3/PIK3R4/SNX16/STAM2/VPS13A/VPS13C/VPS13D/VPS41/VPS54/VPS8/ZFYVE16 | 19 |
| BP | GO:0045089 | positive regulation of innate immune response | 59/2221 | 300/18614 | 7.05E-05 | 0.001937236 | 0.001637187 | AIM2/ALPK1/ANKRD17/AP3B1/BIRC2/BIRC3/BTK/CASP1/CD226/CD36/COLEC12/CTSS/CYLD/DDX3X/DDX60/DHX9/GBP5/HAVCR2/HMGB1/HMGB2/HSP90AA1/HSPD1/IFI16/IFIH1/IL18RAP/IRAK3/IRAK4/LACC1/LYN/MAP3K7/MATR3/MNDA/NAIP/NLRC4/NLRP3/OTUD4/PARP9/PIK3AP1/PJA2/POLR3B/POLR3C/PRKDC/PUM2/RAB11FIP2/RIOK3/RIPK2/RPS6KA3/TBK1/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/TRIM6/USP15/USP27X/XRCC5/ZNFX1 | 59 |
| BP | GO:0060623 | regulation of chromosome condensation | 7/2221 | 11/18614 | 7.27E-05 | 0.001987482 | 0.001679651 | NCAPG/NCAPG2/NCAPH/BAZ1B/SMARCA5/SMC2/SMC4 | 7 |
| BP | GO:0001782 | B cell homeostasis | 13/2221 | 34/18614 | 7.83E-05 | 0.002130217 | 0.001800278 | CASP3/DOCK10/DOCK11/GAPT/HIF1A/IL7R/LYN/MEF2C/NCKAP1L/PPP2R3C/RC3H2/SOS1/SOS2 | 13 |
| BP | GO:0042274 | ribosomal small subunit biogenesis | 22/2221 | 78/18614 | 7.94E-05 | 0.002151556 | 0.001818312 | BMS1/DDX52/HEATR1/LTV1/MPHOSPH10/NGDN/NOL10/NOL11/PRKDC/RIOK1/RIOK2/RIOK3/RRS1/SRFBP1/TSR1/UTP20/UTP23/UTP3/UTP6/WDR3/WDR43/XRCC5 | 22 |
| BP | GO:0034501 | protein localization to kinetochore | 9/2221 | 18/18614 | 8.53E-05 | 0.002290693 | 0.001935898 | CDK1/KNTC1/MTBP/NDC80/SPDL1/TTK/ZWILCH/MIS12/ZW10 | 9 |
| BP | GO:1903083 | protein localization to condensed chromosome | 9/2221 | 18/18614 | 8.53E-05 | 0.002290693 | 0.001935898 | CDK1/KNTC1/MTBP/NDC80/SPDL1/TTK/ZWILCH/MIS12/ZW10 | 9 |
| BP | GO:0044380 | protein localization to cytoskeleton | 18/2221 | 58/18614 | 9.01E-05 | 0.002410197 | 0.002036893 | KIF20B/SPAG5/STIL/TTK/APC/CCDC14/CEP192/CEP350/CEP83/GOLGB1/HNRNPU/HOOK3/HTR2A/MAPRE1/PCM1/PIBF1/SNX10/UBXN2B | 18 |
| BP | GO:0090305 | nucleic acid phosphodiester bond hydrolysis | 50/2221 | 245/18614 | 9.40E-05 | 0.002503549 | 0.002115786 | ATAD5/LACTB2/MGME1/BMS1/CNOT1/CNOT6L/CPSF2/CPSF3/CSTF3/DCLRE1A/DDX1/DICER1/DIS3/DIS3L/DNA2/ENDOD1/ENPP1/ERI1/ERI2/EXOSC9/FANCM/G3BP1/GEN1/N4BP2/NCBP1/NCBP2/NUDT12/NUDT21/PCF11/PNPT1/PNRC2/POP1/RAD50/RBBP8/RNASEL/RRS1/SAMHD1/SDE2/SETMAR/SLFN13/TDP2/TSNAX/TSR1/UTP20/UTP23/WRN/XRN1/XRN2/ZC3H12C/ZRANB3 | 50 |
| BP | GO:0000470 | maturation of LSU-rRNA | 10/2221 | 22/18614 | 9.50E-05 | 0.002506355 | 0.002118158 | DDX18/GTPBP4/MAK16/NIFK/NSA2/RPF2/RPL7L1/RRP15/WDR12/ZNHIT6 | 10 |
| BP | GO:0001832 | blastocyst growth | 10/2221 | 22/18614 | 9.50E-05 | 0.002506355 | 0.002118158 | BRCA2/CHEK1/NCAPG2/COPS2/CTR9/IGF1/NBN/PALB2/RTF1/ZPR1 | 10 |
| BP | GO:0006457 | protein folding | 46/2221 | 220/18614 | 9.67E-05 | 0.002541334 | 0.002147719 | VBP1/ANP32E/ATF6/CANX/CCDC47/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CHORDC1/CLPX/CWC27/DNAJA1/DNAJC10/DNAJC2/DNAJC21/DNAJC3/DNAJC7/FKBP5/GRPEL1/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSP90B1/HSPA13/HSPA4/HSPA4L/HSPA5/HSPA8/HSPA9/HSPD1/HSPH1/LMAN1/MKKS/NKTR/PDIA3/PDIA6/PPIG/RANBP2/RP2/SACS/TCP1/UGGT1 | 46 |
| BP | GO:0002221 | pattern recognition receptor signaling pathway | 41/2221 | 189/18614 | 9.72E-05 | 0.002542156 | 0.002148414 | AIM2/ALPK1/ANKRD17/AP3B1/BIRC2/BIRC3/BTK/CASP1/CD36/COLEC12/CTSS/CYLD/DDX3X/DDX60/HAVCR2/HMGB1/HSPD1/IFIH1/IRAK3/IRAK4/LACC1/LYN/MAP3K7/NAIP/NLRC4/NLRP3/OTUD4/PIK3AP1/PJA2/PUM2/RAB11FIP2/RIOK3/RIPK2/RPS6KA3/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/USP15 | 41 |
| BP | GO:0032886 | regulation of microtubule-based process | 51/2221 | 252/18614 | 0.000100529 | 0.002618095 | 0.002212591 | BORA/BRCA1/KIF15/KIF18A/PLK4/SASS6/SKA3/SPAG5/STIL/TPX2/XPO1/AKAP9/ALMS1/APC/CAMSAP2/CCNL1/CDK5RAP2/CENPJ/CEP120/CEP70/CEP97/CHMP2B/CHORDC1/CKAP2/CKAP5/CLASP2/CLIP1/CLTC/CYLD/DYNC1H1/EPHA3/GEN1/GPSM2/HNRNPU/MACF1/MAP1B/MAP9/MAPRE1/MET/MKKS/MPDZ/NAV3/PHLDB2/ROCK1/ROCK2/SENP6/SPICE1/TAOK1/TPR/TTC21B/WDR47 | 51 |
| BP | GO:0010389 | regulation of G2/M transition of mitotic cell cycle | 26/2221 | 101/18614 | 0.000101624 | 0.002635205 | 0.002227051 | BLM/BRCA1/CDC6/CDK1/CENPF/CHEK1/DTL/FBXO5/KIF14/TICRR/ATM/BRCC3/CCNG1/NAE1/NBN/RAD17/RAD21/RAD50/RBBP8/RRM1/RRM2B/SYF2/TAOK1/TAOK3/TOPBP1/USP47 | 26 |
| BP | GO:0051298 | centrosome duplication | 21/2221 | 74/18614 | 0.000103912 | 0.002682979 | 0.002267425 | BRCA1/BRCA2/CEP135/NDC80/PLK4/SASS6/STIL/XPO1/ALMS1/CCP110/CDK5RAP2/CENPJ/CEP120/CEP152/CEP192/CHMP2B/CHORDC1/CKAP5/GEN1/ROCK2/SPICE1 | 21 |
| BP | GO:0051028 | mRNA transport | 31/2221 | 130/18614 | 0.000110214 | 0.002833534 | 0.002394661 | XPO1/AHCTF1/DHX9/EIF4A3/FMR1/FYTTD1/G3BP2/HNRNPA1/HNRNPA1L2/HNRNPA2B1/HNRNPA3/IWS1/LRPPRC/NCBP1/NCBP2/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/RANBP2/THOC1/THOC2/TPR/UPF2/UPF3B/YTHDC1/ZC3H11A | 31 |
| BP | GO:0007143 | female meiotic nuclear division | 13/2221 | 35/18614 | 0.000110972 | 0.00284087 | 0.002400862 | CCNB2/FBXO5/NCAPH/NDC80/TOP2A/TTK/ATM/MASTL/MLH1/MLH3/ORC4/SPIRE1/SYCP2 | 13 |
| BP | GO:0006383 | transcription by RNA polymerase III | 17/2221 | 54/18614 | 0.000115161 | 0.00292324 | 0.002470474 | DEK/GTF3C6/BAZ1B/BDP1/CHD8/DDX21/DHX36/ERCC6/GTF3C3/ICE1/ICE2/INHBA/IVNS1ABP/POLR3C/SF3B1/SMARCA5/ZNF143 | 17 |
| BP | GO:0072698 | protein localization to microtubule cytoskeleton | 17/2221 | 54/18614 | 0.000115161 | 0.00292324 | 0.002470474 | KIF20B/SPAG5/STIL/TTK/APC/CCDC14/CEP192/CEP350/CEP83/GOLGB1/HNRNPU/HOOK3/MAPRE1/PCM1/PIBF1/SNX10/UBXN2B | 17 |
| BP | GO:0043242 | negative regulation of protein-containing complex disassembly | 22/2221 | 80/18614 | 0.000119857 | 0.003021292 | 0.002553338 | TPX2/ADD3/APC/CAMSAP2/CAPZA2/CKAP2/CLASP2/EPS8/IRAK3/LIMA1/MAP1B/NAV3/PIK3CA/RDX/SCIN/SPTAN1/SVIL/SWAP70/TAOK1/TMOD2/TWF1/WDR47 | 22 |
| BP | GO:1904874 | positive regulation of telomerase RNA localization to Cajal body | 8/2221 | 15/18614 | 0.000120028 | 0.003021292 | 0.002553338 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 57/2221 | 293/18614 | 0.000125794 | 0.003153249 | 0.002664857 | ECT2/AKAP13/ALPK1/ANGPT1/ANKRD17/ASH1L/ATP2C1/AZI2/BIRC2/BIRC3/BTK/CAPN3/CASP1/CD36/CHUK/CLEC4D/CTNNB1/DDX1/DDX21/DHX15/DHX36/ERC1/GOLT1B/IFIT5/IRAK4/MALT1/MAP3K7/MIR15B/MTDH/PPM1B/PRKD1/REL/RIOK3/RIPK1/RIPK2/ROCK1/ROCK2/RORA/STAT1/TAB2/TAB3/TANK/TBK1/TFRC/TLR2/TLR3/TLR4/TLR6/TLR8/TRAF5/TRIM22/TRIM38/TRIM59/TRIM6/UFL1/ZMYND11/ZNF675 | 57 |
| BP | GO:0099022 | vesicle tethering | 12/2221 | 31/18614 | 0.000128098 | 0.003192169 | 0.002697749 | EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/FAM91A1/TBC1D23/TRAPPC11/TRAPPC13/TRAPPC8/TRIP11/WDR11 | 12 |
| BP | GO:0000731 | DNA synthesis involved in DNA repair | 14/2221 | 40/18614 | 0.000128408 | 0.003192169 | 0.002697749 | DTL/RFC3/POLA1/POLD3/POLK/REV1/REV3L/RRM1/RRM2B/SPRTN/USP1/VCP/WRN/ZBTB1 | 14 |
| BP | GO:0016570 | histone modification | 84/2221 | 475/18614 | 0.000131682 | 0.003260072 | 0.002755135 | BRCA1/BRCA2/CDK1/CHEK1/DEK/EZH2/HDAC2/VRK1/ARID4A/ARID4B/ASH1L/BAZ1B/BOD1L1/BRCC3/BRMS1L/CHD4/CLOCK/CTNNB1/CTR9/DDX21/DTX3L/EPC2/ERCC6/HAT1/HCFC2/ING2/ING3/IWS1/JADE1/JAK2/JMJD1C/KAT6A/KDM3A/KDM4C/KDM5A/KDM5B/KDM6A/KDM7A/KMT2C/LEO1/LRRK2/MAP3K7/MECOM/MORF4L2/MSL3P1/MTF2/MYSM1/NAA50/NCOA1/NCOA3/NIPBL/OGT/PAXBP1/PHF20L1/PRKD1/RBBP5/RIF1/RLF/RNF20/RPS6KA5/RTF1/SDR16C5/SETD7/SETDB2/SETMAR/SF3B1/SMARCA5/SMARCAD1/SNW1/SUPT20H/SUV39H2/SUZ12/TAF1/TAF2/TAF7/TBL1XR1/TRIP12/UBR2/UBR5/UFL1/USP15/USP16/USP7/ZZZ3 | 84 |
| BP | GO:0006970 | response to osmotic stress | 23/2221 | 86/18614 | 0.000134685 | 0.003307676 | 0.002795366 | ABCB1/AQP4/CAB39/CAPN3/CASP1/CASP3/CLDN1/DDX3X/FMO1/HSP90AA1/ITGA2/KCNMA1/KMO/LRRC8D/NFAT5/NLRP3/NOLC1/OXSR1/PTGS2/TLR3/USP15/WNK3/XRCC5 | 23 |
| BP | GO:0043414 | macromolecule methylation | 61/2221 | 320/18614 | 0.000134704 | 0.003307676 | 0.002795366 | BRCA1/EZH2/HELLS/PRMT3/ALKBH8/ARID4A/ARID4B/ASH1L/ATF7IP/ATRX/BOD1L1/CTNNB1/CTR9/ETF1/FAM98A/FBXO11/GRHL2/GSPT1/HCFC2/IWS1/KDM6A/KMT2C/KMT2E/LARP7/METTL14/METTL15/METTL18/MTF2/MTRR/NSUN2/NSUN6/OGT/PARP1/PAXBP1/PRMT9/RBBP5/RIF1/RLF/RNF20/RNMT/RTF1/SETD7/SETDB2/SETMAR/SMARCA5/SNW1/SUV39H2/SUZ12/TFB2M/TGS1/THADA/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TRMT6/TYW3/WTAP/ZC3H13/ZDBF2 | 61 |
| BP | GO:1903320 | regulation of protein modification by small protein conjugation or removal | 51/2221 | 255/18614 | 0.000137073 | 0.003352163 | 0.002832962 | BRCA1/BUB1B/FANCI/FBXO5/MAD2L1/MTBP/PRMT3/ANGPT1/ARRDC3/ARRDC4/BIRC2/BIRC3/CAPN3/COPS2/COPS4/CTNNB1/CUL3/DCUN1D3/DDX3X/DNAJA1/DTX3L/FANCM/GCLC/GNL3/GTPBP4/HIF1A/HSP90AA1/HSP90AB1/HSPA5/IVNS1ABP/LRRK2/MALT1/MASTL/MYCBP2/OGT/OTUD4/PLAA/RIPK2/SPOPL/SPRTN/TAF1/TANK/TGFBR1/TOPORS/TRIM44/TRIP12/UBR5/UFL1/USP44/VCP/WDR48 | 51 |
| BP | GO:0002833 | positive regulation of response to biotic stimulus | 62/2221 | 327/18614 | 0.00013947 | 0.003396965 | 0.002870825 | AIM2/ALPK1/ANKRD17/AP3B1/ARG1/BIRC2/BIRC3/BTK/CASP1/CD180/CD226/CD36/COLEC12/CTSS/CYLD/DDX3X/DDX60/DHX9/FBXO38/GBP5/HAVCR2/HMGB1/HMGB2/HSP90AA1/HSPD1/IFI16/IFIH1/IL18RAP/IRAK3/IRAK4/LACC1/LYN/MAP3K7/MATR3/MNDA/NAIP/NLRC4/NLRP3/OTUD4/PARP9/PIK3AP1/PJA2/POLR3B/POLR3C/PRKDC/PUM2/RAB11FIP2/RIOK3/RIPK2/RPS6KA3/TBK1/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/TRIM6/USP15/USP27X/XRCC5/ZNFX1 | 62 |
| BP | GO:0051984 | positive regulation of chromosome segregation | 11/2221 | 27/18614 | 0.000142532 | 0.003457549 | 0.002922026 | CDC6/NCAPG/NCAPG2/NCAPH/RAD18/BECN1/HNRNPU/SMC2/SMC4/SMC5/SMC6 | 11 |
| BP | GO:0031123 | RNA 3'-end processing | 26/2221 | 103/18614 | 0.000143878 | 0.003476187 | 0.002937777 | AHCYL1/CPSF2/CPSF3/CSTF3/DHX36/DKC1/ERI1/ERI2/EXOSC9/INTS12/INTS6/INTS7/LARP7/LEO1/NCBP1/NCBP2/NUDT21/PAPOLA/PAPOLG/PCF11/PNPT1/SSB/TRMT10C/TRNT1/YTHDC1/ZNF473 | 26 |
| BP | GO:0072665 | protein localization to vacuole | 22/2221 | 81/18614 | 0.000146237 | 0.003514835 | 0.002970439 | AP3B1/AP3M1/BECN1/GBP1/GCC2/GNPTAB/HSPA8/NCOA4/NEDD4/PIK3C3/PIK3R4/ROCK2/SH3GLB1/SNX16/STAM2/VPS13A/VPS13C/VPS13D/VPS41/VPS54/VPS8/ZFYVE16 | 22 |
| BP | GO:0046824 | positive regulation of nucleocytoplasmic transport | 18/2221 | 60/18614 | 0.000146646 | 0.003514835 | 0.002970439 | CDK1/ECT2/CTDSPL2/DHX9/EFCAB7/HSP90AA1/IPO5/JAK2/NCBP2/NEDD4/PIK3R1/PRKD1/PTGS2/RIOK2/TPR/UBR5/XPO4/ZPR1 | 18 |
| BP | GO:0032288 | myelin assembly | 10/2221 | 23/18614 | 0.00015013 | 0.003584058 | 0.00302894 | UGT8/ANK2/CNTN1/DICER1/EPB41L3/FIG4/GNPAT/MTMR2/PIKFYVE/TLR2 | 10 |
| BP | GO:1903557 | positive regulation of tumor necrosis factor superfamily cytokine production | 27/2221 | 109/18614 | 0.000152148 | 0.003617882 | 0.003057525 | HDAC2/AKAP12/ARFGEF2/BTK/CD36/CD84/CD86/CYBB/DHX9/FCGR3A/HAVCR2/HMGB1/IFIH1/IFNGR1/JAK2/LPL/LRRK2/MMP8/PIK3R1/PTPN11/PTPRC/RIPK1/RIPK2/TLR1/TLR2/TLR3/TLR4 | 27 |
| BP | GO:1901653 | cellular response to peptide | 69/2221 | 375/18614 | 0.000155238 | 0.003676826 | 0.00310734 | MIRLET7F1/BRIP1/CCNA2/CDC6/AHCYL1/APC/ARG1/ATP2B1/C2CD5/CACNA2D1/CASP4/CD36/DENND4C/ENPP1/EPHA4/FBN1/FER/GCLC/IDE/IGF1/INHBA/ITGA4/ITGB3/JAK2/LPL/LYN/MAP1B/MDM2/MIR15B/MYO5A/NCK1/NCL/NCOA1/NCOA2/NFE2L2/NUCKS1/OGT/OSBPL8/PARP1/PDE3B/PHIP/PIK3C2A/PIK3CA/PIK3R1/PIK3R3/PLCB1/PPARG/PRKCI/PRKDC/PTPN11/PTPN2/RAP1GDS1/RB1/RIPK2/ROCK1/ROCK2/SESN3/SNX6/SOS1/SOS2/STAT1/STXBP4/SYAP1/TBC1D4/TLR4/TLR6/USO1/VCAM1/ZNF106 | 69 |
| BP | GO:0043254 | regulation of protein-containing complex assembly | 74/2221 | 409/18614 | 0.000157551 | 0.003716965 | 0.003141262 | KIF14/ABCA1/ADD3/AIDA/AKAP9/ARFGEF1/ARHGAP18/ARHGAP28/ATF7IP/ATM/ATR/BIRC2/BRCC3/BTK/CAMSAP2/CAND1/CAPZA2/CD36/CDK5RAP2/CKAP5/CLIP1/DDX3X/DLG1/EIF2AK2/EPS8/FER/FERMT2/FMN1/FNIP1/FNIP2/GBP5/HMGB1/HSP90AA1/HSPA5/HSPA8/ICE1/IMPACT/LCP1/MAP1B/MAPRE1/MET/MKKS/MMP1/MPP7/NAV3/NCK1/NCKAP1/NCKAP1L/PARP1/PPP2CA/PRKD1/PSMC6/PTPN11/RASA1/RB1/RDX/RICTOR/RIOK3/SAR1B/SCIN/SENP6/SH3GLB1/SNX9/SPTAN1/SVIL/TFRC/TLR4/TLR6/TMOD2/TWF1/VCP/VPS35/VPS41/VPS8 | 74 |
| BP | GO:0032479 | regulation of type I interferon production | 26/2221 | 104/18614 | 0.00017037 | 0.003979543 | 0.003363171 | CHUK/CYLD/DDX3X/DHX36/DHX9/G3BP1/HAVCR2/HMGB2/HSP90AA1/HSPD1/IFIH1/POLA1/POLR3B/POLR3C/PPM1B/PTPN11/REL/RIOK3/RIPK2/STAT1/TBK1/TLR2/TLR3/TLR4/TLR8/TRIM38 | 26 |
| BP | GO:0032606 | type I interferon production | 26/2221 | 104/18614 | 0.00017037 | 0.003979543 | 0.003363171 | CHUK/CYLD/DDX3X/DHX36/DHX9/G3BP1/HAVCR2/HMGB2/HSP90AA1/HSPD1/IFIH1/POLA1/POLR3B/POLR3C/PPM1B/PTPN11/REL/RIOK3/RIPK2/STAT1/TBK1/TLR2/TLR3/TLR4/TLR8/TRIM38 | 26 |
| BP | GO:0034250 | positive regulation of amide metabolic process | 37/2221 | 169/18614 | 0.000170665 | 0.003979543 | 0.003363171 | GUF1/RMND1/CASP3/CSDE1/DDX3X/DHX29/DHX36/DHX9/DNAJC3/EIF2AK4/EIF3D/EIF3E/EIF4A3/EPHA4/FASTKD2/FMR1/FXR1/GSAP/HNRNPU/IFNGR1/IMPACT/ITGA2/LARP1B/LARP4/METTL14/MIR15B/NCK1/NFE2L2/PLD1/PRKDC/ROCK2/SSB/SYNCRIP/TRMT10C/UPF3B/USP16/YTHDF3 | 37 |
| BP | GO:0050684 | regulation of mRNA processing | 32/2221 | 139/18614 | 0.00017397 | 0.004040952 | 0.003415068 | AHCYL1/CWC22/DDX5/DHX36/DHX9/FMR1/FXR1/HNRNPA1/HNRNPA2B1/HNRNPU/HSPA8/IWS1/LARP7/LEO1/NCBP1/NCBP2/NCL/NSRP1/NUDT21/PAPOLA/PTCD2/RBM25/RBM39/SLTM/SMU1/SNW1/SON/SRPK1/SRPK2/SRSF10/WTAP/YTHDC1 | 32 |
| BP | GO:0008156 | negative regulation of DNA replication | 12/2221 | 32/18614 | 0.00018283 | 0.004218484 | 0.003565103 | BLM/BRCA2/CDC6/FBXO5/GMNN/ATR/GTPBP4/PDS5A/RAD17/SLFN11/TSPYL2/ZRANB3 | 12 |
| BP | GO:0009314 | response to radiation | 80/2221 | 452/18614 | 0.000183016 | 0.004218484 | 0.003565103 | BLM/BRCA1/BRCA2/CHEK1/DTL/ECT2/FANCD2/MSH2/PBK/RAD51AP1/RAD54B/TICRR/XRCC2/ANGPT2/AQP4/ATM/ATR/BRCC3/CASP3/CCDC66/CLOCK/COL3A1/DCUN1D3/DHX36/EIF2AK4/EIF2S1/ERCC4/ERCC5/ERCC6/FBXL3/FIGNL1/HIF1A/HMGCR/HSPA5/IFI16/IMPACT/INTS7/ITGB1/ITGB3/ITGB6/KRAS/LIG4/MAP3K4/MAPK10/MDM2/MMP1/MSH6/NEDD4/NET1/NF1/NIPBL/NUCKS1/PARP1/PDE8B/PIK3R1/POLD3/POLK/PRKDC/PTGS2/PTPRC/PTPRK/REV1/RFWD3/SDE2/SLC1A3/SLC7A11/SMC1A/SPRTN/TAF1/TANK/TOPBP1/TP53BP1/USP1/USP47/VCAM1/WRN/XRCC4/XRCC5/ZBTB1/ZRANB3 | 80 |
| BP | GO:0051653 | spindle localization | 18/2221 | 61/18614 | 0.000185081 | 0.004234473 | 0.003578616 | ASPM/MAD2L1/NDC80/NUSAP1/SPAG5/SPDL1/ACTR2/ACTR3/CDK5RAP2/CLASP2/DYNC1H1/GPSM2/ITGB1/KPNB1/MAPRE1/SPIRE1/UBXN2B/ZW10 | 18 |
| BP | GO:0006356 | regulation of transcription by RNA polymerase I | 15/2221 | 46/18614 | 0.000185117 | 0.004234473 | 0.003578616 | DEK/BAZ1B/DDX21/EIF2AK3/ERCC6/HEATR1/LYAR/NCL/NOL11/PWP1/SF3B1/SMARCA5/UTP15/WDR43/WDR75 | 15 |
| BP | GO:2001020 | regulation of response to DNA damage stimulus | 59/2221 | 311/18614 | 0.00019652 | 0.00447828 | 0.003784661 | ATAD5/BRCA1/BRCA2/CHEK1/DDIAS/DEK/FBXO5/PARPBP/POLQ/RAD51AP1/WDR76/ACTR2/ACTR8/ARID2/ATM/ATR/BAZ1B/BCLAF1/BRCC3/BRD7/DDX5/DHX9/EPC2/ERCC4/ERCC6/ETAA1/FIGNL1/FMR1/FXR1/HMGB1/ING2/ING3/MDM2/MORF4L2/PARP1/PBRM1/PLA2R1/POT1/PPP4R2/PRKDC/RBBP8/RFWD3/RIF1/SETMAR/SKIL/SMARCA5/SMCHD1/SPIRE1/SUPT20H/TAF2/TAF7/THOC1/TP53BP1/TRIP12/UBR5/UCHL5/USP1/USP47/WDR48 | 59 |
| BP | GO:0031334 | positive regulation of protein-containing complex assembly | 41/2221 | 195/18614 | 0.000198849 | 0.004497273 | 0.003800712 | ABCA1/AKAP9/ATM/ATR/BRCC3/BTK/CAND1/CD36/CDK5RAP2/CKAP5/CLIP1/DDX3X/DLG1/FER/FERMT2/FMN1/FNIP1/FNIP2/GBP5/HSP90AA1/ICE1/LCP1/MAP1B/MAPRE1/MET/MMP1/MPP7/NAV3/NCK1/NCKAP1/NCKAP1L/PPP2CA/PRKD1/PSMC6/RICTOR/SH3GLB1/SNX9/TFRC/TLR4/TLR6/VCP | 41 |
| BP | GO:0120032 | regulation of plasma membrane bounded cell projection assembly | 41/2221 | 195/18614 | 0.000198849 | 0.004497273 | 0.003800712 | ANLN/CEP135/ACTR2/ACTR3/APC/ATG3/ATP7A/ATP8B1/CCDC88A/CCP110/CDKL5/CENPJ/CEP120/CEP97/CORO1C/CYLD/DOCK11/EPS8/FAM98A/FER/FMR1/FNBP1L/FXR1/GDI2/HSP90AA1/MNS1/MPHOSPH9/NCKAP1/NLGN1/ODF2L/PIK3CA/PIK3R1/PLD1/RAB3IP/RDX/SDCCAG8/STAP1/SYNE2/TBC1D30/TGFBR1/TWF1 | 41 |
| BP | GO:0032760 | positive regulation of tumor necrosis factor production | 26/2221 | 105/18614 | 0.00020111 | 0.004514469 | 0.003815244 | HDAC2/AKAP12/ARFGEF2/BTK/CD36/CD84/CYBB/DHX9/FCGR3A/HAVCR2/HMGB1/IFIH1/IFNGR1/JAK2/LPL/LRRK2/MMP8/PIK3R1/PTPN11/PTPRC/RIPK1/RIPK2/TLR1/TLR2/TLR3/TLR4 | 26 |
| BP | GO:0070828 | heterochromatin organization | 26/2221 | 105/18614 | 0.00020111 | 0.004514469 | 0.003815244 | EZH2/HDAC2/HELLS/ATF7IP/ATRX/BAZ1A/CTR9/HAT1/HMGB1/KDM5A/L3MBTL3/LMNB1/MECOM/PIK3CA/RB1/RIF1/SETD7/SETDB2/SMARCA5/SMCHD1/SPTY2D1/SUZ12/TPR/UBR2/ZDBF2/ZNFX1 | 26 |
| BP | GO:0034063 | stress granule assembly | 11/2221 | 28/18614 | 0.000209569 | 0.004669507 | 0.003946269 | C9orf72/CSDE1/DDX3X/DYNC1H1/EIF2S1/G3BP1/G3BP2/OGFOD1/PRRC2C/PUM2/YTHDF3 | 11 |
| BP | GO:0070199 | establishment of protein localization to chromosome | 11/2221 | 28/18614 | 0.000209569 | 0.004669507 | 0.003946269 | BRCA2/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/NIPBL/POT1/TCP1 | 11 |
| BP | GO:0006270 | DNA replication initiation | 13/2221 | 37/18614 | 0.000212826 | 0.004724576 | 0.003992809 | CDC6/GMNN/MCM3/MCM6/PRIM2/TICRR/CCNE2/NBN/NOC3L/ORC3/ORC4/POLA1/TOPBP1 | 13 |
| BP | GO:0001732 | formation of cytoplasmic translation initiation complex | 8/2221 | 16/18614 | 0.000214946 | 0.004754091 | 0.004017752 | EIF3M/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF5 | 8 |
| BP | GO:0043434 | response to peptide hormone | 76/2221 | 427/18614 | 0.00021942 | 0.004835275 | 0.004086362 | BRIP1/CCNA2/CDC6/AHCYL1/APC/ARG1/ATP2B1/C2CD5/COL3A1/CTSK/CYBB/DENND4C/EIF2B3/ENPP1/EPM2AIP1/FBN1/FER/GCLC/GCNT1/HADHA/IDE/INHBA/ITGB3/JAK2/KBTBD2/LPL/LRP6/LTA4H/LYN/MAP1B/MIR15B/MYO5A/NCK1/NCL/NCOA1/NCOA2/NFE2L2/NUCKS1/OGT/OSBPL8/PARP1/PCSK1/PDE3B/PHEX/PHIP/PIK3C2A/PIK3CA/PIK3R1/PIK3R3/PLCB1/PNPT1/PPARG/PRKCI/PRKDC/PTGS2/PTPN11/PTPN2/RAP1GDS1/RB1/ROCK1/ROCK2/SESN3/SOS1/SOS2/STAT1/STAT4/STXBP3/STXBP4/SYAP1/TBC1D4/TCF12/TIMP4/TLR2/USO1/VPS13C/ZNF106 | 76 |
| BP | GO:0034605 | cellular response to heat | 19/2221 | 67/18614 | 0.000220584 | 0.004843193 | 0.004093054 | HDAC2/ATM/ATR/CHORDC1/DHX36/DNAJC2/DNAJC7/EIF2S1/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/LYN/NF1/PTGS2/SLU7/TFEC/TPR/VCP | 19 |
| BP | GO:0140013 | meiotic nuclear division | 41/2221 | 196/18614 | 0.000222981 | 0.004871332 | 0.004116835 | ASPM/BRCA2/BRIP1/BUB1/BUB1B/CCNB2/FANCD2/FBXO5/KIF18A/MND1/NCAPH/NDC80/NUF2/RAD51AP1/RAD54B/TOP2A/TTK/ACTR2/ACTR3/ATM/CCNE2/CENPC/ERCC4/FANCM/FIGNL1/ING2/MASTL/MLH1/MLH3/ORC4/PLCB1/RAD21/RAD50/SMC1A/SMC2/SMC3/SMC4/SPIRE1/SYCP2/TOP2B/UBR2 | 41 |
| BP | GO:0051648 | vesicle localization | 44/2221 | 215/18614 | 0.000224823 | 0.004871332 | 0.004116835 | AP1AR/AP3B1/AP3M1/ARFGAP3/BLOC1S6/CCDC186/CDH2/CLASP2/CTNNB1/CUL3/DYNC1H1/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/FAM91A1/FNBP1L/ITGA4/KIF3A/KIF5B/LRRK2/MKKS/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/NLGN1/PIK3CG/RAB1A/RAB27A/SAR1B/SDCBP/SPG11/TANC2/TBC1D23/TRAK2/TRAPPC11/TRAPPC13/TRAPPC8/TRIP11/USO1/WDR11 | 44 |
| BP | GO:1903046 | meiotic cell cycle process | 44/2221 | 215/18614 | 0.000224823 | 0.004871332 | 0.004116835 | ASPM/BRCA2/BRIP1/BUB1/BUB1B/CCNB2/FANCD2/FBXO5/KIF18A/MND1/NCAPH/NDC80/NUF2/RAD51AP1/RAD54B/TOP2A/TTK/ACTR2/ACTR3/ATM/ATRX/CCNE2/CENPC/ERCC4/FANCM/FIGNL1/ING2/MASTL/MLH1/MLH3/MSH6/NSUN2/ORC4/PLCB1/RAD21/RAD50/SMC1A/SMC2/SMC3/SMC4/SPIRE1/SYCP2/TOP2B/UBR2 | 44 |
| BP | GO:0016579 | protein deubiquitination | 35/2221 | 159/18614 | 0.000225915 | 0.004871332 | 0.004116835 | BRCA1/CDK1/BRCC3/CYLD/MYSM1/OTUD4/OTUD6B/PSMD14/SUPT20H/TAF2/TAF7/TANK/UCHL3/UCHL5/USP1/USP13/USP14/USP15/USP16/USP24/USP25/USP27X/USP32/USP34/USP37/USP38/USP44/USP47/USP53/USP7/USP8/USP9X/VCP/YOD1/ZRANB1 | 35 |
| BP | GO:0051092 | positive regulation of NF-kappaB transcription factor activity | 35/2221 | 159/18614 | 0.000225915 | 0.004871332 | 0.004116835 | AIM2/BTK/CAPN3/CD36/CHUK/CLOCK/DHX9/EIF2AK2/ERC1/FER/IL18/IL18RAP/IL1RAP/IRAK3/MALT1/MAP3K13/MAP3K7/MTDH/NLRC4/NLRP3/PRKCI/PRKD1/RIPK1/RIPK2/RPS6KA5/TFRC/TLR2/TLR3/TLR4/TLR6/TRAF5/TRIM22/TRIM38/TRIM6/USP14 | 35 |
| BP | GO:0009167 | purine ribonucleoside monophosphate metabolic process | 14/2221 | 42/18614 | 0.000232236 | 0.004989757 | 0.004216917 | ADK/ATIC/CASK/DLG1/DLG2/GART/GMPS/IMPDH2/MAGI3/MPP1/NT5C2/NT5E/PAICS/PPAT | 14 |
| BP | GO:0002200 | somatic diversification of immune receptors | 21/2221 | 78/18614 | 0.000234319 | 0.005016604 | 0.004239606 | ATAD5/MSH2/POLQ/ATM/HMGB1/HMGB2/HSPD1/LIG4/MLH1/MSH3/MSH6/NBN/PRKDC/PTPRC/RIF1/SAMHD1/SWAP70/TFRC/THOC1/TP53BP1/XRCC4 | 21 |
| BP | GO:1900227 | positive regulation of NLRP3 inflammasome complex assembly | 9/2221 | 20/18614 | 0.000235636 | 0.005026892 | 0.004248301 | BRCC3/BTK/CD36/DDX3X/GBP5/PPP2CA/PRKD1/TLR4/TLR6 | 9 |
| BP | GO:0046677 | response to antibiotic | 15/2221 | 47/18614 | 0.000242178 | 0.005148215 | 0.004350833 | EZH2/ATP7A/CASP3/CYB5R4/HSP90AA1/HSPA5/JAK1/JAK2/KDM5B/MDM2/MEF2C/PLA2G4A/RSRC1/SLC1A3/VPS54 | 15 |
| BP | GO:1902749 | regulation of cell cycle G2/M phase transition | 27/2221 | 112/18614 | 0.000245853 | 0.005205669 | 0.004399388 | ATAD5/BLM/BRCA1/CDC6/CDK1/CENPF/CHEK1/DTL/FBXO5/KIF14/TICRR/ATM/BRCC3/CCNG1/NAE1/NBN/RAD17/RAD21/RAD50/RBBP8/RRM1/RRM2B/SYF2/TAOK1/TAOK3/TOPBP1/USP47 | 27 |
| BP | GO:0018205 | peptidyl-lysine modification | 68/2221 | 374/18614 | 0.000246612 | 0.005205669 | 0.004399388 | BRCA1/BRCA2/CHEK1/DEK/EZH2/HDAC2/ARID4A/ARID4B/ASH1L/ATP7A/BAZ1B/BOD1L1/CAPN3/CTNNB1/CTR9/DDX21/EPC2/ERCC6/ESCO1/GNL3/HAT1/HCFC2/IFIH1/ING3/IWS1/JADE1/KAT6A/KDM6A/KIAA1586/KMT2C/LOX/MAP3K7/MDM2/METTL18/MORF4L2/MSL3P1/MTF2/NAA50/OGT/PHF20L1/PLOD2/RANBP2/RBBP5/RIF1/RLF/RTF1/SDR16C5/SENP1/SENP5/SENP6/SENP7/SETD7/SETDB2/SETMAR/SF3B1/SMARCA5/SMC5/SMC6/SNW1/SUPT20H/SUV39H2/TAF2/TAF7/TOPORS/TRIM38/USPL1/ZNF451/ZZZ3 | 68 |
| BP | GO:0051650 | establishment of vesicle localization | 41/2221 | 197/18614 | 0.000249713 | 0.0052344 | 0.004423669 | AP1AR/AP3B1/AP3M1/ARFGAP3/BLOC1S6/CCDC186/CLASP2/CTNNB1/CUL3/DYNC1H1/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/FAM91A1/FNBP1L/ITGA4/KIF3A/KIF5B/LRRK2/MKKS/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/NLGN1/RAB1A/RAB27A/SAR1B/SDCBP/SPG11/TANC2/TBC1D23/TRAK2/TRAPPC11/TRAPPC13/TRAPPC8/TRIP11/WDR11 | 41 |
| BP | GO:0060491 | regulation of cell projection assembly | 41/2221 | 197/18614 | 0.000249713 | 0.0052344 | 0.004423669 | ANLN/CEP135/ACTR2/ACTR3/APC/ATG3/ATP7A/ATP8B1/CCDC88A/CCP110/CDKL5/CENPJ/CEP120/CEP97/CORO1C/CYLD/DOCK11/EPS8/FAM98A/FER/FMR1/FNBP1L/FXR1/GDI2/HSP90AA1/MNS1/MPHOSPH9/NCKAP1/NLGN1/ODF2L/PIK3CA/PIK3R1/PLD1/RAB3IP/RDX/SDCCAG8/STAP1/SYNE2/TBC1D30/TGFBR1/TWF1 | 41 |
| BP | GO:0090169 | regulation of spindle assembly | 12/2221 | 33/18614 | 0.000256316 | 0.005354148 | 0.00452487 | KIF15/SASS6/SPAG5/STIL/CENPJ/CEP97/CHMP2B/DYNC1H1/GPSM2/HNRNPU/SENP6/TPR | 12 |
| BP | GO:0009411 | response to UV | 34/2221 | 154/18614 | 0.000259836 | 0.00540891 | 0.004571149 | BRCA2/CHEK1/DTL/MSH2/PBK/ATR/CASP3/DCUN1D3/DHX36/EIF2AK4/EIF2S1/ERCC4/ERCC5/ERCC6/IMPACT/MAP3K4/MMP1/MSH6/NEDD4/PARP1/PIK3R1/POLD3/POLK/PTGS2/PTPRK/REV1/SDE2/SPRTN/TAF1/USP1/USP47/WRN/ZBTB1/ZRANB3 | 34 |
| BP | GO:0002183 | cytoplasmic translational initiation | 13/2221 | 38/18614 | 0.000288443 | 0.005983692 | 0.005056906 | EIF3M/DHX29/EIF2B3/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF5/NCBP1/NCBP2/NCK1 | 13 |
| BP | GO:2000045 | regulation of G1/S transition of mitotic cell cycle | 39/2221 | 186/18614 | 0.000297776 | 0.006156074 | 0.005202589 | CDC6/EZH2/KIF14/MTBP/SASS6/STIL/ADAM17/ANKRD17/APC/ARID2/ATM/BRD7/CCNH/CENPJ/CPSF3/DCUN1D3/DDX3X/DLG1/ECD/GIGYF2/GPNMB/INHBA/JADE1/KMT2E/MDM2/MIR15B/MIR30C2/PBRM1/PLCB1/PLRG1/PPP2CA/PRKDC/RB1/RBL2/RDX/RFWD3/RRM1/SDE2/SLFN11 | 39 |
| BP | GO:0042306 | regulation of protein import into nucleus | 17/2221 | 58/18614 | 0.00030271 | 0.006236656 | 0.00527069 | CDK1/ECT2/ANGPT1/CD36/EFCAB7/HSP90AA1/IPO5/JAK2/NF1/NOLC1/PIK3R1/PRKD1/PTGS2/TPR/UBR5/UFM1/ZPR1 | 17 |
| BP | GO:0034085 | establishment of sister chromatid cohesion | 7/2221 | 13/18614 | 0.00030393 | 0.006240412 | 0.005273864 | NAA50/NIPBL/RAD21/SMC1A/SMC3/STAG1/STAG2 | 7 |
| BP | GO:0060236 | regulation of mitotic spindle organization | 14/2221 | 43/18614 | 0.000306884 | 0.00627964 | 0.005307017 | BORA/KIF15/SASS6/STIL/TPX2/CENPJ/CEP97/CHMP2B/CLTC/DYNC1H1/GPSM2/HNRNPU/MAP9/TPR | 14 |
| BP | GO:0032732 | positive regulation of interleukin-1 production | 20/2221 | 74/18614 | 0.000309209 | 0.006305777 | 0.005329106 | HDAC2/AIM2/CASP1/CD36/GBP5/HAVCR2/HMGB1/IFI16/JAK2/LPL/MALT1/MNDA/NAIP/NLRC4/NLRP3/PANX1/RIPK2/TLR4/TLR6/TLR8 | 20 |
| BP | GO:0051321 | meiotic cell cycle | 54/2221 | 284/18614 | 0.000338057 | 0.006870773 | 0.005806592 | ASPM/BRCA2/BRIP1/BUB1/BUB1B/CCNB2/FANCD2/FBXO5/KIF18A/MND1/NCAPH/NDC80/NEK2/NUF2/RAD51AP1/RAD54B/TOP2A/TTK/XRCC2/ACTR2/ACTR3/ANAPC1/ATM/ATRX/CCNE2/CDC27/CENPC/ERCC4/FANCM/FIGNL1/ING2/MASTL/MLH1/MLH3/MNS1/MSH6/NBN/NSUN2/ORC4/PLCB1/PPP2CA/RAD21/RAD50/RBBP8/SMC1A/SMC2/SMC3/SMC4/SPIRE1/STAG2/SYCP2/TOP2B/UBR2/ZW10 | 54 |
| BP | GO:0048872 | homeostasis of number of cells | 57/2221 | 304/18614 | 0.000340856 | 0.006890517 | 0.005823278 | CCNB2/EZH2/NCAPG2/ADAM17/ALAS2/AP3B1/ARID4A/BPGM/BTK/CASP3/CDH2/DOCK10/DOCK11/FAS/FH/FSTL1/GAPT/GIGYF2/HIF1A/HMGB1/HMGB2/HSPA9/IL2RA/IL7R/INHBA/IREB2/JAK2/KMT2E/KRAS/L3MBTL3/LIPA/LYAR/LYN/MEF2C/MERTK/MTHFD1/NCKAP1L/NF1/PDE4B/PIK3CB/PPP2R3C/PRKDC/PTPN11/PTPN2/RACGAP1/RB1/RC3H2/SKIL/SLC4A1/SLC7A11/SOS1/SOS2/STAT1/UBA5/UFL1/VPS54/WDR48 | 57 |
| BP | GO:0006312 | mitotic recombination | 10/2221 | 25/18614 | 0.000342464 | 0.006890517 | 0.005823278 | BRCA2/MSH2/RAD54B/ERCC4/GEN1/MLH1/MSH3/RAD50/SMC5/SMC6 | 10 |
| BP | GO:0060333 | type II interferon-mediated signaling pathway | 10/2221 | 25/18614 | 0.000342464 | 0.006890517 | 0.005823278 | ARG1/IFNGR1/JAK1/JAK2/PARP14/PARP9/PPARG/PTPN2/SP100/STAT1 | 10 |
| BP | GO:0044546 | NLRP3 inflammasome complex assembly | 12/2221 | 34/18614 | 0.00035344 | 0.007064102 | 0.005969977 | AIM2/BRCC3/BTK/CD36/DDX3X/EIF2AK2/GBP5/NLRP3/PPP2CA/PRKD1/TLR4/TLR6 | 12 |
| BP | GO:0051973 | positive regulation of telomerase activity | 12/2221 | 34/18614 | 0.00035344 | 0.007064102 | 0.005969977 | NEK2/CCT2/CCT4/CTNNB1/DKC1/GRHL2/HSP90AA1/HSP90AB1/MAP3K4/POT1/TCP1/XRCC5 | 12 |
| BP | GO:1990778 | protein localization to cell periphery | 63/2221 | 345/18614 | 0.000362459 | 0.007220372 | 0.006102043 | AGR2/ACSL3/ADAM10/AKAP5/ANK2/ANK3/ARL13B/ATP1B1/ATP2C1/BLZF1/C2CD5/CCDC88A/CDH2/CLASP2/CLTC/CNST/DENND4C/DLG1/EFCAB7/EFR3A/EPB41/EPB41L2/EPB41L3/EPHA3/ERBB4/EXOC5/EZR/FCHO2/GBP1/GOLGA4/GPSM2/HECTD1/IFT80/ITGB1/KIF5B/LRP6/LZTFL1/MACF1/MYO5A/NSF/OGT/PIGW/PIK3R1/PKP2/PLS1/PPFIA1/PREPL/PRKCI/RAB8B/RABEP1/RAPGEF2/RAPGEF6/RDX/ROCK1/ROCK2/SEC23A/SLC4A1/SLMAP/SNAP25/TNIK/VPS35/WDR19/WNK3 | 63 |
| BP | GO:1901879 | regulation of protein depolymerization | 22/2221 | 86/18614 | 0.000370583 | 0.007357855 | 0.006218232 | TPX2/ADD3/APC/ASPH/CAMSAP2/CAPZA2/CKAP2/CLASP2/EPS8/LIMA1/MAP1B/NAV3/PIK3CA/RDX/SCIN/SPTAN1/SVIL/SWAP70/TAOK1/TMOD2/TWF1/WDR47 | 22 |
| BP | GO:0007062 | sister chromatid cohesion | 17/2221 | 59/18614 | 0.00037853 | 0.007490911 | 0.00633068 | BUB1/BUB1B/ESCO2/ATRX/CTNNB1/ESCO1/NAA50/NIPBL/PDS5A/PDS5B/RAD21/RB1/SMC1A/SMC3/SMC5/STAG1/STAG2 | 17 |
| BP | GO:0036297 | interstrand cross-link repair | 13/2221 | 39/18614 | 0.000385823 | 0.007610201 | 0.006431493 | FANCD2/FANCI/MCM8/NEIL3/RAD51AP1/ATR/DCLRE1A/ERCC4/ERCC6L2/FANCM/NUCKS1/RFWD3/VCP | 13 |
| BP | GO:2000234 | positive regulation of rRNA processing | 6/2221 | 10/18614 | 0.000392312 | 0.007712898 | 0.006518284 | HEATR1/RIOK1/RIOK2/UTP15/WDR43/WDR75 | 6 |
| BP | GO:0051099 | positive regulation of binding | 37/2221 | 176/18614 | 0.000397752 | 0.007794384 | 0.006587149 | GMNN/CAPRIN2/CLIC2/CTNNB1/DHX9/DPH3/DTX3L/EGF/EIF2S1/EIF3D/EIF3E/EPB41/EPHA4/FMR1/HMGB1/HMGB2/IDE/IGF1/ITGA2/JAK2/KRIT1/LRRK2/MAPRE1/MET/MMP8/NCBP1/NMD3/PARP1/PARP9/PPARG/PPP2CA/RAPGEF2/RB1/RIPK2/TAF1/TRIM6/USP9X | 37 |
| BP | GO:0009126 | purine nucleoside monophosphate metabolic process | 14/2221 | 44/18614 | 0.000401164 | 0.007835722 | 0.006622085 | ADK/ATIC/CASK/DLG1/DLG2/GART/GMPS/IMPDH2/MAGI3/MPP1/NT5C2/NT5E/PAICS/PPAT | 14 |
| BP | GO:0032984 | protein-containing complex disassembly | 47/2221 | 240/18614 | 0.000403871 | 0.007863067 | 0.006645194 | KIF18A/TPX2/ABCE1/ADD3/APC/ARID2/ASPH/ATP2A2/BECN1/CAMSAP2/CAPZA2/CHMP2B/CKAP2/CKAP5/CLASP2/DHX8/EPS8/ETF1/GFM2/GSPT1/HSPA8/IRAK3/KIF2A/KIF5B/LIMA1/MAP1B/NAV3/NSF/OGFOD1/PIK3C3/PIK3CA/PIK3R4/RDX/SCIN/SETX/SPTAN1/STX17/SUPT16H/SVIL/SWAP70/TAOK1/TMOD2/TWF1/VCP/VTA1/WDR47/ZFAND1 | 47 |
| BP | GO:0002224 | toll-like receptor signaling pathway | 19/2221 | 70/18614 | 0.000408168 | 0.007915693 | 0.006689669 | AP3B1/BIRC2/BIRC3/BTK/CD36/CTSS/HSPD1/IRAK3/IRAK4/MAP3K7/OTUD4/RAB11FIP2/RPS6KA3/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8 | 19 |
| BP | GO:0009615 | response to virus | 72/2221 | 408/18614 | 0.000409206 | 0.007915693 | 0.006689669 | ABCC9/AIM2/AZI2/BECN1/BNIP3L/CASP1/CCT5/CHUK/DCLK1/DDX1/DDX21/DDX3X/DDX60/DDX60L/DHX15/DHX36/DHX9/DNAJC3/DTX3L/EIF2AK2/EIF2AK4/ELMOD2/EXOC1/FGL2/FMR1/G3BP1/GBP1/GBP3/HIF1A/HSP90AA1/IFI16/IFIH1/IFIT1B/IFIT3/IFIT5/IFNAR1/IFNGR1/IRAK3/ITGB6/ITGB8/IVNS1ABP/JAK1/JAK2/LGALS8/LYST/NCBP1/NLRP3/PARP9/POLR3B/POLR3C/PPM1B/PTPRC/RIOK3/RNASEL/SAMHD1/SENP7/SLFN11/SLFN13/STAT1/TANK/TBK1/TLR2/TLR3/TLR8/TRIM22/TRIM38/TRIM44/TRIM6/USP27X/ZMYND11/ZNF175/ZNFX1 | 72 |
| BP | GO:0031503 | protein-containing complex localization | 38/2221 | 183/18614 | 0.00043199 | 0.008329644 | 0.007039505 | XPO1/ABCE1/ADAM10/AKAP9/ATM/ATR/CEP112/DLG1/DYNC2H1/ERBB4/EZR/HNRNPU/IFT57/IFT74/IFT80/ITGB3/KIF5B/LCA5/LMNB1/LSG1/LTV1/MDN1/MIOS/NLGN1/NMD3/NUP88/OGT/PCM1/RIOK2/RPGR/RRS1/SDAD1/SNAP25/SSX2IP/TTC21B/VPS35/WDR19/WDR35 | 38 |
| BP | GO:0006301 | postreplication repair | 12/2221 | 35/18614 | 0.000479945 | 0.009224761 | 0.007795982 | BRCA1/DTL/MSH2/RAD18/POLD3/POLK/REV1/REV3L/SPRTN/USP1/VCP/ZBTB1 | 12 |
| BP | GO:0016241 | regulation of macroautophagy | 34/2221 | 159/18614 | 0.000484526 | 0.009283147 | 0.007845325 | ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/BECN1/BNIP3L/C9orf72/CASP3/EXOC1/EXOC4/GNAI3/HIF1A/LRRK2/MAP3K7/MTM1/NEDD4/NPC1/PIK3C3/PIK3CA/PIK3R4/RAB3GAP1/RAB3GAP2/RIPK2/SCFD1/SESN3/SH3GLB1/SNX30/SNX6/SPTLC1/TBK1/VPS13C/VPS13D/VPS26A/VPS35 | 34 |
| BP | GO:0002562 | somatic diversification of immune receptors via germline recombination within a single locus | 19/2221 | 71/18614 | 0.000495831 | 0.009438896 | 0.007976951 | ATAD5/MSH2/ATM/HMGB1/HMGB2/HSPD1/LIG4/MLH1/MSH3/MSH6/NBN/PRKDC/PTPRC/RIF1/SWAP70/TFRC/THOC1/TP53BP1/XRCC4 | 19 |
| BP | GO:0016444 | somatic cell DNA recombination | 19/2221 | 71/18614 | 0.000495831 | 0.009438896 | 0.007976951 | ATAD5/MSH2/ATM/HMGB1/HMGB2/HSPD1/LIG4/MLH1/MSH3/MSH6/NBN/PRKDC/PTPRC/RIF1/SWAP70/TFRC/THOC1/TP53BP1/XRCC4 | 19 |
| BP | GO:0036119 | response to platelet-derived growth factor | 10/2221 | 26/18614 | 0.000497362 | 0.009438896 | 0.007976951 | CCNA2/ATP7A/FER/IQGAP1/ITGB3/PDGFD/RDX/SYAP1/TLR4/YES1 | 10 |
| BP | GO:0035337 | fatty-acyl-CoA metabolic process | 13/2221 | 40/18614 | 0.000509763 | 0.009613595 | 0.008124591 | ELOVL6/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ELOVL2/ELOVL7/FAR1/FAR2/HSD17B4/PPT1/SLC27A2 | 13 |
| BP | GO:1901998 | toxin transport | 13/2221 | 40/18614 | 0.000509763 | 0.009613595 | 0.008124591 | ADAM10/CCT2/CCT3/CCT4/CCT5/CCT8/COPB2/DNAJA1/HSPA5/LRP6/SCFD1/SLC22A3/TCP1 | 13 |
| BP | GO:0045727 | positive regulation of translation | 31/2221 | 141/18614 | 0.000512092 | 0.009627322 | 0.008136192 | GUF1/RMND1/CSDE1/DDX3X/DHX29/DHX36/DHX9/DNAJC3/EIF2AK4/EIF3D/EIF3E/EIF4A3/FASTKD2/FMR1/FXR1/HNRNPU/IMPACT/ITGA2/LARP1B/LARP4/METTL14/MIR15B/NCK1/PLD1/PRKDC/SSB/SYNCRIP/TRMT10C/UPF3B/USP16/YTHDF3 | 31 |
| BP | GO:0001701 | in utero embryonic development | 70/2221 | 398/18614 | 0.000537959 | 0.0100387 | 0.008483854 | BRCA2/CCNB2/CHEK1/MSH2/NCAPG2/NEK2/PLK4/STIL/XRCC2/ADAM10/ADAMTS3/ANGPT1/ATP7A/BIRC6/C5/C6/CHD7/CHD8/CIR1/CNOT1/COL3A1/COPS2/CTNNB1/CTR9/CUL3/EIF2S2/FUT8/GABPA/GGNBP2/GRHL2/HECTD1/HIF1A/IGF1/ITGB1/KDM4C/KIDINS220/LIG4/MATR3/MYO1E/NASP/NBN/NCOA1/NECAB1/NPAT/NSRP1/NSUN2/PALB2/PDGFRA/PHF6/RBBP6/RBBP8/RBPJ/RCN1/RPGRIP1L/RPL7L1/RSPO3/RTCB/RTF1/SEC24D/SKIL/SYF2/TBL1XR1/TGFBR1/VPS54/WDR19/YTHDC1/ZFAND5/ZFP14/ZFPM2/ZPR1 | 70 |
| BP | GO:0006903 | vesicle targeting | 18/2221 | 66/18614 | 0.000538979 | 0.0100387 | 0.008483854 | AP1AR/ARFGAP3/CLASP2/CUL3/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/FAM91A1/NLGN1/SAR1B/TBC1D23/TRAPPC11/TRAPPC13/TRAPPC8/TRIP11/WDR11 | 18 |
| BP | GO:0060760 | positive regulation of response to cytokine stimulus | 18/2221 | 66/18614 | 0.000538979 | 0.0100387 | 0.008483854 | ADAM17/CASP1/CASP4/DHX9/HIF1A/IFIH1/IL1R1/LRRC70/PARP14/PARP9/RIPK1/RIPK2/TBK1/TLR2/TLR4/TRIM44/TRIM6/USP27X | 18 |
| BP | GO:0006177 | GMP biosynthetic process | 7/2221 | 14/18614 | 0.000545291 | 0.01009375 | 0.008530378 | ADK/ATIC/GART/GMPS/IMPDH2/PAICS/PPAT | 7 |
| BP | GO:0070816 | phosphorylation of RNA polymerase II C-terminal domain | 7/2221 | 14/18614 | 0.000545291 | 0.01009375 | 0.008530378 | GTF2H3/CCNH/CCNT1/GTF2H1/NCBP1/NCBP2/PPIL4 | 7 |
| BP | GO:0051607 | defense response to virus | 56/2221 | 303/18614 | 0.000552176 | 0.010189851 | 0.008611593 | ABCC9/AIM2/AZI2/BECN1/BNIP3L/CASP1/DDX1/DDX21/DDX60/DDX60L/DHX15/DHX36/DHX9/DNAJC3/DTX3L/EIF2AK2/EIF2AK4/ELMOD2/EXOC1/FGL2/G3BP1/GBP1/GBP3/HSP90AA1/IFI16/IFIH1/IFIT1B/IFIT3/IFIT5/LYST/NCBP1/PARP9/POLR3B/POLR3C/PPM1B/PTPRC/RIOK3/RNASEL/SAMHD1/SENP7/SLFN11/SLFN13/STAT1/TANK/TBK1/TLR2/TLR3/TLR8/TRIM22/TRIM38/TRIM44/TRIM6/USP27X/ZMYND11/ZNF175/ZNFX1 | 56 |
| BP | GO:0001819 | positive regulation of cytokine production | 83/2221 | 489/18614 | 0.000553899 | 0.01019039 | 0.008612049 | BRCA1/HDAC2/ADAM17/AIM2/AKAP12/ARFGEF2/BTK/C3/C5/CASP1/CD226/CD36/CD84/CD86/CHUK/CYBB/DDX1/DDX21/DDX3X/DHX36/DHX9/EIF2AK2/EIF2AK3/FCGR3A/G3BP1/GBP5/HAVCR2/HGF/HIF1A/HMGB1/HMGB2/HSP90AA1/HSPD1/IFI16/IFIH1/IFNGR1/IL18/IL1R1/IL1RAP/IL6ST/IRAK3/ITK/JAK2/LACC1/LPL/LRRK2/MALT1/MAP3K7/MMP8/MNDA/NAIP/NLRC4/NLRP3/PANX1/PDE4B/PDE4D/PIBF1/PIK3CG/PIK3R1/PLA2R1/PLCB1/POLR3B/POLR3C/PTGS2/PTPN11/PTPRC/RAB1A/RIOK3/RIPK1/RIPK2/ROCK2/RORA/STAT1/SULF1/TBK1/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/TMF1/TRIM6 | 83 |
| BP | GO:0010042 | response to manganese ion | 9/2221 | 22/18614 | 0.000558459 | 0.010211827 | 0.008630166 | ADAM9/ARG1/ATP7A/EIF2AK3/EIF2S1/HSPA5/LRRK2/PTGS2/TFRC | 9 |
| BP | GO:0043555 | regulation of translation in response to stress | 9/2221 | 22/18614 | 0.000558459 | 0.010211827 | 0.008630166 | DDX3X/DNAJC3/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/IMPACT/NCK1/RPS6KA3 | 9 |
| BP | GO:0051988 | regulation of attachment of spindle microtubules to kinetochore | 8/2221 | 18/18614 | 0.000586263 | 0.010655461 | 0.009005088 | ECT2/NEK2/SPAG5/APC/BECN1/HNRNPU/KNSTRN/RACGAP1 | 8 |
| BP | GO:1904872 | regulation of telomerase RNA localization to Cajal body | 8/2221 | 18/18614 | 0.000586263 | 0.010655461 | 0.009005088 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0007179 | transforming growth factor beta receptor signaling pathway | 43/2221 | 218/18614 | 0.000595705 | 0.010794454 | 0.009122552 | MIRLET7F1/HDAC2/ADAM17/ADAM9/ARID4A/ARID4B/BRMS1L/CD109/CILP/COL3A1/FBN1/FERMT2/FUT8/GCNT2/HSP90AB1/HSPA5/ING2/ITGB6/ITGB8/LOX/LTBP1/MAP3K7/MIR15B/MIR30B/MTMR4/OGT/PARP1/PPARG/PTPRK/SDCBP/SKIL/SNW1/SNX25/SNX6/TGFBR1/TRIM33/USP15/USP9X/VEPH1/ZEB1/ZEB2/ZFYVE9/ZNF451 | 43 |
| BP | GO:0140546 | defense response to symbiont | 56/2221 | 304/18614 | 0.000599893 | 0.010837714 | 0.009159112 | ABCC9/AIM2/AZI2/BECN1/BNIP3L/CASP1/DDX1/DDX21/DDX60/DDX60L/DHX15/DHX36/DHX9/DNAJC3/DTX3L/EIF2AK2/EIF2AK4/ELMOD2/EXOC1/FGL2/G3BP1/GBP1/GBP3/HSP90AA1/IFI16/IFIH1/IFIT1B/IFIT3/IFIT5/LYST/NCBP1/PARP9/POLR3B/POLR3C/PPM1B/PTPRC/RIOK3/RNASEL/SAMHD1/SENP7/SLFN11/SLFN13/STAT1/TANK/TBK1/TLR2/TLR3/TLR8/TRIM22/TRIM38/TRIM44/TRIM6/USP27X/ZMYND11/ZNF175/ZNFX1 | 56 |
| BP | GO:0007015 | actin filament organization | 76/2221 | 442/18614 | 0.00063384 | 0.011416714 | 0.009648434 | DIAPH3/ACTR2/ACTR3/ADD3/ALMS1/AP1AR/ARFGEF1/ARHGAP12/ARHGAP18/ARHGAP28/C9orf72/CALD1/CAPZA2/CCDC88A/CD2AP/CGNL1/CLASP2/CORO1C/CUL3/DIAPH2/DLG1/EPS8/EZR/FAT1/FER/FERMT2/FMN1/GAS2L3/HMCN1/HSP90B1/IQGAP2/JAK2/JMY/LCP1/LIMA1/MET/MKKS/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/NCK1/NCKAP1/NCKAP1L/NEB/NOSTRIN/PHLDB2/PIK3CA/PIK3R1/PLS1/PLS3/POF1B/PPFIA1/PPP1R9A/PRKCI/PSTPIP2/RASA1/RDX/RICTOR/ROCK1/ROCK2/RUFY3/SCIN/SNX9/SPIRE1/SPTAN1/SVIL/SWAP70/TGFBR1/TJP1/TMOD2/TPM1/TTC17/TTN/TWF1 | 76 |
| BP | GO:0043122 | regulation of I-kappaB kinase/NF-kappaB signaling | 49/2221 | 258/18614 | 0.000637015 | 0.011439651 | 0.009667818 | ECT2/AKAP13/ALPK1/ANGPT1/ANKRD17/ASH1L/ATP2C1/BIRC2/BIRC3/CAPN3/CASP1/CD36/CHUK/CLEC4D/CTNNB1/DDX1/DDX21/DHX15/DHX36/GOLT1B/IFIT5/IRAK4/MALT1/MAP3K7/MIR15B/MTDH/PPM1B/PRKD1/REL/RIOK3/RIPK1/RIPK2/RORA/STAT1/TAB2/TAB3/TANK/TBK1/TFRC/TLR3/TLR4/TLR6/TRAF5/TRIM22/TRIM38/TRIM59/TRIM6/UFL1/ZMYND11 | 49 |
| BP | GO:0140632 | inflammasome complex assembly | 12/2221 | 36/18614 | 0.000642497 | 0.011503756 | 0.009721994 | AIM2/BRCC3/BTK/CD36/DDX3X/EIF2AK2/GBP5/NLRP3/PPP2CA/PRKD1/TLR4/TLR6 | 12 |
| BP | GO:0031396 | regulation of protein ubiquitination | 42/2221 | 213/18614 | 0.000689714 | 0.012312517 | 0.01040549 | BRCA1/BUB1B/FANCI/FBXO5/MAD2L1/MTBP/PRMT3/ANGPT1/ARRDC3/ARRDC4/BIRC2/BIRC3/CUL3/DCUN1D3/DDX3X/DNAJA1/DTX3L/FANCM/GCLC/GTPBP4/HSP90AA1/HSP90AB1/HSPA5/IVNS1ABP/LRRK2/MALT1/MASTL/MYCBP2/OGT/PLAA/RIPK2/SPOPL/SPRTN/TAF1/TGFBR1/TOPORS/TRIM44/TRIP12/UBR5/UFL1/USP44/WDR48 | 42 |
| BP | GO:0098727 | maintenance of cell number | 37/2221 | 181/18614 | 0.000696116 | 0.012390036 | 0.010471002 | ASPM/EZH2/FANCD2/HDAC2/ARID4A/ARID4B/BRMS1L/CDH2/CNOT1/CTNNB1/CTR9/GNL3/HOOK3/IGF1/ING2/KDM3A/KDM4C/LEO1/LIG4/MED6/METTL14/MTF2/NCOA3/NIPBL/OGT/PCM1/PRRX1/RBPJ/RIF1/RTF1/SMC1A/SMC3/SMC5/WDR43/WDR47/ZC3H13/ZNF322 | 37 |
| BP | GO:0046949 | fatty-acyl-CoA biosynthetic process | 10/2221 | 27/18614 | 0.000706086 | 0.012530417 | 0.010589641 | ELOVL6/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ELOVL2/ELOVL7/PPT1/SLC27A2 | 10 |
| BP | GO:0031507 | heterochromatin formation | 23/2221 | 96/18614 | 0.00075183 | 0.013302969 | 0.011242536 | EZH2/HELLS/ATF7IP/ATRX/BAZ1A/CTR9/HAT1/HMGB1/KDM5A/L3MBTL3/LMNB1/PIK3CA/RB1/RIF1/SETDB2/SMARCA5/SMCHD1/SPTY2D1/SUZ12/TPR/UBR2/ZDBF2/ZNFX1 | 23 |
| BP | GO:0071559 | response to transforming growth factor beta | 52/2221 | 280/18614 | 0.000760545 | 0.013417706 | 0.011339502 | MIRLET7F1/HDAC2/ADAM17/ADAM9/ARG1/ARID4A/ARID4B/BRMS1L/CD109/CILP/CLDN1/COL3A1/CTSK/FBN1/FERMT2/FUT8/GCNT2/HSP90AB1/HSPA5/ING2/ITGB6/ITGB8/LOX/LTBP1/MAP3K7/MEF2C/MIR15B/MIR30B/MTMR4/OGT/PARP1/PDGFD/PPARG/PTPRK/ROCK1/ROCK2/SDCBP/SKIL/SNW1/SNX25/SNX6/SOX5/TGFBR1/TRIM33/USP15/USP9X/VEPH1/YES1/ZEB1/ZEB2/ZFYVE9/ZNF451 | 52 |
| BP | GO:0034975 | protein folding in endoplasmic reticulum | 6/2221 | 11/18614 | 0.000775869 | 0.013608244 | 0.011500528 | CANX/DNAJC10/DNAJC3/HSP90B1/HSPA5/PDIA3 | 6 |
| BP | GO:0070673 | response to interleukin-18 | 6/2221 | 11/18614 | 0.000775869 | 0.013608244 | 0.011500528 | CASP4/CLDN1/CYLD/IL18/IL18RAP/RIPK2 | 6 |
| BP | GO:0006406 | mRNA export from nucleus | 18/2221 | 68/18614 | 0.000794053 | 0.013806428 | 0.011668016 | EIF4A3/FYTTD1/HNRNPA2B1/IWS1/NCBP1/NCBP2/NSUN2/NUP107/NUP133/NUP155/NUP88/NXT2/THOC1/THOC2/TPR/UPF2/YTHDC1/ZC3H11A | 18 |
| BP | GO:0016445 | somatic diversification of immunoglobulins | 18/2221 | 68/18614 | 0.000794053 | 0.013806428 | 0.011668016 | ATAD5/MSH2/POLQ/HSPD1/LIG4/MLH1/MSH3/MSH6/NBN/PRKDC/PTPRC/RIF1/SAMHD1/SWAP70/TFRC/THOC1/TP53BP1/XRCC4 | 18 |
| BP | GO:1904377 | positive regulation of protein localization to cell periphery | 18/2221 | 68/18614 | 0.000794053 | 0.013806428 | 0.011668016 | AGR2/ACSL3/AKAP5/ATP2C1/CNST/DLG1/EFCAB7/EPB41/EPB41L2/EPHA3/EZR/GPSM2/ITGB1/KIF5B/PIK3R1/PLS1/PRKCI/WNK3 | 18 |
| BP | GO:0002253 | activation of immune response | 83/2221 | 495/18614 | 0.000809204 | 0.014029314 | 0.01185638 | AIM2/ALPK1/ANKRD17/AP3B1/BANK1/BIRC2/BIRC3/BMX/BTK/C3/C5/C6/C7/CASP1/CD226/CD36/CD38/CFH/CFHR1/CFHR3/CFI/COLEC12/CR1/CR1L/CTSS/CYLD/DDX3X/DDX60/EIF2B3/ELF1/EZR/GBP1/HAVCR2/HMGB1/HSP90AA1/HSPD1/IFI16/IFIH1/IRAK3/IRAK4/ITK/LACC1/LYN/MALT1/MAP3K7/MATR3/MEF2C/MNDA/NAIP/NCKAP1L/NLRC4/NLRP3/OTUD4/PDE4B/PDE4D/PIK3AP1/PIK3CA/PJA2/PRKDC/PTPN2/PTPRC/PUM2/RAB11FIP2/RABGEF1/RC3H2/RIOK3/RIPK2/RPS6KA3/SLC39A10/SOS1/STAP1/TBK1/TEC/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/USP15/XRCC5/YES1/ZNFX1 | 83 |
| BP | GO:0046599 | regulation of centriole replication | 9/2221 | 23/18614 | 0.000820957 | 0.014151504 | 0.011959645 | BRCA1/PLK4/SASS6/STIL/ALMS1/CDK5RAP2/CENPJ/CEP120/SPICE1 | 9 |
| BP | GO:0046794 | transport of virus | 9/2221 | 23/18614 | 0.000820957 | 0.014151504 | 0.011959645 | ACE2/CTSL/DPP4/EPS15/FMR1/KPNA2/KPNA3/NUP153/PIKFYVE | 9 |
| BP | GO:0071375 | cellular response to peptide hormone stimulus | 56/2221 | 308/18614 | 0.000829731 | 0.014261896 | 0.012052939 | BRIP1/CCNA2/CDC6/AHCYL1/APC/ARG1/ATP2B1/C2CD5/DENND4C/ENPP1/FBN1/FER/GCLC/IDE/INHBA/ITGB3/JAK2/LPL/LYN/MAP1B/MIR15B/MYO5A/NCK1/NCL/NCOA1/NCOA2/NFE2L2/NUCKS1/OGT/OSBPL8/PARP1/PDE3B/PHIP/PIK3C2A/PIK3CA/PIK3R1/PIK3R3/PLCB1/PPARG/PRKCI/PRKDC/PTPN11/PTPN2/RAP1GDS1/RB1/ROCK1/ROCK2/SESN3/SOS1/SOS2/STAT1/STXBP4/SYAP1/TBC1D4/USO1/ZNF106 | 56 |
| BP | GO:0010824 | regulation of centrosome duplication | 14/2221 | 47/18614 | 0.000844641 | 0.01442377 | 0.012189742 | BRCA1/PLK4/SASS6/STIL/XPO1/ALMS1/CDK5RAP2/CENPJ/CEP120/CHMP2B/CHORDC1/GEN1/ROCK2/SPICE1 | 14 |
| BP | GO:0051972 | regulation of telomerase activity | 14/2221 | 47/18614 | 0.000844641 | 0.01442377 | 0.012189742 | NEK2/CCT2/CCT4/CTNNB1/DKC1/GRHL2/HNRNPA2B1/HSP90AA1/HSP90AB1/MAP3K4/PARP4/POT1/TCP1/XRCC5 | 14 |
| BP | GO:0009225 | nucleotide-sugar metabolic process | 12/2221 | 37/18614 | 0.000848739 | 0.01442377 | 0.012189742 | CMAHP/CSGALNACT1/FUT8/GFPT1/GNPDA2/GNPNAT1/PGM3/UAP1/UGDH/UGGT1/UGGT2/UGP2 | 12 |
| BP | GO:0022616 | DNA strand elongation | 12/2221 | 37/18614 | 0.000848739 | 0.01442377 | 0.012189742 | MCM3/RFC3/RFC4/ACTR8/DNA2/NBN/NUCKS1/POLA1/POLD3/POT1/RAD50/UCHL5 | 12 |
| BP | GO:0007099 | centriole replication | 13/2221 | 42/18614 | 0.000860117 | 0.014575962 | 0.012318361 | BRCA1/CEP135/PLK4/SASS6/STIL/ALMS1/CCP110/CDK5RAP2/CENPJ/CEP120/CEP152/CEP192/SPICE1 | 13 |
| BP | GO:0032731 | positive regulation of interleukin-1 beta production | 17/2221 | 63/18614 | 0.000868247 | 0.014672403 | 0.012399864 | AIM2/CASP1/CD36/GBP5/IFI16/JAK2/LPL/MALT1/MNDA/NAIP/NLRC4/NLRP3/PANX1/RIPK2/TLR4/TLR6/TLR8 | 17 |
| BP | GO:0002758 | innate immune response-activating signaling pathway | 41/2221 | 209/18614 | 0.000881389 | 0.014852758 | 0.012552286 | AIM2/ALPK1/ANKRD17/AP3B1/BIRC2/BIRC3/BTK/CASP1/CD36/COLEC12/CTSS/CYLD/DDX3X/DDX60/HAVCR2/HMGB1/HSPD1/IFIH1/IRAK3/IRAK4/LACC1/LYN/MAP3K7/NAIP/NLRC4/NLRP3/OTUD4/PIK3AP1/PJA2/PUM2/RAB11FIP2/RIOK3/RIPK2/RPS6KA3/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/USP15 | 41 |
| BP | GO:0051261 | protein depolymerization | 26/2221 | 115/18614 | 0.000902308 | 0.015035812 | 0.012706987 | KIF18A/TPX2/ADD3/APC/ASPH/CAMSAP2/CAPZA2/CKAP2/CKAP5/CLASP2/EPS8/HSPA8/KIF2A/LIMA1/MAP1B/NAV3/PIK3CA/RDX/SCIN/SPTAN1/SVIL/SWAP70/TAOK1/TMOD2/TWF1/WDR47 | 26 |
| BP | GO:0007076 | mitotic chromosome condensation | 8/2221 | 19/18614 | 0.000907247 | 0.015035812 | 0.012706987 | NCAPG/NCAPH/NUSAP1/BAZ1B/SMARCA5/SMC2/SMC4/TTN | 8 |
| BP | GO:0090670 | RNA localization to Cajal body | 8/2221 | 19/18614 | 0.000907247 | 0.015035812 | 0.012706987 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0090671 | telomerase RNA localization to Cajal body | 8/2221 | 19/18614 | 0.000907247 | 0.015035812 | 0.012706987 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0090672 | telomerase RNA localization | 8/2221 | 19/18614 | 0.000907247 | 0.015035812 | 0.012706987 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0090685 | RNA localization to nucleus | 8/2221 | 19/18614 | 0.000907247 | 0.015035812 | 0.012706987 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/DKC1/TCP1 | 8 |
| BP | GO:0000463 | maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 7/2221 | 15/18614 | 0.000917396 | 0.015038287 | 0.012709079 | DDX18/GTPBP4/NIFK/RPF2/RPL7L1/WDR12/ZNHIT6 | 7 |
| BP | GO:0010457 | centriole-centriole cohesion | 7/2221 | 15/18614 | 0.000917396 | 0.015038287 | 0.012709079 | CEP135/NEK2/CCDC102B/CNTLN/CTNNB1/KIF3A/NIN | 7 |
| BP | GO:0032239 | regulation of nucleobase-containing compound transport | 7/2221 | 15/18614 | 0.000917396 | 0.015038287 | 0.012709079 | DHX9/IWS1/NCBP2/NSUN2/NUP153/RIPK1/TPR | 7 |
| BP | GO:0043558 | regulation of translational initiation in response to stress | 7/2221 | 15/18614 | 0.000917396 | 0.015038287 | 0.012709079 | DNAJC3/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/IMPACT/NCK1 | 7 |
| BP | GO:0048008 | platelet-derived growth factor receptor signaling pathway | 16/2221 | 58/18614 | 0.000940768 | 0.015379505 | 0.012997447 | ARID5B/FER/IQGAP1/ITGB3/JAK2/LOX/MYO1E/PDGFC/PDGFD/PDGFRA/PHF14/PIK3C2A/PTPN11/PTPN2/TIPARP/ZFAND5 | 16 |
| BP | GO:0042113 | B cell activation | 51/2221 | 276/18614 | 0.000954567 | 0.015562813 | 0.013152363 | ATAD5/EZH2/MSH2/ADAM17/ATM/BANK1/BTK/CASP3/CD180/CD38/CD86/CR1/CTPS1/DOCK10/DOCK11/FNIP1/GAPT/HSPD1/IL7R/INHBA/ITGA4/ITGB1/LIG4/LYN/MALT1/MEF2C/MLH1/MNDA/MSH6/NBN/NCKAP1L/PHF14/PIK3R1/PIK3R3/PPP2R3C/PRKDC/PTPN2/PTPRC/RABL3/RBPJ/RIF1/SAMSN1/SLC39A10/SWAP70/TFRC/THOC1/TLR4/TOP2B/TP53BP1/VCAM1/ZBTB1 | 51 |
| BP | GO:0071346 | cellular response to type II interferon | 26/2221 | 116/18614 | 0.001033385 | 0.016792314 | 0.014191433 | ACTR2/ACTR3/AQP4/ARG1/CASP1/CLDN1/GBP1/GBP2/GBP5/IFNGR1/JAK1/JAK2/KIF5B/MRC1/PARP14/PARP9/PPARG/PTPN2/SP100/STAT1/STXBP3/STXBP4/SYNCRIP/TLR2/TLR3/TLR4 | 26 |
| BP | GO:0009408 | response to heat | 25/2221 | 110/18614 | 0.001035563 | 0.016792314 | 0.014191433 | HDAC2/ATM/ATR/CHORDC1/DHX36/DNAJA1/DNAJC2/DNAJC7/EIF2B3/EIF2S1/GCLC/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/IGF1/LYN/NF1/PSIP1/PTGS2/SCN9A/SLU7/TFEC/TPR/VCP | 25 |
| BP | GO:0010970 | transport along microtubule | 35/2221 | 172/18614 | 0.001040343 | 0.016824467 | 0.014218606 | KIF4A/AP3B1/AP3M1/ARHGAP21/BLOC1S6/DLG2/DST/DYNC1H1/DYNC2H1/HIF1A/HNRNPU/HSPA8/IFT57/IFT74/IFT80/KIF3A/KIF5B/LCA5/LRPPRC/MAP1B/OPA1/PCM1/RAB1A/RAB27B/RABGEF1/RHOT1/RPGR/SPG11/SSX2IP/SYBU/SYNE2/TRAK2/TTC21B/WDR19/WDR35 | 35 |
| BP | GO:1990776 | response to angiotensin | 11/2221 | 33/18614 | 0.001072907 | 0.017304582 | 0.014624358 | BRIP1/CDC6/AHCYL1/COL3A1/CYBB/INHBA/NFE2L2/PTGS2/RAP1GDS1/ROCK1/ROCK2 | 11 |
| BP | GO:0032386 | regulation of intracellular transport | 59/2221 | 332/18614 | 0.001091252 | 0.017553397 | 0.014834635 | CDK1/ECT2/KIF20B/SPAG5/XPO1/AKAP5/ANGPT1/ANK3/BNIP3L/C2CD5/CD36/CEP290/CTDSPL2/DHX9/DNAJC13/DYNC1H1/EFCAB7/EZR/GCC2/HSP90AA1/ICE1/IPO5/IWS1/JAK2/LCP1/LMAN1/LRRK2/MAP1B/MTMR2/NCBP2/NEDD4/NF1/NOLC1/NSUN2/NUP153/PCM1/PIK3R1/PPP1R12A/PRKD1/PTGS2/PTPN11/RDX/RIOK2/RUFY3/SAR1B/SCFD1/SCP2/SH3GLB1/SP100/TPR/TTC21B/UBR5/UFM1/USP7/VPS35/XPO4/YOD1/ZFAND1/ZPR1 | 59 |
| BP | GO:0044786 | cell cycle DNA replication | 13/2221 | 43/18614 | 0.001099852 | 0.017644558 | 0.014911677 | ATAD5/BLM/BRCA2/FBXO5/GMNN/MCM3/MCM6/ATRX/DBF4/DNA2/POLA1/WRN/ZPR1 | 13 |
| BP | GO:0061458 | reproductive system development | 55/2221 | 305/18614 | 0.001118365 | 0.017882949 | 0.015113144 | ASPM/BRCA2/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ASH1L/ATM/ATRX/C3/CASP3/CHD7/CSDE1/CTNNA1/CTNNB1/CYP7B1/DLG1/EIF2S2/FER/FNDC3A/FRS2/HMGB2/HSD17B4/HSPA5/IDH1/ING2/INHBA/KDM5B/LRP2/MERTK/MKKS/NASP/NCOA4/NIPBL/NRIP1/NUP107/PDGFRA/PLAG1/PLEKHA5/PTPN11/RHOBTB3/SCAPER/SULF1/SYCP2/TGFBR1/TIPARP/TLR3/TMF1/TNC/TNFAIP6/WDR19/WDR48/ZFPM2 | 55 |
| BP | GO:0031346 | positive regulation of cell projection organization | 62/2221 | 353/18614 | 0.001120657 | 0.017882949 | 0.015113144 | ANLN/CEP135/EZH2/ABL2/ACTR2/ACTR3/APC/ATP7A/CAPRIN1/CAPRIN2/CCDC88A/CCP110/CDKL5/CENPJ/CEP120/CNR1/CNTN1/CORO1C/DHX36/DOCK11/EPHA3/EPHA4/EPS8/FAM98A/FBXO38/FIG4/FMR1/FNBP1L/GOLGA4/HGF/HSP90AA1/HSPA5/ITGA2/ITGA6/KIDINS220/LRP8/LYN/MACF1/MAP1B/MAP3K13/MNS1/NCK1/NCKAP1/NFE2L2/NIN/NLGN1/PIK3CA/PIK3R1/PLXNC1/PRKCI/PRKD1/PTPRD/RAB8B/RAPGEF2/RGS2/RUFY3/SETX/SKIL/TENM3/TGFBR1/TWF1/VLDLR | 62 |
| BP | GO:0009161 | ribonucleoside monophosphate metabolic process | 16/2221 | 59/18614 | 0.001149972 | 0.018302204 | 0.015467463 | ADK/ATIC/CASK/DLG1/DLG2/DPYD/GART/GMPS/IMPDH2/MAGI3/MPP1/NT5C2/NT5E/PAICS/PPAT/UMPS | 16 |
| BP | GO:0032465 | regulation of cytokinesis | 22/2221 | 93/18614 | 0.001159807 | 0.018410021 | 0.015558581 | BRCA2/CDC6/ECT2/KIF14/KIF20A/KIF20B/KIF23/PRC1/AHCTF1/BECN1/BIRC6/CCP110/CUL3/KLHL13/MAP9/PIK3C3/PIK3R4/PKN2/PRPF40A/RACGAP1/SH3GLB1/SVIL | 22 |
| BP | GO:0043244 | regulation of protein-containing complex disassembly | 27/2221 | 123/18614 | 0.001167033 | 0.018475976 | 0.015614321 | TPX2/ADD3/APC/ASPH/CAMSAP2/CAPZA2/CKAP2/CLASP2/EPS8/ETF1/GSPT1/IRAK3/LIMA1/MAP1B/NAV3/OGFOD1/PIK3CA/RDX/SCIN/SETX/SPTAN1/SVIL/SWAP70/TAOK1/TMOD2/TWF1/WDR47 | 27 |
| BP | GO:0007265 | Ras protein signal transduction | 59/2221 | 333/18614 | 0.001175446 | 0.018513573 | 0.015646094 | CCNA2/KIF14/ABCA1/ABL2/AKAP13/ARFGEF1/ARFGEF2/ARHGAP29/ARHGAP42/ARHGEF12/CCDC125/COL3A1/CTNNAL1/CUL3/DENND4A/DENND4C/DOCK5/EPS8/G3BP1/G3BP2/GPSM2/IGF1/ITGB1/KPNB1/KRAS/MAP4K4/MET/NCKAP1/NET1/NF1/OGT/PIK3CB/PIK3CG/PLD1/PSD3/RABGEF1/RABL3/RACGAP1/RALGPS2/RAPGEF2/RAPGEF4/RAPGEF5/RAPGEF6/RASA2/RASGEF1B/RASGRF2/RASGRP3/RB1/RDX/RGL1/RIT1/ROCK1/ROCK2/SDCBP/SHOC2/SOS1/SOS2/SSX2IP/USP8 | 59 |
| BP | GO:0036120 | cellular response to platelet-derived growth factor stimulus | 9/2221 | 24/18614 | 0.001175563 | 0.018513573 | 0.015646094 | CCNA2/ATP7A/IQGAP1/ITGB3/PDGFD/RDX/SYAP1/TLR4/YES1 | 9 |
| BP | GO:0042176 | regulation of protein catabolic process | 63/2221 | 361/18614 | 0.00121107 | 0.019022968 | 0.016076591 | DTL/MAD2L1/PBK/XPO1/ADAM9/ANKIB1/APC/ARIH1/EZR/FBXL5/FBXO11/FMR1/GCLC/HECTD1/HMGCR/HSP90AA1/HSP90AB1/IDE/IRAK3/LRP2/LRRK2/MDM2/MIR181B1/MTM1/MYCBP2/NEDD4/NFE2L2/NSF/NUB1/OGT/PHF20L1/PSMC1/PSMC2/PSMC6/PSMD1/PSMD14/PSMD2/PTPN3/RDX/RNF14/RNF19A/RNF217/ROCK1/RYBP/SDCBP/SNX9/SOCS4/TAF1/TIMP4/TIPARP/TMF1/TMTC3/UBR3/UCHL5/UFL1/USP13/USP14/USP25/USP7/USP8/USP9X/VCP/VPS35 | 63 |
| BP | GO:0006986 | response to unfolded protein | 30/2221 | 142/18614 | 0.001236436 | 0.019370833 | 0.016370577 | AGR2/ATF6/CREBRF/DNAJA1/DNAJC10/DNAJC3/EDEM3/EIF2AK2/EIF2AK3/EIF2S1/HSP90AA1/HSP90AB1/HSPA13/HSPA4/HSPA4L/HSPA5/HSPA8/HSPA9/HSPD1/HSPH1/NCK1/NFE2L2/PARP8/PIK3R1/PTPN2/STT3B/UBXN4/UFL1/VCP/YOD1 | 30 |
| BP | GO:0019058 | viral life cycle | 57/2221 | 320/18614 | 0.001240004 | 0.01937627 | 0.016375172 | CDK1/DEK/TOP2A/ACE2/CD86/CHMP2B/CLDN1/CR1/CTSL/CXADR/DDX3X/DPP4/EIF2AK2/EIF2AK4/EPS15/FAM111A/FMR1/GYPA/HMGB1/HSP90AB1/HSPA8/HTATSF1/HTR2A/IDE/IFI16/IFIH1/IFIT5/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/KPNA2/KPNA3/MRC1/NEDD4/NPC1/NUCKS1/NUP153/PIK3C3/PIKFYVE/PKN2/RAB1A/RNASEL/SRPK1/SRPK2/TFRC/TOP2B/TRIM22/TRIM38/TRIM59/TRIM6/VCP/VTA1/WWP1/ZNF502/ZNFX1 | 57 |
| BP | GO:0046605 | regulation of centrosome cycle | 15/2221 | 54/18614 | 0.001243513 | 0.019380765 | 0.016378971 | BRCA1/PLK4/SASS6/STIL/XPO1/ALMS1/CCNL1/CDK5RAP2/CENPJ/CEP120/CHMP2B/CHORDC1/GEN1/ROCK2/SPICE1 | 15 |
| BP | GO:0010506 | regulation of autophagy | 61/2221 | 348/18614 | 0.001285002 | 0.019975634 | 0.016881704 | WDR41/ABL2/ATF6/ATM/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/BECN1/BNIP3L/C9orf72/CASP3/DNM1L/EIF4G2/ERCC4/EXOC1/EXOC4/GNAI3/HERC1/HGF/HIF1A/HMGB1/IFI16/ITPR1/LRRK2/MAP3K7/MET/MTDH/MTM1/MTMR4/NEDD4/NPC1/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3R4/PRKD1/RAB3GAP1/RAB3GAP2/RB1CC1/RIPK2/ROCK1/SCFD1/SESN3/SH3GLB1/SNX30/SNX6/SPTLC1/TAB2/TAB3/TBK1/TRIM22/TRIM38/TRIM6/UFL1/USP13/VPS13C/VPS13D/VPS26A/VPS35 | 61 |
| BP | GO:0030010 | establishment of cell polarity | 32/2221 | 155/18614 | 0.001300089 | 0.020158081 | 0.017035892 | KIF20B/MAD2L1/NDC80/SPAG5/SPDL1/ABL2/ARFGEF1/CDK5RAP2/DOCK2/DOCK7/DOCK8/FAT1/FRMD4B/GPSM2/HSP90AA1/HSP90AB1/ITGB1/KRIT1/MAP1B/MAPRE1/MPP7/MYO9A/PHLDB2/PRKCI/RAB11FIP2/RICTOR/ROCK1/ROCK2/RUFY3/SDCCAG8/UBXN2B/ZW10 | 32 |
| BP | GO:0031058 | positive regulation of histone modification | 21/2221 | 88/18614 | 0.001319515 | 0.020406691 | 0.017245996 | BRCA1/DEK/BAZ1B/CTNNB1/CTR9/DDX21/ERCC6/ING2/LRRK2/MTF2/NIPBL/OGT/PAXBP1/PRKD1/RIF1/RNF20/RTF1/SDR16C5/SF3B1/SMARCA5/SNW1 | 21 |
| BP | GO:0000245 | spliceosomal complex assembly | 22/2221 | 94/18614 | 0.001346649 | 0.020772923 | 0.017555505 | CRNKL1/DDX1/DDX23/DDX46/GCFC2/HTATSF1/LUC7L3/NCBP1/PRPF39/PSIP1/PTBP2/SCAF11/SETX/SF3A3/SF3B1/SLU7/SNRNP200/SNRPA1/SRPK1/SRPK2/SRSF10/YTHDC1 | 22 |
| BP | GO:0006607 | NLS-bearing protein import into nucleus | 8/2221 | 20/18614 | 0.001354988 | 0.020794924 | 0.017574098 | IPO5/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/RANBP2/RGPD1 | 8 |
| BP | GO:0008334 | histone mRNA metabolic process | 8/2221 | 20/18614 | 0.001354988 | 0.020794924 | 0.017574098 | ATM/CPSF2/CPSF3/NCBP1/NCBP2/SSB/XRN1/ZNF473 | 8 |
| BP | GO:0048608 | reproductive structure development | 54/2221 | 301/18614 | 0.001390473 | 0.021038374 | 0.017779841 | ASPM/BRCA2/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ASH1L/ATM/ATRX/C3/CASP3/CHD7/CSDE1/CTNNA1/CTNNB1/CYP7B1/DLG1/EIF2S2/FER/FNDC3A/FRS2/HMGB2/HSD17B4/HSPA5/IDH1/ING2/INHBA/KDM5B/LRP2/MERTK/MKKS/NASP/NCOA4/NIPBL/NRIP1/NUP107/PDGFRA/PLAG1/PTPN11/RHOBTB3/SCAPER/SULF1/SYCP2/TGFBR1/TIPARP/TLR3/TMF1/TNC/TNFAIP6/WDR19/WDR48/ZFPM2 | 54 |
| BP | GO:0030261 | chromosome condensation | 13/2221 | 44/18614 | 0.00139285 | 0.021038374 | 0.017779841 | CDK1/NCAPG/NCAPG2/NCAPH/NUSAP1/TOP2A/AIFM1/BAZ1B/SMARCA5/SMC2/SMC4/SMC5/TTN | 13 |
| BP | GO:0002328 | pro-B cell differentiation | 6/2221 | 12/18614 | 0.001395331 | 0.021038374 | 0.017779841 | FNIP1/LIG4/NUDT21/PRKDC/SOS1/SOS2 | 6 |
| BP | GO:0046831 | regulation of RNA export from nucleus | 6/2221 | 12/18614 | 0.001395331 | 0.021038374 | 0.017779841 | DHX9/IWS1/NCBP2/NSUN2/NUP153/TPR | 6 |
| BP | GO:0098911 | regulation of ventricular cardiac muscle cell action potential | 6/2221 | 12/18614 | 0.001395331 | 0.021038374 | 0.017779841 | DLG1/DSC2/DSG2/DSP/PKP2/RYR2 | 6 |
| BP | GO:0140719 | constitutive heterochromatin formation | 6/2221 | 12/18614 | 0.001395331 | 0.021038374 | 0.017779841 | EZH2/HELLS/ATRX/HAT1/RIF1/SMCHD1 | 6 |
| BP | GO:1903441 | protein localization to ciliary membrane | 6/2221 | 12/18614 | 0.001395331 | 0.021038374 | 0.017779841 | ARL13B/EFCAB7/IFT80/LZTFL1/RABEP1/WDR19 | 6 |
| BP | GO:0071560 | cellular response to transforming growth factor beta stimulus | 50/2221 | 274/18614 | 0.001408669 | 0.021186376 | 0.01790492 | MIRLET7F1/HDAC2/ADAM17/ADAM9/ARG1/ARID4A/ARID4B/BRMS1L/CD109/CILP/CLDN1/COL3A1/CTSK/FBN1/FERMT2/FUT8/GCNT2/HSP90AB1/HSPA5/ING2/ITGB6/ITGB8/LOX/LTBP1/MAP3K7/MEF2C/MIR15B/MIR30B/MTMR4/OGT/PARP1/PDGFD/PPARG/PTPRK/SDCBP/SKIL/SNW1/SNX25/SNX6/SOX5/TGFBR1/TRIM33/USP15/USP9X/VEPH1/YES1/ZEB1/ZEB2/ZFYVE9/ZNF451 | 50 |
| BP | GO:0086004 | regulation of cardiac muscle cell contraction | 11/2221 | 34/18614 | 0.001417 | 0.021228832 | 0.0179408 | AKAP9/ANK2/ATP2A2/DLG1/DSC2/DSG2/DSP/PDE4B/PDE4D/PKP2/RYR2 | 11 |
| BP | GO:1902806 | regulation of cell cycle G1/S phase transition | 41/2221 | 214/18614 | 0.001418549 | 0.021228832 | 0.0179408 | CDC6/EZH2/KIF14/MTBP/SASS6/STIL/ADAM17/ANKRD17/APC/ARID2/ATM/BRD7/CCNH/CENPJ/CPSF3/DCUN1D3/DDX3X/DLG1/ECD/GIGYF2/GPNMB/INHBA/JADE1/KMT2E/MDM2/MIR15B/MIR30C2/PBRM1/PLCB1/PLRG1/PPP2CA/PRKDC/RB1/RBL2/RDX/RFWD3/RRM1/SDE2/SLFN11/STXBP4/TAF1 | 41 |
| BP | GO:0040001 | establishment of mitotic spindle localization | 12/2221 | 39/18614 | 0.001428011 | 0.021264635 | 0.017971057 | MAD2L1/NDC80/NUSAP1/SPDL1/CDK5RAP2/CLASP2/GPSM2/ITGB1/KPNB1/MAPRE1/UBXN2B/ZW10 | 12 |
| BP | GO:0042307 | positive regulation of protein import into nucleus | 12/2221 | 39/18614 | 0.001428011 | 0.021264635 | 0.017971057 | CDK1/ECT2/EFCAB7/HSP90AA1/IPO5/JAK2/PIK3R1/PRKD1/PTGS2/TPR/UBR5/ZPR1 | 12 |
| BP | GO:0016236 | macroautophagy | 57/2221 | 322/18614 | 0.001439461 | 0.021382214 | 0.018070425 | ATG3/ATM/ATP2A2/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/BECN1/BNIP3L/C9orf72/CASP3/CHMP2B/EXOC1/EXOC4/GNAI3/HIF1A/LGALS8/LRBA/LRRK2/MAP3K7/MTM1/NEDD4/NPC1/OGT/PIK3C3/PIK3CA/PIK3R4/PIKFYVE/PLAA/RAB1A/RAB3GAP1/RAB3GAP2/RB1CC1/RIPK2/SCFD1/SESN3/SH3GLB1/SNX30/SNX6/SPG11/SPTLC1/STAM2/STX17/TBK1/UBA5/UBXN2B/UFL1/UFM1/VCP/VPS13C/VPS13D/VPS26A/VPS35/VPS41/VTA1/WDFY3/YOD1 | 57 |
| BP | GO:2000232 | regulation of rRNA processing | 7/2221 | 16/18614 | 0.001463745 | 0.021689391 | 0.018330025 | HEATR1/METTL18/RIOK1/RIOK2/UTP15/WDR43/WDR75 | 7 |
| BP | GO:0015931 | nucleobase-containing compound transport | 42/2221 | 221/18614 | 0.001471671 | 0.021753246 | 0.01838399 | XPO1/XPOT/ABCC4/AHCTF1/CKAP5/CR1/DHX9/EIF4A3/FMR1/FYTTD1/G3BP2/HNRNPA1/HNRNPA1L2/HNRNPA2B1/HNRNPA3/IWS1/KPNB1/LRPPRC/NCBP1/NCBP2/NSUN2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/PHAX/PNPT1/RANBP2/RIPK1/SLC25A32/SSB/THOC1/THOC2/TPR/UPF2/UPF3B/XPO5/YTHDC1/ZC3H11A | 42 |
| BP | GO:0006979 | response to oxidative stress | 73/2221 | 434/18614 | 0.001482482 | 0.021859346 | 0.018473656 | CDK1/ECT2/EZH2/FANCD2/GSKIP/HDAC2/MELK/ADAM9/AIFM1/ARG1/ATP2A2/ATP7A/BECN1/BTK/CA3/CASP3/CD36/CD38/CHUK/CTNNB1/EIF2S1/ERCC6/ERCC6L2/ETFDH/FER/FUT8/GCLC/GPX8/HBA2/HBB/HGF/HIF1A/HP/IDH1/IL18RAP/IMPACT/IPCEF1/JAK2/LRRK2/MCTP1/MET/NCOA7/NET1/NFE2L2/OSER1/OXR1/OXSR1/PARP1/PDGFD/PDGFRA/PLA2R1/PNPLA8/PNPT1/PON2/PRKD1/PSIP1/PTGS2/PTPRK/PYROXD1/RIPK1/RRM2B/SESN3/SETX/SLC7A11/STAT1/TLR4/TLR6/TPM1/VNN1/VRK2/WRN/ZNF277/ZNF622 | 73 |
| BP | GO:1900087 | positive regulation of G1/S transition of mitotic cell cycle | 15/2221 | 55/18614 | 0.001524102 | 0.022418087 | 0.018945857 | CDC6/MTBP/SASS6/STIL/ADAM17/ANKRD17/CENPJ/CPSF3/DDX3X/KMT2E/MDM2/PLCB1/PLRG1/RDX/RRM1 | 15 |
| BP | GO:0048017 | inositol lipid-mediated signaling | 35/2221 | 176/18614 | 0.001581268 | 0.023202212 | 0.019608532 | CEP55/ANGPT1/BECN1/EGF/ERBB4/EXOC1/EZR/FCGR3A/FLT1/HGF/HTR2A/IGF1/IL18/JAK2/KBTBD2/NEDD4/NF1/OGT/PDGFC/PDGFD/PDGFRA/PIK3AP1/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIP5K1B/PLCB1/PLCB4/PLCH1/PLD1/PREX2/PTPN13 | 35 |
| BP | GO:0032259 | methylation | 63/2221 | 365/18614 | 0.001599496 | 0.023412581 | 0.019786318 | BRCA1/EZH2/HELLS/PRMT3/ALKBH8/ARID4A/ARID4B/ASH1L/ATF7IP/ATRX/BOD1L1/CTNNB1/CTR9/ETF1/FAM98A/FBXO11/GRHL2/GSPT1/HCFC2/IWS1/KDM6A/KMT2C/KMT2E/LARP7/MECOM/METTL14/METTL15/METTL18/MTF2/MTR/MTRR/NSUN2/NSUN6/OGT/PARP1/PAXBP1/PRMT9/RBBP5/RIF1/RLF/RNF20/RNMT/RTF1/SETD7/SETDB2/SETMAR/SMARCA5/SNW1/SUV39H2/SUZ12/TFB2M/TGS1/THADA/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TRMT6/TYW3/WTAP/ZC3H13/ZDBF2 | 63 |
| BP | GO:0010569 | regulation of double-strand break repair via homologous recombination | 18/2221 | 72/18614 | 0.001622779 | 0.023695731 | 0.020025612 | CHEK1/PARPBP/POLQ/RAD51AP1/ACTR2/ARID2/EPC2/ERCC6/FIGNL1/ING3/MORF4L2/PARP1/PPP4R2/RBBP8/RIF1/SMCHD1/TP53BP1/WDR48 | 18 |
| BP | GO:0019985 | translesion synthesis | 9/2221 | 25/18614 | 0.001644181 | 0.023892246 | 0.020191691 | DTL/POLD3/POLK/REV1/REV3L/SPRTN/USP1/VCP/ZBTB1 | 9 |
| BP | GO:2000114 | regulation of establishment of cell polarity | 9/2221 | 25/18614 | 0.001644181 | 0.023892246 | 0.020191691 | KIF20B/ABL2/ARFGEF1/DOCK8/KRIT1/RICTOR/ROCK1/ROCK2/RUFY3 | 9 |
| BP | GO:0007254 | JNK cascade | 34/2221 | 170/18614 | 0.001654626 | 0.023952889 | 0.02024294 | AIDA/CYLD/DNAJA1/ERCC6/FKTN/HIPK3/HMGB1/IRAK4/LRRK2/MAP3K13/MAP3K7/MAP4K4/MAPK10/MECOM/MMP8/NAIP/NCOR1/PDCD4/PJA2/PLCB1/RB1CC1/RIPK1/RIPK2/SDCBP/SEMA3A/TAOK1/TAOK3/TLR3/TLR4/TNIK/TRAF5/ZMYND11/ZNF622/ZNF675 | 34 |
| BP | GO:0002244 | hematopoietic progenitor cell differentiation | 28/2221 | 132/18614 | 0.001656317 | 0.023952889 | 0.02024294 | ANLN/ESCO2/TOP2A/AGPAT5/AP3B1/CHD2/DHX36/EIF2AK2/FNIP1/HSPA9/INHBA/LIG4/LYN/METTL14/MLLT3/NFE2L2/NUDT21/PDGFRA/PRKDC/PRRC2C/PTPRC/PUS7/RRS1/SOS1/SOS2/UFL1/XRCC5/ZBTB1 | 28 |
| BP | GO:0046854 | phosphatidylinositol phosphate biosynthetic process | 16/2221 | 61/18614 | 0.001687576 | 0.024346418 | 0.020575518 | ATM/BECN1/EFR3A/FIG4/IMPA1/INPP4B/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/PIKFYVE/SOCS4 | 16 |
| BP | GO:0034599 | cellular response to oxidative stress | 52/2221 | 290/18614 | 0.001704301 | 0.024528886 | 0.020729724 | CDK1/ECT2/EZH2/FANCD2/GSKIP/HDAC2/MELK/AIFM1/ARG1/ATP2A2/ATP7A/BECN1/BTK/CD36/CHUK/CTNNB1/EIF2S1/ERCC6L2/FER/FUT8/GPX8/HGF/HIF1A/IL18RAP/IMPACT/JAK2/LRRK2/MET/NCOA7/NET1/NFE2L2/OSER1/OXR1/PARP1/PDGFD/PDGFRA/PLA2R1/PNPLA8/PNPT1/PRKD1/PTPRK/PYROXD1/RIPK1/SETX/SLC7A11/TLR4/TLR6/TPM1/VNN1/VRK2/ZNF277/ZNF622 | 52 |
| BP | GO:0035966 | response to topologically incorrect protein | 33/2221 | 164/18614 | 0.001728897 | 0.024764396 | 0.020928757 | AGR2/ATF6/CREBRF/CUL3/DNAJA1/DNAJC10/DNAJC3/EDEM3/EIF2AK2/EIF2AK3/EIF2S1/HSP90AA1/HSP90AB1/HSPA13/HSPA4/HSPA4L/HSPA5/HSPA8/HSPA9/HSPD1/HSPH1/NCK1/NFE2L2/PARP8/PIK3R1/PTPN2/STT3B/UBXN4/UFL1/UGGT1/UGGT2/VCP/YOD1 | 33 |
| BP | GO:0051494 | negative regulation of cytoskeleton organization | 33/2221 | 164/18614 | 0.001728897 | 0.024764396 | 0.020928757 | BRCA1/TPX2/ADD3/APC/ARFGEF1/ARHGAP28/CAMSAP2/CAPZA2/CDK5RAP2/CGNL1/CKAP2/CLASP2/EPS8/LIMA1/MAP1B/MAPRE1/MET/MKKS/NAV3/PHLDB2/PIK3CA/PIK3R1/PPFIA1/RDX/SCIN/SPTAN1/SVIL/SWAP70/TAOK1/TJP1/TMOD2/TWF1/WDR47 | 33 |
| BP | GO:0019827 | stem cell population maintenance | 35/2221 | 177/18614 | 0.001749678 | 0.025002527 | 0.021130005 | ASPM/FANCD2/HDAC2/ARID4A/ARID4B/BRMS1L/CDH2/CNOT1/CTNNB1/CTR9/GNL3/HOOK3/ING2/KDM3A/KDM4C/LEO1/LIG4/MED6/METTL14/MTF2/NCOA3/NIPBL/OGT/PCM1/PRRX1/RBPJ/RIF1/RTF1/SMC1A/SMC3/SMC5/WDR43/WDR47/ZC3H13/ZNF322 | 35 |
| BP | GO:0022406 | membrane docking | 21/2221 | 90/18614 | 0.001782862 | 0.025416349 | 0.021479732 | AHCYL1/ATP2A2/BLOC1S6/CEP83/CFTR/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/EZR/PDZD8/RAB3IP/RAB8B/ROCK1/SNAP25/STX17/STXBP3/SYTL2/USO1/VCAM1 | 21 |
| BP | GO:1990830 | cellular response to leukemia inhibitory factor | 23/2221 | 102/18614 | 0.001799566 | 0.025590981 | 0.021627316 | HELLS/ADAM23/ARID5B/BCLAF1/CACYBP/EPS8/HK2/HNRNPU/KDM3A/KDM5B/MAT2A/MIR224/MTF2/NCL/PCOLCE2/PIGA/RIF1/RNMT/SMARCA5/SNX10/TFRC/WDR35/XRCC5 | 23 |
| BP | GO:0090501 | RNA phosphodiester bond hydrolysis | 32/2221 | 158/18614 | 0.00180362 | 0.025590981 | 0.021627316 | LACTB2/BMS1/CNOT1/CNOT6L/CPSF2/CPSF3/CSTF3/DICER1/DIS3/DIS3L/ERI1/ERI2/EXOSC9/NCBP1/NCBP2/NUDT12/NUDT21/PCF11/PNPT1/POP1/RNASEL/RRS1/SAMHD1/SDE2/SLFN13/TSNAX/TSR1/UTP20/UTP23/XRN1/XRN2/ZC3H12C | 32 |
| BP | GO:1901532 | regulation of hematopoietic progenitor cell differentiation | 12/2221 | 40/18614 | 0.001821545 | 0.025784509 | 0.021790869 | DHX36/EIF2AK2/FNIP1/HSPA9/METTL14/NFE2L2/NUDT21/PRKDC/PUS7/SOS1/SOS2/ZBTB1 | 12 |
| BP | GO:0002262 | myeloid cell homeostasis | 34/2221 | 171/18614 | 0.00183356 | 0.025893651 | 0.021883107 | NCAPG2/ADAM17/ALAS2/ARID4A/BPGM/BTK/CASP3/HIF1A/HMGB1/HMGB2/HSPA9/INHBA/IREB2/JAK2/KMT2E/L3MBTL3/LIPA/LYAR/LYN/MERTK/MTHFD1/NCKAP1L/NF1/PDE4B/PIK3CB/PRKDC/PTPN2/RACGAP1/RB1/SLC4A1/SLC7A11/STAT1/UBA5/UFL1 | 34 |
| BP | GO:0051293 | establishment of spindle localization | 15/2221 | 56/18614 | 0.001855761 | 0.026145807 | 0.022096208 | MAD2L1/NDC80/NUSAP1/SPAG5/SPDL1/CDK5RAP2/CLASP2/DYNC1H1/GPSM2/ITGB1/KPNB1/MAPRE1/SPIRE1/UBXN2B/ZW10 | 15 |
| BP | GO:2000779 | regulation of double-strand break repair | 28/2221 | 133/18614 | 0.001864046 | 0.026201172 | 0.022142998 | CHEK1/DEK/PARPBP/POLQ/RAD51AP1/ACTR2/ARID2/ATR/BRD7/EPC2/ERCC6/FIGNL1/ING3/MORF4L2/PARP1/PBRM1/POT1/PPP4R2/PRKDC/RBBP8/RIF1/SETMAR/SMCHD1/SPIRE1/TP53BP1/TRIP12/UBR5/WDR48 | 28 |
| BP | GO:0007034 | vacuolar transport | 33/2221 | 165/18614 | 0.001918905 | 0.026909395 | 0.022741527 | AP3B1/AP3M1/BECN1/C9orf72/CHMP2B/DTX3L/GCC2/GNPTAB/HOOK1/HOOK3/HSPA8/LRRK2/LYST/MTM1/NCOA4/NEDD4/NPC1/PIK3C3/PIK3R4/SCYL2/SNX16/STAM2/UEVLD/VCP/VPS13A/VPS13C/VPS13D/VPS35/VPS41/VPS54/VPS8/VTA1/ZFYVE16 | 33 |
| BP | GO:0006605 | protein targeting | 58/2221 | 333/18614 | 0.001935201 | 0.027074806 | 0.022881319 | SSR1/AIFM1/AKAP6/ANK3/AP3B1/AP3M1/AP4E1/ATG3/BECN1/BNIP3L/C2CD5/CHM/GCC2/GNPTAB/GRPEL1/HSP90AA1/HSPA4/HSPA5/HSPA8/HSPD1/LMAN1/LRRK2/NCOA4/NEDD4/NLGN1/PEX1/PIK3C3/PIK3R4/PIKFYVE/PMPCB/PRKCI/RAB3IP/RAB8B/RABGEF1/RASSF9/SDCBP/SEC62/SEC63/SH3GLB1/SNX16/SRP54/SRP72/SRPRB/SSR3/STXBP4/TIMM21/TOMM34/TRAK2/USP9X/VPS13A/VPS13C/VPS13D/VPS41/VPS54/VPS8/YWHAB/ZDHHC21/ZFYVE16 | 58 |
| BP | GO:0000729 | DNA double-strand break processing | 8/2221 | 21/18614 | 0.001961838 | 0.027307348 | 0.023077843 | BLM/BRIP1/DNA2/NBN/RAD50/RBBP8/SETMAR/SMARCAD1 | 8 |
| BP | GO:0051315 | attachment of mitotic spindle microtubules to kinetochore | 8/2221 | 21/18614 | 0.001961838 | 0.027307348 | 0.023077843 | CENPE/NDC80/NUF2/BECN1/CENPC/HNRNPU/MAPRE1/MIS12 | 8 |
| BP | GO:1901989 | positive regulation of cell cycle phase transition | 26/2221 | 121/18614 | 0.001965439 | 0.027307348 | 0.023077843 | ATAD5/CDC6/CDK1/DLGAP5/DTL/EZH2/FBXO5/MTBP/SASS6/STIL/ADAM17/ANKRD17/CENPJ/CPSF3/CUL3/DDX3X/KMT2E/MDM2/PLCB1/PLRG1/RB1/RDX/RRM1/RRM2B/STXBP4/THOC1 | 26 |
| BP | GO:0032869 | cellular response to insulin stimulus | 40/2221 | 211/18614 | 0.001970948 | 0.027320794 | 0.023089207 | APC/ATP2B1/C2CD5/DENND4C/ENPP1/FER/GCLC/IDE/LPL/MIR15B/MYO5A/NCK1/NCL/NCOA1/NCOA2/NUCKS1/OGT/OSBPL8/PARP1/PDE3B/PHIP/PIK3C2A/PIK3CA/PIK3R1/PIK3R3/PPARG/PRKCI/PRKDC/PTPN11/PTPN2/RB1/SESN3/SOS1/SOS2/STAT1/STXBP4/SYAP1/TBC1D4/USO1/ZNF106 | 40 |
| BP | GO:0009299 | mRNA transcription | 14/2221 | 51/18614 | 0.002021339 | 0.02780502 | 0.023498433 | AP3B1/DDX5/HIPK3/HLTF/NCBP1/NCBP2/NCOA1/NCOA2/PPARG/TAF1/TAF2/TAF4B/TAF7/ZBTB1 | 14 |
| BP | GO:0032873 | negative regulation of stress-activated MAPK cascade | 14/2221 | 51/18614 | 0.002021339 | 0.02780502 | 0.023498433 | PBK/AIDA/CYLD/DLG1/DNAJA1/EZR/FKTN/HIPK3/MECOM/NCOR1/PDCD4/TAOK3/ZMYND11/ZNF675 | 14 |
| BP | GO:0070303 | negative regulation of stress-activated protein kinase signaling cascade | 14/2221 | 51/18614 | 0.002021339 | 0.02780502 | 0.023498433 | PBK/AIDA/CYLD/DLG1/DNAJA1/EZR/FKTN/HIPK3/MECOM/NCOR1/PDCD4/TAOK3/ZMYND11/ZNF675 | 14 |
| BP | GO:0016447 | somatic recombination of immunoglobulin gene segments | 16/2221 | 62/18614 | 0.002026922 | 0.02780502 | 0.023498433 | ATAD5/MSH2/HSPD1/LIG4/MLH1/MSH3/MSH6/NBN/PRKDC/PTPRC/RIF1/SWAP70/TFRC/THOC1/TP53BP1/XRCC4 | 16 |
| BP | GO:0048015 | phosphatidylinositol-mediated signaling | 34/2221 | 172/18614 | 0.00202899 | 0.02780502 | 0.023498433 | CEP55/ANGPT1/BECN1/EGF/ERBB4/EXOC1/EZR/FCGR3A/FLT1/HGF/HTR2A/IGF1/IL18/JAK2/KBTBD2/NEDD4/NF1/OGT/PDGFC/PDGFD/PDGFRA/PIK3AP1/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIP5K1B/PLCB1/PLCB4/PLCH1/PREX2/PTPN13 | 34 |
| BP | GO:0045814 | negative regulation of gene expression, epigenetic | 24/2221 | 109/18614 | 0.002038856 | 0.02787672 | 0.023559028 | EZH2/HELLS/ATF7IP/ATRX/BAZ1A/CTR9/HAT1/HMGB1/KDM5A/L3MBTL3/LMNB1/PIK3CA/RB1/RIF1/SETDB2/SMARCA5/SMCHD1/SPTY2D1/SUZ12/TPR/UBR2/USP7/ZDBF2/ZNFX1 | 24 |
| BP | GO:0032868 | response to insulin | 49/2221 | 272/18614 | 0.002060177 | 0.02798184 | 0.023647867 | APC/ATP2B1/C2CD5/CTSK/DENND4C/ENPP1/EPM2AIP1/FER/GCLC/GCNT1/HADHA/IDE/KBTBD2/LPL/LYN/MIR15B/MYO5A/NCK1/NCL/NCOA1/NCOA2/NUCKS1/OGT/OSBPL8/PARP1/PDE3B/PHIP/PIK3C2A/PIK3CA/PIK3R1/PIK3R3/PPARG/PRKCI/PRKDC/PTPN11/PTPN2/RB1/SESN3/SOS1/SOS2/STAT1/STXBP3/STXBP4/SYAP1/TBC1D4/TLR2/USO1/VPS13C/ZNF106 | 49 |
| BP | GO:0043547 | positive regulation of GTPase activity | 49/2221 | 272/18614 | 0.002060177 | 0.02798184 | 0.023647867 | ARHGAP11A/ECT2/EZH2/WDR41/ARAP2/ARHGAP29/ARHGAP42/C9orf72/CCDC125/CDKL5/CORO1C/DOCK10/DOCK11/DOCK7/DOCK8/DOCK9/EVI5/FERMT2/ITGA6/ITGB1/MAP4K4/MYO9A/NET1/NF1/RAB11FIP2/RAB3GAP1/RALGAPA1/RALGAPA2/RALGPS2/RAP1GDS1/RAPGEF2/RAPGEF4/RAPGEF5/RAPGEF6/RASGEF1B/RASGRF2/RASGRP3/RGL1/RGS1/SIPA1L1/SNX13/SNX9/SOS1/SOS2/TBC1D15/TBC1D30/TBC1D4/TBC1D8B/ZC3H15 | 49 |
| BP | GO:1990823 | response to leukemia inhibitory factor | 23/2221 | 103/18614 | 0.002060498 | 0.02798184 | 0.023647867 | HELLS/ADAM23/ARID5B/BCLAF1/CACYBP/EPS8/HK2/HNRNPU/KDM3A/KDM5B/MAT2A/MIR224/MTF2/NCL/PCOLCE2/PIGA/RIF1/RNMT/SMARCA5/SNX10/TFRC/WDR35/XRCC5 | 23 |
| BP | GO:0018209 | peptidyl-serine modification | 57/2221 | 327/18614 | 0.00206656 | 0.028000956 | 0.023664021 | CDK1/PBK/TTK/VRK1/AKAP9/ANGPT1/ATM/ATR/CAB39/CAPRIN2/CHUK/DCLK1/DMD/DOCK7/EIF2AK3/FNIP1/FNIP2/GALNT1/GALNT3/GGNBP2/HGF/HIPK3/HSP90AA1/HSP90AB1/LRRK2/MAP3K13/MASTL/NCK1/PDE4D/PIK3CA/PIKFYVE/PKN2/POGLUT1/PRKACB/PRKCI/PRKD1/PRKDC/PTGS2/PWP1/RICTOR/RIPK1/RIPK2/ROCK1/ROCK2/RPS6KA3/SGK3/SRPK2/STK32A/STK38L/TAF1/TBK1/TFRC/TGFBR1/TLK1/TOP1/TRIM6/VRK2 | 57 |
| BP | GO:0071900 | regulation of protein serine/threonine kinase activity | 63/2221 | 369/18614 | 0.002093829 | 0.02830668 | 0.023922393 | BLM/CCNA2/CCNB2/CDC6/CDKN3/EZH2/ACSL1/ADAM17/ADAM9/AIDA/AKAP13/APC/BCCIP/CAB39/CASP3/CCNE2/CCNG1/CCNH/CCNT1/CCNT2/CDK5RAP2/CHORDC1/DDX3X/DNAJA1/EGF/EPHA4/ETAA1/FERMT2/FLT1/GTF2H1/GTPBP4/HIPK3/HMGCR/HTR2A/IPO5/IPO7/IRAK3/LRP6/LRRK2/LYN/MAP3K13/MAP3K4/MAP3K7/MEF2C/NF1/PDCD4/PDGFC/PDGFD/PIK3CB/PIK3CG/PPARG/PPP2CA/PRKAR2B/PTPRC/RAPGEF2/RB1/RGS2/SOS1/SYAP1/TAOK3/TLR4/TLR6/ZNF675 | 63 |
| BP | GO:0043123 | positive regulation of I-kappaB kinase/NF-kappaB signaling | 37/2221 | 192/18614 | 0.002117897 | 0.028567869 | 0.024143128 | ECT2/AKAP13/ALPK1/ANKRD17/ATP2C1/BIRC2/BIRC3/CASP1/CD36/CHUK/CLEC4D/CTNNB1/DDX1/DDX21/DHX15/DHX36/GOLT1B/IFIT5/IRAK4/MALT1/MAP3K7/MTDH/PRKD1/REL/RIPK1/RIPK2/TAB2/TAB3/TBK1/TFRC/TLR3/TLR4/TLR6/TRAF5/TRIM22/TRIM38/TRIM6 | 37 |
| BP | GO:0034976 | response to endoplasmic reticulum stress | 47/2221 | 259/18614 | 0.002157977 | 0.028999696 | 0.024508072 | AGR2/UBXN8/AIFM1/ATF6/ATP2A2/CANX/CASP4/CCDC47/CFTR/DDX3X/DNAJC10/DNAJC3/EDEM3/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/ERLIN1/HSP90B1/HSPA5/ITPR1/LRRK2/NCK1/NFE2L2/OPA1/PARP8/PDIA3/PDIA6/PIK3R1/PSMC6/PTPN2/RASGRF2/SEL1L/STT3B/TMTC3/UBA5/UBE4A/UBXN4/UFL1/UFM1/UGGT1/UGGT2/USP13/USP14/USP25/VCP/YOD1 | 47 |
| BP | GO:1902808 | positive regulation of cell cycle G1/S phase transition | 17/2221 | 68/18614 | 0.002159552 | 0.028999696 | 0.024508072 | CDC6/EZH2/MTBP/SASS6/STIL/ADAM17/ANKRD17/CENPJ/CPSF3/DDX3X/KMT2E/MDM2/PLCB1/PLRG1/RDX/RRM1/STXBP4 | 17 |
| BP | GO:0098534 | centriole assembly | 13/2221 | 46/18614 | 0.002174314 | 0.029132897 | 0.024620642 | BRCA1/CEP135/PLK4/SASS6/STIL/ALMS1/CCP110/CDK5RAP2/CENPJ/CEP120/CEP152/CEP192/SPICE1 | 13 |
| BP | GO:0018108 | peptidyl-tyrosine phosphorylation | 63/2221 | 370/18614 | 0.002236607 | 0.029701621 | 0.025101279 | HDAC2/MELK/NCAPG2/PBK/TTK/ABL2/ADAM17/ANGPT1/BANK1/BAZ1B/BMX/BTK/CD36/CLK4/CNTN1/EGF/EIF2AK2/EPHA3/EPHA4/ERBB4/FER/FGF7/FLT1/FRK/GGNBP2/HGF/HIPK3/HTR2A/IBTK/IGF1/IL18/IL6ST/ITGB3/ITK/JAK1/JAK2/LRP8/LYN/MERTK/MET/NCL/OSBP/PARP14/PARP9/PDGFC/PDGFD/PDGFRA/PIBF1/PPP2CA/PTPN11/PTPN2/PTPN4/PTPRC/RICTOR/RIPK2/ROS1/RPS6KA5/SAMSN1/SNX6/SOCS4/TEC/TTN/YES1 | 63 |
| BP | GO:0007131 | reciprocal meiotic recombination | 15/2221 | 57/18614 | 0.002245407 | 0.029701621 | 0.025101279 | BRIP1/FANCD2/MND1/RAD51AP1/RAD54B/TOP2A/ATM/ERCC4/FANCM/MLH1/MLH3/RAD21/RAD50/TOP2B/UBR2 | 15 |
| BP | GO:0010332 | response to gamma radiation | 15/2221 | 57/18614 | 0.002245407 | 0.029701621 | 0.025101279 | BRCA2/FANCD2/XRCC2/ATM/ATR/DCUN1D3/ERCC6/HSPA5/LIG4/MDM2/PARP1/PRKDC/PTPRC/WRN/XRCC5 | 15 |
| BP | GO:0031124 | mRNA 3'-end processing | 15/2221 | 57/18614 | 0.002245407 | 0.029701621 | 0.025101279 | AHCYL1/CPSF2/CPSF3/CSTF3/DHX36/LEO1/NCBP1/NCBP2/NUDT21/PAPOLA/PAPOLG/PCF11/PNPT1/YTHDC1/ZNF473 | 15 |
| BP | GO:0140527 | reciprocal homologous recombination | 15/2221 | 57/18614 | 0.002245407 | 0.029701621 | 0.025101279 | BRIP1/FANCD2/MND1/RAD51AP1/RAD54B/TOP2A/ATM/ERCC4/FANCM/MLH1/MLH3/RAD21/RAD50/TOP2B/UBR2 | 15 |
| BP | GO:0007026 | negative regulation of microtubule depolymerization | 9/2221 | 26/18614 | 0.00225132 | 0.029701621 | 0.025101279 | TPX2/APC/CAMSAP2/CKAP2/CLASP2/MAP1B/NAV3/TAOK1/WDR47 | 9 |
| BP | GO:0014829 | vascular associated smooth muscle contraction | 9/2221 | 26/18614 | 0.00225132 | 0.029701621 | 0.025101279 | ARHGAP42/ATP2B1/CD38/DOCK5/HTR2A/MKKS/PIK3C2A/RAP1GDS1/ZDHHC21 | 9 |
| BP | GO:0001824 | blastocyst development | 25/2221 | 116/18614 | 0.002273833 | 0.029933001 | 0.025296822 | BRCA2/CHEK1/NCAPG2/NEK2/CNOT1/COPS2/CTR9/CUL3/GABPA/IGF1/KDM4C/MATR3/NASP/NBN/NECAB1/PALB2/PHF6/RBBP8/RPL7L1/RTF1/SKIL/TBL1XR1/TGFBR1/ZFP14/ZPR1 | 25 |
| BP | GO:0007163 | establishment or maintenance of cell polarity | 42/2221 | 226/18614 | 0.002284685 | 0.030010181 | 0.025362047 | KIF20B/MAD2L1/NDC80/SPAG5/SPDL1/ABL2/ACTR2/ACTR3/ARFGEF1/CDK5RAP2/CKAP5/CLASP2/CTNNA1/DLG1/DLG2/DOCK2/DOCK7/DOCK8/DST/FAT1/FRMD4B/GPSM2/HSP90AA1/HSP90AB1/ITGB1/KRIT1/MAP1B/MAPRE1/MPP7/MYO9A/NCKAP1L/PHLDB2/PRKCI/RAB11FIP2/RICTOR/ROCK1/ROCK2/RPGRIP1L/RUFY3/SDCCAG8/UBXN2B/ZW10 | 42 |
| BP | GO:0071236 | cellular response to antibiotic | 6/2221 | 13/18614 | 0.002330818 | 0.030549456 | 0.025817797 | EZH2/ATP7A/HSPA5/MDM2/MEF2C/PLA2G4A | 6 |
| BP | GO:0034968 | histone lysine methylation | 23/2221 | 104/18614 | 0.002352902 | 0.030676922 | 0.02592552 | BRCA1/EZH2/ARID4A/ARID4B/ASH1L/BOD1L1/CTNNB1/CTR9/HCFC2/IWS1/KDM6A/KMT2C/MTF2/OGT/RBBP5/RIF1/RLF/RTF1/SETD7/SETDB2/SETMAR/SNW1/SUV39H2 | 23 |
| BP | GO:1902904 | negative regulation of supramolecular fiber organization | 33/2221 | 167/18614 | 0.002353529 | 0.030676922 | 0.02592552 | TPX2/VBP1/ADD3/APC/ARFGEF1/ARHGAP28/CAMSAP2/CAPZA2/CGNL1/CKAP2/CLASP2/EPS8/HSPA8/LIMA1/MAP1B/MAPRE1/MET/MKKS/NAV3/PHLDB2/PIK3CA/PIK3R1/PPFIA1/RDX/SCIN/SPTAN1/SVIL/SWAP70/TAOK1/TJP1/TMOD2/TWF1/WDR47 | 33 |
| BP | GO:0016556 | mRNA modification | 10/2221 | 31/18614 | 0.002373461 | 0.030676922 | 0.02592552 | DKC1/METTL14/NSUN2/PUS3/PUS7/PUS7L/TRMT10C/TRMT6/WTAP/ZC3H13 | 10 |
| BP | GO:0098901 | regulation of cardiac muscle cell action potential | 10/2221 | 31/18614 | 0.002373461 | 0.030676922 | 0.02592552 | AKAP9/ANK2/ATP2A2/CXADR/DLG1/DSC2/DSG2/DSP/PKP2/RYR2 | 10 |
| BP | GO:1900225 | regulation of NLRP3 inflammasome complex assembly | 10/2221 | 31/18614 | 0.002373461 | 0.030676922 | 0.02592552 | BRCC3/BTK/CD36/DDX3X/EIF2AK2/GBP5/PPP2CA/PRKD1/TLR4/TLR6 | 10 |
| BP | GO:0000460 | maturation of 5.8S rRNA | 11/2221 | 36/18614 | 0.002376238 | 0.030676922 | 0.02592552 | ERI1/ERI2/EXOSC9/MAK16/MPHOSPH6/NSA2/PRKDC/RRP15/RRS1/UTP20/WDR12 | 11 |
| BP | GO:0010737 | protein kinase A signaling | 11/2221 | 36/18614 | 0.002376238 | 0.030676922 | 0.02592552 | AKAP12/AKAP5/AKAP6/EZR/LCP1/LRRK2/MYOM1/PJA2/PRKACB/RDX/TTN | 11 |
| BP | GO:1901570 | fatty acid derivative biosynthetic process | 14/2221 | 52/18614 | 0.002467383 | 0.031785388 | 0.026862302 | ELOVL6/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSS3/ELOVL2/ELOVL7/FAR1/FAR2/PAM/PPT1/SLC27A2 | 14 |
| BP | GO:0018105 | peptidyl-serine phosphorylation | 54/2221 | 309/18614 | 0.002516473 | 0.032348502 | 0.027338197 | CDK1/PBK/TTK/VRK1/AKAP9/ANGPT1/ATM/ATR/CAB39/CAPRIN2/CHUK/DCLK1/DMD/DOCK7/EIF2AK3/FNIP1/FNIP2/GGNBP2/HGF/HIPK3/HSP90AA1/HSP90AB1/LRRK2/MAP3K13/MASTL/NCK1/PDE4D/PIK3CA/PIKFYVE/PKN2/PRKACB/PRKCI/PRKD1/PRKDC/PTGS2/PWP1/RICTOR/RIPK1/RIPK2/ROCK1/ROCK2/RPS6KA3/SGK3/SRPK2/STK32A/STK38L/TAF1/TBK1/TFRC/TGFBR1/TLK1/TOP1/TRIM6/VRK2 | 54 |
| BP | GO:0018212 | peptidyl-tyrosine modification | 63/2221 | 372/18614 | 0.002547934 | 0.032683099 | 0.02762097 | HDAC2/MELK/NCAPG2/PBK/TTK/ABL2/ADAM17/ANGPT1/BANK1/BAZ1B/BMX/BTK/CD36/CLK4/CNTN1/EGF/EIF2AK2/EPHA3/EPHA4/ERBB4/FER/FGF7/FLT1/FRK/GGNBP2/HGF/HIPK3/HTR2A/IBTK/IGF1/IL18/IL6ST/ITGB3/ITK/JAK1/JAK2/LRP8/LYN/MERTK/MET/NCL/OSBP/PARP14/PARP9/PDGFC/PDGFD/PDGFRA/PIBF1/PPP2CA/PTPN11/PTPN2/PTPN4/PTPRC/RICTOR/RIPK2/ROS1/RPS6KA5/SAMSN1/SNX6/SOCS4/TEC/TTN/YES1 | 63 |
| BP | GO:0070192 | chromosome organization involved in meiotic cell cycle | 18/2221 | 75/18614 | 0.002644828 | 0.033853802 | 0.028610349 | BRIP1/BUB1/BUB1B/FANCD2/MND1/NCAPH/ATM/ATRX/CCNE2/MLH1/MLH3/RAD21/RAD50/SMC1A/SMC2/SMC3/SMC4/SYCP2 | 18 |
| BP | GO:1901976 | regulation of cell cycle checkpoint | 13/2221 | 47/18614 | 0.002682718 | 0.034265882 | 0.028958603 | BRCA1/BRCA2/MAD2L1/NDC80/WDR76/BRCC3/CDK5RAP2/ETAA1/GEN1/RFWD3/THOC1/TPR/USP44 | 13 |
| BP | GO:1901992 | positive regulation of mitotic cell cycle phase transition | 22/2221 | 99/18614 | 0.00271478 | 0.034601936 | 0.029242608 | CDC6/CDK1/DLGAP5/DTL/FBXO5/MTBP/SASS6/STIL/ADAM17/ANKRD17/CENPJ/CPSF3/CUL3/DDX3X/KMT2E/MDM2/PLCB1/PLRG1/RB1/RDX/RRM1/RRM2B | 22 |
| BP | GO:0033627 | cell adhesion mediated by integrin | 20/2221 | 87/18614 | 0.00272996 | 0.034721857 | 0.029343955 | ADAM17/ADAM9/DPP4/FBN1/IFT74/ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/LYN/MMRN1/NCKAP1L/PDE3B/PIK3CG/PTPN11/SWAP70 | 20 |
| BP | GO:0031440 | regulation of mRNA 3'-end processing | 8/2221 | 22/18614 | 0.002763769 | 0.03507771 | 0.029644691 | AHCYL1/DHX36/LEO1/NCBP1/NCBP2/NUDT21/PAPOLA/YTHDC1 | 8 |
| BP | GO:0051258 | protein polymerization | 49/2221 | 276/18614 | 0.002798661 | 0.035445779 | 0.029955751 | DIAPH3/FBXO5/TPX2/ADD3/AKAP9/ARFGEF1/ARHGAP18/ARHGAP28/CAMSAP2/CAPZA2/CDK5RAP2/CENPJ/CEP192/CKAP5/CLASP2/CLIP1/DIAPH2/DLG1/DNM1L/EPS8/FER/FMN1/HSP90AA1/JAK2/MAP1B/MAP7D3/MAPRE1/MET/MKKS/NAV3/NCK1/NCKAP1/NCKAP1L/NEDD1/NIN/ORC4/PSTPIP2/RASA1/RDX/RICTOR/SCIN/SNX9/SPIRE1/SPTAN1/SVIL/TMOD2/TRIM6/TTC17/TWF1 | 49 |
| BP | GO:0061512 | protein localization to cilium | 17/2221 | 70/18614 | 0.003004163 | 0.03796858 | 0.032087808 | ARL13B/ATP6V1D/CC2D2A/CCDC66/CCDC88A/DYNC2H1/EFCAB7/FSIP2/GDI2/IFT80/INVS/LZTFL1/RABEP1/SNX10/TTC21B/WDR19/WDR35 | 17 |
| BP | GO:0006378 | mRNA polyadenylation | 11/2221 | 37/18614 | 0.003022487 | 0.038120088 | 0.032215849 | AHCYL1/CPSF2/CPSF3/CSTF3/LEO1/NUDT21/PAPOLA/PAPOLG/PCF11/PNPT1/YTHDC1 | 11 |
| BP | GO:0006661 | phosphatidylinositol biosynthetic process | 27/2221 | 131/18614 | 0.003048273 | 0.038284783 | 0.032355036 | ATM/BECN1/BMX/EFR3A/FIG4/HTR2A/IMPA1/INPP4B/MTM1/MTMR2/MTMR4/MTMR6/PIGA/PIGN/PIGW/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/PIKFYVE/PIP5K1B/SACM1L/SOCS4 | 27 |
| BP | GO:0006888 | endoplasmic reticulum to Golgi vesicle-mediated transport | 27/2221 | 131/18614 | 0.003048273 | 0.038284783 | 0.032355036 | ARCN1/COPA/COPB1/COPB2/CUL3/ERGIC2/GOLT1B/GOPC/KDELR3/LMAN1/LRRK2/MIA3/RAB1A/SAR1B/SCFD1/SEC23A/SEC23B/SEC24D/SEC31A/STX17/TRAPPC11/TRAPPC13/TRAPPC8/TRIP11/USO1/VCP/ZW10 | 27 |
| BP | GO:0070302 | regulation of stress-activated protein kinase signaling cascade | 37/2221 | 196/18614 | 0.003058257 | 0.038330152 | 0.032393378 | PBK/AIDA/CYLD/DLG1/DNAJA1/EIF2AK2/EZR/FAS/FKTN/HGF/HIPK3/HMGB1/LYN/MAP3K4/MAP4K4/MECOM/MIR181B1/MMP8/NAIP/NCOR1/PDCD4/PJA2/PLCB1/RB1CC1/RIPK1/RIPK2/SDCBP/SEMA3A/TAOK1/TAOK3/TLR3/TLR4/TNIK/TRAF5/ZMYND11/ZNF622/ZNF675 | 37 |
| BP | GO:0051235 | maintenance of location | 59/2221 | 347/18614 | 0.003120828 | 0.038923866 | 0.032895135 | ASPM/ABCA1/AKAP6/AKAP9/ANK2/ANK3/ARHGAP21/C3/CAPN3/CCDC88A/CD36/CHD7/CLIC2/DMD/ENPP1/FBN1/G3BP2/GPSM2/HK2/HNRNPU/HSP90B1/HSPA5/HTR2A/IBTK/ITGAV/ITGB3/ITPR1/ITPR2/KDELR3/LMAN1/LPL/LTBP1/LYN/MSR1/NRIP1/OSBPL11/OSBPL8/PDE4D/PLCB1/PLCB4/PLCH1/PLIN2/PPARG/PRKD1/PTPN2/PTPRC/RYR2/SCIN/SP100/SQLE/STARD4/SYNE1/TOPORS/TTC39B/TWF1/VPS13A/VPS13C/VPS13D/YWHAB | 59 |
| BP | GO:0009266 | response to temperature stimulus | 35/2221 | 183/18614 | 0.003123464 | 0.038923866 | 0.032895135 | HDAC2/ACADM/ATM/ATP2B1/ATR/CHORDC1/DHX36/DNAJA1/DNAJC2/DNAJC3/DNAJC7/EIF2AK3/EIF2AK4/EIF2B3/EIF2S1/GCLC/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSPD1/HTR2A/IGF1/LPL/LXN/LYN/NF1/PSIP1/PTGS2/SCN9A/SLU7/TFEC/TPR/VCP/WDR47 | 35 |
| BP | GO:0006637 | acyl-CoA metabolic process | 21/2221 | 94/18614 | 0.003131508 | 0.038923866 | 0.032895135 | ELOVL6/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/BAAT/DLD/ELOVL2/ELOVL7/FAR1/FAR2/HMGCS1/HSD17B4/PPT1/SLC27A2/SUCLA2/SUCLG2/TDO2 | 21 |
| BP | GO:0035383 | thioester metabolic process | 21/2221 | 94/18614 | 0.003131508 | 0.038923866 | 0.032895135 | ELOVL6/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/BAAT/DLD/ELOVL2/ELOVL7/FAR1/FAR2/HMGCS1/HSD17B4/PPT1/SLC27A2/SUCLA2/SUCLG2/TDO2 | 21 |
| BP | GO:0007030 | Golgi organization | 31/2221 | 157/18614 | 0.003169485 | 0.039314684 | 0.03322542 | CDK1/VRK1/AKAP9/ARFGEF1/ARHGAP21/ATP8B1/ATP8B4/BLZF1/CAMSAP2/CLASP2/COG5/COG6/DYNC2H1/GCC2/GOLGA5/GOLGB1/HOOK1/LMAN1/LRRK2/LYSMD3/PRKD1/RAB1A/STX17/SYNE1/TRAPPC11/TRAPPC8/TRIP11/UBXN2B/USO1/VPS13B/ZW10 | 31 |
| BP | GO:0072659 | protein localization to plasma membrane | 50/2221 | 285/18614 | 0.003271841 | 0.040463761 | 0.034196522 | AGR2/ACSL3/AKAP5/ANK2/ANK3/ATP1B1/ATP2C1/BLZF1/C2CD5/CCDC88A/CDH2/CLASP2/CLTC/CNST/DENND4C/DLG1/EFR3A/EPB41L3/EPHA3/EXOC5/EZR/FCHO2/GBP1/GOLGA4/HECTD1/ITGB1/KIF5B/LRP6/MACF1/MYO5A/NSF/PIGW/PIK3R1/PKP2/PLS1/PPFIA1/PREPL/PRKCI/RAB8B/RAPGEF2/RAPGEF6/RDX/ROCK1/ROCK2/SEC23A/SLC4A1/SLMAP/TNIK/VPS35/WNK3 | 50 |
| BP | GO:0019081 | viral translation | 7/2221 | 18/18614 | 0.0032823 | 0.040463761 | 0.034196522 | CSDE1/DHX9/EIF2AK4/EIF3A/EIF3D/EIF3L/SSB | 7 |
| BP | GO:0036499 | PERK-mediated unfolded protein response | 7/2221 | 18/18614 | 0.0032823 | 0.040463761 | 0.034196522 | AGR2/EIF2AK3/EIF2S1/HSPA5/NCK1/NFE2L2/PTPN2 | 7 |
| BP | GO:0060759 | regulation of response to cytokine stimulus | 34/2221 | 177/18614 | 0.003298628 | 0.040581899 | 0.034296363 | ADAM17/ANGPT1/ARG1/CASP1/CASP4/CYLD/DHX9/HIF1A/IFIH1/IL1R1/IRAK3/LRRC70/NAIP/OTUD4/PARP14/PARP9/PPARG/PTPN11/PTPN2/PTPRC/RABGEF1/RIPK1/RIPK2/SAMHD1/STAP1/TBK1/TLR2/TLR4/TRIM44/TRIM6/USP27X/VRK2/YTHDF3/ZNF675 | 34 |
| BP | GO:0098781 | ncRNA transcription | 16/2221 | 65/18614 | 0.003402525 | 0.041649853 | 0.035198907 | GTF3C6/ATRX/ELL2/ERCC6/GTF3C3/ICE1/ICE2/LARP7/NCL/NIFK/NOL11/POLR1B/PWP1/TAF1B/USPL1/ZNF143 | 16 |
| BP | GO:1905515 | non-motile cilium assembly | 16/2221 | 65/18614 | 0.003402525 | 0.041649853 | 0.035198907 | CEP135/ARL13B/CC2D2A/CENPJ/CEP350/DYNC2H1/EXOC5/GORAB/IFT57/IFT74/IFT80/MAPRE1/MKKS/PCM1/PIBF1/RPGRIP1L | 16 |
| BP | GO:0007041 | lysosomal transport | 27/2221 | 132/18614 | 0.003406205 | 0.041649853 | 0.035198907 | AP3B1/AP3M1/BECN1/C9orf72/CHMP2B/DTX3L/GCC2/GNPTAB/HOOK1/HOOK3/HSPA8/LRRK2/LYST/MTM1/NCOA4/NEDD4/NPC1/PIK3C3/PIK3R4/SCYL2/SNX16/UEVLD/VCP/VPS35/VPS41/VPS54/ZFYVE16 | 27 |
| BP | GO:0046546 | development of primary male sexual characteristics | 29/2221 | 145/18614 | 0.003481598 | 0.042485383 | 0.035905026 | ASPM/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ATRX/CSDE1/CTNNA1/EIF2S2/FER/FNDC3A/HMGB2/HSD17B4/ING2/INHBA/LHFPL2/LRP2/NASP/NCOA4/PDGFRA/RHOBTB3/SCAPER/TGFBR1/TLR3/TMF1/WDR48/ZFPM2 | 29 |
| BP | GO:0000956 | nuclear-transcribed mRNA catabolic process | 26/2221 | 126/18614 | 0.003538842 | 0.043096509 | 0.036421496 | ATM/CNOT1/CNOT6L/CSDE1/DDX5/DHX36/DHX9/DIS3/EIF3E/EIF4A3/ETF1/EXOSC9/GSPT1/HNRNPU/MLH1/NBAS/NCBP1/NCBP2/PNRC2/RC3H2/SSB/SYNCRIP/UPF2/UPF3B/XRN1/XRN2 | 26 |
| BP | GO:0071459 | protein localization to chromosome, centromeric region | 12/2221 | 43/18614 | 0.003563079 | 0.043304011 | 0.03659686 | BUB1B/CDK1/KNTC1/MTBP/NDC80/SPDL1/TTK/ZWILCH/MIS12/RB1/SMC5/ZW10 | 12 |
| BP | GO:0002753 | cytosolic pattern recognition receptor signaling pathway | 21/2221 | 95/18614 | 0.003577853 | 0.043377559 | 0.036659016 | ALPK1/ANKRD17/BIRC2/BIRC3/COLEC12/CYLD/DDX3X/DDX60/HAVCR2/HMGB1/IFIH1/IRAK4/LACC1/MAP3K7/PIK3AP1/PUM2/RIOK3/RIPK2/TLR4/TLR8/USP15 | 21 |
| BP | GO:0002312 | B cell activation involved in immune response | 20/2221 | 89/18614 | 0.003611007 | 0.043377559 | 0.036659016 | ATAD5/MSH2/CD180/CR1/DOCK10/DOCK11/GAPT/HSPD1/LIG4/MLH1/MSH6/NBN/PHF14/PTPRC/RIF1/SWAP70/TFRC/THOC1/TLR4/TP53BP1 | 20 |
| BP | GO:0030242 | autophagy of peroxisome | 5/2221 | 10/18614 | 0.003612393 | 0.043377559 | 0.036659016 | ACBD5/ATM/PIK3C3/PIK3R4/RB1CC1 | 5 |
| BP | GO:0030953 | astral microtubule organization | 5/2221 | 10/18614 | 0.003612393 | 0.043377559 | 0.036659016 | CENPJ/CEP120/DLG1/EZR/KPNB1 | 5 |
| BP | GO:0031442 | positive regulation of mRNA 3'-end processing | 5/2221 | 10/18614 | 0.003612393 | 0.043377559 | 0.036659016 | DHX36/LEO1/NCBP1/NCBP2/NUDT21 | 5 |
| BP | GO:0033314 | mitotic DNA replication checkpoint signaling | 5/2221 | 10/18614 | 0.003612393 | 0.043377559 | 0.036659016 | CDC6/TICRR/NAE1/RAD17/TOPBP1 | 5 |
| BP | GO:0034341 | response to type II interferon | 28/2221 | 139/18614 | 0.003640265 | 0.043461612 | 0.036730051 | ACTR2/ACTR3/AQP4/ARG1/CASP1/CLDN1/GBP1/GBP2/GBP5/IFNGR1/JAK1/JAK2/KIF5B/KYNU/MRC1/NUB1/PARP14/PARP9/PPARG/PTPN2/SP100/STAT1/STXBP3/STXBP4/SYNCRIP/TLR2/TLR3/TLR4 | 28 |
| BP | GO:0046328 | regulation of JNK cascade | 28/2221 | 139/18614 | 0.003640265 | 0.043461612 | 0.036730051 | AIDA/CYLD/DNAJA1/FKTN/HIPK3/HMGB1/MAP4K4/MECOM/MMP8/NAIP/NCOR1/PDCD4/PJA2/PLCB1/RB1CC1/RIPK1/RIPK2/SDCBP/SEMA3A/TAOK1/TAOK3/TLR3/TLR4/TNIK/TRAF5/ZMYND11/ZNF622/ZNF675 | 28 |
| BP | GO:0001833 | inner cell mass cell proliferation | 6/2221 | 14/18614 | 0.003669963 | 0.043461612 | 0.036730051 | BRCA2/CHEK1/NCAPG2/COPS2/PALB2/ZPR1 | 6 |
| BP | GO:0006999 | nuclear pore organization | 6/2221 | 14/18614 | 0.003669963 | 0.043461612 | 0.036730051 | AHCTF1/NUP107/NUP133/NUP153/NUP205/TPR | 6 |
| BP | GO:0060009 | Sertoli cell development | 6/2221 | 14/18614 | 0.003669963 | 0.043461612 | 0.036730051 | ARID4A/ARID4B/ATRX/FER/FNDC3A/HSD17B4 | 6 |
| BP | GO:1904424 | regulation of GTP binding | 6/2221 | 14/18614 | 0.003669963 | 0.043461612 | 0.036730051 | ARHGAP28/C9orf72/CCPG1/EIF2S1/EPHA4/MET | 6 |
| BP | GO:1905214 | regulation of RNA binding | 6/2221 | 14/18614 | 0.003669963 | 0.043461612 | 0.036730051 | EIF3D/EIF3E/EIF4A3/FMR1/NCBP1/NUCKS1 | 6 |
| BP | GO:0016571 | histone methylation | 27/2221 | 133/18614 | 0.003799019 | 0.044682113 | 0.037761515 | BRCA1/EZH2/ARID4A/ARID4B/ASH1L/BOD1L1/CTNNB1/CTR9/HCFC2/IWS1/KDM6A/KMT2C/MTF2/OGT/PAXBP1/RBBP5/RIF1/RLF/RNF20/RTF1/SETD7/SETDB2/SETMAR/SMARCA5/SNW1/SUV39H2/SUZ12 | 27 |
| BP | GO:0000462 | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 11/2221 | 38/18614 | 0.003802733 | 0.044682113 | 0.037761515 | BMS1/HEATR1/NGDN/NOL10/RRS1/TSR1/UTP20/UTP23/UTP3/UTP6/WDR43 | 11 |
| BP | GO:0032435 | negative regulation of proteasomal ubiquitin-dependent protein catabolic process | 11/2221 | 38/18614 | 0.003802733 | 0.044682113 | 0.037761515 | PBK/HSP90AB1/MTM1/OGT/PHF20L1/RYBP/SDCBP/UCHL5/USP14/USP7/USP9X | 11 |
| BP | GO:0033260 | nuclear DNA replication | 11/2221 | 38/18614 | 0.003802733 | 0.044682113 | 0.037761515 | ATAD5/BLM/BRCA2/GMNN/MCM3/MCM6/ATRX/DBF4/DNA2/POLA1/WRN | 11 |
| BP | GO:0071711 | basement membrane organization | 10/2221 | 33/18614 | 0.003964627 | 0.046493554 | 0.03929239 | CLASP2/COL3A1/CTSS/FLRT2/HMCN1/ITGB1/LAMA2/LAMB1/LAMC1/PHLDB2 | 10 |
| BP | GO:0071470 | cellular response to osmotic stress | 13/2221 | 49/18614 | 0.003990893 | 0.046623461 | 0.039402176 | CAB39/CAPN3/CASP1/CASP3/DDX3X/LRRC8D/NFAT5/NLRP3/OXSR1/PTGS2/USP15/WNK3/XRCC5 | 13 |
| BP | GO:0032878 | regulation of establishment or maintenance of cell polarity | 9/2221 | 28/18614 | 0.003991204 | 0.046623461 | 0.039402176 | KIF20B/ABL2/ARFGEF1/DOCK8/KRIT1/RICTOR/ROCK1/ROCK2/RUFY3 | 9 |
| BP | GO:1902017 | regulation of cilium assembly | 16/2221 | 66/18614 | 0.004003883 | 0.046680932 | 0.039450745 | CEP135/ATG3/CCDC88A/CCP110/CDKL5/CENPJ/CEP120/CEP97/CYLD/GDI2/MNS1/MPHOSPH9/ODF2L/SDCCAG8/SYNE2/TBC1D30 | 16 |
| BP | GO:0007292 | female gamete generation | 30/2221 | 153/18614 | 0.004067211 | 0.047327544 | 0.039997207 | ASPM/BRCA2/CCNB2/FBXO5/MCM8/NCAPH/NDC80/TOP2A/TTK/ATM/CTNNB1/DDX20/DIAPH2/IGF1/INHBA/MASTL/MLH1/MLH3/NRIP1/ORC4/PANX1/PTGS2/RGS2/SOS1/SPIRE1/SYCP2/TAF4B/TNFAIP6/USP9X/YTHDC1 | 30 |
| BP | GO:0002260 | lymphocyte homeostasis | 17/2221 | 72/18614 | 0.004105881 | 0.047593407 | 0.040221892 | CCNB2/CASP3/DOCK10/DOCK11/FAS/GAPT/HIF1A/IL2RA/IL7R/LYN/MEF2C/NCKAP1L/PPP2R3C/RC3H2/SKIL/SOS1/SOS2 | 17 |
| BP | GO:0045911 | positive regulation of DNA recombination | 17/2221 | 72/18614 | 0.004105881 | 0.047593407 | 0.040221892 | ATAD5/MSH2/RAD51AP1/ACTR2/ARID2/EPC2/ERCC6/ING3/MLH1/MORF4L2/PARP1/PTPRC/RBBP8/RIF1/TFRC/TP53BP1/WDR48 | 17 |
| BP | GO:0008088 | axo-dendritic transport | 18/2221 | 78/18614 | 0.004155641 | 0.047985285 | 0.040553074 | KIF4A/AP3B1/AP3M1/BLOC1S6/DLG2/DST/DYNC1H1/HIF1A/HNRNPU/HSPA8/KIF3A/KIF5B/OPA1/RAB27B/RABGEF1/SPG11/SYBU/TRAK2 | 18 |
| BP | GO:0055117 | regulation of cardiac muscle contraction | 18/2221 | 78/18614 | 0.004155641 | 0.047985285 | 0.040553074 | ACE2/AKAP9/ANK2/ATP1B1/ATP2A2/CLIC2/DLG1/DMD/DSC2/DSG2/DSP/HSP90AA1/PDE4B/PDE4D/PIK3CG/PKP2/RGS2/RYR2 | 18 |
| BP | GO:0032970 | regulation of actin filament-based process | 64/2221 | 387/18614 | 0.004171879 | 0.048080505 | 0.040633545 | ECT2/ABL2/ADD3/AKAP13/AKAP9/ALMS1/ANK2/AP1AR/ARFGEF1/ARHGAP18/ARHGAP28/ATP2A2/C9orf72/CAPZA2/CCDC88A/CD2AP/CGNL1/CLASP2/DLG1/DSC2/DSG2/DSP/EPHA3/EPS8/FER/FERMT2/FMN1/IQGAP1/IQGAP2/ITGB3/LIMA1/MET/MKKS/NCK1/NCKAP1/NCKAP1L/NEB/PAM/PDE4B/PDE4D/PDGFRA/PHLDB2/PIK3CA/PIK3R1/PKP2/PPFIA1/RASA1/RDX/RICTOR/ROCK1/ROCK2/RYR2/SCIN/SNX9/SPTAN1/STAP1/SVIL/SWAP70/TAOK1/TGFBR1/TJP1/TMOD2/TPM1/TWF1 | 64 |
| BP | GO:0033674 | positive regulation of kinase activity | 70/2221 | 430/18614 | 0.0041876 | 0.048169413 | 0.040708683 | BORA/CDC6/CENPE/ECT2/EZH2/KIF14/TPX2/ACSL1/ADAM17/ADAM9/AKAP13/ANGPT1/CAB39/CCDC88A/CD86/DDX3X/DLG1/EGF/EPHA4/ERBB4/ETAA1/FERMT2/FLT1/HSP90AA1/HSP90AB1/HTR2A/IGF1/IL18/IQGAP1/ITGB3/JAK2/LRP8/LRRK2/LYN/MALT1/MAP3K13/MAP3K4/MAP3K7/MEF2C/MERTK/MET/NBN/OSBPL8/PDGFC/PDGFD/PDGFRA/PFKFB2/PIBF1/PIK3CG/PIK3R4/PPP2CA/PPP2R3C/PRKD1/PTPRC/RAD50/RANBP2/RAPGEF2/ROS1/SNX9/SYAP1/TAB2/TAOK3/TLR3/TLR4/TLR6/TNFSF15/TOM1L1/VLDLR/XRCC5/ZNF622 | 70 |
| BP | GO:0032872 | regulation of stress-activated MAPK cascade | 36/2221 | 193/18614 | 0.004224612 | 0.048502418 | 0.04099011 | PBK/AIDA/CYLD/DLG1/DNAJA1/EIF2AK2/EZR/FAS/FKTN/HGF/HIPK3/HMGB1/MAP3K4/MAP4K4/MECOM/MIR181B1/MMP8/NAIP/NCOR1/PDCD4/PJA2/PLCB1/RB1CC1/RIPK1/RIPK2/SDCBP/SEMA3A/TAOK1/TAOK3/TLR3/TLR4/TNIK/TRAF5/ZMYND11/ZNF622/ZNF675 | 36 |
| BP | GO:0061462 | protein localization to lysosome | 14/2221 | 55/18614 | 0.004313075 | 0.049423731 | 0.041768726 | AP3B1/AP3M1/BECN1/GCC2/GNPTAB/HSPA8/NCOA4/NEDD4/PIK3C3/PIK3R4/ROCK2/SNX16/VPS54/ZFYVE16 | 14 |
| BP | GO:0030835 | negative regulation of actin filament depolymerization | 12/2221 | 44/18614 | 0.004376915 | 0.049870308 | 0.042146134 | ADD3/CAPZA2/EPS8/LIMA1/PIK3CA/RDX/SCIN/SPTAN1/SVIL/SWAP70/TMOD2/TWF1 | 12 |
| BP | GO:0045022 | early endosome to late endosome transport | 12/2221 | 44/18614 | 0.004376915 | 0.049870308 | 0.042146134 | BECN1/DNAJC13/EEA1/EZR/HOOK1/HOOK3/KIF16B/MTMR2/PIK3C3/PIK3R4/RDX/SNX16 | 12 |
| BP | GO:1904646 | cellular response to amyloid-beta | 12/2221 | 44/18614 | 0.004376915 | 0.049870308 | 0.042146134 | MIRLET7F1/CACNA2D1/CASP4/CD36/EPHA4/IGF1/ITGA4/PARP1/SNX6/TLR4/TLR6/VCAM1 | 12 |
| BP | GO:0032147 | activation of protein kinase activity | 23/2221 | 109/18614 | 0.004396085 | 0.049994039 | 0.042250702 | BORA/ECT2/KIF14/TPX2/ANGPT1/CAB39/CCDC88A/CD86/DLG1/IGF1/IL18/ITGB3/JAK2/MALT1/MAP3K7/OSBPL8/PDGFC/PIBF1/PPP2R3C/TLR3/TLR6/TNFSF15/TOM1L1 | 23 |
| BP | GO:2001022 | positive regulation of response to DNA damage stimulus | 32/2221 | 167/18614 | 0.004437935 | 0.050374744 | 0.042572441 | BRCA1/RAD51AP1/ACTR2/ACTR8/ARID2/ATM/ATR/BCLAF1/BRCC3/BRD7/DDX5/DHX9/EPC2/ERCC6/FMR1/FXR1/HMGB1/ING3/MORF4L2/PARP1/PBRM1/PLA2R1/PRKDC/RBBP8/RIF1/SETMAR/SKIL/SMCHD1/SPIRE1/UCHL5/USP1/WDR48 | 32 |
| BP | GO:0031056 | regulation of histone modification | 28/2221 | 141/18614 | 0.00448541 | 0.050755584 | 0.042894295 | BRCA1/CHEK1/DEK/BAZ1B/CTNNB1/CTR9/DDX21/ERCC6/ING2/IWS1/LRRK2/MTF2/NIPBL/OGT/PAXBP1/PRKD1/RIF1/RNF20/RTF1/SDR16C5/SETD7/SF3B1/SMARCA5/SNW1/TAF7/TRIP12/UBR5/ZZZ3 | 28 |
| BP | GO:0050729 | positive regulation of inflammatory response | 30/2221 | 154/18614 | 0.00448836 | 0.050755584 | 0.042894295 | SUCNR1/AIM2/BTK/C3/CASP1/CASP4/CLOCK/CNR1/DHX9/IL18/IL6ST/ITGA2/JAK2/LPL/LRRK2/MIR142/MIR181B1/MMP8/NAIP/NLRC4/NLRP3/OSMR/PDCD4/PIK3CG/PTGS2/RIPK1/STAP1/TLR2/TLR3/TLR4 | 30 |
| BP | GO:0098900 | regulation of action potential | 15/2221 | 61/18614 | 0.004541556 | 0.051260791 | 0.043321252 | AKAP9/ANK2/ATP2A2/CACNA2D1/CD36/CNR1/CXADR/DLG1/DSC2/DSG2/DSP/FMR1/PKP2/RYR2/SCN9A | 15 |
| BP | GO:0061136 | regulation of proteasomal protein catabolic process | 36/2221 | 194/18614 | 0.004605943 | 0.051876599 | 0.04384168 | PBK/XPO1/ANKIB1/ARIH1/FMR1/GCLC/HECTD1/HSP90AB1/LRRK2/MDM2/MTM1/NFE2L2/NUB1/OGT/PHF20L1/PSMC1/PSMC2/PSMC6/PSMD14/RNF14/RNF19A/RNF217/RYBP/SDCBP/SOCS4/TAF1/TMF1/TMTC3/UCHL5/UFL1/USP13/USP14/USP25/USP7/USP9X/VCP | 36 |
| BP | GO:0034109 | homotypic cell-cell adhesion | 21/2221 | 97/18614 | 0.004630607 | 0.051876599 | 0.04384168 | ANK3/CXADR/DSC2/DSG2/DSP/HBB/IL6ST/ITGB3/JAK1/JAK2/LYN/METAP1/MMRN1/PDGFRA/PIK3CB/PIK3CG/PKP2/RDX/SLC7A11/STXBP3/VCL | 21 |
| BP | GO:0099175 | regulation of postsynapse organization | 21/2221 | 97/18614 | 0.004630607 | 0.051876599 | 0.04384168 | ADAM10/CAPRIN1/CAPRIN2/CDH2/CDKL5/DHX36/EPHA4/HSPA8/IL1RAP/LRP8/LRRK2/LRRTM2/MIR30B/NF1/NLGN1/NRCAM/PTPRD/RPS6KA5/SIPA1L1/TANC2/VPS35 | 21 |
| BP | GO:1903321 | negative regulation of protein modification by small protein conjugation or removal | 21/2221 | 97/18614 | 0.004630607 | 0.051876599 | 0.04384168 | BUB1B/FBXO5/MAD2L1/PRMT3/CAPN3/CTNNB1/DCUN1D3/DNAJA1/DTX3L/GCLC/GTPBP4/IVNS1ABP/OGT/PLAA/SPOPL/TAF1/TRIM44/TRIP12/UBR5/UFL1/USP44 | 21 |
| BP | GO:0002755 | MyD88-dependent toll-like receptor signaling pathway | 7/2221 | 19/18614 | 0.004667747 | 0.052002159 | 0.043947794 | BTK/HSPD1/IRAK3/IRAK4/MAP3K7/TLR4/TLR6 | 7 |
| BP | GO:0006379 | mRNA cleavage | 7/2221 | 19/18614 | 0.004667747 | 0.052002159 | 0.043947794 | CPSF2/CPSF3/CSTF3/NCBP1/NCBP2/NUDT21/PCF11 | 7 |
| BP | GO:0045947 | negative regulation of translational initiation | 7/2221 | 19/18614 | 0.004667747 | 0.052002159 | 0.043947794 | BANK1/EIF2AK3/EIF2AK4/EIF2S1/EIF3E/FMR1/TPR | 7 |
| BP | GO:0043631 | RNA polyadenylation | 11/2221 | 39/18614 | 0.00473566 | 0.052564075 | 0.044422677 | AHCYL1/CPSF2/CPSF3/CSTF3/LEO1/NUDT21/PAPOLA/PAPOLG/PCF11/PNPT1/YTHDC1 | 11 |
| BP | GO:0046329 | negative regulation of JNK cascade | 11/2221 | 39/18614 | 0.00473566 | 0.052564075 | 0.044422677 | AIDA/CYLD/DNAJA1/FKTN/HIPK3/MECOM/NCOR1/PDCD4/TAOK3/ZMYND11/ZNF675 | 11 |
| BP | GO:0019362 | pyridine nucleotide metabolic process | 18/2221 | 79/18614 | 0.004794768 | 0.052927197 | 0.044729557 | ME1/ME2/ALDH1L2/CD38/FMO1/FMO5/IDH1/KMO/KYNU/LDHB/MDH1/NNT/NUDT12/PARP9/PGD/RPE/SLC5A8/VCP | 18 |
| BP | GO:0046496 | nicotinamide nucleotide metabolic process | 18/2221 | 79/18614 | 0.004794768 | 0.052927197 | 0.044729557 | ME1/ME2/ALDH1L2/CD38/FMO1/FMO5/IDH1/KMO/KYNU/LDHB/MDH1/NNT/NUDT12/PARP9/PGD/RPE/SLC5A8/VCP | 18 |
| BP | GO:2000736 | regulation of stem cell differentiation | 18/2221 | 79/18614 | 0.004794768 | 0.052927197 | 0.044729557 | EZH2/HDAC2/CHD4/DHX36/EIF2AK2/HNRNPU/HSPA9/KDM3A/KDM4C/NFE2L2/NSUN2/NUDT21/PDGFRA/PRKDC/PUS7/PWP1/SOX5/TRIM6 | 18 |
| BP | GO:0002285 | lymphocyte activation involved in immune response | 38/2221 | 208/18614 | 0.00481949 | 0.05310266 | 0.044877843 | ATAD5/MSH2/ATP7A/CD180/CD86/CLEC4D/CR1/DOCK10/DOCK11/EIF2AK4/ENTPD7/FCGR3A/FGL2/GAPT/HAVCR2/HMGB1/HSPD1/IL18/LCP1/LIG4/MALT1/MLH1/MSH6/NBN/NCKAP1L/NLRP3/PHF14/PTPRC/RAB27A/RC3H2/RIF1/RIPK2/RORA/SWAP70/TFRC/THOC1/TLR4/TP53BP1 | 38 |
| BP | GO:0040029 | epigenetic regulation of gene expression | 35/2221 | 188/18614 | 0.004891042 | 0.053792521 | 0.045460854 | BRCA1/CHEK1/EZH2/HELLS/ARID4A/ARID4B/ATF7IP/ATRX/BAZ1A/BRD7/CTR9/HAT1/HMGB1/HNRNPU/IFI16/KDM5A/L3MBTL3/LMNB1/LRIF1/OGT/PIK3CA/RB1/RBBP5/RIF1/SETDB2/SMARCA5/SMCHD1/SPTY2D1/SUZ12/TPR/UBR2/USP7/YTHDC1/ZDBF2/ZNFX1 | 35 |
| BP | GO:0038061 | NIK/NF-kappaB signaling | 28/2221 | 142/18614 | 0.004966248 | 0.054519979 | 0.04607564 | BIRC2/BIRC3/CD86/CHUK/CYLD/DDX3X/DICER1/EIF2AK2/HAVCR2/IL18/MALT1/MAP3K7/MIR15B/MIR30C2/MMP8/NFAT5/NLRP3/PDCD4/PPM1B/RC3H2/REL/TLR2/TLR3/TLR4/TLR6/TNFSF15/TRIM44/UACA | 28 |
| BP | GO:0050869 | negative regulation of B cell activation | 10/2221 | 34/18614 | 0.005026138 | 0.055076947 | 0.046546342 | ATM/BANK1/BTK/CASP3/CR1/INHBA/LYN/MNDA/SAMSN1/THOC1 | 10 |
| BP | GO:0032528 | microvillus organization | 8/2221 | 24/18614 | 0.005112122 | 0.055917322 | 0.047256556 | ATP8B1/EZR/PLD1/PLS1/PTPN11/RAPGEF2/RAPGEF6/TNIK | 8 |
| BP | GO:0000469 | cleavage involved in rRNA processing | 9/2221 | 29/18614 | 0.005184212 | 0.056276243 | 0.047559885 | BMS1/ERI1/ERI2/EXOSC9/RRS1/SDE2/TSR1/UTP20/UTP23 | 9 |
| BP | GO:0010575 | positive regulation of vascular endothelial growth factor production | 9/2221 | 29/18614 | 0.005184212 | 0.056276243 | 0.047559885 | BRCA1/C3/C5/EIF2AK3/HIF1A/IL6ST/PTGS2/RORA/SULF1 | 9 |
| BP | GO:0006479 | protein methylation | 34/2221 | 182/18614 | 0.005191708 | 0.056276243 | 0.047559885 | BRCA1/EZH2/PRMT3/ARID4A/ARID4B/ASH1L/BOD1L1/CTNNB1/CTR9/ETF1/FAM98A/FBXO11/GSPT1/HCFC2/IWS1/KDM6A/KMT2C/METTL18/MTF2/OGT/PAXBP1/PRMT9/RBBP5/RIF1/RLF/RNF20/RTF1/SETD7/SETDB2/SETMAR/SMARCA5/SNW1/SUV39H2/SUZ12 | 34 |
| BP | GO:0008213 | protein alkylation | 34/2221 | 182/18614 | 0.005191708 | 0.056276243 | 0.047559885 | BRCA1/EZH2/PRMT3/ARID4A/ARID4B/ASH1L/BOD1L1/CTNNB1/CTR9/ETF1/FAM98A/FBXO11/GSPT1/HCFC2/IWS1/KDM6A/KMT2C/METTL18/MTF2/OGT/PAXBP1/PRMT9/RBBP5/RIF1/RLF/RNF20/RTF1/SETD7/SETDB2/SETMAR/SMARCA5/SNW1/SUV39H2/SUZ12 | 34 |
| BP | GO:0043484 | regulation of RNA splicing | 34/2221 | 182/18614 | 0.005191708 | 0.056276243 | 0.047559885 | CCNL1/CLK4/CWC22/DDX5/FMR1/FXR1/HNRNPA1/HNRNPA2B1/HNRNPH2/HNRNPH3/HNRNPU/HSPA8/LARP7/NCBP1/NCL/NSRP1/PIK3R1/PTBP2/RBM25/RBM39/SETX/SLC38A2/SMU1/SNW1/SON/SRPK1/SRPK2/SRSF10/SUPT20H/WTAP/YTHDC1/ZNF326/ZNF638/ZPR1 | 34 |
| BP | GO:0007019 | microtubule depolymerization | 12/2221 | 45/18614 | 0.00533295 | 0.057496462 | 0.04859111 | KIF18A/TPX2/APC/CAMSAP2/CKAP2/CKAP5/CLASP2/KIF2A/MAP1B/NAV3/TAOK1/WDR47 | 12 |
| BP | GO:0032781 | positive regulation of ATP-dependent activity | 12/2221 | 45/18614 | 0.00533295 | 0.057496462 | 0.04859111 | MSH2/ATP1B1/DHX9/DNAJC10/HNRNPU/MSH3/MSH6/POT1/RYR2/SETMAR/TOR1AIP2/TPM1 | 12 |
| BP | GO:1902116 | negative regulation of organelle assembly | 12/2221 | 45/18614 | 0.00533295 | 0.057496462 | 0.04859111 | BRCA1/BECN1/CCP110/CDK5RAP2/CEP97/GDI2/LRRK2/MPHOSPH9/MTM1/ODF2L/SCFD1/TBC1D30 | 12 |
| BP | GO:0009791 | post-embryonic development | 20/2221 | 92/18614 | 0.005366544 | 0.057755146 | 0.048809727 | ACADM/ACO1/ARID5B/ASH1L/ATM/ATRX/CCDC47/FBN1/GIGYF2/IREB2/ITPR1/JAK2/KDM5B/MYO1E/RC3H2/SCN9A/SEMA3C/TGFBR1/TIPARP/VPS54 | 20 |
| BP | GO:2000134 | negative regulation of G1/S transition of mitotic cell cycle | 19/2221 | 86/18614 | 0.005458024 | 0.05817943 | 0.049168297 | EZH2/APC/ATM/BRD7/DCUN1D3/DLG1/GIGYF2/GPNMB/INHBA/JADE1/MDM2/MIR15B/MIR30C2/PRKDC/RB1/RBL2/RFWD3/SDE2/SLFN11 | 19 |
| BP | GO:0006997 | nucleus organization | 28/2221 | 143/18614 | 0.00548949 | 0.05817943 | 0.049168297 | CDK1/CHEK1/VRK1/AHCTF1/CHMP2B/GOLM1/HMGB2/KDM3A/LMNB1/NOLC1/NUP107/NUP133/NUP153/NUP155/NUP205/PITPNB/POLR1B/PSME4/SERBP1/SMARCA5/SRPK1/SRPK2/SYNE1/TMF1/TPR/UBXN2B/USPL1/ZPR1 | 28 |
| BP | GO:0006271 | DNA strand elongation involved in DNA replication | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | MCM3/RFC3/RFC4/DNA2/POLA1/POLD3 | 6 |
| BP | GO:0007135 | meiosis II | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | BUB1/BUB1B/MASTL/RAD21/SMC1A/SMC3 | 6 |
| BP | GO:0010225 | response to UV-C | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | BRCA2/DCUN1D3/ERCC5/IMPACT/MAP3K4/WRN | 6 |
| BP | GO:0061983 | meiosis II cell cycle process | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | BUB1/BUB1B/MASTL/RAD21/SMC1A/SMC3 | 6 |
| BP | GO:0072520 | seminiferous tubule development | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | BRIP1/KIF18A/ATRX/ING2/SCAPER/WDR48 | 6 |
| BP | GO:0090110 | COPII-coated vesicle cargo loading | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | MIA3/RAB1A/SEC23A/SEC23B/SEC24D/SEC31A | 6 |
| BP | GO:0098760 | response to interleukin-7 | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | ATIC/BTK/HSPD1/IL7R/PDIA3/STIP1 | 6 |
| BP | GO:0098761 | cellular response to interleukin-7 | 6/2221 | 15/18614 | 0.005505008 | 0.05817943 | 0.049168297 | ATIC/BTK/HSPD1/IL7R/PDIA3/STIP1 | 6 |
| BP | GO:0140056 | organelle localization by membrane tethering | 18/2221 | 80/18614 | 0.005512346 | 0.05817943 | 0.049168297 | AHCYL1/ATP2A2/BLOC1S6/CEP83/CFTR/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/PDZD8/RAB3IP/RAB8B/SNAP25/STX17/STXBP3/SYTL2/USO1 | 18 |
| BP | GO:0051403 | stress-activated MAPK cascade | 42/2221 | 237/18614 | 0.005526723 | 0.058229012 | 0.049210199 | PBK/AIDA/CYLD/DLG1/DNAJA1/EIF2AK2/ERCC6/EZR/FAS/FKTN/HGF/HIPK3/HMGB1/IRAK4/LRRK2/MAP3K13/MAP3K4/MAP3K7/MAP4K4/MAPK10/MECOM/MIR181B1/MMP8/NAIP/NCOR1/PDCD4/PJA2/PLCB1/RB1CC1/RIPK1/RIPK2/SDCBP/SEMA3A/TAOK1/TAOK3/TLR3/TLR4/TNIK/TRAF5/ZMYND11/ZNF622/ZNF675 | 42 |
| BP | GO:0002764 | immune response-regulating signaling pathway | 72/2221 | 450/18614 | 0.005687913 | 0.059822524 | 0.050556899 | AIM2/ALPK1/ANKRD17/AP3B1/BANK1/BIRC2/BIRC3/BMX/BTK/CASP1/CD226/CD36/CD38/CLEC4D/COLEC12/CR1/CTSS/CYLD/DDX3X/DDX60/EIF2B3/ELF1/EZR/FCGR3A/FER/GBP1/HAVCR2/HMGB1/HSPD1/IFIH1/IRAK3/IRAK4/ITK/LACC1/LYN/MALT1/MAP3K1/MAP3K7/MAPK10/MEF2C/MNDA/NAIP/NCKAP1L/NLRC4/NLRP3/OTUD4/PDE4B/PDE4D/PIK3AP1/PIK3CA/PJA2/PTPN2/PTPRC/PUM2/RAB11FIP2/RABGEF1/RC3H2/RIOK3/RIPK2/RPS6KA3/SLC39A10/SOS1/STAP1/TEC/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/USP15/YES1 | 72 |
| BP | GO:0061351 | neural precursor cell proliferation | 29/2221 | 150/18614 | 0.005744262 | 0.060227186 | 0.050898885 | ASPM/KIF14/MELK/SHCBP1/CDH2/CDON/CEP120/CTNNA1/CTNNB1/DOCK7/EGF/FRS2/HIF1A/HOOK3/ITGB1/LNX2/LRP2/LRRK2/LYN/NAP1L1/NBN/NF1/ORC3/PCM1/PTBP2/RACGAP1/RORA/SOX5/WDR47 | 29 |
| BP | GO:0032784 | regulation of DNA-templated transcription elongation | 22/2221 | 105/18614 | 0.00574641 | 0.060227186 | 0.050898885 | EZH2/CCNT1/CCNT2/CTNNB1/ELL2/ERCC6/HNRNPU/HTATSF1/INTS12/INTS6/INTS7/LARP7/LEO1/MED23/MED6/NCBP1/NCBP2/SUPT16H/THOC1/WDR43/ZMYND11/ZNF326 | 22 |
| BP | GO:0060612 | adipose tissue development | 13/2221 | 51/18614 | 0.005771297 | 0.060382823 | 0.051030416 | ACAT1/ARID5B/ARRDC3/NCOA1/NCOA2/OXCT1/PIK3CA/PPARG/PUM2/RASAL2/SH3PXD2B/TBL1XR1/VPS13B | 13 |
| BP | GO:0016233 | telomere capping | 11/2221 | 40/18614 | 0.005841013 | 0.060900411 | 0.051467837 | NEK2/ATM/DCLRE1A/ERCC4/MAP3K4/NBN/POT1/PRKDC/RAD50/TNKS2/USP7 | 11 |
| BP | GO:1903115 | regulation of actin filament-based movement | 11/2221 | 40/18614 | 0.005841013 | 0.060900411 | 0.051467837 | AKAP9/ANK2/ATP2A2/DLG1/DSC2/DSG2/DSP/PDE4B/PDE4D/PKP2/RYR2 | 11 |
| BP | GO:0010998 | regulation of translational initiation by eIF2 alpha phosphorylation | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | DNAJC3/EIF2AK2/EIF2AK3/EIF2AK4/NCK1 | 5 |
| BP | GO:0019065 | receptor-mediated endocytosis of virus by host cell | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | ACE2/CTSL/DPP4/EPS15/PIKFYVE | 5 |
| BP | GO:0036490 | regulation of translation in response to endoplasmic reticulum stress | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | DDX3X/DNAJC3/EIF2AK3/EIF2AK4/NCK1 | 5 |
| BP | GO:0042276 | error-prone translesion synthesis | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | POLD3/POLK/REV1/REV3L/USP1 | 5 |
| BP | GO:0046349 | amino sugar biosynthetic process | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | GFPT1/GNPDA2/GNPNAT1/PGM3/UAP1 | 5 |
| BP | GO:0046710 | GDP metabolic process | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | CASK/DLG1/DLG2/MAGI3/MPP1 | 5 |
| BP | GO:0097278 | complement-dependent cytotoxicity | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | C3/CFH/CR1/CR1L/RAB27A | 5 |
| BP | GO:0110011 | regulation of basement membrane organization | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | CLASP2/LAMA2/LAMB1/LAMC1/PHLDB2 | 5 |
| BP | GO:1903564 | regulation of protein localization to cilium | 5/2221 | 11/18614 | 0.005976163 | 0.061352556 | 0.051849952 | CCDC66/CCDC88A/EFCAB7/GDI2/LZTFL1 | 5 |
| BP | GO:0031098 | stress-activated protein kinase signaling cascade | 43/2221 | 245/18614 | 0.006003148 | 0.061524601 | 0.05199535 | PBK/AIDA/CYLD/DLG1/DNAJA1/EIF2AK2/ERCC6/EZR/FAS/FKTN/HGF/HIPK3/HMGB1/IRAK4/LRRK2/LYN/MAP3K13/MAP3K4/MAP3K7/MAP4K4/MAPK10/MECOM/MIR181B1/MMP8/NAIP/NCOR1/PDCD4/PJA2/PLCB1/RB1CC1/RIPK1/RIPK2/SDCBP/SEMA3A/TAOK1/TAOK3/TLR3/TLR4/TNIK/TRAF5/ZMYND11/ZNF622/ZNF675 | 43 |
| BP | GO:0008584 | male gonad development | 28/2221 | 144/18614 | 0.006057939 | 0.061980548 | 0.052380677 | ASPM/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ATRX/CSDE1/CTNNA1/EIF2S2/FER/FNDC3A/HMGB2/HSD17B4/ING2/INHBA/LRP2/NASP/NCOA4/PDGFRA/RHOBTB3/SCAPER/TGFBR1/TLR3/TMF1/WDR48/ZFPM2 | 28 |
| BP | GO:0034644 | cellular response to UV | 20/2221 | 93/18614 | 0.006088127 | 0.062183658 | 0.052552328 | CHEK1/PBK/ATR/DHX36/EIF2AK4/EIF2S1/ERCC4/IMPACT/MMP1/NEDD4/PARP1/PIK3R1/POLD3/POLK/PTGS2/PTPRK/SDE2/TAF1/USP47/ZBTB1 | 20 |
| BP | GO:0032205 | negative regulation of telomere maintenance | 10/2221 | 35/18614 | 0.006297999 | 0.064109583 | 0.054179956 | ATM/ERCC4/HNRNPA1/HNRNPU/NBN/PARP1/POT1/RAD50/TNKS2/XRN1 | 10 |
| BP | GO:0035633 | maintenance of blood-brain barrier | 10/2221 | 35/18614 | 0.006297999 | 0.064109583 | 0.054179956 | ANGPT1/CLDN1/DMD/ITGB1/LAMA2/LAMC1/PTGS2/TJP1/VCL/WNK3 | 10 |
| BP | GO:0042789 | mRNA transcription by RNA polymerase II | 12/2221 | 46/18614 | 0.006447763 | 0.064795435 | 0.05475958 | AP3B1/HLTF/NCBP1/NCBP2/NCOA1/NCOA2/PPARG/TAF1/TAF2/TAF4B/TAF7/ZBTB1 | 12 |
| BP | GO:0045910 | negative regulation of DNA recombination | 12/2221 | 46/18614 | 0.006447763 | 0.064795435 | 0.05475958 | BLM/MSH2/PARPBP/POLQ/MLH1/MSH3/MSH6/RIF1/SMCHD1/THOC1/TP53BP1/ZRANB3 | 12 |
| BP | GO:0070266 | necroptotic process | 12/2221 | 46/18614 | 0.006447763 | 0.064795435 | 0.05475958 | AIFM1/BIRC2/BIRC3/CYLD/DNM1L/FAS/OGT/PARP1/PYGL/RIPK1/TLR3/TRPM7 | 12 |
| BP | GO:0001780 | neutrophil homeostasis | 7/2221 | 20/18614 | 0.00645154 | 0.064795435 | 0.05475958 | BTK/HMGB1/MERTK/MTHFD1/PDE4B/PIK3CB/SLC7A11 | 7 |
| BP | GO:0008340 | determination of adult lifespan | 7/2221 | 20/18614 | 0.00645154 | 0.064795435 | 0.05475958 | MSH2/RAD54B/ATM/IDE/LRRK2/MSH6/TFCP2L1 | 7 |
| BP | GO:0009168 | purine ribonucleoside monophosphate biosynthetic process | 7/2221 | 20/18614 | 0.00645154 | 0.064795435 | 0.05475958 | ADK/ATIC/GART/GMPS/IMPDH2/PAICS/PPAT | 7 |
| BP | GO:0010878 | cholesterol storage | 7/2221 | 20/18614 | 0.00645154 | 0.064795435 | 0.05475958 | ABCA1/CD36/LPL/MSR1/PPARG/STARD4/TTC39B | 7 |
| BP | GO:0046931 | pore complex assembly | 7/2221 | 20/18614 | 0.00645154 | 0.064795435 | 0.05475958 | ADAM10/AHCTF1/CCT3/CCT8/NUP107/NUP153/NUP205 | 7 |
| BP | GO:0051222 | positive regulation of protein transport | 52/2221 | 309/18614 | 0.00648521 | 0.065025042 | 0.054953624 | CDK1/ECT2/KIF20B/ACSL3/ACSL4/ADAM9/AKAP5/ANK3/ATP2C1/C2CD5/CD2AP/CD38/CEP290/CFTR/CNST/CTDSPL2/DNM1L/EFCAB7/EXOC1/EXPH5/EZR/HIF1A/HSP90AA1/ICE1/IGF1/IPO5/ITPR1/JAK2/MYOM1/OSBP/OXCT1/PCM1/PCSK1/PFKFB2/PIK3R1/PLCB1/PPARG/PRKD1/PTGS2/RAPGEF4/RUFY3/SAR1B/SH3GLB1/TLR2/TLR4/TPR/TTN/UBR5/VPS35/XPO4/ZFAND1/ZPR1 | 52 |
| BP | GO:0000302 | response to reactive oxygen species | 37/2221 | 205/18614 | 0.006545583 | 0.065521181 | 0.055372918 | CDK1/ECT2/EZH2/HDAC2/ADAM9/AIFM1/ARG1/ATP7A/BECN1/BTK/CASP3/CD36/CHUK/ERCC6/ERCC6L2/FER/HBA2/HBB/HGF/HIF1A/HP/IL18RAP/IMPACT/LRRK2/MET/NET1/NFE2L2/OSER1/PDGFD/PDGFRA/PTPRK/RIPK1/SESN3/SETX/STAT1/TPM1/ZNF277 | 37 |
| BP | GO:0031114 | regulation of microtubule depolymerization | 9/2221 | 30/18614 | 0.006635614 | 0.066041874 | 0.055812964 | TPX2/APC/CAMSAP2/CKAP2/CLASP2/MAP1B/NAV3/TAOK1/WDR47 | 9 |
| BP | GO:0043032 | positive regulation of macrophage activation | 9/2221 | 30/18614 | 0.006635614 | 0.066041874 | 0.055812964 | HAVCR2/HSPD1/LRRK2/MIR142/MMP8/PLA2G4A/STAP1/TLR4/TLR6 | 9 |
| BP | GO:0070498 | interleukin-1-mediated signaling pathway | 9/2221 | 30/18614 | 0.006635614 | 0.066041874 | 0.055812964 | IL1R1/IRAK3/IRAK4/MAP3K7/OTUD4/PLCB1/RPS6KA5/VRK2/ZNF675 | 9 |
| BP | GO:0099111 | microtubule-based transport | 38/2221 | 212/18614 | 0.006641512 | 0.066041874 | 0.055812964 | KIF4A/AP3B1/AP3M1/AQP4/ARHGAP21/BLOC1S6/DLG2/DNAH5/DST/DYNC1H1/DYNC2H1/HIF1A/HNRNPU/HSPA8/IFT57/IFT74/IFT80/KIF3A/KIF5B/LCA5/LRPPRC/MAP1B/OFD1/OPA1/PCM1/RAB1A/RAB27B/RABGEF1/RHOT1/RPGR/SPG11/SSX2IP/SYBU/SYNE2/TRAK2/TTC21B/WDR19/WDR35 | 38 |
| BP | GO:0006760 | folic acid-containing compound metabolic process | 8/2221 | 25/18614 | 0.006744095 | 0.066731043 | 0.056395391 | ALDH1L2/ATIC/GART/MTHFD1/MTHFD1L/MTHFD2/MTRR/SLC25A32 | 8 |
| BP | GO:0034453 | microtubule anchoring | 8/2221 | 25/18614 | 0.006744095 | 0.066731043 | 0.056395391 | BCCIP/CEP350/CLASP2/GCC2/HOOK3/KIF3A/NIN/PCM1 | 8 |
| BP | GO:0035336 | long-chain fatty-acyl-CoA metabolic process | 8/2221 | 25/18614 | 0.006744095 | 0.066731043 | 0.056395391 | ELOVL6/ACSL1/ACSL3/ACSL4/ELOVL2/ELOVL7/FAR1/FAR2 | 8 |
| BP | GO:1990928 | response to amino acid starvation | 13/2221 | 52/18614 | 0.006872602 | 0.067890923 | 0.057375623 | BECN1/EIF2A/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/FAS/IMPACT/MIOS/PRKD1/SESN3/SH3GLB1/SLC38A2 | 13 |
| BP | GO:0060271 | cilium assembly | 60/2221 | 367/18614 | 0.006923222 | 0.068278855 | 0.05770347 | CEP135/PLK4/ABCC4/ACTR2/ACTR3/AHI1/ALPK1/ARL13B/ATG3/ATP6V1D/CC2D2A/CCDC66/CCDC88A/CCP110/CDKL5/CENPJ/CEP120/CEP162/CEP290/CEP350/CEP70/CEP83/CEP97/CYLD/DNAH5/DYNC2H1/EXOC5/FNBP1L/FSIP2/GDI2/GORAB/IFT57/IFT74/IFT80/IQCB1/IQCG/KIAA0586/KIF3A/MAPRE1/MKKS/MNS1/MPHOSPH9/ODF2L/OFD1/PCM1/PIBF1/RAB3IP/RP2/RPGR/RPGRIP1L/SDCCAG8/SNX10/SPAG1/SSX2IP/SYNE2/TBC1D30/TTC21B/WDR11/WDR19/WDR35 | 60 |
| BP | GO:0051701 | biological process involved in interaction with host | 37/2221 | 206/18614 | 0.007085313 | 0.06976308 | 0.05895781 | CDK1/ACE2/BECN1/CD86/CHMP2B/CLDN1/CR1/CTSL/CXADR/DPP4/EPS15/EXOC2/GYPA/HMGB1/HSP90AB1/HTR2A/IDE/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/KPNA3/MRC1/NPC1/NUP153/PIKFYVE/TCP1/TFRC/THOC1/THOC2/TRIM22/TRIM38/TRIM59/TRIM6/WWP1/ZNF502 | 37 |
| BP | GO:0031062 | positive regulation of histone methylation | 11/2221 | 41/18614 | 0.00713946 | 0.070005301 | 0.059162515 | BRCA1/CTNNB1/CTR9/MTF2/OGT/PAXBP1/RIF1/RNF20/RTF1/SMARCA5/SNW1 | 11 |
| BP | GO:1902275 | regulation of chromatin organization | 11/2221 | 41/18614 | 0.00713946 | 0.070005301 | 0.059162515 | MKI67/ATF7IP/BAZ1A/CTR9/HNRNPU/L3MBTL3/MLLT3/PIK3CA/SETDB2/TLK1/TPR | 11 |
| BP | GO:0090329 | regulation of DNA-templated DNA replication | 14/2221 | 58/18614 | 0.007144823 | 0.070005301 | 0.059162515 | BLM/BRCA2/FBXO5/GMNN/MCM3/MCM6/RFC3/RFC4/TICRR/ATRX/DBF4/NBN/SLFN11/ZRANB3 | 14 |
| BP | GO:0051568 | histone H3-K4 methylation | 15/2221 | 64/18614 | 0.007292123 | 0.071332379 | 0.060284048 | BRCA1/ARID4A/ASH1L/BOD1L1/CTNNB1/CTR9/HCFC2/KDM6A/KMT2C/OGT/RBBP5/RLF/RTF1/SETMAR/SNW1 | 15 |
| BP | GO:0150076 | neuroinflammatory response | 17/2221 | 76/18614 | 0.007305978 | 0.071351894 | 0.06030054 | ATM/BPGM/IFNGR1/IGF1/IL18/ITGB1/JAK2/LRRK2/MIR142/MIR181B1/MMP8/PTGS2/PTPRC/STAP1/TLR2/TLR3/VPS54 | 17 |
| BP | GO:0043112 | receptor metabolic process | 16/2221 | 70/18614 | 0.007338918 | 0.071473347 | 0.060403182 | AP1AR/ARFGEF2/BECN1/DTX3L/FUT8/KIF16B/MTMR2/NEDD4/NSF/PEX1/PIK3R4/PTPN2/REP15/SH3GLB1/SNX25/USP9X | 16 |
| BP | GO:0010508 | positive regulation of autophagy | 28/2221 | 146/18614 | 0.007342176 | 0.071473347 | 0.060403182 | ATF6/BECN1/BNIP3L/C9orf72/GNAI3/HIF1A/HMGB1/LRRK2/MAP3K7/MTDH/PIK3C2A/PIK3CB/PRKD1/RAB3GAP1/RAB3GAP2/RB1CC1/RIPK2/ROCK1/SESN3/SH3GLB1/SNX30/SPTLC1/TBK1/TRIM22/TRIM38/TRIM6/UFL1/VPS13D | 28 |
| BP | GO:0016197 | endosomal transport | 43/2221 | 248/18614 | 0.007450339 | 0.072409111 | 0.06119401 | ABCA1/ACAP2/AKAP5/ALMS1/ANKRD50/CCDC93/CHMP2B/CLTC/CORO1C/DCLK1/EEA1/EPS15/ERC1/EVI5/GCC2/GOLT1B/HEATR5A/HEATR5B/ITSN1/ITSN2/LRRK2/LYST/PIKFYVE/PREPL/RASSF9/RHOBTB3/SNX2/SNX30/SNX6/SNX9/SPAG9/STAM2/TBC1D23/TMEM87A/USP7/VCP/VPS13B/VPS26A/VPS35/VPS54/VTA1/ZFYVE16/ZFYVE9 | 43 |
| BP | GO:0046718 | viral entry into host cell | 29/2221 | 153/18614 | 0.007614121 | 0.073881531 | 0.062438374 | CDK1/ACE2/CD86/CLDN1/CR1/CTSL/CXADR/DPP4/EPS15/GYPA/HMGB1/HTR2A/IDE/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/KPNA3/MRC1/NPC1/NUP153/PIKFYVE/TFRC/TRIM22/TRIM38/TRIM59/TRIM6/WWP1 | 29 |
| BP | GO:0006984 | ER-nucleus signaling pathway | 12/2221 | 47/18614 | 0.007738635 | 0.074838781 | 0.06324736 | AGR2/ATF6/ATP2A2/CCDC47/EIF2A/EIF2AK3/EIF2S1/ERLIN1/HSPA5/NCK1/NFE2L2/PTPN2 | 12 |
| BP | GO:0098927 | vesicle-mediated transport between endosomal compartments | 12/2221 | 47/18614 | 0.007738635 | 0.074838781 | 0.06324736 | BECN1/DNAJC13/EEA1/EZR/HOOK1/HOOK3/KIF16B/MTMR2/PIK3C3/PIK3R4/RDX/SNX16 | 12 |
| BP | GO:0006282 | regulation of DNA repair | 38/2221 | 214/18614 | 0.007750093 | 0.074838781 | 0.06324736 | BRCA1/CHEK1/DEK/PARPBP/POLQ/RAD51AP1/ACTR2/ACTR8/ARID2/ATR/BRCC3/BRD7/DHX9/EPC2/ERCC6/FIGNL1/HMGB1/ING3/MORF4L2/PARP1/PBRM1/POT1/PPP4R2/PRKDC/RBBP8/RIF1/SETMAR/SMCHD1/SPIRE1/SUPT20H/TAF2/TAF7/TP53BP1/TRIP12/UBR5/UCHL5/USP1/WDR48 | 38 |
| BP | GO:0043648 | dicarboxylic acid metabolic process | 20/2221 | 95/18614 | 0.00776971 | 0.074907974 | 0.063305836 | ME1/ME2/AASDHPPT/ALDH18A1/ALDH1L2/ATIC/FH/GCLC/IDH1/KMO/KYNU/MDH1/MTHFD1/MTHFD1L/MTHFD2/MTRR/SLC25A12/SLC25A32/SLC7A11/SUCLA2 | 20 |
| BP | GO:0035520 | monoubiquitinated protein deubiquitination | 10/2221 | 36/18614 | 0.007806369 | 0.075140986 | 0.063502758 | MYSM1/SUPT20H/TAF2/TAF7/USP1/USP15/USP16/USP47/USP7/USP9X | 10 |
| BP | GO:0044409 | entry into host | 30/2221 | 160/18614 | 0.00785929 | 0.075529533 | 0.063831124 | CDK1/ACE2/CD86/CLDN1/CR1/CTSL/CXADR/DPP4/EPS15/EXOC2/GYPA/HMGB1/HTR2A/IDE/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/KPNA3/MRC1/NPC1/NUP153/PIKFYVE/TFRC/TRIM22/TRIM38/TRIM59/TRIM6/WWP1 | 30 |
| BP | GO:0015671 | oxygen transport | 6/2221 | 16/18614 | 0.007929766 | 0.075722974 | 0.063994605 | BPGM/HBA2/HBB/HBD/HBG2/IPCEF1 | 6 |
| BP | GO:0030033 | microvillus assembly | 6/2221 | 16/18614 | 0.007929766 | 0.075722974 | 0.063994605 | ATP8B1/EZR/PLD1/RAPGEF2/RAPGEF6/TNIK | 6 |
| BP | GO:0034134 | toll-like receptor 2 signaling pathway | 6/2221 | 16/18614 | 0.007929766 | 0.075722974 | 0.063994605 | LYN/PIK3AP1/PJA2/RIPK2/TLR1/TLR6 | 6 |
| BP | GO:2000104 | negative regulation of DNA-templated DNA replication | 6/2221 | 16/18614 | 0.007929766 | 0.075722974 | 0.063994605 | BLM/BRCA2/FBXO5/GMNN/SLFN11/ZRANB3 | 6 |
| BP | GO:0009259 | ribonucleotide metabolic process | 73/2221 | 464/18614 | 0.00805804 | 0.076825945 | 0.064926742 | ELOVL6/OLA1/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/ADK/ATIC/ATP1B1/ATP6V1A/ATP6V1B2/BAAT/BPGM/CASK/CLPX/CTPS1/DLD/DLG1/DLG2/DNM1L/DPYD/ELOVL2/ELOVL7/ENPP1/ENTPD7/FAR1/FAR2/FIGNL1/GART/GMPS/GNAI3/HIF1A/HK2/HMGCR/HMGCS1/HSD17B4/HSPA8/HTR2A/IGF1/IMPDH2/LRRK2/MAGI3/MFN1/MPP1/MTHFD1/NCOR1/NDUFS1/NT5C2/NT5E/OGT/OPA1/PAICS/PARP1/PDE4B/PDE4D/PDE8B/PFKFB2/PPAT/PPT1/RORA/SLC25A12/SLC25A13/SLC27A2/SLC4A1/SUCLA2/SUCLG2/SULT1B1/TDO2/UMPS/VCP | 73 |
| BP | GO:0048024 | regulation of mRNA splicing, via spliceosome | 22/2221 | 108/18614 | 0.008084603 | 0.076957238 | 0.065037699 | CWC22/DDX5/FMR1/FXR1/HNRNPA1/HNRNPA2B1/HNRNPU/HSPA8/LARP7/NCBP1/NCL/NSRP1/RBM25/RBM39/SMU1/SNW1/SON/SRPK1/SRPK2/SRSF10/WTAP/YTHDC1 | 22 |
| BP | GO:0010883 | regulation of lipid storage | 13/2221 | 53/18614 | 0.008133994 | 0.077305065 | 0.065331653 | ABCA1/C3/CD36/ITGAV/ITGB3/LPL/MSR1/OSBPL11/OSBPL8/PLIN2/PPARG/PTPN2/TTC39B | 13 |
| BP | GO:0071496 | cellular response to external stimulus | 54/2221 | 327/18614 | 0.008217466 | 0.077975201 | 0.065897995 | BRIP1/CHEK1/AIFM1/ATP2B1/BECN1/CASP1/CASP5/CASP8AP2/CTSK/DSC2/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/ERCC6/FAS/FNIP1/GCLC/HNRNPA1/HSPA5/HSPA8/IFI16/IMPACT/ITGA2/ITGA4/ITGB3/JMY/LPL/LRRK2/LYN/MAP3K1/MAP3K2/MIOS/NCOA1/NFE2L2/PHEX/PIK3C3/PIK3R4/PLIN2/POSTN/PRKD1/PTGS2/PTPRC/RICTOR/SESN3/SH3GLB1/SLC38A2/SNW1/TLR3/TLR4/TLR8/VCAM1/VPS41/WRN | 54 |
| BP | GO:0046488 | phosphatidylinositol metabolic process | 29/2221 | 154/18614 | 0.008339297 | 0.079006632 | 0.066769672 | AGPAT5/ATM/BECN1/BMX/EFR3A/FIG4/HTR2A/IMPA1/INPP4B/MTM1/MTMR2/MTMR4/MTMR6/PIGA/PIGN/PIGW/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/PIKFYVE/PIP5K1B/PLCB1/SACM1L/SOCS4 | 29 |
| BP | GO:0051654 | establishment of mitochondrion localization | 9/2221 | 31/18614 | 0.008379222 | 0.079260061 | 0.066983849 | DNM1L/HIF1A/KIF5B/LRPPRC/MAP1B/OPA1/RHOT1/SYBU/TRAK2 | 9 |
| BP | GO:0030522 | intracellular receptor signaling pathway | 50/2221 | 299/18614 | 0.008437995 | 0.079690703 | 0.067347791 | BRCA1/EZH2/ALPK1/ANKRD17/BIRC2/BIRC3/CLOCK/CNOT1/COLEC12/CYLD/CYP7B1/DDX3X/DDX5/DDX60/DNAJA1/HAVCR2/HMGB1/IFIH1/IRAK4/JAK2/KDM3A/KDM4C/LACC1/MAP3K7/NCOA1/NCOA2/NCOA4/NCOR1/NEDD4/NR1D2/PARP1/PIK3AP1/PPARG/PUM2/RIOK3/RIPK2/RNF14/RNF6/RORA/SNW1/TAF7/TLR4/TLR8/TMF1/UBA5/UBR5/UFL1/UFM1/UFSP2/USP15 | 50 |
| BP | GO:0010324 | membrane invagination | 15/2221 | 65/18614 | 0.008459003 | 0.079763887 | 0.06740964 | ABCA1/ARHGAP12/BECN1/BIN2/C3/CD36/CLCN3/FCHO2/FNBP1L/ITGA2/MSR1/NCKAP1L/SNX9/SPIRE1/STAP1 | 15 |
| BP | GO:0032434 | regulation of proteasomal ubiquitin-dependent protein catabolic process | 27/2221 | 141/18614 | 0.008533958 | 0.080344745 | 0.067900532 | PBK/XPO1/ANKIB1/ARIH1/GCLC/HECTD1/HSP90AB1/LRRK2/MDM2/MTM1/NFE2L2/NUB1/OGT/PHF20L1/RNF14/RNF19A/RNF217/RYBP/SDCBP/SOCS4/TAF1/UCHL5/UFL1/USP14/USP7/USP9X/VCP | 27 |
| BP | GO:1904375 | regulation of protein localization to cell periphery | 25/2221 | 128/18614 | 0.00863643 | 0.080861652 | 0.068337377 | AGR2/ACSL3/ADAM10/AKAP5/ATP2C1/CLTC/CNST/DLG1/EFCAB7/EPB41/EPB41L2/EPHA3/EZR/GBP1/GPSM2/HECTD1/ITGB1/KIF5B/LZTFL1/OGT/PIK3R1/PLS1/PPFIA1/PRKCI/WNK3 | 25 |
| BP | GO:0030488 | tRNA methylation | 11/2221 | 42/18614 | 0.008652419 | 0.080861652 | 0.068337377 | ALKBH8/NSUN2/NSUN6/THADA/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TRMT6/TYW3 | 11 |
| BP | GO:0002888 | positive regulation of myeloid leukocyte mediated immunity | 7/2221 | 21/18614 | 0.008696391 | 0.080861652 | 0.068337377 | ARG1/BTK/C3/DDX1/DDX21/DHX36/STAP1 | 7 |
| BP | GO:0007413 | axonal fasciculation | 7/2221 | 21/18614 | 0.008696391 | 0.080861652 | 0.068337377 | CASP3/CNR1/CNTN4/EPHA3/EPHA4/NCAM2/NRCAM | 7 |
| BP | GO:0010888 | negative regulation of lipid storage | 7/2221 | 21/18614 | 0.008696391 | 0.080861652 | 0.068337377 | ABCA1/ITGAV/ITGB3/OSBPL8/PPARG/PTPN2/TTC39B | 7 |
| BP | GO:0099515 | actin filament-based transport | 7/2221 | 21/18614 | 0.008696391 | 0.080861652 | 0.068337377 | FNBP1L/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/SYNE2 | 7 |
| BP | GO:0106030 | neuron projection fasciculation | 7/2221 | 21/18614 | 0.008696391 | 0.080861652 | 0.068337377 | CASP3/CNR1/CNTN4/EPHA3/EPHA4/NCAM2/NRCAM | 7 |
| BP | GO:1903428 | positive regulation of reactive oxygen species biosynthetic process | 7/2221 | 21/18614 | 0.008696391 | 0.080861652 | 0.068337377 | CD36/CLCN3/MMP8/RAB27A/SLC5A3/TLR4/TLR6 | 7 |
| BP | GO:0044346 | fibroblast apoptotic process | 8/2221 | 26/18614 | 0.008740884 | 0.081024894 | 0.068475336 | XRCC2/API5/CASP3/CHD8/CUL3/MIR181B1/PIK3CA/PIK3CG | 8 |
| BP | GO:1904353 | regulation of telomere capping | 8/2221 | 26/18614 | 0.008740884 | 0.081024894 | 0.068475336 | NEK2/ATM/ERCC4/MAP3K4/NBN/RAD50/TNKS2/USP7 | 8 |
| BP | GO:0019693 | ribose phosphate metabolic process | 74/2221 | 473/18614 | 0.008758862 | 0.081066639 | 0.068510615 | ELOVL6/OLA1/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/ADK/ATIC/ATP1B1/ATP6V1A/ATP6V1B2/BAAT/BPGM/CASK/CLPX/CTPS1/DLD/DLG1/DLG2/DNM1L/DPYD/ELOVL2/ELOVL7/ENPP1/ENTPD7/FAR1/FAR2/FIGNL1/GART/GMPS/GNAI3/HIF1A/HK2/HMGCR/HMGCS1/HSD17B4/HSPA8/HTR2A/IGF1/IMPDH2/LRRK2/MAGI3/MFN1/MPP1/MTHFD1/NCOR1/NDUFS1/NT5C2/NT5E/OGT/OPA1/PAICS/PARP1/PDE4B/PDE4D/PDE8B/PFKFB2/PPAT/PPT1/PYGL/RORA/SLC25A12/SLC25A13/SLC27A2/SLC4A1/SUCLA2/SUCLG2/SULT1B1/TDO2/UMPS/VCP | 74 |
| BP | GO:0046661 | male sex differentiation | 31/2221 | 168/18614 | 0.008804958 | 0.081368092 | 0.068765378 | ASPM/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ATRX/CSDE1/CTNNA1/CTNNB1/EIF2S2/FER/FNDC3A/HMGB2/HSD17B4/ING2/INHBA/LHFPL2/LRP2/NASP/NCOA4/PDGFRA/RHOBTB3/SCAPER/SYCP2/TGFBR1/TLR3/TMF1/WDR48/ZFPM2 | 31 |
| BP | GO:0017015 | regulation of transforming growth factor beta receptor signaling pathway | 28/2221 | 148/18614 | 0.008843373 | 0.081597745 | 0.068959461 | MIRLET7F1/HDAC2/ADAM17/ARID4A/ARID4B/BRMS1L/CD109/CILP/FBN1/HSP90AB1/HSPA5/ING2/LOX/LTBP1/MIR15B/MIR30B/MTMR4/OGT/PPARG/SDCBP/SNW1/SNX25/SNX6/TRIM33/VEPH1/ZEB1/ZEB2/ZNF451 | 28 |
| BP | GO:0045732 | positive regulation of protein catabolic process | 37/2221 | 209/18614 | 0.008932195 | 0.082291091 | 0.069545417 | DTL/ADAM9/ANKIB1/APC/ARIH1/EZR/FBXL5/FBXO11/FMR1/GCLC/HECTD1/HSP90AA1/IDE/LRP2/LRRK2/MDM2/MIR181B1/NEDD4/NFE2L2/NSF/NUB1/PSMC1/PSMC2/PSMC6/RDX/RNF14/RNF19A/RNF217/SNX9/SOCS4/TAF1/TIPARP/TMTC3/UBR3/USP13/VCP/VPS35 | 37 |
| BP | GO:0036503 | ERAD pathway | 22/2221 | 109/18614 | 0.009017332 | 0.082821788 | 0.069993917 | UBXN8/ATF6/CANX/CCDC47/DNAJC10/EDEM3/ERLIN1/HSP90B1/HSPA5/NFE2L2/PSMC6/SEL1L/STT3B/UBE4A/UBXN4/UGGT1/UGGT2/USP13/USP14/USP25/VCP/YOD1 | 22 |
| BP | GO:0120034 | positive regulation of plasma membrane bounded cell projection assembly | 22/2221 | 109/18614 | 0.009017332 | 0.082821788 | 0.069993917 | ANLN/CEP135/ACTR2/ACTR3/APC/ATP7A/CCDC88A/CCP110/CENPJ/CEP120/DOCK11/EPS8/FAM98A/FMR1/FNBP1L/HSP90AA1/MNS1/NCKAP1/NLGN1/PIK3CA/PIK3R1/TGFBR1 | 22 |
| BP | GO:0001510 | RNA methylation | 19/2221 | 90/18614 | 0.00904139 | 0.082916158 | 0.070073671 | ALKBH8/LARP7/METTL14/METTL15/NSUN2/NSUN6/RNMT/TFB2M/TGS1/THADA/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TRMT6/TYW3/WTAP/ZC3H13 | 19 |
| BP | GO:0033865 | nucleoside bisphosphate metabolic process | 24/2221 | 122/18614 | 0.009094424 | 0.083022841 | 0.07016383 | ELOVL6/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/BAAT/DLD/ELOVL2/ELOVL7/ENPP1/FAR1/FAR2/HMGCR/HMGCS1/HSD17B4/PPT1/SLC27A2/SUCLA2/SUCLG2/SULT1B1/TDO2 | 24 |
| BP | GO:0033875 | ribonucleoside bisphosphate metabolic process | 24/2221 | 122/18614 | 0.009094424 | 0.083022841 | 0.07016383 | ELOVL6/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/BAAT/DLD/ELOVL2/ELOVL7/ENPP1/FAR1/FAR2/HMGCR/HMGCS1/HSD17B4/PPT1/SLC27A2/SUCLA2/SUCLG2/SULT1B1/TDO2 | 24 |
| BP | GO:0034032 | purine nucleoside bisphosphate metabolic process | 24/2221 | 122/18614 | 0.009094424 | 0.083022841 | 0.07016383 | ELOVL6/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/BAAT/DLD/ELOVL2/ELOVL7/ENPP1/FAR1/FAR2/HMGCR/HMGCS1/HSD17B4/PPT1/SLC27A2/SUCLA2/SUCLG2/SULT1B1/TDO2 | 24 |
| BP | GO:0035987 | endodermal cell differentiation | 12/2221 | 48/18614 | 0.009223432 | 0.083413926 | 0.070494342 | COL12A1/COL5A2/COL8A1/CTNNB1/CTR9/INHBA/ITGA4/ITGAV/LAMB1/LEO1/MMP8/RTF1 | 12 |
| BP | GO:0016446 | somatic hypermutation of immunoglobulin genes | 5/2221 | 12/18614 | 0.009248186 | 0.083413926 | 0.070494342 | MSH2/POLQ/MLH1/MSH6/SAMHD1 | 5 |
| BP | GO:0018342 | protein prenylation | 5/2221 | 12/18614 | 0.009248186 | 0.083413926 | 0.070494342 | CHM/CHML/PGGT1B/PTAR1/RABGGTB | 5 |
| BP | GO:0036363 | transforming growth factor beta activation | 5/2221 | 12/18614 | 0.009248186 | 0.083413926 | 0.070494342 | HSP90AB1/ITGAV/ITGB6/ITGB8/LTBP1 | 5 |
| BP | GO:0097354 | prenylation | 5/2221 | 12/18614 | 0.009248186 | 0.083413926 | 0.070494342 | CHM/CHML/PGGT1B/PTAR1/RABGGTB | 5 |
| BP | GO:1902946 | protein localization to early endosome | 5/2221 | 12/18614 | 0.009248186 | 0.083413926 | 0.070494342 | DTX3L/EGF/EZR/RDX/ROCK2 | 5 |
| BP | GO:1905456 | regulation of lymphoid progenitor cell differentiation | 5/2221 | 12/18614 | 0.009248186 | 0.083413926 | 0.070494342 | FNIP1/NUDT21/SOS1/SOS2/ZBTB1 | 5 |
| BP | GO:1905668 | positive regulation of protein localization to endosome | 5/2221 | 12/18614 | 0.009248186 | 0.083413926 | 0.070494342 | DTX3L/EGF/EZR/RDX/ROCK2 | 5 |
| BP | GO:0002757 | immune response-activating signaling pathway | 67/2221 | 423/18614 | 0.009301666 | 0.083770695 | 0.070795852 | AIM2/ALPK1/ANKRD17/AP3B1/BANK1/BIRC2/BIRC3/BMX/BTK/CASP1/CD226/CD36/CD38/COLEC12/CR1/CTSS/CYLD/DDX3X/DDX60/EIF2B3/ELF1/EZR/GBP1/HAVCR2/HMGB1/HSPD1/IFIH1/IRAK3/IRAK4/ITK/LACC1/LYN/MALT1/MAP3K7/MEF2C/MNDA/NAIP/NCKAP1L/NLRC4/NLRP3/OTUD4/PDE4B/PDE4D/PIK3AP1/PIK3CA/PJA2/PTPN2/PTPRC/PUM2/RAB11FIP2/RABGEF1/RC3H2/RIOK3/RIPK2/RPS6KA3/SLC39A10/SOS1/STAP1/TEC/TLR1/TLR2/TLR3/TLR4/TLR6/TLR8/USP15/YES1 | 67 |
| BP | GO:0009150 | purine ribonucleotide metabolic process | 70/2221 | 445/18614 | 0.009346623 | 0.084049755 | 0.07103169 | ELOVL6/OLA1/AASS/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSM3/ADK/ATIC/ATP1B1/ATP6V1A/ATP6V1B2/BAAT/BPGM/CASK/CLPX/DLD/DLG1/DLG2/DNM1L/ELOVL2/ELOVL7/ENPP1/ENTPD7/FAR1/FAR2/FIGNL1/GART/GMPS/GNAI3/HIF1A/HK2/HMGCR/HMGCS1/HSD17B4/HSPA8/HTR2A/IGF1/IMPDH2/LRRK2/MAGI3/MFN1/MPP1/MTHFD1/NCOR1/NDUFS1/NT5C2/NT5E/OGT/OPA1/PAICS/PARP1/PDE4B/PDE4D/PDE8B/PFKFB2/PPAT/PPT1/RORA/SLC25A12/SLC25A13/SLC27A2/SLC4A1/SUCLA2/SUCLG2/SULT1B1/TDO2/VCP | 70 |
| BP | GO:0006354 | DNA-templated transcription elongation | 25/2221 | 129/18614 | 0.009530816 | 0.08524011 | 0.072037677 | EZH2/CCNT1/CCNT2/CTNNB1/CTR9/ELL2/ERCC6/HNRNPU/HTATSF1/INTS12/INTS6/INTS7/LARP7/LEO1/MED23/MED6/NCBP1/NCBP2/RTF1/SUPT16H/TCEA1/THOC1/WDR43/ZMYND11/ZNF326 | 25 |
| BP | GO:0042542 | response to hydrogen peroxide | 25/2221 | 129/18614 | 0.009530816 | 0.08524011 | 0.072037677 | CDK1/ECT2/EZH2/HDAC2/ADAM9/AIFM1/ARG1/BECN1/CASP3/HBA2/HBB/HGF/HP/IL18RAP/IMPACT/LRRK2/MET/NET1/NFE2L2/OSER1/PDGFD/RIPK1/SETX/STAT1/ZNF277 | 25 |
| BP | GO:0045931 | positive regulation of mitotic cell cycle | 25/2221 | 129/18614 | 0.009530816 | 0.08524011 | 0.072037677 | BRCA2/CDC6/CDK1/DLGAP5/DTL/FBXO5/MTBP/SASS6/STIL/ADAM17/ANKRD17/CENPJ/CPSF3/CUL3/DDX3X/KMT2E/MDM2/PKN2/PLCB1/PLRG1/PTPN11/RB1/RDX/RRM1/RRM2B | 25 |
| BP | GO:0002204 | somatic recombination of immunoglobulin genes involved in immune response | 13/2221 | 54/18614 | 0.009570601 | 0.08524011 | 0.072037677 | ATAD5/MSH2/HSPD1/LIG4/MLH1/MSH6/NBN/PTPRC/RIF1/SWAP70/TFRC/THOC1/TP53BP1 | 13 |
| BP | GO:0002208 | somatic diversification of immunoglobulins involved in immune response | 13/2221 | 54/18614 | 0.009570601 | 0.08524011 | 0.072037677 | ATAD5/MSH2/HSPD1/LIG4/MLH1/MSH6/NBN/PTPRC/RIF1/SWAP70/TFRC/THOC1/TP53BP1 | 13 |
| BP | GO:0045190 | isotype switching | 13/2221 | 54/18614 | 0.009570601 | 0.08524011 | 0.072037677 | ATAD5/MSH2/HSPD1/LIG4/MLH1/MSH6/NBN/PTPRC/RIF1/SWAP70/TFRC/THOC1/TP53BP1 | 13 |
| BP | GO:0071402 | cellular response to lipoprotein particle stimulus | 10/2221 | 37/18614 | 0.009578177 | 0.08524011 | 0.072037677 | ABCA1/ADAM17/CD36/ITGB1/LPL/MIA3/NPC1/PPARG/TLR4/TLR6 | 10 |
| BP | GO:0098876 | vesicle-mediated transport to the plasma membrane | 28/2221 | 149/18614 | 0.00968337 | 0.085991262 | 0.072672486 | ACAP2/ACSL3/AKAP5/ANK3/ANKRD50/ARFGEF2/ATP2C1/BLZF1/CCDC93/CNST/EPS15/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/GOLGA4/GOPC/MACF1/NSF/PREPL/RABEP1/SNAP25/SNX30/STEAP2/VPS13B/VPS26A/VPS35 | 28 |
| BP | GO:0099518 | vesicle cytoskeletal trafficking | 16/2221 | 72/18614 | 0.009691169 | 0.085991262 | 0.072672486 | AP3B1/AP3M1/BLOC1S6/CCDC186/DYNC1H1/FNBP1L/KIF3A/KIF5B/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/RAB1A/TANC2/TRAK2 | 16 |
| BP | GO:1903078 | positive regulation of protein localization to plasma membrane | 14/2221 | 60/18614 | 0.009739698 | 0.086277285 | 0.072914209 | AGR2/ACSL3/AKAP5/ATP2C1/CNST/DLG1/EPHA3/EZR/ITGB1/KIF5B/PIK3R1/PLS1/PRKCI/WNK3 | 14 |
| BP | GO:0033157 | regulation of intracellular protein transport | 39/2221 | 224/18614 | 0.009752087 | 0.086277285 | 0.072914209 | CDK1/ECT2/KIF20B/XPO1/AKAP5/ANGPT1/ANK3/BNIP3L/C2CD5/CD36/CEP290/CTDSPL2/EFCAB7/GCC2/HSP90AA1/ICE1/IPO5/JAK2/LCP1/LMAN1/LRRK2/NF1/NOLC1/PCM1/PIK3R1/PRKD1/PTGS2/PTPN11/RUFY3/SAR1B/SH3GLB1/SP100/TPR/UBR5/UFM1/XPO4/YOD1/ZFAND1/ZPR1 | 39 |
| BP | GO:0042147 | retrograde transport, endosome to Golgi | 20/2221 | 97/18614 | 0.009809546 | 0.086658191 | 0.073236118 | CLTC/ERC1/EVI5/GCC2/GOLT1B/HEATR5A/HEATR5B/LRRK2/PIKFYVE/PREPL/RHOBTB3/SNX2/SNX6/SPAG9/TBC1D23/TMEM87A/USP7/VPS26A/VPS35/VPS54 | 20 |
| BP | GO:0018022 | peptidyl-lysine methylation | 24/2221 | 123/18614 | 0.010055184 | 0.088697931 | 0.074959933 | BRCA1/EZH2/ARID4A/ARID4B/ASH1L/BOD1L1/CTNNB1/CTR9/HCFC2/IWS1/KDM6A/KMT2C/METTL18/MTF2/OGT/RBBP5/RIF1/RLF/RTF1/SETD7/SETDB2/SETMAR/SNW1/SUV39H2 | 24 |
| BP | GO:0032388 | positive regulation of intracellular transport | 35/2221 | 197/18614 | 0.010196952 | 0.089816788 | 0.075905495 | CDK1/ECT2/KIF20B/SPAG5/AKAP5/ANK3/C2CD5/CEP290/CTDSPL2/DHX9/DYNC1H1/EFCAB7/EZR/HSP90AA1/ICE1/IPO5/JAK2/MTMR2/NCBP2/NEDD4/PCM1/PIK3R1/PRKD1/PTGS2/RDX/RIOK2/RUFY3/SAR1B/SCP2/SH3GLB1/TPR/UBR5/XPO4/ZFAND1/ZPR1 | 35 |
| BP | GO:0034655 | nucleobase-containing compound catabolic process | 70/2221 | 447/18614 | 0.010330306 | 0.090858364 | 0.076785746 | ACAT1/ADAL/AIFM1/ATM/CDADC1/CNOT1/CNOT6L/CSDE1/DDX5/DHX36/DHX9/DICER1/DIS3/DIS3L/DKC1/DNA2/DPYD/EIF3E/EIF4A3/ENPP1/ENTPD1/ENTPD7/ETF1/EXOSC9/FASTKD2/FMR1/FXR1/GIGYF2/GSPT1/HNRNPU/LRPPRC/MBD4/METTL14/MLH1/NBAS/NCBP1/NCBP2/NSUN2/NT5C2/NT5E/NUDT12/PDE4B/PDE4D/PDE8B/PHAX/PNPT1/PNRC2/POP1/PUM2/RC3H2/RNASEL/ROCK1/ROCK2/SAMHD1/SERBP1/SETMAR/SLFN13/SSB/SUCLA2/SUCLG2/SYNCRIP/TRAF5/UPF2/UPF3B/VCP/VPS54/XRN1/XRN2/YTHDF3/ZPR1 | 70 |
| BP | GO:0044782 | cilium organization | 63/2221 | 396/18614 | 0.01039288 | 0.090955966 | 0.076868232 | CEP135/CEP78/PLK4/ABCC4/ACTR2/ACTR3/AHI1/ALPK1/ARL13B/ATG3/ATP6V1D/CC2D2A/CCDC66/CCDC88A/CCP110/CDKL5/CENPJ/CEP120/CEP162/CEP290/CEP350/CEP70/CEP83/CEP97/CYLD/DNAH5/DYNC2H1/EXOC5/FNBP1L/FSIP2/GDI2/GORAB/IFT57/IFT74/IFT80/IQCB1/IQCG/KIAA0586/KIF3A/LCA5/MAPRE1/MKKS/MNS1/MPHOSPH9/ODF2L/OFD1/PCM1/PIBF1/RAB3IP/RP2/RPGR/RPGRIP1L/SDCCAG8/SNX10/SPAG1/SSX2IP/SYNE2/TBC1D30/TTC17/TTC21B/WDR11/WDR19/WDR35 | 63 |
| BP | GO:0006739 | NADP metabolic process | 11/2221 | 43/18614 | 0.010401879 | 0.090955966 | 0.076868232 | ME1/ME2/ALDH1L2/FMO1/FMO5/IDH1/MDH1/NNT/NUDT12/PGD/RPE | 11 |
| BP | GO:0006904 | vesicle docking involved in exocytosis | 11/2221 | 43/18614 | 0.010401879 | 0.090955966 | 0.076868232 | BLOC1S6/CFTR/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/RAB8B/SNAP25/STXBP3/SYTL2 | 11 |
| BP | GO:0090503 | RNA phosphodiester bond hydrolysis, exonucleolytic | 11/2221 | 43/18614 | 0.010401879 | 0.090955966 | 0.076868232 | CNOT1/CNOT6L/CPSF3/DIS3/DIS3L/ERI1/ERI2/EXOSC9/PNPT1/XRN1/XRN2 | 11 |
| BP | GO:0010743 | regulation of macrophage derived foam cell differentiation | 9/2221 | 32/18614 | 0.010449564 | 0.090976231 | 0.076885358 | ABCA1/ABCA5/CD36/IL18/ITGAV/ITGB3/LPL/MSR1/PPARG | 9 |
| BP | GO:0042558 | pteridine-containing compound metabolic process | 9/2221 | 32/18614 | 0.010449564 | 0.090976231 | 0.076885358 | ALDH1L2/ATIC/GART/MTHFD1/MTHFD1L/MTHFD2/MTR/MTRR/SLC25A32 | 9 |
| BP | GO:0045671 | negative regulation of osteoclast differentiation | 9/2221 | 32/18614 | 0.010449564 | 0.090976231 | 0.076885358 | CTNNB1/FBN1/LRRC17/NF1/PIK3R1/TLR3/TLR4/TNFAIP6/ZNF675 | 9 |
| BP | GO:0031397 | negative regulation of protein ubiquitination | 18/2221 | 85/18614 | 0.010527042 | 0.091386267 | 0.077231885 | BUB1B/FBXO5/MAD2L1/PRMT3/DNAJA1/DTX3L/GCLC/GTPBP4/IVNS1ABP/OGT/PLAA/SPOPL/TAF1/TRIM44/TRIP12/UBR5/UFL1/USP44 | 18 |
| BP | GO:0072524 | pyridine-containing compound metabolic process | 18/2221 | 85/18614 | 0.010527042 | 0.091386267 | 0.077231885 | ME1/ME2/ALDH1L2/CD38/FMO1/FMO5/IDH1/KMO/KYNU/LDHB/MDH1/NNT/NUDT12/PARP9/PGD/RPE/SLC5A8/VCP | 18 |
| BP | GO:0086001 | cardiac muscle cell action potential | 17/2221 | 79/18614 | 0.010829395 | 0.093875564 | 0.079335627 | AKAP9/ANK2/ANK3/ATP1B1/ATP2A2/CACNA2D1/CXADR/DLG1/DMD/DSC2/DSG2/DSP/NUP155/PKP2/RYR2/SCN1A/SLMAP | 17 |
| BP | GO:0034198 | cellular response to amino acid starvation | 12/2221 | 49/18614 | 0.010920472 | 0.094313059 | 0.07970536 | BECN1/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/FAS/IMPACT/MIOS/PRKD1/SESN3/SH3GLB1/SLC38A2 | 12 |
| BP | GO:0042149 | cellular response to glucose starvation | 12/2221 | 49/18614 | 0.010920472 | 0.094313059 | 0.07970536 | BECN1/EIF2AK3/HNRNPA1/HSPA5/IFI16/IMPACT/NFE2L2/PIK3C3/PIK3R4/PLIN2/SESN3/SH3GLB1 | 12 |
| BP | GO:0016050 | vesicle organization | 59/2221 | 368/18614 | 0.010982085 | 0.094313059 | 0.07970536 | FBXO5/ABCA1/AP3B1/AP3M1/ARFGAP3/ARFGEF2/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/BLOC1S6/C2CD5/CD2AP/CHMP2B/CLCN3/CORO1C/CUL3/DNAJC13/EEA1/EPS15/FNBP1L/GNAI3/HOOK1/HOOK3/HPS3/LYST/MIA3/OSBP/PIK3C3/PIKFYVE/PRKCI/RAB1A/RAB27A/RAB8B/SAMD9/SAR1B/SDCBP/SEC23A/SEC23B/SEC24D/SEC31A/SNAP25/SNX10/SPG11/STAM2/STX17/TBC1D4/TMF1/TRAPPC11/TRAPPC13/TRAPPC8/USO1/USP8/VPS13B/VPS41/VPS8/VTA1/ZEB2/ZFYVE16 | 59 |
| BP | GO:0000478 | endonucleolytic cleavage involved in rRNA processing | 6/2221 | 17/18614 | 0.011036635 | 0.094313059 | 0.07970536 | BMS1/RRS1/SDE2/TSR1/UTP20/UTP23 | 6 |
| BP | GO:0000479 | endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 6/2221 | 17/18614 | 0.011036635 | 0.094313059 | 0.07970536 | BMS1/RRS1/SDE2/TSR1/UTP20/UTP23 | 6 |
| BP | GO:0006895 | Golgi to endosome transport | 6/2221 | 17/18614 | 0.011036635 | 0.094313059 | 0.07970536 | AP1AR/EPS15/KIF16B/MON2/VPS13A/VPS13C | 6 |
| BP | GO:0031053 | primary miRNA processing | 6/2221 | 17/18614 | 0.011036635 | 0.094313059 | 0.07970536 | DDX3X/DDX5/HNRNPA2B1/NCBP1/NCBP2/PUS10 | 6 |
| BP | GO:0033151 | V(D)J recombination | 6/2221 | 17/18614 | 0.011036635 | 0.094313059 | 0.07970536 | ATM/HMGB1/HMGB2/LIG4/PRKDC/XRCC4 | 6 |
| BP | GO:0036005 | response to macrophage colony-stimulating factor | 6/2221 | 17/18614 | 0.011036635 | 0.094313059 | 0.07970536 | FER/PTPN2/SPP1/STAP1/TLR2/TLR4 | 6 |
| BP | GO:0080009 | mRNA methylation | 6/2221 | 17/18614 | 0.011036635 | 0.094313059 | 0.07970536 | METTL14/NSUN2/TRMT10C/TRMT6/WTAP/ZC3H13 | 6 |
| BP | GO:0034643 | establishment of mitochondrion localization, microtubule-mediated | 8/2221 | 27/18614 | 0.011148019 | 0.09499502 | 0.080281696 | HIF1A/KIF5B/LRPPRC/MAP1B/OPA1/RHOT1/SYBU/TRAK2 | 8 |
| BP | GO:0047497 | mitochondrion transport along microtubule | 8/2221 | 27/18614 | 0.011148019 | 0.09499502 | 0.080281696 | HIF1A/KIF5B/LRPPRC/MAP1B/OPA1/RHOT1/SYBU/TRAK2 | 8 |
| BP | GO:0014065 | phosphatidylinositol 3-kinase signaling | 27/2221 | 144/18614 | 0.011248399 | 0.0955417 | 0.080743703 | CEP55/ANGPT1/BECN1/EGF/ERBB4/FCGR3A/FLT1/HGF/HTR2A/IGF1/IL18/JAK2/KBTBD2/NEDD4/NF1/PDGFC/PDGFD/PDGFRA/PIK3AP1/PIK3C2A/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIP5K1B/PREX2/PTPN13 | 27 |
| BP | GO:0045137 | development of primary sexual characteristics | 40/2221 | 233/18614 | 0.011260976 | 0.0955417 | 0.080743703 | ASPM/BRCA2/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ATM/ATRX/CASP3/CSDE1/CTNNA1/EIF2S2/FER/FNDC3A/HMGB2/HSD17B4/HSPA5/IDH1/ING2/INHBA/LHFPL2/LRP2/MKKS/NASP/NCOA4/NRIP1/NUP107/PDGFRA/RHOBTB3/SCAPER/TGFBR1/TIPARP/TLR3/TMF1/TNFAIP6/WDR19/WDR48/ZFPM2 | 40 |
| BP | GO:0002274 | myeloid leukocyte activation | 41/2221 | 240/18614 | 0.011263525 | 0.0955417 | 0.080743703 | SUCNR1/ADAM10/ADAM9/ATM/BTK/C12orf4/CD226/CD84/CLEC4D/CNR1/DOCK2/FCGR3A/FER/HAVCR2/HMGB1/HSPD1/IFNGR1/IL18/IL18RAP/ITGB6/ITGB8/JAK2/KMT2E/LRRK2/LYN/MIR142/MMP8/PIK3CG/PJA2/PLA2G4A/PTPRC/RABGEF1/RBPJ/RORA/STAP1/STXBP3/TLR1/TLR2/TLR3/TLR4/TLR6 | 41 |
| BP | GO:0042326 | negative regulation of phosphorylation | 61/2221 | 383/18614 | 0.011275699 | 0.0955417 | 0.080743703 | GSKIP/NCAPG2/PBK/AIDA/ANGPT1/APC/C9orf72/CASP3/CD109/CDK5RAP2/CHORDC1/CORO1C/DMD/DNAJA1/DNAJC10/DNAJC3/ENPP1/GGNBP2/HGF/HIPK3/HMGCR/HNRNPU/IBTK/IMPACT/INHBA/IPO5/IPO7/IRAK3/LRP6/LRRK2/LYN/NCK1/NCOR1/NF1/PARP14/PDCD4/PDE4D/PIBF1/PIK3CB/PPARG/PPP2CA/PRKAR2B/PRKDC/PTPN13/PTPN2/PTPRC/PTPRO/PWP1/RABGEF1/RB1/RGS2/ROCK1/SAMSN1/SLC4A1/SNX25/SNX6/SOCS4/SPAG9/STAP1/TAF7/ZNF675 | 61 |
| BP | GO:0009127 | purine nucleoside monophosphate biosynthetic process | 7/2221 | 22/18614 | 0.011464948 | 0.096601018 | 0.081638948 | ADK/ATIC/GART/GMPS/IMPDH2/PAICS/PPAT | 7 |
| BP | GO:0015669 | gas transport | 7/2221 | 22/18614 | 0.011464948 | 0.096601018 | 0.081638948 | AQP4/BPGM/HBA2/HBB/HBD/HBG2/IPCEF1 | 7 |
| BP | GO:0042026 | protein refolding | 7/2221 | 22/18614 | 0.011464948 | 0.096601018 | 0.081638948 | DNAJA1/HSP90AA1/HSPA13/HSPA5/HSPA8/HSPA9/HSPD1 | 7 |
| BP | GO:0051567 | histone H3-K9 methylation | 7/2221 | 22/18614 | 0.011464948 | 0.096601018 | 0.081638948 | BRCA1/ARID4A/ARID4B/RIF1/SETD7/SETDB2/SUV39H2 | 7 |
| BP | GO:0044270 | cellular nitrogen compound catabolic process | 75/2221 | 486/18614 | 0.011484022 | 0.096626401 | 0.0816604 | ACADL/ACAT1/ADAL/AIFM1/ATM/CDADC1/CNOT1/CNOT6L/CSDE1/DDX5/DHX36/DHX9/DICER1/DIS3/DIS3L/DKC1/DNA2/DPYD/EIF3E/EIF4A3/ENPP1/ENTPD1/ENTPD7/ETF1/EXOSC9/FASTKD2/FMR1/FXR1/GIGYF2/GSPT1/HNRNPU/KMO/KYNU/LRPPRC/MBD4/METTL14/MLH1/NBAS/NCBP1/NCBP2/NSUN2/NT5C2/NT5E/NUDT12/PDE4B/PDE4D/PDE8B/PHAX/PNPT1/PNRC2/POP1/PUM2/RC3H2/RNASEL/ROCK1/ROCK2/SAMHD1/SERBP1/SETMAR/SLFN13/SSB/SUCLA2/SUCLG2/SYNCRIP/TDO2/TET2/TRAF5/UPF2/UPF3B/VCP/VPS54/XRN1/XRN2/YTHDF3/ZPR1 | 75 |
| BP | GO:0030048 | actin filament-based movement | 25/2221 | 131/18614 | 0.011545523 | 0.096985894 | 0.081964212 | ABCC9/AKAP9/ANK2/ATP2A2/CACNA2D1/DLG1/DSC2/DSG2/DSP/FNBP1L/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/NUP155/PDE4B/PDE4D/PIK3CA/PKP2/ROCK1/RYR2/SCN1A/SYNE2/TPM1 | 25 |
| BP | GO:1903844 | regulation of cellular response to transforming growth factor beta stimulus | 28/2221 | 151/18614 | 0.01155899 | 0.096985894 | 0.081964212 | MIRLET7F1/HDAC2/ADAM17/ARID4A/ARID4B/BRMS1L/CD109/CILP/FBN1/HSP90AB1/HSPA5/ING2/LOX/LTBP1/MIR15B/MIR30B/MTMR4/OGT/PPARG/SDCBP/SNW1/SNX25/SNX6/TRIM33/VEPH1/ZEB1/ZEB2/ZNF451 | 28 |
| BP | GO:0051098 | regulation of binding | 59/2221 | 369/18614 | 0.011593985 | 0.097144026 | 0.082097853 | GMNN/HDAC2/NEK2/ANGPT1/ARHGAP28/ATP2A2/BTAF1/C9orf72/CAPRIN2/CCPG1/CDON/CFHR1/CLIC2/CTNNB1/DHX9/DPH3/DTX3L/EGF/EIF2S1/EIF3D/EIF3E/EIF4A3/EPB41/EPHA4/ERCC4/FMR1/GTPBP4/HMGB1/HMGB2/IDE/IFI16/IGF1/ITGA2/ITGA4/JAK2/KRIT1/LOX/LRRK2/MAPRE1/MET/MMP8/NCBP1/NMD3/NUCKS1/PARP1/PARP9/PPARG/PPP2CA/RAPGEF2/RB1/RIPK2/ROCK1/RSF1/SP100/TAF1/TGFBR1/TRIM6/USP9X/ZNF675 | 59 |
| BP | GO:0010742 | macrophage derived foam cell differentiation | 10/2221 | 38/18614 | 0.011640836 | 0.09740093 | 0.082314966 | ABCA1/ABCA5/CD36/IL18/ITGAV/ITGB3/LPL/MSR1/PPARG/STAT1 | 10 |
| BP | GO:0007548 | sex differentiation | 47/2221 | 283/18614 | 0.011743081 | 0.09811997 | 0.082922637 | ASPM/BRCA2/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ATM/ATRX/CASP3/CDKL2/CHD7/CSDE1/CTNNA1/CTNNB1/EIF2S2/FER/FNDC3A/HMGB2/HSD17B4/HSPA5/IDH1/ING2/INHBA/LHFPL2/LRP2/MERTK/MKKS/NASP/NCOA4/NIPBL/NRIP1/NUP107/PDGFRA/PTPN11/RHOBTB3/SCAPER/SYCP2/TGFBR1/TIPARP/TLR3/TMF1/TNFAIP6/WDR19/WDR48/ZFPM2 | 47 |
| BP | GO:0001933 | negative regulation of protein phosphorylation | 55/2221 | 341/18614 | 0.012211165 | 0.101889551 | 0.086108366 | GSKIP/NCAPG2/PBK/AIDA/ANGPT1/APC/C9orf72/CASP3/CD109/CDK5RAP2/CHORDC1/CORO1C/DMD/DNAJA1/DNAJC10/DNAJC3/ENPP1/GGNBP2/HGF/HIPK3/HMGCR/IBTK/IMPACT/IPO5/IPO7/IRAK3/LRP6/LRRK2/LYN/NCK1/NF1/PARP14/PDCD4/PDE4D/PIBF1/PIK3CB/PPARG/PPP2CA/PRKAR2B/PRKDC/PTPN13/PTPN2/PTPRC/PTPRO/PWP1/RABGEF1/RB1/RGS2/SAMSN1/SNX25/SNX6/SOCS4/SPAG9/TAF7/ZNF675 | 55 |
| BP | GO:1990138 | neuron projection extension | 31/2221 | 172/18614 | 0.012266238 | 0.102207324 | 0.08637692 | ALCAM/C9orf72/CDKL5/CTNNB1/DCLK1/EIF2AK4/FLRT3/GOLGA4/HSP90AA1/HSP90AB1/IFRD1/IMPACT/IQGAP1/ITGA4/ITGB1/ITSN2/LLPH/MACF1/MAP1B/MAP3K13/NRCAM/PLAA/RNF6/RUFY3/SEMA3A/SEMA3C/SEMA3D/SPAG9/SPG11/USP9X/VCL | 31 |
| BP | GO:0007229 | integrin-mediated signaling pathway | 22/2221 | 112/18614 | 0.01234895 | 0.102754197 | 0.086839091 | ADAM10/ADAM9/COL3A1/CTNNA1/CUL3/DST/FERMT2/FUT8/ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/LAMA2/LAMB1/LAMC1/PRKD1/PTPN11/TEC | 22 |
| BP | GO:0043620 | regulation of DNA-templated transcription in response to stress | 11/2221 | 44/18614 | 0.0124102 | 0.103121223 | 0.08714927 | CHEK1/ATF6/BCLAF1/HIF1A/HSPA5/IMPACT/NCK1/NEDD4/NFE2L2/RBPJ/RPS6KA3 | 11 |
| BP | GO:0034614 | cellular response to reactive oxygen species | 28/2221 | 152/18614 | 0.012601575 | 0.104432962 | 0.08825784 | CDK1/ECT2/EZH2/HDAC2/AIFM1/ARG1/ATP7A/BECN1/BTK/CD36/CHUK/ERCC6L2/FER/HGF/IL18RAP/IMPACT/LRRK2/MET/NET1/NFE2L2/OSER1/PDGFD/PDGFRA/PTPRK/RIPK1/SETX/TPM1/ZNF277 | 28 |
| BP | GO:0046700 | heterocycle catabolic process | 75/2221 | 488/18614 | 0.012602781 | 0.104432962 | 0.08825784 | ACAT1/ADAL/AIFM1/ATM/CDADC1/CNOT1/CNOT6L/CSDE1/DDX5/DHX36/DHX9/DICER1/DIS3/DIS3L/DKC1/DNA2/DPYD/EIF3E/EIF4A3/ENPP1/ENTPD1/ENTPD7/ETF1/EXOSC9/FASTKD2/FMR1/FXR1/GIGYF2/GSPT1/HNRNPU/KMO/KYNU/LRPPRC/MBD4/METTL14/MLH1/NBAS/NCBP1/NCBP2/NFE2L2/NSUN2/NT5C2/NT5E/NUDT12/PDE4B/PDE4D/PDE8B/PHAX/PNPT1/PNRC2/POP1/PUM2/RC3H2/RNASEL/ROCK1/ROCK2/SAMHD1/SERBP1/SETMAR/SLFN13/SSB/SUCLA2/SUCLG2/SYNCRIP/TDO2/TET2/TRAF5/UPF2/UPF3B/VCP/VPS54/XRN1/XRN2/YTHDF3/ZPR1 | 75 |
| BP | GO:0044403 | biological process involved in symbiotic interaction | 51/2221 | 313/18614 | 0.012782153 | 0.105706937 | 0.089334495 | CDK1/ACE2/ARG1/BECN1/CCNT1/CD86/CFHR1/CHD1/CHMP2B/CLDN1/CR1/CTSL/CXADR/DPP4/EEA1/EIF2AK4/EPS15/EXOC2/FMR1/GYPA/HMGB1/HSP90AB1/HSPA8/HSPD1/HTR2A/IDE/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/JAK2/KPNA3/MRC1/NPC1/NUCKS1/NUP153/PIK3C3/PIKFYVE/ROCK2/SNW1/TCP1/TFRC/THOC1/THOC2/TRIM22/TRIM38/TRIM59/TRIM6/WWP1/ZNF502 | 51 |
| BP | GO:0006898 | receptor-mediated endocytosis | 43/2221 | 256/18614 | 0.012795983 | 0.105706937 | 0.089334495 | HMMR/ACE2/AHI1/ANGPT1/C3/CANX/CD2AP/CD36/CLTC/CTSL/DNAJC13/DPP4/EGF/EPS15/EZR/FCHO2/FMR1/FNBP1L/ITGA4/ITGAV/ITGB1/ITGB3/ITSN1/ITSN2/LRP2/LRP6/LRRTM2/MKLN1/MRC1/MSR1/MTMR2/NEDD4/PIK3CB/PIKFYVE/PLA2R1/PPT1/RABGEF1/SCYL2/SDCBP/SNAP25/SNX9/TFRC/VLDLR | 43 |
| BP | GO:0070301 | cellular response to hydrogen peroxide | 19/2221 | 93/18614 | 0.012809235 | 0.105706937 | 0.089334495 | CDK1/ECT2/EZH2/HDAC2/AIFM1/ARG1/BECN1/HGF/IL18RAP/IMPACT/LRRK2/MET/NET1/NFE2L2/OSER1/PDGFD/RIPK1/SETX/ZNF277 | 19 |
| BP | GO:0016925 | protein sumoylation | 15/2221 | 68/18614 | 0.012866689 | 0.106011757 | 0.089592103 | CAPN3/CTNNB1/GNL3/IFIH1/KIAA1586/MDM2/RANBP2/SENP1/SENP5/SENP6/SMC5/SMC6/TOPORS/TRIM38/ZNF451 | 15 |
| BP | GO:0071404 | cellular response to low-density lipoprotein particle stimulus | 9/2221 | 33/18614 | 0.012881415 | 0.106011757 | 0.089592103 | ABCA1/CD36/ITGB1/LPL/MIA3/NPC1/PPARG/TLR4/TLR6 | 9 |
| BP | GO:0008406 | gonad development | 39/2221 | 228/18614 | 0.012918453 | 0.106171332 | 0.089726962 | ASPM/BRCA2/BRIP1/KIF18A/MSH2/ARID4A/ARID4B/ARID5B/ATM/ATRX/CASP3/CSDE1/CTNNA1/EIF2S2/FER/FNDC3A/HMGB2/HSD17B4/HSPA5/IDH1/ING2/INHBA/LRP2/MKKS/NASP/NCOA4/NRIP1/NUP107/PDGFRA/RHOBTB3/SCAPER/TGFBR1/TIPARP/TLR3/TMF1/TNFAIP6/WDR19/WDR48/ZFPM2 | 39 |
| BP | GO:0043030 | regulation of macrophage activation | 14/2221 | 62/18614 | 0.013021742 | 0.106874215 | 0.090320979 | ATM/CD84/HAVCR2/HSPD1/LRRK2/MIR142/MMP8/PJA2/PLA2G4A/PTPRC/RORA/STAP1/TLR4/TLR6 | 14 |
| BP | GO:0021987 | cerebral cortex development | 24/2221 | 126/18614 | 0.013439598 | 0.109887474 | 0.092867529 | ARHGAP11B/ASPM/KIF14/ATIC/CCDC141/CDH2/CDON/CEP120/COL3A1/CTNNB1/FAT4/FBXO45/FOXP2/GART/HIF1A/LAMB1/LRP8/MKKS/NF1/PLCB1/SLC38A2/SYNE2/TACC1/WDR47 | 24 |
| BP | GO:0002566 | somatic diversification of immune receptors via somatic mutation | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | MSH2/POLQ/MLH1/MSH6/SAMHD1 | 5 |
| BP | GO:0010745 | negative regulation of macrophage derived foam cell differentiation | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | ABCA1/ABCA5/ITGAV/ITGB3/PPARG | 5 |
| BP | GO:0036006 | cellular response to macrophage colony-stimulating factor stimulus | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | FER/PTPN2/STAP1/TLR2/TLR4 | 5 |
| BP | GO:0038203 | TORC2 signaling | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | NCKAP1L/RICTOR/SESN3/SYAP1/USP9X | 5 |
| BP | GO:0060100 | positive regulation of phagocytosis, engulfment | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | C3/CD36/ITGA2/NCKAP1L/STAP1 | 5 |
| BP | GO:0071481 | cellular response to X-ray | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | ATM/NIPBL/NUCKS1/TP53BP1/XRCC5 | 5 |
| BP | GO:0075509 | endocytosis involved in viral entry into host cell | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | ACE2/CTSL/DPP4/EPS15/PIKFYVE | 5 |
| BP | GO:1905155 | positive regulation of membrane invagination | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | C3/CD36/ITGA2/NCKAP1L/STAP1 | 5 |
| BP | GO:1905666 | regulation of protein localization to endosome | 5/2221 | 13/18614 | 0.013571541 | 0.109887474 | 0.092867529 | DTX3L/EGF/EZR/RDX/ROCK2 | 5 |
| BP | GO:0019080 | viral gene expression | 20/2221 | 100/18614 | 0.013653168 | 0.110251625 | 0.093175278 | CANX/CCNT1/CCNT2/CHD1/CSDE1/DHX9/EIF2AK4/EIF3A/EIF3D/EIF3L/FUT8/GALNT1/LARP7/MGAT4A/NUCKS1/PARP9/RSF1/SNW1/SSB/ST6GALNAC3 | 20 |
| BP | GO:0030512 | negative regulation of transforming growth factor beta receptor signaling pathway | 20/2221 | 100/18614 | 0.013653168 | 0.110251625 | 0.093175278 | MIRLET7F1/HDAC2/ADAM17/ARID4A/ARID4B/BRMS1L/CD109/CILP/FBN1/HSPA5/ING2/LTBP1/MIR15B/MTMR4/OGT/PPARG/SNX25/SNX6/VEPH1/ZNF451 | 20 |
| BP | GO:0006473 | protein acetylation | 36/2221 | 208/18614 | 0.013798218 | 0.111273564 | 0.094038934 | BRCA1/BRCA2/CHEK1/DEK/ESCO2/HDAC2/BAZ1B/CLOCK/DDX21/DDX3X/EPC2/ERCC6/ESCO1/HAT1/ING3/IWS1/JADE1/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA15/NAA25/NAA35/NAA50/OGT/PHF20L1/SDR16C5/SF3B1/SMARCA5/SMC5/SUPT20H/TAF2/TAF7/TAOK1/ZZZ3 | 36 |
| BP | GO:1903311 | regulation of mRNA metabolic process | 53/2221 | 329/18614 | 0.013995268 | 0.111877901 | 0.094549668 | AHCYL1/CNOT1/CNOT6L/CSDE1/CWC22/DDX5/DHX36/DHX9/DIS3/EIF4A3/EXOSC9/FASTKD2/FMR1/FXR1/GIGYF2/HNRNPA1/HNRNPA2B1/HNRNPU/HSPA8/IWS1/LARP7/LEO1/METTL14/MLH1/NBAS/NCBP1/NCBP2/NCL/NSRP1/NUDT21/PAPOLA/PNPT1/PTCD2/PUM2/RBM25/RBM39/RC3H2/RNASEL/ROCK1/ROCK2/SERBP1/SLTM/SMU1/SNW1/SON/SRPK1/SRPK2/SRSF10/SYNCRIP/TRAF5/WTAP/YTHDC1/YTHDF3 | 53 |
| BP | GO:0016540 | protein autoprocessing | 8/2221 | 28/18614 | 0.014010745 | 0.111877901 | 0.094549668 | CASP1/CASP4/CTSE/CTSL/FAM111A/PARP1/PCSK1/SPRTN | 8 |
| BP | GO:0032801 | receptor catabolic process | 8/2221 | 28/18614 | 0.014010745 | 0.111877901 | 0.094549668 | BECN1/DTX3L/KIF16B/MTMR2/NEDD4/PIK3R4/SH3GLB1/SNX25 | 8 |
| BP | GO:0150146 | cell junction disassembly | 8/2221 | 28/18614 | 0.014010745 | 0.111877901 | 0.094549668 | C3/EPHA4/FER/ITGB1/MAP4K4/PIK3R1/PLXNC1/TGFBR1 | 8 |
| BP | GO:1905820 | positive regulation of chromosome separation | 8/2221 | 28/18614 | 0.014010745 | 0.111877901 | 0.094549668 | DLGAP5/NCAPG/NCAPG2/NCAPH/CUL3/RB1/SMC2/SMC4 | 8 |
| BP | GO:0031111 | negative regulation of microtubule polymerization or depolymerization | 10/2221 | 39/18614 | 0.014021931 | 0.111877901 | 0.094549668 | TPX2/APC/CAMSAP2/CKAP2/CLASP2/MAP1B/MAPRE1/NAV3/TAOK1/WDR47 | 10 |
| BP | GO:0090077 | foam cell differentiation | 10/2221 | 39/18614 | 0.014021931 | 0.111877901 | 0.094549668 | ABCA1/ABCA5/CD36/IL18/ITGAV/ITGB3/LPL/MSR1/PPARG/STAT1 | 10 |
| BP | GO:1905168 | positive regulation of double-strand break repair via homologous recombination | 10/2221 | 39/18614 | 0.014021931 | 0.111877901 | 0.094549668 | RAD51AP1/ACTR2/ARID2/EPC2/ERCC6/ING3/MORF4L2/PARP1/RBBP8/WDR48 | 10 |
| BP | GO:0045936 | negative regulation of phosphate metabolic process | 68/2221 | 439/18614 | 0.014322187 | 0.114122219 | 0.096446374 | GSKIP/NCAPG2/PBK/AIDA/ANGPT1/APC/C9orf72/CASP3/CD109/CDK5RAP2/CHORDC1/CORO1C/DMD/DNAJA1/DNAJC10/DNAJC3/ENPP1/GGNBP2/HGF/HIPK3/HMGCR/HNRNPU/IBTK/IMPACT/INHBA/IPO5/IPO7/IQGAP1/IRAK3/LRP6/LRRK2/LYN/MASTL/NCK1/NCKAP1L/NCOR1/NF1/PARP1/PARP14/PDCD4/PDE4D/PIBF1/PIK3CB/PPARG/PPP2CA/PRKAR2B/PRKDC/PTPN13/PTPN2/PTPRC/PTPRO/PWP1/RABGEF1/RB1/RGS2/ROCK1/ROCK2/SAMSN1/SLC4A1/SNX25/SNX6/SOCS4/SPAG9/STAP1/SWAP70/TAF7/YWHAB/ZNF675 | 68 |
| BP | GO:0007018 | microtubule-based movement | 65/2221 | 417/18614 | 0.014381107 | 0.114440135 | 0.09671505 | CENPE/DLGAP5/KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF4A/ACTR2/ACTR3/AP3B1/AP3M1/AQP4/ARHGAP21/ASH1L/BLOC1S6/DLG2/DNAH14/DNAH5/DNAJA1/DST/DYNC1H1/DYNC2H1/FSIP2/HIF1A/HNRNPU/HSPA8/IFT57/IFT74/IFT80/ING2/IQCG/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B/KPNB1/KTN1/LCA5/LRPPRC/LZTFL1/MAP1B/MKKS/MNS1/OFD1/OPA1/PCM1/RAB1A/RAB27B/RABGEF1/RHOT1/RPGR/SPG11/SSX2IP/SYBU/SYNE2/TMF1/TRAK2/TTC21B/VPS13A/WDR19/WDR35 | 65 |
| BP | GO:0031330 | negative regulation of cellular catabolic process | 42/2221 | 251/18614 | 0.014620784 | 0.115919164 | 0.097964999 | PBK/BECN1/CNR1/CSDE1/DHX36/DHX9/DKC1/EIF4G2/FMR1/HERC1/HGF/HNRNPU/HP/HSP90AB1/LRPPRC/LRRK2/MET/MTM1/MTMR2/NBAS/NPC1/NSUN2/OGT/PHAX/PHF20L1/PIK3CA/PIK3CG/PTPN3/ROCK1/RYBP/SCFD1/SDCBP/SYNCRIP/TAB2/TAB3/TAF1/TIMP4/TRAF5/UCHL5/USP14/USP7/USP9X | 42 |
| BP | GO:0061077 | chaperone-mediated protein folding | 15/2221 | 69/18614 | 0.014677404 | 0.115919164 | 0.097964999 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CHORDC1/DNAJC7/FKBP5/HSPA13/HSPA5/HSPA8/HSPA9/HSPH1/TCP1 | 15 |
| BP | GO:0062208 | positive regulation of pattern recognition receptor signaling pathway | 11/2221 | 45/18614 | 0.014699899 | 0.115919164 | 0.097964999 | ANKRD17/DDX3X/DDX60/HMGB1/PJA2/PUM2/TLR1/TLR2/TLR3/TLR4/USP15 | 11 |
| BP | GO:0031109 | microtubule polymerization or depolymerization | 24/2221 | 127/18614 | 0.014750934 | 0.115919164 | 0.097964999 | FBXO5/KIF18A/SKA3/TPX2/AKAP9/APC/CAMSAP2/CDK5RAP2/CENPJ/CEP192/CKAP2/CKAP5/CLASP2/CLIP1/KIF2A/MAP1B/MAP7D3/MAPRE1/MET/NAV3/NEDD1/NIN/TAOK1/WDR47 | 24 |
| BP | GO:0031589 | cell-substrate adhesion | 57/2221 | 359/18614 | 0.014768855 | 0.115919164 | 0.097964999 | AGR2/KIF14/ADAM9/ADAMTS9/ANGPT1/ANGPT2/AP1AR/CASK/CCDC80/CD36/CD96/CLASP2/COL3A1/COL8A1/CORO1C/CTNNB1/DOCK5/ECM2/EGFL6/EPHA3/FER/FERMT2/FMN1/GBP1/GCNT2/ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/JAK2/LAMB1/LAMC1/MACF1/MAP4K4/MERTK/MKLN1/NF1/PHLDB2/PIK3CB/PIK3R1/PKP2/PPFIA1/PTPRK/PTPRO/RAB1A/RASA1/ROCK1/ROCK2/SLK/TRPM7/UTRN/VCAM1/VCL | 57 |
| BP | GO:1903050 | regulation of proteolysis involved in protein catabolic process | 39/2221 | 230/18614 | 0.014791367 | 0.115919164 | 0.097964999 | PBK/XPO1/ANKIB1/ARIH1/EGF/EPHA4/FMR1/GCLC/HECTD1/HSP90AB1/L3MBTL3/LRRK2/MDM2/MTM1/NFE2L2/NUB1/OGT/PHF20L1/PSMC1/PSMC2/PSMC6/PSMD14/RNF14/RNF19A/RNF217/RYBP/SDCBP/SOCS4/TAF1/TMF1/TMTC3/UCHL5/UFL1/USP13/USP14/USP25/USP7/USP9X/VCP | 39 |
| BP | GO:0006353 | DNA-templated transcription termination | 7/2221 | 23/18614 | 0.014818391 | 0.115919164 | 0.097964999 | DHX9/MTERF1/MTERF2/PCF11/SETX/TTF2/XRN2 | 7 |
| BP | GO:0038095 | Fc-epsilon receptor signaling pathway | 7/2221 | 23/18614 | 0.014818391 | 0.115919164 | 0.097964999 | BTK/FER/LYN/MAP3K1/MAP3K7/MAPK10/SOS1 | 7 |
| BP | GO:0046823 | negative regulation of nucleocytoplasmic transport | 7/2221 | 23/18614 | 0.014818391 | 0.115919164 | 0.097964999 | ANGPT1/CD36/NF1/NUP153/SP100/TPR/UFM1 | 7 |
| BP | GO:0097150 | neuronal stem cell population maintenance | 7/2221 | 23/18614 | 0.014818391 | 0.115919164 | 0.097964999 | ASPM/FANCD2/CDH2/HOOK3/PCM1/PRRX1/WDR47 | 7 |
| BP | GO:0000076 | DNA replication checkpoint signaling | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | CDC6/TICRR/DNA2/NAE1/RAD17/TOPBP1 | 6 |
| BP | GO:0008356 | asymmetric cell division | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | ASPM/ACTR2/ACTR3/DOCK7/ING2/SOX5 | 6 |
| BP | GO:0010885 | regulation of cholesterol storage | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | ABCA1/CD36/LPL/MSR1/PPARG/TTC39B | 6 |
| BP | GO:0030730 | sequestering of triglyceride | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | ENPP1/LPL/OSBPL11/OSBPL8/PLIN2/PPARG | 6 |
| BP | GO:0046112 | nucleobase biosynthetic process | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | CTPS1/GART/GMPS/PAICS/PPAT/UMPS | 6 |
| BP | GO:0050746 | regulation of lipoprotein metabolic process | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | ITGAV/ITGB3/RAB3GAP1/RAB3GAP2/RABL3/RB1CC1 | 6 |
| BP | GO:0051770 | positive regulation of nitric-oxide synthase biosynthetic process | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | AKAP12/JAK2/LRRK2/STAT1/TLR2/TLR4 | 6 |
| BP | GO:1902018 | negative regulation of cilium assembly | 6/2221 | 18/18614 | 0.014913802 | 0.115919164 | 0.097964999 | CCP110/CEP97/GDI2/MPHOSPH9/ODF2L/TBC1D30 | 6 |
| BP | GO:0010563 | negative regulation of phosphorus metabolic process | 68/2221 | 440/18614 | 0.015020668 | 0.116190346 | 0.098194179 | GSKIP/NCAPG2/PBK/AIDA/ANGPT1/APC/C9orf72/CASP3/CD109/CDK5RAP2/CHORDC1/CORO1C/DMD/DNAJA1/DNAJC10/DNAJC3/ENPP1/GGNBP2/HGF/HIPK3/HMGCR/HNRNPU/IBTK/IMPACT/INHBA/IPO5/IPO7/IQGAP1/IRAK3/LRP6/LRRK2/LYN/MASTL/NCK1/NCKAP1L/NCOR1/NF1/PARP1/PARP14/PDCD4/PDE4D/PIBF1/PIK3CB/PPARG/PPP2CA/PRKAR2B/PRKDC/PTPN13/PTPN2/PTPRC/PTPRO/PWP1/RABGEF1/RB1/RGS2/ROCK1/ROCK2/SAMSN1/SLC4A1/SNX25/SNX6/SOCS4/SPAG9/STAP1/SWAP70/TAF7/YWHAB/ZNF675 | 68 |
| BP | GO:0051646 | mitochondrion localization | 12/2221 | 51/18614 | 0.015025946 | 0.116190346 | 0.098194179 | DNM1L/HIF1A/KIF5B/LRPPRC/LRRK2/MAP1B/MFN1/MTM1/OPA1/RHOT1/SYBU/TRAK2 | 12 |
| BP | GO:1901799 | negative regulation of proteasomal protein catabolic process | 12/2221 | 51/18614 | 0.015025946 | 0.116190346 | 0.098194179 | PBK/HSP90AB1/MTM1/OGT/PHF20L1/RYBP/SDCBP/UCHL5/USP14/USP25/USP7/USP9X | 12 |
| BP | GO:2000059 | negative regulation of ubiquitin-dependent protein catabolic process | 12/2221 | 51/18614 | 0.015025946 | 0.116190346 | 0.098194179 | PBK/HSP90AB1/MTM1/OGT/PHF20L1/RYBP/SDCBP/TAF1/UCHL5/USP14/USP7/USP9X | 12 |
| BP | GO:0031060 | regulation of histone methylation | 13/2221 | 57/18614 | 0.015088039 | 0.116520721 | 0.098473383 | BRCA1/CTNNB1/CTR9/IWS1/MTF2/OGT/PAXBP1/RIF1/RNF20/RTF1/SETD7/SMARCA5/SNW1 | 13 |
| BP | GO:0051017 | actin filament bundle assembly | 29/2221 | 161/18614 | 0.015159484 | 0.116922381 | 0.098812832 | ALMS1/ARHGAP28/CALD1/CCDC88A/CGNL1/CLASP2/CUL3/EPS8/EZR/FERMT2/HSP90B1/LCP1/LIMA1/MET/MKKS/MYO1B/PHLDB2/PIK3R1/PLS1/PLS3/PPFIA1/RDX/ROCK1/ROCK2/SPIRE1/SWAP70/TGFBR1/TJP1/TPM1 | 29 |
| BP | GO:0002702 | positive regulation of production of molecular mediator of immune response | 25/2221 | 134/18614 | 0.015197585 | 0.117066159 | 0.098934341 | ATAD5/MSH2/BTK/CD226/CD36/CD86/DDX1/DDX21/DHX36/IL18/IL1R1/LACC1/MALT1/MAP3K7/MLH1/NLRP3/PANX1/PTPRC/RIF1/RIPK2/TFRC/TLR3/TLR4/TP53BP1/TRIM6 | 25 |
| BP | GO:0022604 | regulation of cell morphogenesis | 41/2221 | 245/18614 | 0.015669967 | 0.120544949 | 0.101874319 | ARHGAP15/ARHGAP18/BRWD1/BRWD3/CAPRIN1/CAPRIN2/CDKL5/CORO1C/DHX36/DLG1/EPB41/EPB41L3/EPHA4/EPS8/EZR/FERMT2/FGD4/FGD6/FMNL2/ITSN2/LARP4/LRP8/MACF1/MAP3K13/MKLN1/MYO9A/PALMD/PDZD8/PHIP/PLAA/PLXNC1/PRKDC/PRPF40A/PTPRD/RASA1/RDX/SPAG9/STRIP2/TPM1/ZMYM4/ZRANB1 | 41 |
| BP | GO:0000132 | establishment of mitotic spindle orientation | 9/2221 | 34/18614 | 0.015709315 | 0.120544949 | 0.101874319 | MAD2L1/NDC80/SPDL1/CDK5RAP2/GPSM2/ITGB1/MAPRE1/UBXN2B/ZW10 | 9 |
| BP | GO:0055094 | response to lipoprotein particle | 9/2221 | 34/18614 | 0.015709315 | 0.120544949 | 0.101874319 | ABCA1/CD36/ITGB1/LPL/MIA3/NPC1/PPARG/TLR4/TLR6 | 9 |
| BP | GO:0002700 | regulation of production of molecular mediator of immune response | 33/2221 | 189/18614 | 0.015755919 | 0.120748548 | 0.102046383 | ATAD5/MSH2/ANGPT1/ARG1/BTK/CD226/CD36/CD86/CD96/CR1/DDX1/DDX21/DHX36/IL18/IL1R1/IRAK3/LACC1/MALT1/MAP3K7/MLH1/NLRP3/PANX1/PTPRC/RABGEF1/RIF1/RIPK2/SPINK5/TFRC/THOC1/TLR3/TLR4/TP53BP1/TRIM6 | 33 |
| BP | GO:0046474 | glycerophospholipid biosynthetic process | 36/2221 | 210/18614 | 0.015882672 | 0.121553877 | 0.102726979 | ACSL3/AGPAT5/ATM/BECN1/BMX/DGKH/EFR3A/FABP3/FAR1/FIG4/GNPAT/HTR2A/IMPA1/INPP4B/LIPH/MTM1/MTMR2/MTMR4/MTMR6/PIGA/PIGN/PIGW/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/PIKFYVE/PIP5K1B/PLA2G4A/PLD1/SACM1L/SOCS4 | 36 |
| BP | GO:0030900 | forebrain development | 62/2221 | 397/18614 | 0.015901413 | 0.121553877 | 0.102726979 | ARHGAP11B/ASPM/EZH2/KIF14/STIL/ARL13B/ATIC/ATP7A/ATRX/C21orf91/CASP3/CCDC141/CDH2/CDON/CEP120/CHD7/COL3A1/CORO1C/CTNNB1/DCLK1/DNAH5/DOCK7/DYNC2H1/ERBB4/FAT4/FBXO45/FOXP2/FRS2/GART/HERC1/HIF1A/HOOK3/INHBA/KRAS/LAMB1/LRP2/LRP8/LRRK2/METTL14/MKKS/NF1/NIN/PCM1/PCSK1/PLCB1/RAB3GAP1/RAPGEF2/RBPJ/RPGRIP1L/SCYL2/SEMA3A/SLC38A2/SLC7A11/SYNE2/TACC1/TOP2B/TTC21B/UBA6/UCHL5/WDR47/XRN2/ZEB1 | 62 |
| BP | GO:0009123 | nucleoside monophosphate metabolic process | 16/2221 | 76/18614 | 0.016161475 | 0.123228686 | 0.104142384 | ADK/ATIC/CASK/DLG1/DLG2/DPYD/GART/GMPS/IMPDH2/MAGI3/MPP1/NT5C2/NT5E/PAICS/PPAT/UMPS | 16 |
| BP | GO:0086003 | cardiac muscle cell contraction | 16/2221 | 76/18614 | 0.016161475 | 0.123228686 | 0.104142384 | ABCC9/AKAP9/ANK2/ATP2A2/CACNA2D1/DLG1/DSC2/DSG2/DSP/NUP155/PDE4B/PDE4D/PIK3CA/PKP2/RYR2/SCN1A | 16 |
| BP | GO:0030518 | intracellular steroid hormone receptor signaling pathway | 22/2221 | 115/18614 | 0.016597314 | 0.126391698 | 0.106815492 | BRCA1/CLOCK/CNOT1/CYP7B1/DDX5/DNAJA1/JAK2/KDM3A/KDM4C/NCOA4/NCOR1/NEDD4/PARP1/RNF14/RNF6/TAF7/TMF1/UBA5/UBR5/UFL1/UFM1/UFSP2 | 22 |
| BP | GO:0002366 | leukocyte activation involved in immune response | 48/2221 | 296/18614 | 0.016641985 | 0.12657166 | 0.10696758 | ATAD5/MSH2/SUCNR1/ATP7A/BTK/C12orf4/CD180/CD84/CD86/CLEC4D/CR1/DOCK10/DOCK11/DOCK2/EIF2AK4/ENTPD7/FCGR3A/FER/FGL2/GAPT/HAVCR2/HMGB1/HSPD1/IL18/LCP1/LIG4/LYN/MALT1/MLH1/MSH6/NBN/NCKAP1L/NLRP3/PHF14/PIK3CG/PTPRC/RAB27A/RABGEF1/RC3H2/RIF1/RIPK2/RORA/STXBP3/SWAP70/TFRC/THOC1/TLR4/TP53BP1 | 48 |
| BP | GO:1902903 | regulation of supramolecular fiber organization | 59/2221 | 376/18614 | 0.016717672 | 0.126986757 | 0.107318386 | TPX2/VBP1/ADD3/AKAP13/AKAP9/ALMS1/AP1AR/APC/ARFGEF1/ARHGAP18/ARHGAP28/C9orf72/CAMSAP2/CAPZA2/CCDC88A/CDK5RAP2/CGNL1/CKAP2/CKAP5/CLASP2/CLIP1/DLG1/EPS8/FER/FERMT2/FMN1/HSPA8/LIMA1/MAP1B/MAPRE1/MET/MKKS/NAV3/NCK1/NCKAP1/NCKAP1L/PHLDB2/PIK3CA/PIK3R1/PPFIA1/RASA1/RB1/RDX/RICTOR/ROCK1/ROCK2/SCIN/SNX9/SPTAN1/SVIL/SWAP70/TAOK1/TGFBR1/TJP1/TMOD2/TPM1/TWF1/USP8/WDR47 | 59 |
| BP | GO:0000184 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 10/2221 | 40/18614 | 0.016748904 | 0.127063562 | 0.107383294 | EIF3E/EIF4A3/ETF1/GSPT1/NBAS/NCBP1/NCBP2/PNRC2/UPF2/UPF3B | 10 |
| BP | GO:0001508 | action potential | 26/2221 | 142/18614 | 0.016975774 | 0.128622487 | 0.108700765 | AKAP6/AKAP9/ANK2/ANK3/ATP1B1/ATP2A2/CACNA2D1/CD36/CNR1/CXADR/DLG1/DMD/DSC2/DSG2/DSP/FMR1/KCND2/NRCAM/NUP155/PKP2/PTPN3/RYR2/SCN1A/SCN9A/SLMAP/USP53 | 26 |
| BP | GO:0002520 | immune system development | 34/2221 | 197/18614 | 0.016998067 | 0.1286294 | 0.108706607 | ATAD5/CCNB2/MSH2/POLQ/ADAM17/ATM/CTNNB1/HAVCR2/HMGB1/HMGB2/HSPD1/IL2RA/IL7R/IRAK3/LIG4/LRRC17/LYN/MLH1/MSH3/MSH6/NBN/PPP2R3C/PRKDC/PTPRC/RC3H2/RIF1/SAMHD1/SWAP70/TFRC/TGFBR1/THOC1/TP53BP1/XRCC4/ZBTB1 | 34 |
| BP | GO:0048278 | vesicle docking | 14/2221 | 64/18614 | 0.017099832 | 0.129236921 | 0.109220032 | BLOC1S6/CEP83/CFTR/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/RAB8B/SNAP25/STX17/STXBP3/SYTL2/USO1 | 14 |
| BP | GO:0016574 | histone ubiquitination | 11/2221 | 46/18614 | 0.017293428 | 0.130209339 | 0.110041837 | BRCA1/BRCA2/BRCC3/CTR9/DTX3L/LEO1/RNF20/SUZ12/TRIP12/UBR2/UBR5 | 11 |
| BP | GO:0035384 | thioester biosynthetic process | 11/2221 | 46/18614 | 0.017293428 | 0.130209339 | 0.110041837 | ELOVL6/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/DLD/ELOVL2/ELOVL7/PPT1/SLC27A2 | 11 |
| BP | GO:0071616 | acyl-CoA biosynthetic process | 11/2221 | 46/18614 | 0.017293428 | 0.130209339 | 0.110041837 | ELOVL6/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/DLD/ELOVL2/ELOVL7/PPT1/SLC27A2 | 11 |
| BP | GO:0061647 | histone H3-K9 modification | 8/2221 | 29/18614 | 0.017373234 | 0.130392266 | 0.110196432 | BRCA1/CHEK1/ARID4A/ARID4B/RIF1/SETD7/SETDB2/SUV39H2 | 8 |
| BP | GO:1904385 | cellular response to angiotensin | 8/2221 | 29/18614 | 0.017373234 | 0.130392266 | 0.110196432 | BRIP1/CDC6/AHCYL1/INHBA/NFE2L2/RAP1GDS1/ROCK1/ROCK2 | 8 |
| BP | GO:0099024 | plasma membrane invagination | 13/2221 | 58/18614 | 0.017382746 | 0.130392266 | 0.110196432 | ABCA1/ARHGAP12/BECN1/BIN2/C3/CD36/CLCN3/ITGA2/MSR1/NCKAP1L/SNX9/SPIRE1/STAP1 | 13 |
| BP | GO:0002762 | negative regulation of myeloid leukocyte differentiation | 12/2221 | 52/18614 | 0.017471949 | 0.130784455 | 0.110527876 | CTNNB1/FBN1/INHBA/LRRC17/LYN/NF1/PIK3R1/PTPN2/TLR3/TLR4/TNFAIP6/ZNF675 | 12 |
| BP | GO:0030433 | ubiquitin-dependent ERAD pathway | 17/2221 | 83/18614 | 0.017478508 | 0.130784455 | 0.110527876 | UBXN8/CANX/CCDC47/DNAJC10/EDEM3/ERLIN1/HSP90B1/HSPA5/NFE2L2/PSMC6/SEL1L/STT3B/UBE4A/UBXN4/USP14/VCP/YOD1 | 17 |
| BP | GO:0042116 | macrophage activation | 21/2221 | 109/18614 | 0.017580294 | 0.131382666 | 0.111033433 | SUCNR1/ATM/CD84/FCGR3A/HAVCR2/HSPD1/IFNGR1/JAK2/LRRK2/MIR142/MMP8/PJA2/PLA2G4A/PTPRC/RORA/STAP1/TLR1/TLR2/TLR3/TLR4/TLR6 | 21 |
| BP | GO:0050803 | regulation of synapse structure or activity | 40/2221 | 240/18614 | 0.01790377 | 0.133634095 | 0.112936149 | ADAM10/CAPRIN1/CAPRIN2/CDH2/CDKL5/CHD4/CTNNB1/CTTNBP2/DHX36/EPHA4/FLRT2/FLRT3/HSPA8/IL1RAP/ITGB1/LRP8/LRRK2/LRRTM2/MEF2C/MIR30B/MYCBP2/NEDD4/NF1/NLGN1/NRCAM/OGT/PLXNC1/PPT1/PTPN13/PTPRD/PTPRO/ROCK1/RPS6KA5/SIPA1L1/SLC7A11/TANC2/THBS2/TLR2/VCP/VPS35 | 40 |
| BP | GO:1901568 | fatty acid derivative metabolic process | 16/2221 | 77/18614 | 0.018207948 | 0.135736082 | 0.114712569 | ELOVL6/ACACA/ACAT1/ACSL1/ACSL3/ACSL4/ACSS3/ELOVL2/ELOVL7/FAR1/FAR2/HSD17B4/OXCT1/PAM/PPT1/SLC27A2 | 16 |
| BP | GO:0150115 | cell-substrate junction organization | 20/2221 | 103/18614 | 0.018599236 | 0.138240564 | 0.116829144 | CLASP2/CORO1C/DST/EPHA3/FERMT2/FMN1/ITGA2/ITGA6/ITGB3/LAMC1/MACF1/MAP4K4/PHLDB2/PIK3R1/PTPRK/RAB8B/ROCK1/ROCK2/SLK/VCL | 20 |
| BP | GO:0008654 | phospholipid biosynthetic process | 42/2221 | 255/18614 | 0.018767388 | 0.138240564 | 0.116829144 | ABCA8/ACSL3/AGPAT5/ATM/BECN1/BMX/DGKH/EFR3A/FABP3/FAR1/FIG4/GNPAT/HMGCS1/HTR2A/IDH1/IDI1/IMPA1/INPP4B/LIPH/MTM1/MTMR2/MTMR4/MTMR6/OSBP/PIGA/PIGN/PIGW/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/PIKFYVE/PIP5K1B/PLA2G4A/PLD1/SACM1L/SOCS4/SPTLC1 | 42 |
| BP | GO:0002320 | lymphoid progenitor cell differentiation | 7/2221 | 24/18614 | 0.01881509 | 0.138240564 | 0.116829144 | FNIP1/LIG4/NUDT21/PRKDC/SOS1/SOS2/ZBTB1 | 7 |
| BP | GO:0006730 | one-carbon metabolic process | 7/2221 | 24/18614 | 0.01881509 | 0.138240564 | 0.116829144 | AHCYL1/AHCYL2/ALDH1L2/MAT2A/MTHFD1/MTHFD1L/MTHFD2 | 7 |
| BP | GO:0007097 | nuclear migration | 7/2221 | 24/18614 | 0.01881509 | 0.138240564 | 0.116829144 | CEP120/DOCK7/DYNC1H1/HOOK3/LMNB1/PCM1/SYNE2 | 7 |
| BP | GO:0010839 | negative regulation of keratinocyte proliferation | 7/2221 | 24/18614 | 0.01881509 | 0.138240564 | 0.116829144 | CASK/CD109/IFT57/IFT74/IFT80/PTPRK/ZEB1 | 7 |
| BP | GO:0035458 | cellular response to interferon-beta | 7/2221 | 24/18614 | 0.01881509 | 0.138240564 | 0.116829144 | AIM2/IFI16/MNDA/PNPT1/STAT1/TLR3/TRIM6 | 7 |
| BP | GO:0060999 | positive regulation of dendritic spine development | 9/2221 | 35/18614 | 0.018967078 | 0.138240564 | 0.116829144 | C21orf91/CAPRIN1/CAPRIN2/DHX36/FMR1/LLPH/LRP8/MAPK6/NLGN1 | 9 |
| BP | GO:0000722 | telomere maintenance via recombination | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | BRCA2/ERCC4/RAD50/SMC5/SMC6 | 5 |
| BP | GO:0006047 | UDP-N-acetylglucosamine metabolic process | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | GFPT1/GNPDA2/GNPNAT1/PGM3/UAP1 | 5 |
| BP | GO:0006167 | AMP biosynthetic process | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | ADK/ATIC/GART/PAICS/PPAT | 5 |
| BP | GO:0007100 | mitotic centrosome separation | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | CHEK1/KIF11/NEK2/MAP9/UBXN2B | 5 |
| BP | GO:0015670 | carbon dioxide transport | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | AQP4/HBA2/HBB/HBD/HBG2 | 5 |
| BP | GO:0016078 | tRNA catabolic process | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | DICER1/EXOSC9/NSUN2/POP1/SLFN13 | 5 |
| BP | GO:0018206 | peptidyl-methionine modification | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | METAP1/METAP2/NAA15/NAA25/NAA35 | 5 |
| BP | GO:0043201 | response to leucine | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | PIK3C3/PIK3CA/SESN3/UBR1/UBR2 | 5 |
| BP | GO:0043650 | dicarboxylic acid biosynthetic process | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | KMO/KYNU/MTHFD1/MTHFD1L/SLC25A12 | 5 |
| BP | GO:0045144 | meiotic sister chromatid segregation | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | BUB1/BUB1B/RAD21/SMC1A/SMC3 | 5 |
| BP | GO:0051177 | meiotic sister chromatid cohesion | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | BUB1/BUB1B/RAD21/SMC1A/SMC3 | 5 |
| BP | GO:0051231 | spindle elongation | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | KIF11/KIF23/KIF4A/PRC1/RACGAP1 | 5 |
| BP | GO:0051255 | spindle midzone assembly | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | KIF23/KIF4A/PRC1/MLH1/RACGAP1 | 5 |
| BP | GO:0060330 | regulation of response to type II interferon | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | ARG1/PARP14/PARP9/PPARG/PTPN2 | 5 |
| BP | GO:0060334 | regulation of type II interferon-mediated signaling pathway | 5/2221 | 14/18614 | 0.019072418 | 0.138240564 | 0.116829144 | ARG1/PARP14/PARP9/PPARG/PTPN2 | 5 |
| BP | GO:0050807 | regulation of synapse organization | 39/2221 | 234/18614 | 0.019197451 | 0.138979379 | 0.117453528 | ADAM10/CAPRIN1/CAPRIN2/CDH2/CDKL5/CHD4/CTNNB1/CTTNBP2/DHX36/EPHA4/FLRT2/FLRT3/HSPA8/IL1RAP/ITGB1/LRP8/LRRK2/LRRTM2/MEF2C/MIR30B/MYCBP2/NEDD4/NF1/NLGN1/NRCAM/OGT/PLXNC1/PTPN13/PTPRD/PTPRO/ROCK1/RPS6KA5/SIPA1L1/SLC7A11/TANC2/THBS2/TLR2/VCP/VPS35 | 39 |
| BP | GO:0045739 | positive regulation of DNA repair | 24/2221 | 130/18614 | 0.019303003 | 0.139575564 | 0.117957372 | BRCA1/RAD51AP1/ACTR2/ACTR8/ARID2/BRCC3/BRD7/DHX9/EPC2/ERCC6/HMGB1/ING3/MORF4L2/PARP1/PBRM1/PRKDC/RBBP8/RIF1/SETMAR/SMCHD1/SPIRE1/UCHL5/USP1/WDR48 | 24 |
| BP | GO:0006368 | transcription elongation by RNA polymerase II | 21/2221 | 110/18614 | 0.01936056 | 0.139823683 | 0.118167062 | EZH2/CCNT1/CTNNB1/CTR9/ELL2/ERCC6/HNRNPU/INTS12/INTS6/INTS7/LARP7/LEO1/MED23/MED6/NCBP1/NCBP2/RTF1/SUPT16H/TCEA1/WDR43/ZMYND11 | 21 |
| BP | GO:0032507 | maintenance of protein location in cell | 14/2221 | 65/18614 | 0.019471824 | 0.140223716 | 0.118505135 | ANK3/CCDC88A/HK2/HNRNPU/HSPA5/KDELR3/SCIN/SP100/SYNE1/TOPORS/TWF1/VPS13A/VPS13C/VPS13D | 14 |
| BP | GO:0098930 | axonal transport | 14/2221 | 65/18614 | 0.019471824 | 0.140223716 | 0.118505135 | KIF4A/AP3B1/AP3M1/BLOC1S6/DLG2/DST/DYNC1H1/HIF1A/KIF3A/KIF5B/OPA1/RAB27B/SYBU/TRAK2 | 14 |
| BP | GO:0044000 | movement in host | 32/2221 | 185/18614 | 0.019519231 | 0.140223716 | 0.118505135 | CDK1/ACE2/CD86/CHMP2B/CLDN1/CR1/CTSL/CXADR/DPP4/EPS15/EXOC2/GYPA/HMGB1/HTR2A/IDE/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/KPNA3/MRC1/NPC1/NUP153/PIKFYVE/TFRC/TRIM22/TRIM38/TRIM59/TRIM6/WWP1/ZNF502 | 32 |
| BP | GO:0009226 | nucleotide-sugar biosynthetic process | 6/2221 | 19/18614 | 0.01964275 | 0.140223716 | 0.118505135 | GFPT1/GNPDA2/GNPNAT1/PGM3/UAP1/UGDH | 6 |
| BP | GO:0009301 | snRNA transcription | 6/2221 | 19/18614 | 0.01964275 | 0.140223716 | 0.118505135 | ELL2/ICE1/ICE2/LARP7/USPL1/ZNF143 | 6 |
| BP | GO:0030050 | vesicle transport along actin filament | 6/2221 | 19/18614 | 0.01964275 | 0.140223716 | 0.118505135 | FNBP1L/MYO1B/MYO1E/MYO5A/MYO5C/MYO6 | 6 |
| BP | GO:0035338 | long-chain fatty-acyl-CoA biosynthetic process | 6/2221 | 19/18614 | 0.01964275 | 0.140223716 | 0.118505135 | ELOVL6/ACSL1/ACSL3/ACSL4/ELOVL2/ELOVL7 | 6 |
| BP | GO:0044070 | regulation of monoatomic anion transport | 6/2221 | 19/18614 | 0.01964275 | 0.140223716 | 0.118505135 | ABCB1/AHCYL1/ATP8B1/CFTR/GOPC/RIPK1 | 6 |
| BP | GO:0098543 | detection of other organism | 6/2221 | 19/18614 | 0.01964275 | 0.140223716 | 0.118505135 | NAIP/NLRC4/TLR1/TLR2/TLR4/TLR6 | 6 |
| BP | GO:1902807 | negative regulation of cell cycle G1/S phase transition | 19/2221 | 97/18614 | 0.019649035 | 0.140223716 | 0.118505135 | EZH2/APC/ATM/BRD7/DCUN1D3/DLG1/GIGYF2/GPNMB/INHBA/JADE1/MDM2/MIR15B/MIR30C2/PRKDC/RB1/RBL2/RFWD3/SDE2/SLFN11 | 19 |
| BP | GO:0051294 | establishment of spindle orientation | 10/2221 | 41/18614 | 0.019848724 | 0.14131352 | 0.119426145 | MAD2L1/NDC80/SPAG5/SPDL1/CDK5RAP2/GPSM2/ITGB1/MAPRE1/UBXN2B/ZW10 | 10 |
| BP | GO:0150077 | regulation of neuroinflammatory response | 10/2221 | 41/18614 | 0.019848724 | 0.14131352 | 0.119426145 | ATM/IGF1/IL18/LRRK2/MIR142/MIR181B1/MMP8/PTGS2/PTPRC/STAP1 | 10 |
| BP | GO:0051960 | regulation of nervous system development | 70/2221 | 461/18614 | 0.019927707 | 0.141402897 | 0.119501679 | ASPM/EZH2/HDAC2/KIF14/XRCC2/CAPRIN1/CAPRIN2/CDKL5/CDON/CHD7/CTNNA1/CTNNB1/DHX36/DICER1/DLG1/DOCK7/EIF2AK3/EPHA4/FIG4/FLRT2/FLRT3/GOLGA4/HGF/HIF1A/HLTF/HMGB2/HOOK3/IFRD1/IL1RAP/IL6ST/ITGB1/KRAS/LIG4/LRP2/LRP8/LRRTM2/LYN/MACF1/MAP1B/MAP3K13/MIR142/MIR181B1/MTMR2/NAP1L1/NF1/NIN/NLGN1/PCM1/PLAG1/PLXNC1/PRKCI/PRTG/PTPN13/PTPRD/RAPGEF2/RB1/RNF6/RUFY3/SEMA3A/SEMA3C/SEMA3D/SKIL/SLC25A12/SNW1/SPP1/THBS2/TLR2/UFL1/XRCC5/ZPR1 | 70 |
| BP | GO:0001961 | positive regulation of cytokine-mediated signaling pathway | 13/2221 | 59/18614 | 0.019931791 | 0.141402897 | 0.119501679 | ADAM17/CASP1/CASP4/HIF1A/IL1R1/PARP14/PARP9/RIPK1/RIPK2/TBK1/TRIM44/TRIM6/USP27X | 13 |
| BP | GO:0031122 | cytoplasmic microtubule organization | 13/2221 | 59/18614 | 0.019931791 | 0.141402897 | 0.119501679 | CAMSAP2/CCDC88A/CENPJ/CEP120/CLIP1/DLG1/DYNC1H1/EZR/HOOK1/HOOK3/KPNB1/PCM1/SLK | 13 |
| BP | GO:0045862 | positive regulation of proteolysis | 57/2221 | 365/18614 | 0.020100742 | 0.142433526 | 0.120372678 | HDAC2/ADAM9/AIFM1/AIM2/ANKIB1/ARIH1/ASPH/CAPN3/CASP1/CASP8AP2/CR1/CTSK/CTSL/CTSS/CYCS/DDX3X/EGF/EIF2AK3/EPHA4/FAS/FMR1/GCLC/HECTD1/HMGB1/HSPD1/IFI16/IFT57/JAK2/L3MBTL3/LRRK2/LYN/MALT1/MDM2/NFE2L2/NLRC4/NLRP3/NUB1/OGT/PPARG/PSMC1/PSMC2/PSMC6/RIPK2/RNF14/RNF19A/RNF217/ROCK2/SENP1/SNX9/SOCS4/TAF1/TANK/TMTC3/TNFSF15/UACA/USP13/VCP | 57 |
| BP | GO:0030834 | regulation of actin filament depolymerization | 12/2221 | 53/18614 | 0.020205009 | 0.142724289 | 0.120618406 | ADD3/CAPZA2/EPS8/LIMA1/PIK3CA/RDX/SCIN/SPTAN1/SVIL/SWAP70/TMOD2/TWF1 | 12 |
| BP | GO:0097300 | programmed necrotic cell death | 12/2221 | 53/18614 | 0.020205009 | 0.142724289 | 0.120618406 | AIFM1/BIRC2/BIRC3/CYLD/DNM1L/FAS/OGT/PARP1/PYGL/RIPK1/TLR3/TRPM7 | 12 |
| BP | GO:0042073 | intraciliary transport | 11/2221 | 47/18614 | 0.020212948 | 0.142724289 | 0.120618406 | DYNC2H1/IFT57/IFT74/IFT80/LCA5/PCM1/RPGR/SSX2IP/TTC21B/WDR19/WDR35 | 11 |
| BP | GO:0051091 | positive regulation of DNA-binding transcription factor activity | 44/2221 | 271/18614 | 0.020715222 | 0.145635744 | 0.12307892 | AIM2/ARID5B/BTK/CAPN3/CD36/CHUK/CLOCK/CTNNB1/DHX9/EIF2AK2/ERC1/FER/IL18/IL18RAP/IL1RAP/IRAK3/JAK2/JMY/LRP6/LRP8/MALT1/MAP3K13/MAP3K7/MTDH/NLRC4/NLRP3/PPARG/PRKCI/PRKD1/RIPK1/RIPK2/RPS6KA5/TAF1/TFRC/TLR2/TLR3/TLR4/TLR6/TP53BP1/TRAF5/TRIM22/TRIM38/TRIM6/USP14 | 44 |
| BP | GO:0001959 | regulation of cytokine-mediated signaling pathway | 29/2221 | 165/18614 | 0.020721257 | 0.145635744 | 0.12307892 | ADAM17/ANGPT1/ARG1/CASP1/CASP4/CYLD/HIF1A/IL1R1/IRAK3/NAIP/OTUD4/PARP14/PARP9/PPARG/PTPN11/PTPN2/PTPRC/RABGEF1/RIPK1/RIPK2/SAMHD1/STAP1/TBK1/TRIM44/TRIM6/USP27X/VRK2/YTHDF3/ZNF675 | 29 |
| BP | GO:0061572 | actin filament bundle organization | 29/2221 | 165/18614 | 0.020721257 | 0.145635744 | 0.12307892 | ALMS1/ARHGAP28/CALD1/CCDC88A/CGNL1/CLASP2/CUL3/EPS8/EZR/FERMT2/HSP90B1/LCP1/LIMA1/MET/MKKS/MYO1B/PHLDB2/PIK3R1/PLS1/PLS3/PPFIA1/RDX/ROCK1/ROCK2/SPIRE1/SWAP70/TGFBR1/TJP1/TPM1 | 29 |
| BP | GO:0060996 | dendritic spine development | 18/2221 | 91/18614 | 0.020722107 | 0.145635744 | 0.12307892 | HDAC2/PRMT3/C21orf91/CAPRIN1/CAPRIN2/DHX36/DOCK10/EPHA4/FMR1/LLPH/LRP8/LRRK2/MAPK6/MEF2C/NLGN1/SIPA1L1/TANC2/UBA6 | 18 |
| BP | GO:0045216 | cell-cell junction organization | 36/2221 | 214/18614 | 0.020810961 | 0.14608955 | 0.123462438 | ECT2/UGT8/ACE2/ADAM10/ANK2/APC/CDH2/CDH6/CLDN1/CTNNA1/CTNNB1/CXADR/DLG1/DSG2/DSP/EPB41L3/EPHA4/FER/FERMT2/GNPAT/GRHL2/MIR142/MPDZ/MPP7/PKN2/PKP2/POF1B/PRKCI/PTPRO/RDX/ROCK1/ROCK2/STRN/TGFBR1/TJP1/VCL | 36 |
| BP | GO:0002263 | cell activation involved in immune response | 48/2221 | 300/18614 | 0.020836244 | 0.146096558 | 0.12346836 | ATAD5/MSH2/SUCNR1/ATP7A/BTK/C12orf4/CD180/CD84/CD86/CLEC4D/CR1/DOCK10/DOCK11/DOCK2/EIF2AK4/ENTPD7/FCGR3A/FER/FGL2/GAPT/HAVCR2/HMGB1/HSPD1/IL18/LCP1/LIG4/LYN/MALT1/MLH1/MSH6/NBN/NCKAP1L/NLRP3/PHF14/PIK3CG/PTPRC/RAB27A/RABGEF1/RC3H2/RIF1/RIPK2/RORA/STXBP3/SWAP70/TFRC/THOC1/TLR4/TP53BP1 | 48 |
| BP | GO:0043405 | regulation of MAP kinase activity | 32/2221 | 186/18614 | 0.020962021 | 0.146807359 | 0.124069069 | EZH2/ADAM9/AIDA/AKAP13/DNAJA1/EGF/EPHA4/FLT1/HIPK3/HMGCR/HTR2A/IRAK3/LRRK2/LYN/MAP3K13/MAP3K4/MAP3K7/MEF2C/NF1/PDCD4/PDGFC/PDGFD/PIK3CB/PIK3CG/PPARG/PTPRC/RGS2/SOS1/TAOK3/TLR4/TLR6/ZNF675 | 32 |
| BP | GO:0045860 | positive regulation of protein kinase activity | 57/2221 | 366/18614 | 0.021124545 | 0.147773558 | 0.124885619 | BORA/CDC6/CENPE/ECT2/EZH2/KIF14/TPX2/ACSL1/ADAM17/ADAM9/AKAP13/ANGPT1/CAB39/CCDC88A/CD86/DDX3X/DLG1/EGF/EPHA4/ETAA1/FERMT2/FLT1/HSP90AA1/HSP90AB1/HTR2A/IGF1/IL18/IQGAP1/ITGB3/JAK2/LRP8/LRRK2/MALT1/MAP3K13/MAP3K4/MAP3K7/MEF2C/OSBPL8/PDGFC/PDGFD/PIBF1/PIK3CG/PPP2CA/PPP2R3C/PTPRC/RAPGEF2/SNX9/SYAP1/TAB2/TAOK3/TLR3/TLR4/TLR6/TNFSF15/TOM1L1/VLDLR/XRCC5 | 57 |
| BP | GO:0000380 | alternative mRNA splicing, via spliceosome | 15/2221 | 72/18614 | 0.021301847 | 0.148840778 | 0.125787542 | DDX5/DHX9/FMR1/FXR1/HNRNPA1/HNRNPU/NCBP1/NCBP2/NSRP1/RBM25/RSRC1/SLU7/SMU1/WTAP/YTHDC1 | 15 |
| BP | GO:0060048 | cardiac muscle contraction | 25/2221 | 138/18614 | 0.021432786 | 0.149581948 | 0.126413915 | ABCC9/ACE2/AKAP9/ANK2/ATP1B1/ATP2A2/CACNA2D1/CLIC2/DLG1/DMD/DSC2/DSG2/DSP/HSP90AA1/NUP155/PDE4B/PDE4D/PIK3CA/PIK3CG/PKP2/RGS2/RYR2/SCN1A/TPM1/TTN | 25 |
| BP | GO:0009895 | negative regulation of catabolic process | 53/2221 | 337/18614 | 0.021488092 | 0.149794161 | 0.126593259 | MAD2L1/PBK/BECN1/CNR1/CSDE1/DHX36/DHX9/DKC1/EIF4G2/FMR1/HERC1/HGF/HMGCR/HNRNPU/HP/HSP90AB1/IRAK3/LRPPRC/LRRK2/MET/MTM1/MTMR2/MYCBP2/NBAS/NCOR1/NPC1/NSUN2/OGT/PDE3B/PHAX/PHF20L1/PIK3CA/PIK3CG/PTPN3/ROCK1/RYBP/SCFD1/SDCBP/SLC25A12/SLC4A1/SYNCRIP/TAB2/TAB3/TAF1/TIMP4/TRAF5/UCHL5/USP14/USP25/USP7/USP8/USP9X/VPS35 | 53 |
| BP | GO:0034620 | cellular response to unfolded protein | 19/2221 | 98/18614 | 0.02173408 | 0.151271319 | 0.127841627 | AGR2/ATF6/DNAJC10/EIF2AK2/EIF2AK3/EIF2S1/HSPA13/HSPA5/HSPA8/HSPA9/HSPD1/NCK1/NFE2L2/PARP8/PIK3R1/PTPN2/UFL1/VCP/YOD1 | 19 |
| BP | GO:0035264 | multicellular organism growth | 26/2221 | 145/18614 | 0.021750281 | 0.151271319 | 0.127841627 | STIL/XRCC2/ARID5B/ATM/ATRX/CHD7/COL3A1/ERCC6/EZR/GIGYF2/GRHL2/MKKS/NIPBL/PALB2/PIK3CA/PLAG1/PLS1/PTPN11/RASAL2/RBBP6/RC3H2/SOS1/TBL1XR1/TNKS2/WDR11/WDR48 | 26 |
| BP | GO:0035967 | cellular response to topologically incorrect protein | 22/2221 | 118/18614 | 0.021917848 | 0.152260711 | 0.128677777 | AGR2/ATF6/CUL3/DNAJC10/EIF2AK2/EIF2AK3/EIF2S1/HSPA13/HSPA5/HSPA8/HSPA9/HSPD1/NCK1/NFE2L2/PARP8/PIK3R1/PTPN2/UFL1/UGGT1/UGGT2/VCP/YOD1 | 22 |
| BP | GO:1903051 | negative regulation of proteolysis involved in protein catabolic process | 14/2221 | 66/18614 | 0.022084034 | 0.153238232 | 0.129503895 | PBK/EPHA4/HSP90AB1/MTM1/OGT/PHF20L1/RYBP/SDCBP/TAF1/UCHL5/USP14/USP25/USP7/USP9X | 14 |
| BP | GO:0072331 | signal transduction by p53 class mediator | 30/2221 | 173/18614 | 0.022428091 | 0.155446306 | 0.131369971 | ATAD5/BRCA2/CHEK1/MSH2/ATM/ATR/ATRX/DDX5/IFI16/ING2/JMY/KAT6A/MDM2/MIR186/MYO6/NBN/PAK1IP1/PLA2R1/RPF2/RPS6KA6/RRM2B/RRS1/SNW1/SP100/TAF1/TOPORS/TP53BP2/USP15/USP7/ZNF385B | 30 |
| BP | GO:0006699 | bile acid biosynthetic process | 9/2221 | 36/18614 | 0.022687315 | 0.156798606 | 0.13251282 | ABCD3/BAAT/CYP7B1/OSBP/OSBPL3/OSBPL9/SCP2/SLC27A2/STARD4 | 9 |
| BP | GO:0060218 | hematopoietic stem cell differentiation | 9/2221 | 36/18614 | 0.022687315 | 0.156798606 | 0.13251282 | CHD2/EIF2AK2/HSPA9/MLLT3/NFE2L2/PRKDC/PUS7/UFL1/XRCC5 | 9 |
| BP | GO:0045185 | maintenance of protein location | 18/2221 | 92/18614 | 0.022980864 | 0.156798606 | 0.13251282 | ANK3/CCDC88A/FBN1/G3BP2/HK2/HNRNPU/HSPA5/KDELR3/LTBP1/SCIN/SP100/SYNE1/TOPORS/TWF1/VPS13A/VPS13C/VPS13D/YWHAB | 18 |
| BP | GO:0060998 | regulation of dendritic spine development | 12/2221 | 54/18614 | 0.023243411 | 0.156798606 | 0.13251282 | HDAC2/C21orf91/CAPRIN1/CAPRIN2/DHX36/FMR1/LLPH/LRP8/MAPK6/MEF2C/NLGN1/TANC2 | 12 |
| BP | GO:1904645 | response to amyloid-beta | 12/2221 | 54/18614 | 0.023243411 | 0.156798606 | 0.13251282 | MIRLET7F1/CACNA2D1/CASP4/CD36/EPHA4/IGF1/ITGA4/PARP1/SNX6/TLR4/TLR6/VCAM1 | 12 |
| BP | GO:0042177 | negative regulation of protein catabolic process | 21/2221 | 112/18614 | 0.023338234 | 0.156798606 | 0.13251282 | MAD2L1/PBK/HMGCR/HSP90AB1/IRAK3/MTM1/MYCBP2/OGT/PHF20L1/PTPN3/ROCK1/RYBP/SDCBP/TIMP4/UCHL5/USP14/USP25/USP7/USP8/USP9X/VPS35 | 21 |
| BP | GO:0002714 | positive regulation of B cell mediated immunity | 10/2221 | 42/18614 | 0.02334757 | 0.156798606 | 0.13251282 | ATAD5/MSH2/BTK/C3/CD226/MLH1/PTPRC/RIF1/TFRC/TP53BP1 | 10 |
| BP | GO:0002891 | positive regulation of immunoglobulin mediated immune response | 10/2221 | 42/18614 | 0.02334757 | 0.156798606 | 0.13251282 | ATAD5/MSH2/BTK/C3/CD226/MLH1/PTPRC/RIF1/TFRC/TP53BP1 | 10 |
| BP | GO:0006458 | 'de novo' protein folding | 10/2221 | 42/18614 | 0.02334757 | 0.156798606 | 0.13251282 | CCT2/DNAJC2/DNAJC7/HSPA13/HSPA5/HSPA8/HSPA9/HSPD1/HSPH1/UGGT1 | 10 |
| BP | GO:0045429 | positive regulation of nitric oxide biosynthetic process | 10/2221 | 42/18614 | 0.02334757 | 0.156798606 | 0.13251282 | CD36/HBB/HSP90AA1/HSP90AB1/JAK2/MIR181B1/MMP8/PTGS2/TLR4/TLR6 | 10 |
| BP | GO:0032956 | regulation of actin cytoskeleton organization | 54/2221 | 346/18614 | 0.023388241 | 0.156798606 | 0.13251282 | ECT2/ABL2/ADD3/AKAP13/ALMS1/AP1AR/ARFGEF1/ARHGAP18/ARHGAP28/C9orf72/CAPZA2/CCDC88A/CD2AP/CGNL1/CLASP2/DLG1/EPHA3/EPS8/FER/FERMT2/FMN1/IQGAP1/IQGAP2/ITGB3/LIMA1/MET/MKKS/NCK1/NCKAP1/NCKAP1L/NEB/PAM/PDGFRA/PHLDB2/PIK3CA/PIK3R1/PPFIA1/RASA1/RDX/RICTOR/ROCK1/ROCK2/SCIN/SNX9/SPTAN1/STAP1/SVIL/SWAP70/TAOK1/TGFBR1/TJP1/TMOD2/TPM1/TWF1 | 54 |
| BP | GO:0003056 | regulation of vascular associated smooth muscle contraction | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | ARHGAP42/ATP2B1/DOCK5/ZDHHC21 | 4 |
| BP | GO:0009113 | purine nucleobase biosynthetic process | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | GART/GMPS/PAICS/PPAT | 4 |
| BP | GO:0033523 | histone H2B ubiquitination | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | CTR9/DTX3L/LEO1/RNF20 | 4 |
| BP | GO:0043653 | mitochondrial fragmentation involved in apoptotic process | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | ATG3/DNM1L/ERBB4/VPS35 | 4 |
| BP | GO:0048304 | positive regulation of isotype switching to IgG isotypes | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | ATAD5/MSH2/MLH1/PTPRC | 4 |
| BP | GO:0051660 | establishment of centrosome localization | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | MAD2L1/CEP83/DLG1/EZR | 4 |
| BP | GO:0060368 | regulation of Fc receptor mediated stimulatory signaling pathway | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | CD226/LYN/PTPRC/RABGEF1 | 4 |
| BP | GO:0070339 | response to bacterial lipopeptide | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | CD36/TLR1/TLR2/TLR6 | 4 |
| BP | GO:0070391 | response to lipoteichoic acid | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | CD36/RIPK2/TLR2/TLR4 | 4 |
| BP | GO:0071220 | cellular response to bacterial lipoprotein | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | CD36/TLR1/TLR2/TLR6 | 4 |
| BP | GO:0071221 | cellular response to bacterial lipopeptide | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | CD36/TLR1/TLR2/TLR6 | 4 |
| BP | GO:0071223 | cellular response to lipoteichoic acid | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | CD36/RIPK2/TLR2/TLR4 | 4 |
| BP | GO:0090394 | negative regulation of excitatory postsynaptic potential | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | EIF4A3/LRRK2/MIR30B/MTMR2 | 4 |
| BP | GO:1900246 | positive regulation of RIG-I signaling pathway | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | ANKRD17/DDX60/PUM2/USP15 | 4 |
| BP | GO:1903959 | regulation of monoatomic anion transmembrane transport | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | ABCB1/CFTR/GOPC/RIPK1 | 4 |
| BP | GO:1903980 | positive regulation of microglial cell activation | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | LRRK2/MIR142/MMP8/STAP1 | 4 |
| BP | GO:1905216 | positive regulation of RNA binding | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | EIF3D/EIF3E/FMR1/NCBP1 | 4 |
| BP | GO:2000659 | regulation of interleukin-1-mediated signaling pathway | 4/2221 | 10/18614 | 0.023448017 | 0.156798606 | 0.13251282 | IL1R1/OTUD4/VRK2/ZNF675 | 4 |
| BP | GO:0030318 | melanocyte differentiation | 7/2221 | 25/18614 | 0.023509366 | 0.156798606 | 0.13251282 | ADAMTS9/BLOC1S6/ENPP1/MEF2C/RAB27A/USP13/ZEB2 | 7 |
| BP | GO:0046856 | phosphatidylinositol dephosphorylation | 7/2221 | 25/18614 | 0.023509366 | 0.156798606 | 0.13251282 | FIG4/INPP4B/MTM1/MTMR2/MTMR4/MTMR6/SACM1L | 7 |
| BP | GO:0051016 | barbed-end actin filament capping | 7/2221 | 25/18614 | 0.023509366 | 0.156798606 | 0.13251282 | ADD3/CAPZA2/EPS8/RDX/SCIN/SVIL/TWF1 | 7 |
| BP | GO:0070423 | nucleotide-binding oligomerization domain containing signaling pathway | 7/2221 | 25/18614 | 0.023509366 | 0.156798606 | 0.13251282 | BIRC2/BIRC3/CYLD/LACC1/MAP3K7/RIPK2/TLR4 | 7 |
| BP | GO:2000001 | regulation of DNA damage checkpoint | 7/2221 | 25/18614 | 0.023509366 | 0.156798606 | 0.13251282 | BRCA1/BRCA2/WDR76/BRCC3/ETAA1/RFWD3/THOC1 | 7 |
| BP | GO:0071260 | cellular response to mechanical stimulus | 15/2221 | 73/18614 | 0.02394736 | 0.159430413 | 0.134736999 | CHEK1/CASP1/CASP5/CASP8AP2/FAS/GCLC/ITGA2/ITGB3/MAP3K1/MAP3K2/PTGS2/SLC38A2/TLR3/TLR4/TLR8 | 15 |
| BP | GO:0002718 | regulation of cytokine production involved in immune response | 22/2221 | 119/18614 | 0.023956964 | 0.159430413 | 0.134736999 | ANGPT1/ARG1/BTK/CD226/CD36/CD96/DDX1/DDX21/DHX36/IL18/IL1R1/IRAK3/LACC1/MALT1/MAP3K7/NLRP3/PANX1/RABGEF1/RIPK2/TLR3/TLR4/TRIM6 | 22 |
| BP | GO:0003300 | cardiac muscle hypertrophy | 19/2221 | 99/18614 | 0.023984507 | 0.159437339 | 0.134742852 | EZH2/HDAC2/AKAP13/AKAP6/ATP2A2/BECN1/IGF1/IL6ST/MIR15B/PARP1/PPARG/RAP1GDS1/RGS2/ROCK1/ROCK2/RYR2/SORBS2/TTN/TWF1 | 19 |
| BP | GO:0019915 | lipid storage | 17/2221 | 86/18614 | 0.024256189 | 0.160887797 | 0.135968656 | ABCA1/C3/CD36/ENPP1/ITGAV/ITGB3/LPL/MSR1/NRIP1/OSBPL11/OSBPL8/PLIN2/PPARG/PTPN2/SQLE/STARD4/TTC39B | 17 |
| BP | GO:2000781 | positive regulation of double-strand break repair | 17/2221 | 86/18614 | 0.024256189 | 0.160887797 | 0.135968656 | RAD51AP1/ACTR2/ARID2/BRD7/EPC2/ERCC6/ING3/MORF4L2/PARP1/PBRM1/PRKDC/RBBP8/RIF1/SETMAR/SMCHD1/SPIRE1/WDR48 | 17 |
| BP | GO:0048588 | developmental cell growth | 38/2221 | 231/18614 | 0.02483102 | 0.164519181 | 0.139037592 | AKAP13/AKAP6/ALCAM/C9orf72/CDKL5/CTNNB1/DCLK1/EIF2AK4/FLRT3/GOLGA4/HSP90AA1/HSP90AB1/IFRD1/IGF1/IMPACT/IQGAP1/ITGA4/ITGB1/ITSN2/LLPH/MACF1/MAP1B/MAP3K13/NIN/NRCAM/PLAA/RGS2/RNF6/RUFY3/SEMA3A/SEMA3C/SEMA3D/SORBS2/SPAG9/SPG11/SPP1/USP9X/VCL | 38 |
| BP | GO:1903008 | organelle disassembly | 25/2221 | 140/18614 | 0.025219116 | 0.166364103 | 0.140596763 | CDK1/VRK1/ASCC3/ATG3/BECN1/BNIP3L/CTSK/DNM1L/GFM2/HIF1A/HK2/KIF5B/LRBA/MTIF2/OGT/PLIN2/RB1CC1/SNX30/UBA5/UFL1/UFM1/VCP/VPS13C/VPS13D/ZFAND1 | 25 |
| BP | GO:0006144 | purine nucleobase metabolic process | 6/2221 | 20/18614 | 0.025296126 | 0.166364103 | 0.140596763 | ADK/DPYD/GART/GMPS/PAICS/PPAT | 6 |
| BP | GO:0039535 | regulation of RIG-I signaling pathway | 6/2221 | 20/18614 | 0.025296126 | 0.166364103 | 0.140596763 | ANKRD17/BIRC2/BIRC3/DDX60/PUM2/USP15 | 6 |
| BP | GO:0071243 | cellular response to arsenic-containing substance | 6/2221 | 20/18614 | 0.025296126 | 0.166364103 | 0.140596763 | DDX3X/DHX36/HNRNPA1/SLC38A2/VCP/ZFAND1 | 6 |
| BP | GO:1903978 | regulation of microglial cell activation | 6/2221 | 20/18614 | 0.025296126 | 0.166364103 | 0.140596763 | ATM/LRRK2/MIR142/MMP8/PTPRC/STAP1 | 6 |
| BP | GO:2000269 | regulation of fibroblast apoptotic process | 6/2221 | 20/18614 | 0.025296126 | 0.166364103 | 0.140596763 | XRCC2/API5/CHD8/MIR181B1/PIK3CA/PIK3CG | 6 |
| BP | GO:0002720 | positive regulation of cytokine production involved in immune response | 16/2221 | 80/18614 | 0.025546251 | 0.166364103 | 0.140596763 | CD226/CD36/DDX1/DDX21/DHX36/IL18/IL1R1/LACC1/MALT1/MAP3K7/NLRP3/PANX1/RIPK2/TLR3/TLR4/TRIM6 | 16 |
| BP | GO:2000142 | regulation of DNA-templated transcription initiation | 16/2221 | 80/18614 | 0.025546251 | 0.166364103 | 0.140596763 | ATF7IP/BCLAF1/CAND1/DHX36/ERCC6/HMGB1/MED13/MED23/MED6/PSMC6/SETX/TAF1/TAF2/TAF4B/TAF7/ZNF451 | 16 |
| BP | GO:0002230 | positive regulation of defense response to virus by host | 8/2221 | 31/18614 | 0.025764294 | 0.166364103 | 0.140596763 | AIM2/DTX3L/EIF2AK4/HSP90AA1/PARP9/STAT1/TRIM44/TRIM6 | 8 |
| BP | GO:1903203 | regulation of oxidative stress-induced neuron death | 8/2221 | 31/18614 | 0.025764294 | 0.166364103 | 0.140596763 | CTNNB1/HIF1A/NCOA7/OXR1/PARP1/SLC7A11/TLR4/TLR6 | 8 |
| BP | GO:0034113 | heterotypic cell-cell adhesion | 13/2221 | 61/18614 | 0.025855389 | 0.166364103 | 0.140596763 | CXADR/DSC2/DSG2/DSP/GCNT2/ITGA4/ITGAV/ITGB1/ITGB3/NRCAM/PKP2/PTPRC/VCAM1 | 13 |
| BP | GO:0001325 | formation of extrachromosomal circular DNA | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | BLM/DNA2/NBN/WRN/XRCC5 | 5 |
| BP | GO:0010889 | regulation of sequestering of triglyceride | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | LPL/OSBPL11/OSBPL8/PLIN2/PPARG | 5 |
| BP | GO:0015846 | polyamine transport | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | ATP13A3/ATP13A4/SLC18B1/SLC22A3/TAF7 | 5 |
| BP | GO:0030174 | regulation of DNA-templated DNA replication initiation | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | GMNN/MCM3/MCM6/TICRR/NBN | 5 |
| BP | GO:0042532 | negative regulation of tyrosine phosphorylation of STAT protein | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | GGNBP2/PARP14/PIBF1/PPP2CA/PTPN2 | 5 |
| BP | GO:0046500 | S-adenosylmethionine metabolic process | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | AHCYL1/AHCYL2/AMD1/MAT2A/MTRR | 5 |
| BP | GO:0046653 | tetrahydrofolate metabolic process | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | ATIC/GART/MTHFD1/MTHFD1L/MTHFD2 | 5 |
| BP | GO:0048291 | isotype switching to IgG isotypes | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | ATAD5/MSH2/HSPD1/MLH1/PTPRC | 5 |
| BP | GO:0048820 | hair follicle maturation | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | CTNNB1/NF1/NSUN2/RBPJ/SPINK5 | 5 |
| BP | GO:0051299 | centrosome separation | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | CHEK1/KIF11/NEK2/MAP9/UBXN2B | 5 |
| BP | GO:0060099 | regulation of phagocytosis, engulfment | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | C3/CD36/ITGA2/NCKAP1L/STAP1 | 5 |
| BP | GO:0086069 | bundle of His cell to Purkinje myocyte communication | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | CACNA2D1/DSC2/DSG2/DSP/PKP2 | 5 |
| BP | GO:0090656 | t-circle formation | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | BLM/DNA2/NBN/WRN/XRCC5 | 5 |
| BP | GO:0090737 | telomere maintenance via telomere trimming | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | BLM/DNA2/NBN/WRN/XRCC5 | 5 |
| BP | GO:1905153 | regulation of membrane invagination | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | C3/CD36/ITGA2/NCKAP1L/STAP1 | 5 |
| BP | GO:2000767 | positive regulation of cytoplasmic translation | 5/2221 | 15/18614 | 0.025856123 | 0.166364103 | 0.140596763 | CSDE1/DHX36/DHX9/HNRNPU/SYNCRIP | 5 |
| BP | GO:0006401 | RNA catabolic process | 50/2221 | 319/18614 | 0.026338439 | 0.169286379 | 0.143066421 | ATM/CNOT1/CNOT6L/CSDE1/DDX5/DHX36/DHX9/DICER1/DIS3/DIS3L/DKC1/DNA2/EIF3E/EIF4A3/ETF1/EXOSC9/FASTKD2/FMR1/FXR1/GIGYF2/GSPT1/HNRNPU/LRPPRC/METTL14/MLH1/NBAS/NCBP1/NCBP2/NSUN2/NUDT12/PHAX/PNPT1/PNRC2/POP1/PUM2/RC3H2/RNASEL/ROCK1/ROCK2/SERBP1/SLFN13/SSB/SYNCRIP/TRAF5/UPF2/UPF3B/XRN1/XRN2/YTHDF3/ZPR1 | 50 |
| BP | GO:0140888 | interferon-mediated signaling pathway | 19/2221 | 100/18614 | 0.026407907 | 0.169551728 | 0.143290671 | ARG1/AZI2/IFNAR1/IFNGR1/JAK1/JAK2/PARP14/PARP9/PPARG/PTPN11/PTPN2/SAMHD1/SP100/STAT1/TANK/TBK1/TRIM6/USP27X/YTHDF3 | 19 |
| BP | GO:0003229 | ventricular cardiac muscle tissue development | 12/2221 | 55/18614 | 0.026604941 | 0.170634672 | 0.144205883 | ADAMTS9/CHD7/DSG2/DSP/LRP2/PKP2/PTCD2/RBPJ/RYR2/TGFBR1/TPM1/ZFPM2 | 12 |
| BP | GO:0009303 | rRNA transcription | 9/2221 | 37/18614 | 0.026900966 | 0.172019788 | 0.145376466 | GTF3C6/ERCC6/GTF3C3/NCL/NIFK/NOL11/POLR1B/PWP1/TAF1B | 9 |
| BP | GO:0034243 | regulation of transcription elongation by RNA polymerase II | 17/2221 | 87/18614 | 0.026906686 | 0.172019788 | 0.145376466 | EZH2/CCNT1/CTNNB1/ELL2/ERCC6/HNRNPU/INTS12/INTS6/INTS7/LARP7/LEO1/MED23/MED6/NCBP1/NCBP2/WDR43/ZMYND11 | 17 |
| BP | GO:0046785 | microtubule polymerization | 17/2221 | 87/18614 | 0.026906686 | 0.172019788 | 0.145376466 | FBXO5/TPX2/AKAP9/CAMSAP2/CDK5RAP2/CENPJ/CEP192/CKAP5/CLASP2/CLIP1/MAP1B/MAP7D3/MAPRE1/MET/NAV3/NEDD1/NIN | 17 |
| BP | GO:0061982 | meiosis I cell cycle process | 24/2221 | 134/18614 | 0.027001118 | 0.17244026 | 0.145731813 | BRCA2/BRIP1/CCNB2/FANCD2/FBXO5/MND1/NDC80/RAD51AP1/RAD54B/TOP2A/ATM/CCNE2/CENPC/ERCC4/FANCM/ING2/MLH1/MLH3/MSH6/RAD21/RAD50/SYCP2/TOP2B/UBR2 | 24 |
| BP | GO:0006911 | phagocytosis, engulfment | 11/2221 | 49/18614 | 0.027115783 | 0.172622806 | 0.145886085 | ABCA1/ARHGAP12/BECN1/BIN2/C3/CD36/CLCN3/ITGA2/MSR1/NCKAP1L/STAP1 | 11 |
| BP | GO:0008206 | bile acid metabolic process | 11/2221 | 49/18614 | 0.027115783 | 0.172622806 | 0.145886085 | ABCD3/ATP8B1/BAAT/CYP7B1/NPC1/OSBP/OSBPL3/OSBPL9/SCP2/SLC27A2/STARD4 | 11 |
| BP | GO:0061028 | establishment of endothelial barrier | 11/2221 | 49/18614 | 0.027115783 | 0.172622806 | 0.145886085 | CLDN1/EZR/PDE4D/PLCB1/RAPGEF2/RDX/ROCK1/ROCK2/TJP1/VCL/ZDHHC21 | 11 |
| BP | GO:0019674 | NAD metabolic process | 10/2221 | 43/18614 | 0.027270506 | 0.173058402 | 0.146254214 | ME1/CD38/KMO/KYNU/LDHB/MDH1/NUDT12/PARP9/SLC5A8/VCP | 10 |
| BP | GO:0031952 | regulation of protein autophosphorylation | 10/2221 | 43/18614 | 0.027270506 | 0.173058402 | 0.146254214 | DDX3X/ENPP1/GPNMB/IMPACT/NBN/PDGFC/PDGFD/PTPRC/RAD50/TOM1L1 | 10 |
| BP | GO:0090114 | COPII-coated vesicle budding | 10/2221 | 43/18614 | 0.027270506 | 0.173058402 | 0.146254214 | CUL3/MIA3/RAB1A/SAR1B/SEC23A/SEC23B/SEC24D/SEC31A/TRAPPC11/TRAPPC8 | 10 |
| BP | GO:0051495 | positive regulation of cytoskeleton organization | 32/2221 | 190/18614 | 0.027592432 | 0.174548968 | 0.147513913 | PLK4/SASS6/SPAG5/STIL/AKAP9/CCDC88A/CDK5RAP2/CENPJ/CEP120/CKAP5/CLIP1/DLG1/DYNC1H1/FER/FERMT2/FMN1/GPSM2/MAP1B/MAPRE1/MET/NAV3/NCK1/NCKAP1/NCKAP1L/RICTOR/ROCK2/SCIN/SNX9/STAP1/SWAP70/TGFBR1/TPM1 | 32 |
| BP | GO:0071706 | tumor necrosis factor superfamily cytokine production | 32/2221 | 190/18614 | 0.027592432 | 0.174548968 | 0.147513913 | HDAC2/AKAP12/ANGPT1/ARFGEF2/BTK/CD36/CD84/CD86/CYBB/DHX9/DICER1/FCGR3A/GPNMB/HAVCR2/HMGB1/IFIH1/IFNGR1/IGF1/IRAK3/JAK2/LPL/LRRK2/MMP8/PIK3R1/PTPN11/PTPRC/RIPK1/RIPK2/TLR1/TLR2/TLR3/TLR4 | 32 |
| BP | GO:1903555 | regulation of tumor necrosis factor superfamily cytokine production | 32/2221 | 190/18614 | 0.027592432 | 0.174548968 | 0.147513913 | HDAC2/AKAP12/ANGPT1/ARFGEF2/BTK/CD36/CD84/CD86/CYBB/DHX9/DICER1/FCGR3A/GPNMB/HAVCR2/HMGB1/IFIH1/IFNGR1/IGF1/IRAK3/JAK2/LPL/LRRK2/MMP8/PIK3R1/PTPN11/PTPRC/RIPK1/RIPK2/TLR1/TLR2/TLR3/TLR4 | 32 |
| BP | GO:0030041 | actin filament polymerization | 28/2221 | 162/18614 | 0.027744746 | 0.175328142 | 0.148172404 | DIAPH3/ADD3/ARFGEF1/ARHGAP18/ARHGAP28/CAPZA2/DIAPH2/DLG1/EPS8/FER/FMN1/JAK2/MKKS/NCK1/NCKAP1/NCKAP1L/PSTPIP2/RASA1/RDX/RICTOR/SCIN/SNX9/SPIRE1/SPTAN1/SVIL/TMOD2/TTC17/TWF1 | 28 |
| BP | GO:0051651 | maintenance of location in cell | 38/2221 | 233/18614 | 0.028021781 | 0.176893006 | 0.149494894 | ASPM/AKAP6/AKAP9/ANK2/ANK3/ARHGAP21/CAPN3/CCDC88A/CHD7/CLIC2/DMD/GPSM2/HK2/HNRNPU/HSP90B1/HSPA5/HTR2A/IBTK/ITGB3/ITPR1/ITPR2/KDELR3/LYN/PDE4D/PLCB1/PLCB4/PLCH1/PRKD1/PTPRC/RYR2/SCIN/SP100/SYNE1/TOPORS/TWF1/VPS13A/VPS13C/VPS13D | 38 |
| BP | GO:0032943 | mononuclear cell proliferation | 49/2221 | 313/18614 | 0.028192377 | 0.177783374 | 0.150247357 | ATAD5/HELLS/ARG1/ATM/AZI2/BTK/CASP3/CD180/CD38/CD86/CR1/CTNNB1/CTPS1/DLG1/DOCK2/DOCK8/FCGR3A/GAPT/GPNMB/HAVCR2/HMGB1/HSPD1/IGF1/IL18/IL2RA/IL6ST/IL7R/IMPDH2/JAK2/LYN/MALT1/MEF2C/MIR30B/MNDA/NCK1/NCKAP1L/PDCD1LG2/PIK3CG/PTPRC/RC3H2/RIPK2/SLC39A10/SOS1/SOS2/TBK1/TFRC/TLR4/TNFSF8/VCAM1 | 49 |
| BP | GO:0002367 | cytokine production involved in immune response | 22/2221 | 121/18614 | 0.028468651 | 0.179337599 | 0.151560856 | ANGPT1/ARG1/BTK/CD226/CD36/CD96/DDX1/DDX21/DHX36/IL18/IL1R1/IRAK3/LACC1/MALT1/MAP3K7/NLRP3/PANX1/RABGEF1/RIPK2/TLR3/TLR4/TRIM6 | 22 |
| BP | GO:0008286 | insulin receptor signaling pathway | 23/2221 | 128/18614 | 0.028909518 | 0.181801166 | 0.153642853 | APC/C2CD5/ENPP1/FER/IDE/MIR15B/NCK1/NCL/NUCKS1/OGT/OSBPL8/PHIP/PIK3C2A/PIK3CA/PIK3R1/PIK3R3/PTPN11/PTPN2/SESN3/SOS1/SOS2/STXBP4/ZNF106 | 23 |
| BP | GO:0035872 | nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway | 7/2221 | 26/18614 | 0.028950385 | 0.181801166 | 0.153642853 | BIRC2/BIRC3/CYLD/LACC1/MAP3K7/RIPK2/TLR4 | 7 |
| BP | GO:0070102 | interleukin-6-mediated signaling pathway | 7/2221 | 26/18614 | 0.028950385 | 0.181801166 | 0.153642853 | CTR9/FER/IL6ST/JAK1/JAK2/PTPN2/RIPK1 | 7 |
| BP | GO:0002819 | regulation of adaptive immune response | 34/2221 | 205/18614 | 0.029090792 | 0.182492392 | 0.154227018 | ATAD5/MSH2/ARG1/BTK/C3/CD226/CR1/CR1L/EIF2AK4/FBXO38/HAVCR2/HMGB1/HSPD1/IL18/IL1R1/IL6ST/IL7R/JAK2/MALT1/MAP3K7/MEF2C/MLH1/NCKAP1L/NLRP3/PLA2G4A/PTPRC/RC3H2/RIF1/RIPK2/SAMSN1/TFRC/THOC1/TP53BP1/ZBTB1 | 34 |
| BP | GO:0032271 | regulation of protein polymerization | 32/2221 | 191/18614 | 0.029479965 | 0.184741114 | 0.156127446 | ADD3/AKAP9/ARFGEF1/ARHGAP18/ARHGAP28/CAMSAP2/CAPZA2/CDK5RAP2/CKAP5/CLIP1/DLG1/EPS8/FER/FMN1/HSP90AA1/MAP1B/MAPRE1/MET/MKKS/NAV3/NCK1/NCKAP1/NCKAP1L/RASA1/RDX/RICTOR/SCIN/SNX9/SPTAN1/SVIL/TMOD2/TWF1 | 32 |
| BP | GO:0032273 | positive regulation of protein polymerization | 17/2221 | 88/18614 | 0.029768115 | 0.186198926 | 0.157359464 | AKAP9/CDK5RAP2/CKAP5/CLIP1/DLG1/FER/FMN1/HSP90AA1/MAP1B/MAPRE1/MET/NAV3/NCK1/NCKAP1/NCKAP1L/RICTOR/SNX9 | 17 |
| BP | GO:0007584 | response to nutrient | 27/2221 | 156/18614 | 0.029774496 | 0.186198926 | 0.157359464 | BRIP1/ACSL1/AGL/ARG1/ATP2B1/BECN1/CNR1/CYBB/GCLC/GNPAT/ITGA2/KYNU/LPL/MAP1B/NCOA1/OGT/OXCT1/PHEX/POSTN/PPARG/PTGS2/SLC16A1/SNW1/SPP1/STAT1/TFRC/VCAM1 | 27 |
| BP | GO:0002381 | immunoglobulin production involved in immunoglobulin-mediated immune response | 15/2221 | 75/18614 | 0.029964674 | 0.186805678 | 0.15787224 | ATAD5/MSH2/BTK/GAPT/HSPD1/LIG4/MLH1/MSH6/NBN/PTPRC/RIF1/SWAP70/TFRC/THOC1/TP53BP1 | 15 |
| BP | GO:0016239 | positive regulation of macroautophagy | 15/2221 | 75/18614 | 0.029964674 | 0.186805678 | 0.15787224 | BECN1/BNIP3L/C9orf72/GNAI3/HIF1A/MAP3K7/RAB3GAP1/RAB3GAP2/RIPK2/SESN3/SH3GLB1/SNX30/SPTLC1/TBK1/VPS13D | 15 |
| BP | GO:0030968 | endoplasmic reticulum unfolded protein response | 15/2221 | 75/18614 | 0.029964674 | 0.186805678 | 0.15787224 | AGR2/ATF6/DNAJC10/EIF2AK2/EIF2AK3/EIF2S1/HSPA5/NCK1/NFE2L2/PARP8/PIK3R1/PTPN2/UFL1/VCP/YOD1 | 15 |
| BP | GO:2001233 | regulation of apoptotic signaling pathway | 58/2221 | 381/18614 | 0.030297453 | 0.188547265 | 0.159344081 | ATAD5/BRCA1/DDIAS/HELLS/AATF/BCLAF1/BECN1/BIRC6/CTNNA1/CTNNB1/CTSK/CTSL/CTSS/CYLD/DDX3X/DNAJA1/DNM1L/EIF2AK3/FAS/FIGNL1/GCLC/GNAI3/HGF/HIF1A/HMGB2/IGF1/ING2/INHBA/ITGA6/ITGAV/IVNS1ABP/JAK2/LRRK2/MDM2/MIR186/NCK1/NF1/NFE2L2/OPA1/PARP1/PDIA3/PHIP/PIK3CB/PTGS2/PTPN2/PTPRC/RB1/RB1CC1/RIPK1/RRM2B/SGK3/SKIL/SP100/TGFBR1/USP15/USP47/VNN1/ZMYND11 | 58 |
| BP | GO:0051058 | negative regulation of small GTPase mediated signal transduction | 12/2221 | 56/18614 | 0.030306716 | 0.188547265 | 0.159344081 | ABL2/ARHGAP12/ARHGAP42/CCDC125/CD2AP/CGNL1/CUL3/ITGB1/MET/NF1/RABGEF1/RASA2 | 12 |
| BP | GO:0031647 | regulation of protein stability | 50/2221 | 322/18614 | 0.030631198 | 0.1903691 | 0.16088374 | MCM8/NDC80/VBP1/ANK2/ASPH/ATF7IP/ATP1B1/CAPN3/CASP3/CCNH/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CDKN2AIP/CUL3/EPHA4/FBXL3/GTPBP4/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSPA8/HSPD1/IGF1/LRRK2/MDM2/NAA15/NAPG/PIK3R1/PRKDC/RABL3/RPAP3/SEL1L/SH3GLB1/SPAG1/STXBP4/TAF1/TCP1/TRIM44/USP13/USP25/USP27X/USP7/USP8/USP9X/VPS35 | 50 |
| BP | GO:0050821 | protein stabilization | 35/2221 | 213/18614 | 0.030699019 | 0.190470904 | 0.160969777 | MCM8/VBP1/ANK2/ATF7IP/ATP1B1/CCNH/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/EPHA4/GTPBP4/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSPD1/IGF1/NAA15/NAPG/PIK3R1/RABL3/RPAP3/SEL1L/SPAG1/STXBP4/TAF1/TCP1/TRIM44/USP13/USP27X/USP7/USP9X | 35 |
| BP | GO:0006099 | tricarboxylic acid cycle | 8/2221 | 32/18614 | 0.030869204 | 0.190470904 | 0.160969777 | ACO1/FH/IDH1/IREB2/MDH1/NNT/SUCLA2/SUCLG2 | 8 |
| BP | GO:0006298 | mismatch repair | 8/2221 | 32/18614 | 0.030869204 | 0.190470904 | 0.160969777 | MCM8/MSH2/HMGB1/MLH1/MLH3/MSH3/MSH6/POLD3 | 8 |
| BP | GO:0031116 | positive regulation of microtubule polymerization | 8/2221 | 32/18614 | 0.030869204 | 0.190470904 | 0.160969777 | AKAP9/CDK5RAP2/CKAP5/CLIP1/MAP1B/MAPRE1/MET/NAV3 | 8 |
| BP | GO:0035456 | response to interferon-beta | 8/2221 | 32/18614 | 0.030869204 | 0.190470904 | 0.160969777 | AIM2/IFI16/MNDA/PNPT1/STAT1/TLR3/TRIM6/XAF1 | 8 |
| BP | GO:0046685 | response to arsenic-containing substance | 8/2221 | 32/18614 | 0.030869204 | 0.190470904 | 0.160969777 | ATR/DDX3X/DHX36/GCLC/HNRNPA1/SLC38A2/VCP/ZFAND1 | 8 |
| BP | GO:0140058 | neuron projection arborization | 8/2221 | 32/18614 | 0.030869204 | 0.190470904 | 0.160969777 | LRP2/LRRK2/MACF1/MAP3K13/MYO9A/NLGN1/ROCK1/SEMA3A | 8 |
| BP | GO:0000959 | mitochondrial RNA metabolic process | 11/2221 | 50/18614 | 0.031139922 | 0.191552441 | 0.1618838 | FASTKD2/LRPPRC/MTERF1/MTERF2/PNPT1/TFAM/TFB2M/TRMT10C/TRMT5/TRNT1/WARS2 | 11 |
| BP | GO:0002821 | positive regulation of adaptive immune response | 23/2221 | 129/18614 | 0.031346618 | 0.191552441 | 0.1618838 | ATAD5/MSH2/BTK/C3/CD226/EIF2AK4/FBXO38/HSPD1/IL18/IL1R1/IL6ST/JAK2/MALT1/MAP3K7/MLH1/NLRP3/PLA2G4A/PTPRC/RIF1/RIPK2/TFRC/TP53BP1/ZBTB1 | 23 |
| BP | GO:0007127 | meiosis I | 23/2221 | 129/18614 | 0.031346618 | 0.191552441 | 0.1618838 | BRCA2/BRIP1/CCNB2/FANCD2/FBXO5/MND1/NDC80/RAD51AP1/RAD54B/TOP2A/ATM/CCNE2/CENPC/ERCC4/FANCM/ING2/MLH1/MLH3/RAD21/RAD50/SYCP2/TOP2B/UBR2 | 23 |
| BP | GO:0019079 | viral genome replication | 23/2221 | 129/18614 | 0.031346618 | 0.191552441 | 0.1618838 | DEK/TOP2A/DDX3X/EIF2AK2/EIF2AK4/FAM111A/FMR1/HSPA8/HTATSF1/IFI16/IFIH1/IFIT5/NUCKS1/PIK3C3/PKN2/RNASEL/SRPK1/SRPK2/TOP2B/TRIM38/TRIM6/VCP/ZNFX1 | 23 |
| BP | GO:0006513 | protein monoubiquitination | 16/2221 | 82/18614 | 0.031541249 | 0.191552441 | 0.1618838 | BRCA1/BRCA2/DTL/RAD18/BIRC2/BRCC3/CTR9/CUL1/CUL3/DTX3L/FANCM/KBTBD8/LEO1/RNF20/TOPORS/WDR48 | 16 |
| BP | GO:2001021 | negative regulation of response to DNA damage stimulus | 16/2221 | 82/18614 | 0.031541249 | 0.191552441 | 0.1618838 | ATAD5/DDIAS/FBXO5/PARPBP/POLQ/ERCC4/ERCC6/ING2/MDM2/RIF1/SMCHD1/THOC1/TP53BP1/TRIP12/UBR5/USP47 | 16 |
| BP | GO:0021955 | central nervous system neuron axonogenesis | 9/2221 | 38/18614 | 0.031636869 | 0.191552441 | 0.1618838 | DCLK1/EPHA4/FBXO45/HSP90AA1/HSP90AB1/MYCBP2/NIN/SPG11/WDR47 | 9 |
| BP | GO:0043001 | Golgi to plasma membrane protein transport | 9/2221 | 38/18614 | 0.031636869 | 0.191552441 | 0.1618838 | ACSL3/ANK3/ATP2C1/BLZF1/CNST/GOLGA4/MACF1/NSF/PREPL | 9 |
| BP | GO:0043618 | regulation of transcription from RNA polymerase II promoter in response to stress | 9/2221 | 38/18614 | 0.031636869 | 0.191552441 | 0.1618838 | CHEK1/ATF6/HIF1A/HSPA5/IMPACT/NCK1/NEDD4/NFE2L2/RBPJ | 9 |
| BP | GO:0090148 | membrane fission | 10/2221 | 44/18614 | 0.031641184 | 0.191552441 | 0.1618838 | CHMP2B/CORO1C/DNM1L/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/SH3GLB1/STAM2 | 10 |
| BP | GO:1904407 | positive regulation of nitric oxide metabolic process | 10/2221 | 44/18614 | 0.031641184 | 0.191552441 | 0.1618838 | CD36/HBB/HSP90AA1/HSP90AB1/JAK2/MIR181B1/MMP8/PTGS2/TLR4/TLR6 | 10 |
| BP | GO:2000785 | regulation of autophagosome assembly | 10/2221 | 44/18614 | 0.031641184 | 0.191552441 | 0.1618838 | BECN1/C9orf72/LRRK2/MTM1/PIKFYVE/RAB3GAP1/RAB3GAP2/SCFD1/SH3GLB1/SNX30 | 10 |
| BP | GO:0010952 | positive regulation of peptidase activity | 31/2221 | 185/18614 | 0.031660414 | 0.191552441 | 0.1618838 | AIFM1/AIM2/ASPH/CASP1/CASP8AP2/CR1/CTSK/CTSL/CTSS/CYCS/DDX3X/EIF2AK3/EPHA4/FAS/HMGB1/HSPD1/IFI16/IFT57/JAK2/LYN/MALT1/NLRC4/NLRP3/PPARG/RIPK2/ROCK2/SENP1/TANK/TNFSF15/UACA/VCP | 31 |
| BP | GO:0032640 | tumor necrosis factor production | 31/2221 | 185/18614 | 0.031660414 | 0.191552441 | 0.1618838 | HDAC2/AKAP12/ANGPT1/ARFGEF2/BTK/CD36/CD84/CYBB/DHX9/DICER1/FCGR3A/GPNMB/HAVCR2/HMGB1/IFIH1/IFNGR1/IGF1/IRAK3/JAK2/LPL/LRRK2/MMP8/PIK3R1/PTPN11/PTPRC/RIPK1/RIPK2/TLR1/TLR2/TLR3/TLR4 | 31 |
| BP | GO:0032680 | regulation of tumor necrosis factor production | 31/2221 | 185/18614 | 0.031660414 | 0.191552441 | 0.1618838 | HDAC2/AKAP12/ANGPT1/ARFGEF2/BTK/CD36/CD84/CYBB/DHX9/DICER1/FCGR3A/GPNMB/HAVCR2/HMGB1/IFIH1/IFNGR1/IGF1/IRAK3/JAK2/LPL/LRRK2/MMP8/PIK3R1/PTPN11/PTPRC/RIPK1/RIPK2/TLR1/TLR2/TLR3/TLR4 | 31 |
| BP | GO:0014897 | striated muscle hypertrophy | 19/2221 | 102/18614 | 0.031803449 | 0.191552441 | 0.1618838 | EZH2/HDAC2/AKAP13/AKAP6/ATP2A2/BECN1/IGF1/IL6ST/MIR15B/PARP1/PPARG/RAP1GDS1/RGS2/ROCK1/ROCK2/RYR2/SORBS2/TTN/TWF1 | 19 |
| BP | GO:1905477 | positive regulation of protein localization to membrane | 19/2221 | 102/18614 | 0.031803449 | 0.191552441 | 0.1618838 | AGR2/ACSL3/AKAP5/ANK3/ATP2C1/C2CD5/CNST/DLG1/EFCAB7/EPHA3/EZR/ITGB1/KIF5B/PIK3R1/PLS1/PRKCI/SLC5A3/TNFAIP6/WNK3 | 19 |
| BP | GO:0007252 | I-kappaB phosphorylation | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | CHUK/ERC1/MAP3K7/TLR2/TLR3/TLR4 | 6 |
| BP | GO:0009067 | aspartate family amino acid biosynthetic process | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | AASDHPPT/AASS/MTHFD1/MTR/MTRR/PLOD2 | 6 |
| BP | GO:0009083 | branched-chain amino acid catabolic process | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | ACADSB/ACAT1/DBT/DLD/HIBCH/MCCC1 | 6 |
| BP | GO:0035020 | regulation of Rac protein signal transduction | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | KRAS/NF1/OGT/PIK3CB/PIK3CG/SSX2IP | 6 |
| BP | GO:0051571 | positive regulation of histone H3-K4 methylation | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | BRCA1/CTNNB1/CTR9/OGT/RTF1/SNW1 | 6 |
| BP | GO:0060008 | Sertoli cell differentiation | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | ARID4A/ARID4B/ATRX/FER/FNDC3A/HSD17B4 | 6 |
| BP | GO:0090231 | regulation of spindle checkpoint | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | MAD2L1/NDC80/CDK5RAP2/GEN1/TPR/USP44 | 6 |
| BP | GO:0090266 | regulation of mitotic cell cycle spindle assembly checkpoint | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | MAD2L1/NDC80/CDK5RAP2/GEN1/TPR/USP44 | 6 |
| BP | GO:0150105 | protein localization to cell-cell junction | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | CGNL1/DSP/JAK1/MPP7/TJP1/VCL | 6 |
| BP | GO:1901659 | glycosyl compound biosynthetic process | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | ADAL/ADK/NT5E/PGM2/TRMT12/TYW3 | 6 |
| BP | GO:1903504 | regulation of mitotic spindle checkpoint | 6/2221 | 21/18614 | 0.03193602 | 0.191552441 | 0.1618838 | MAD2L1/NDC80/CDK5RAP2/GEN1/TPR/USP44 | 6 |
| BP | GO:0007043 | cell-cell junction assembly | 27/2221 | 157/18614 | 0.032010792 | 0.191618831 | 0.161939906 | ECT2/UGT8/ACE2/ANK2/APC/CDH2/CDH6/CLDN1/CTNNA1/CTNNB1/DLG1/EPB41L3/FER/GNPAT/GRHL2/MIR142/MPDZ/MPP7/PKN2/PKP2/POF1B/PTPRO/ROCK1/ROCK2/STRN/TJP1/VCL | 27 |
| BP | GO:0010976 | positive regulation of neuron projection development | 27/2221 | 157/18614 | 0.032010792 | 0.191618831 | 0.161939906 | EZH2/ABL2/CAPRIN1/CAPRIN2/CNR1/CNTN1/DHX36/EPHA3/FBXO38/FIG4/HGF/HSPA5/ITGA6/KIDINS220/LRP8/LYN/NCK1/NFE2L2/NLGN1/PRKCI/PRKD1/RAPGEF2/RGS2/SETX/TENM3/TWF1/VLDLR | 27 |
| BP | GO:0045017 | glycerolipid biosynthetic process | 40/2221 | 250/18614 | 0.032492649 | 0.194309915 | 0.164214182 | ACSL1/ACSL3/AGPAT5/ATM/BECN1/BMX/C3/DGKH/EFR3A/FABP3/FAR1/FIG4/GK/GNPAT/HTR2A/IMPA1/INPP4B/LIPH/LPL/MTM1/MTMR2/MTMR4/MTMR6/PIGA/PIGN/PIGW/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/PIKFYVE/PIP5K1B/PLA2G4A/PLD1/SACM1L/SOCS4 | 40 |
| BP | GO:0002712 | regulation of B cell mediated immunity | 13/2221 | 63/18614 | 0.032979753 | 0.195079065 | 0.164864202 | ATAD5/MSH2/BTK/C3/CD226/CR1/CR1L/MLH1/PTPRC/RIF1/TFRC/THOC1/TP53BP1 | 13 |
| BP | GO:0002889 | regulation of immunoglobulin mediated immune response | 13/2221 | 63/18614 | 0.032979753 | 0.195079065 | 0.164864202 | ATAD5/MSH2/BTK/C3/CD226/CR1/CR1L/MLH1/PTPRC/RIF1/TFRC/THOC1/TP53BP1 | 13 |
| BP | GO:0006073 | cellular glucan metabolic process | 15/2221 | 76/18614 | 0.033358903 | 0.195079065 | 0.164864202 | ACADM/AGL/ENPP1/EPM2AIP1/GBE1/IGF1/IL6ST/MGAM/MIR15B/PGM2/PHKA1/PHKB/PYGL/RB1CC1/UGP2 | 15 |
| BP | GO:0044042 | glucan metabolic process | 15/2221 | 76/18614 | 0.033358903 | 0.195079065 | 0.164864202 | ACADM/AGL/ENPP1/EPM2AIP1/GBE1/IGF1/IL6ST/MGAM/MIR15B/PGM2/PHKA1/PHKB/PYGL/RB1CC1/UGP2 | 15 |
| BP | GO:0006188 | IMP biosynthetic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | ATIC/GART/PAICS/PPAT | 4 |
| BP | GO:0006568 | tryptophan metabolic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | ATP7A/KMO/KYNU/TDO2 | 4 |
| BP | GO:0008611 | ether lipid biosynthetic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | AGPS/FAR1/GNPAT/PLA2G4A | 4 |
| BP | GO:0032490 | detection of molecule of bacterial origin | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | TLR1/TLR2/TLR4/TLR6 | 4 |
| BP | GO:0032493 | response to bacterial lipoprotein | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | CD36/TLR1/TLR2/TLR6 | 4 |
| BP | GO:0039530 | MDA-5 signaling pathway | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | ANKRD17/DDX60/IFIH1/RIOK3 | 4 |
| BP | GO:0042451 | purine nucleoside biosynthetic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | ADAL/ADK/NT5E/PGM2 | 4 |
| BP | GO:0042455 | ribonucleoside biosynthetic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | ADAL/ADK/NT5E/PGM2 | 4 |
| BP | GO:0046129 | purine ribonucleoside biosynthetic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | ADAL/ADK/NT5E/PGM2 | 4 |
| BP | GO:0046504 | glycerol ether biosynthetic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | AGPS/FAR1/GNPAT/PLA2G4A | 4 |
| BP | GO:0051256 | mitotic spindle midzone assembly | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | KIF23/KIF4A/PRC1/RACGAP1 | 4 |
| BP | GO:0070601 | centromeric sister chromatid cohesion | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | BUB1/BUB1B/CTNNB1/NAA50 | 4 |
| BP | GO:0070934 | CRD-mediated mRNA stabilization | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | CSDE1/DHX9/HNRNPU/SYNCRIP | 4 |
| BP | GO:0072697 | protein localization to cell cortex | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | EPB41/EPB41L2/EZR/GPSM2 | 4 |
| BP | GO:0075522 | IRES-dependent viral translational initiation | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | CSDE1/EIF3A/EIF3D/SSB | 4 |
| BP | GO:0075733 | intracellular transport of virus | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | FMR1/KPNA2/KPNA3/NUP153 | 4 |
| BP | GO:0097384 | cellular lipid biosynthetic process | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | AGPS/FAR1/GNPAT/PLA2G4A | 4 |
| BP | GO:1902415 | regulation of mRNA binding | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | EIF3D/EIF3E/EIF4A3/FMR1 | 4 |
| BP | GO:1902915 | negative regulation of protein polyubiquitination | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | PLAA/TRIM44/TRIP12/UBR5 | 4 |
| BP | GO:1903059 | regulation of protein lipidation | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | RAB3GAP1/RAB3GAP2/RABL3/RB1CC1 | 4 |
| BP | GO:1903897 | regulation of PERK-mediated unfolded protein response | 4/2221 | 11/18614 | 0.033431934 | 0.195079065 | 0.164864202 | AGR2/HSPA5/NCK1/PTPN2 | 4 |
| BP | GO:0007044 | cell-substrate junction assembly | 18/2221 | 96/18614 | 0.03392242 | 0.196513808 | 0.166076724 | CLASP2/CORO1C/DST/EPHA3/FERMT2/FMN1/ITGA2/ITGA6/ITGB3/LAMC1/MACF1/MAP4K4/PHLDB2/PTPRK/ROCK1/ROCK2/SLK/VCL | 18 |
| BP | GO:0030218 | erythrocyte differentiation | 23/2221 | 130/18614 | 0.033935432 | 0.196513808 | 0.166076724 | NCAPG2/ALAS2/ARID4A/BPGM/CASP3/HIF1A/HMGB2/HSPA9/INHBA/JAK2/KMT2E/L3MBTL3/LYAR/LYN/NCKAP1L/PRKDC/PTPN2/RACGAP1/RB1/SLC4A1/STAT1/UBA5/UFL1 | 23 |
| BP | GO:0050864 | regulation of B cell activation | 23/2221 | 130/18614 | 0.033935432 | 0.196513808 | 0.166076724 | ATAD5/MSH2/ATM/BANK1/BTK/CASP3/CD38/CR1/INHBA/LYN/MEF2C/MLH1/MNDA/NCKAP1L/PPP2R3C/PTPRC/RIF1/SAMSN1/SLC39A10/TFRC/THOC1/TLR4/TP53BP1 | 23 |
| BP | GO:0000212 | meiotic spindle organization | 5/2221 | 16/18614 | 0.034004467 | 0.196513808 | 0.166076724 | ASPM/CCNB2/FBXO5/NDC80/ATRX | 5 |
| BP | GO:0006825 | copper ion transport | 5/2221 | 16/18614 | 0.034004467 | 0.196513808 | 0.166076724 | ATP7A/CP/SLC31A1/STEAP2/STEAP4 | 5 |
| BP | GO:0016045 | detection of bacterium | 5/2221 | 16/18614 | 0.034004467 | 0.196513808 | 0.166076724 | NAIP/NLRC4/TLR1/TLR2/TLR6 | 5 |
| BP | GO:0042795 | snRNA transcription by RNA polymerase II | 5/2221 | 16/18614 | 0.034004467 | 0.196513808 | 0.166076724 | ELL2/ICE1/ICE2/LARP7/ZNF143 | 5 |
| BP | GO:0043508 | negative regulation of JUN kinase activity | 5/2221 | 16/18614 | 0.034004467 | 0.196513808 | 0.166076724 | AIDA/DNAJA1/HIPK3/PDCD4/ZNF675 | 5 |
| BP | GO:0097401 | synaptic vesicle lumen acidification | 5/2221 | 16/18614 | 0.034004467 | 0.196513808 | 0.166076724 | ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/CLCN3 | 5 |
| BP | GO:1900044 | regulation of protein K63-linked ubiquitination | 5/2221 | 16/18614 | 0.034004467 | 0.196513808 | 0.166076724 | BIRC2/DDX3X/PLAA/TRIP12/UBR5 | 5 |
| BP | GO:0018394 | peptidyl-lysine acetylation | 29/2221 | 172/18614 | 0.034181767 | 0.197348858 | 0.166782437 | BRCA1/BRCA2/CHEK1/DEK/HDAC2/BAZ1B/DDX21/EPC2/ERCC6/ESCO1/HAT1/ING3/IWS1/JADE1/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA50/OGT/PHF20L1/SDR16C5/SF3B1/SMARCA5/SMC5/SUPT20H/TAF2/TAF7/ZZZ3 | 29 |
| BP | GO:0001706 | endoderm formation | 12/2221 | 57/18614 | 0.03436503 | 0.197837342 | 0.167195262 | COL12A1/COL5A2/COL8A1/CTNNB1/CTR9/INHBA/ITGA4/ITGAV/LAMB1/LEO1/MMP8/RTF1 | 12 |
| BP | GO:0043388 | positive regulation of DNA binding | 12/2221 | 57/18614 | 0.03436503 | 0.197837342 | 0.167195262 | CTNNB1/EGF/HMGB1/HMGB2/IGF1/ITGA2/JAK2/MMP8/PARP1/PPARG/RB1/TRIM6 | 12 |
| BP | GO:0072523 | purine-containing compound catabolic process | 12/2221 | 57/18614 | 0.03436503 | 0.197837342 | 0.167195262 | ACAT1/ADAL/DPYD/NT5C2/NT5E/NUDT12/PDE4B/PDE4D/PDE8B/SAMHD1/SUCLA2/SUCLG2 | 12 |
| BP | GO:1902882 | regulation of response to oxidative stress | 19/2221 | 103/18614 | 0.034790116 | 0.200093058 | 0.169101601 | CD36/CTNNB1/FUT8/HGF/HIF1A/LRRK2/MCTP1/MET/NCOA7/NFE2L2/OXR1/PARP1/PNPLA8/RIPK1/SESN3/SLC7A11/TLR4/TLR6/VNN1 | 19 |
| BP | GO:0000209 | protein polyubiquitination | 39/2221 | 244/18614 | 0.034855526 | 0.200277787 | 0.169257719 | BRCA1/DTL/ANAPC1/ANKIB1/ARIH1/BIRC2/CDC27/CTNNB1/CUL1/CUL3/DDX3X/DTX3L/DZIP3/FBXO38/HECTD1/MDM2/NEDD4/PLAA/RC3H2/RNF14/RNF19A/RNF20/RNF217/RNF6/SHPRH/TAF1/TNKS2/TOPORS/TPP2/TRAF5/TRIM2/TRIM22/TRIM38/TRIM44/TRIM6/TRIP12/TTC3/UBE4A/UBR5 | 39 |
| BP | GO:0009081 | branched-chain amino acid metabolic process | 7/2221 | 27/18614 | 0.035181213 | 0.201097999 | 0.169950891 | ACADSB/ACAT1/BCAT1/DBT/DLD/HIBCH/MCCC1 | 7 |
| BP | GO:0031954 | positive regulation of protein autophosphorylation | 7/2221 | 27/18614 | 0.035181213 | 0.201097999 | 0.169950891 | DDX3X/GPNMB/NBN/PDGFC/PDGFD/RAD50/TOM1L1 | 7 |
| BP | GO:0036010 | protein localization to endosome | 7/2221 | 27/18614 | 0.035181213 | 0.201097999 | 0.169950891 | AKAP11/DTX3L/EGF/EZR/RDX/ROCK2/VPS35 | 7 |
| BP | GO:1904357 | negative regulation of telomere maintenance via telomere lengthening | 7/2221 | 27/18614 | 0.035181213 | 0.201097999 | 0.169950891 | ERCC4/HNRNPA1/HNRNPU/PARP1/POT1/TNKS2/XRN1 | 7 |
| BP | GO:2001032 | regulation of double-strand break repair via nonhomologous end joining | 7/2221 | 27/18614 | 0.035181213 | 0.201097999 | 0.169950891 | DEK/ERCC6/POT1/PRKDC/RIF1/SETMAR/SMCHD1 | 7 |
| BP | GO:0032722 | positive regulation of chemokine production | 14/2221 | 70/18614 | 0.035198835 | 0.201097999 | 0.169950891 | ADAM17/C5/CD84/DDX3X/EIF2AK2/HAVCR2/HIF1A/HMGB1/IL18/LPL/RIPK2/TLR2/TLR3/TLR4 | 14 |
| BP | GO:0002696 | positive regulation of leukocyte activation | 57/2221 | 377/18614 | 0.03538391 | 0.20196357 | 0.170682399 | ATAD5/MSH2/ABL2/AP3B1/ARID2/BLOC1S6/BRD7/BTK/CD226/CD38/CD86/CLEC4D/CR1/DOCK8/DPP4/FCGR3A/HAVCR2/HMGB1/HSPD1/HSPH1/IGF1/IL18/IL2RA/IL6ST/IL7R/JAK2/LRRK2/LYN/MALT1/MEF2C/MIR142/MIR30B/MLH1/MMP8/NCK1/NCKAP1L/NLRP3/PBRM1/PDCD1LG2/PIK3CA/PLA2G4A/PPP2R3C/PRKDC/PTPN11/PTPRC/RIF1/RIPK2/SLC39A10/STAP1/TFRC/TLR4/TLR6/TP53BP1/VCAM1/VNN1/YES1/ZBTB1 | 57 |
| BP | GO:0090263 | positive regulation of canonical Wnt signaling pathway | 20/2221 | 110/18614 | 0.035478491 | 0.202119885 | 0.170814503 | ASPM/GSKIP/CAPRIN2/DDX3X/EGF/LRRK2/PPM1B/RBPJ/RSPO3/SCEL/TBL1XR1/TNKS2/TTC21B/UBR5/USP34/USP47/USP8/VCP/VPS35/ZEB2 | 20 |
| BP | GO:1901222 | regulation of NIK/NF-kappaB signaling | 20/2221 | 110/18614 | 0.035478491 | 0.202119885 | 0.170814503 | BIRC2/CD86/CYLD/DDX3X/EIF2AK2/HAVCR2/IL18/MIR15B/MIR30C2/MMP8/NFAT5/NLRP3/PDCD4/PPM1B/RC3H2/TLR2/TLR3/TLR4/TRIM44/UACA | 20 |
| BP | GO:0051302 | regulation of cell division | 31/2221 | 187/18614 | 0.036048066 | 0.205170451 | 0.173392581 | ASPM/BLM/BRCA2/CDC6/ECT2/KIF14/KIF20A/KIF20B/KIF23/PRC1/AHCTF1/BECN1/BIRC6/CCP110/CUL3/FGF7/KLHL13/MACC1/MAP9/MLLT3/NCOA3/PDGFC/PDGFD/PIK3C3/PIK3R4/PKN2/PRPF40A/RACGAP1/SH3GLB1/SVIL/ZZZ3 | 31 |
| BP | GO:0048701 | embryonic cranial skeleton morphogenesis | 10/2221 | 45/18614 | 0.036481552 | 0.207010464 | 0.174947603 | EIF4A3/GRHL2/MMP16/MTHFD1/MTHFD1L/NIPBL/PDGFRA/PRRX1/TGFBR1/WDR19 | 10 |
| BP | GO:2000058 | regulation of ubiquitin-dependent protein catabolic process | 29/2221 | 173/18614 | 0.036548827 | 0.207010464 | 0.174947603 | PBK/XPO1/ANKIB1/ARIH1/EGF/GCLC/HECTD1/HSP90AB1/L3MBTL3/LRRK2/MDM2/MTM1/NFE2L2/NUB1/OGT/PHF20L1/RNF14/RNF19A/RNF217/RYBP/SDCBP/SOCS4/TAF1/UCHL5/UFL1/USP14/USP7/USP9X/VCP | 29 |
| BP | GO:2001242 | regulation of intrinsic apoptotic signaling pathway | 29/2221 | 173/18614 | 0.036548827 | 0.207010464 | 0.174947603 | ATAD5/DDIAS/HELLS/BCLAF1/BECN1/CYLD/DDX3X/DNAJA1/DNM1L/EIF2AK3/FIGNL1/HIF1A/ING2/IVNS1ABP/LRRK2/MDM2/MIR186/NCK1/NFE2L2/OPA1/PARP1/PIK3CB/PTGS2/PTPN2/RRM2B/SKIL/USP15/USP47/VNN1 | 29 |
| BP | GO:0021591 | ventricular system development | 8/2221 | 33/18614 | 0.036625296 | 0.207010464 | 0.174947603 | CENPF/CORO1C/DNAH5/RAPGEF2/RPGRIP1L/SLC7A11/TTC21B/UCHL5 | 8 |
| BP | GO:0035459 | vesicle cargo loading | 8/2221 | 33/18614 | 0.036625296 | 0.207010464 | 0.174947603 | AP3B1/AP3M1/MIA3/RAB1A/SEC23A/SEC23B/SEC24D/SEC31A | 8 |
| BP | GO:0051497 | negative regulation of stress fiber assembly | 8/2221 | 33/18614 | 0.036625296 | 0.207010464 | 0.174947603 | ARHGAP28/CGNL1/CLASP2/MET/PHLDB2/PIK3R1/PPFIA1/TJP1 | 8 |
| BP | GO:1901889 | negative regulation of cell junction assembly | 8/2221 | 33/18614 | 0.036625296 | 0.207010464 | 0.174947603 | CLASP2/CORO1C/MIR142/PHLDB2/PTPN13/ROCK1/ROCK2/TLR2 | 8 |
| BP | GO:0032612 | interleukin-1 production | 23/2221 | 131/18614 | 0.036681043 | 0.207010464 | 0.174947603 | HDAC2/AIM2/AQP4/CASP1/CD36/GBP5/HAVCR2/HMGB1/IFI16/IGF1/JAK2/LPL/MALT1/MIR142/MNDA/NAIP/NLRC4/NLRP3/PANX1/RIPK2/TLR4/TLR6/TLR8 | 23 |
| BP | GO:0032652 | regulation of interleukin-1 production | 23/2221 | 131/18614 | 0.036681043 | 0.207010464 | 0.174947603 | HDAC2/AIM2/AQP4/CASP1/CD36/GBP5/HAVCR2/HMGB1/IFI16/IGF1/JAK2/LPL/MALT1/MIR142/MNDA/NAIP/NLRC4/NLRP3/PANX1/RIPK2/TLR4/TLR6/TLR8 | 23 |
| BP | GO:0045740 | positive regulation of DNA replication | 9/2221 | 39/18614 | 0.03692135 | 0.207650616 | 0.175488605 | ATAD5/CDK1/ATRX/BAZ1A/DBF4/DHX9/DNA2/EGF/SMARCA5 | 9 |
| BP | GO:0097242 | amyloid-beta clearance | 9/2221 | 39/18614 | 0.03692135 | 0.207650616 | 0.175488605 | C3/CD36/CLTC/HMGCR/IDE/IFNGR1/LRP2/MSR1/ROCK1 | 9 |
| BP | GO:0016064 | immunoglobulin mediated immune response | 25/2221 | 145/18614 | 0.036932314 | 0.207650616 | 0.175488605 | ATAD5/MSH2/BTK/C3/C5/C6/C7/CD226/CFI/CR1/CR1L/FCGR3A/GAPT/HSPD1/LIG4/MLH1/MSH6/NBN/PTPRC/RIF1/SWAP70/TFRC/THOC1/TLR8/TP53BP1 | 25 |
| BP | GO:0030832 | regulation of actin filament length | 26/2221 | 152/18614 | 0.03693254 | 0.207650616 | 0.175488605 | ADD3/ARFGEF1/ARHGAP18/ARHGAP28/CAPZA2/DLG1/EPS8/FER/FMN1/LIMA1/MKKS/NCK1/NCKAP1/NCKAP1L/NEB/PIK3CA/RASA1/RDX/RICTOR/SCIN/SNX9/SPTAN1/SVIL/SWAP70/TMOD2/TWF1 | 26 |
| BP | GO:0043297 | apical junction assembly | 15/2221 | 77/18614 | 0.037024457 | 0.207973047 | 0.175761096 | ECT2/APC/CLDN1/CTNNA1/DLG1/GRHL2/MIR142/MPP7/PKN2/POF1B/ROCK1/ROCK2/STRN/TJP1/VCL | 15 |
| BP | GO:0006942 | regulation of striated muscle contraction | 18/2221 | 97/18614 | 0.037174583 | 0.208621543 | 0.17630915 | ACE2/AKAP9/ANK2/ATP1B1/ATP2A2/CLIC2/DLG1/DMD/DSC2/DSG2/DSP/HSP90AA1/PDE4B/PDE4D/PIK3CG/PKP2/RGS2/RYR2 | 18 |
| BP | GO:0014896 | muscle hypertrophy | 19/2221 | 104/18614 | 0.037978735 | 0.212935759 | 0.179955157 | EZH2/HDAC2/AKAP13/AKAP6/ATP2A2/BECN1/IGF1/IL6ST/MIR15B/PARP1/PPARG/RAP1GDS1/RGS2/ROCK1/ROCK2/RYR2/SORBS2/TTN/TWF1 | 19 |
| BP | GO:0030042 | actin filament depolymerization | 12/2221 | 58/18614 | 0.038795192 | 0.217310868 | 0.183652627 | ADD3/CAPZA2/EPS8/LIMA1/PIK3CA/RDX/SCIN/SPTAN1/SVIL/SWAP70/TMOD2/TWF1 | 12 |
| BP | GO:0002703 | regulation of leukocyte mediated immunity | 39/2221 | 246/18614 | 0.038920254 | 0.217808605 | 0.184073272 | ATAD5/MSH2/ARG1/BTK/C12orf4/C3/CD226/CD84/CD96/CR1/CR1L/DDX1/DDX21/DHX36/FBXO38/FER/HAVCR2/HMGB1/HSPD1/IL18/IL18RAP/IL1R1/IL7R/LYN/MALT1/MAP3K7/MLH1/NCKAP1L/NLRP3/PTPRC/RABGEF1/RIF1/STAP1/TFRC/THOC1/TLR3/TLR4/TP53BP1/ZBTB1 | 39 |
| BP | GO:0003208 | cardiac ventricle morphogenesis | 14/2221 | 71/18614 | 0.039206244 | 0.219205172 | 0.185253531 | CHD7/DSP/GRHL2/HIF1A/LRP2/MEF2C/PKP2/PTCD2/RBPJ/RYR2/SEMA3C/TGFBR1/TPM1/ZFPM2 | 14 |
| BP | GO:0002064 | epithelial cell development | 34/2221 | 210/18614 | 0.039499442 | 0.219900469 | 0.185841137 | ARID4A/ARID4B/ATRX/C1GALT1/CDH2/CLDN1/CLOCK/EXPH5/EZR/FAT1/FER/FNDC3A/FRS2/GRHL2/HIF1A/HSD17B4/IFT74/IL6ST/IQGAP1/MET/MYO1E/PDE4D/PLCB1/POF1B/RAPGEF2/RDX/ROCK1/ROCK2/ROS1/TFCP2L1/TJP1/VCL/VSIG1/ZDHHC21 | 34 |
| BP | GO:0007160 | cell-matrix adhesion | 38/2221 | 239/18614 | 0.039530507 | 0.219900469 | 0.185841137 | ADAM9/ADAMTS9/CASK/CD36/CD96/CLASP2/COL3A1/CORO1C/CTNNB1/ECM2/EPHA3/FERMT2/FMN1/ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/MACF1/MAP4K4/MKLN1/NF1/PHLDB2/PIK3CB/PIK3R1/PPFIA1/PTPRK/RASA1/ROCK1/ROCK2/SLK/TRPM7/UTRN/VCAM1/VCL | 38 |
| BP | GO:0035024 | negative regulation of Rho protein signal transduction | 6/2221 | 22/18614 | 0.039612673 | 0.219900469 | 0.185841137 | ABL2/ARHGAP42/CCDC125/CUL3/ITGB1/MET | 6 |
| BP | GO:0051767 | nitric-oxide synthase biosynthetic process | 6/2221 | 22/18614 | 0.039612673 | 0.219900469 | 0.185841137 | AKAP12/JAK2/LRRK2/STAT1/TLR2/TLR4 | 6 |
| BP | GO:0051769 | regulation of nitric-oxide synthase biosynthetic process | 6/2221 | 22/18614 | 0.039612673 | 0.219900469 | 0.185841137 | AKAP12/JAK2/LRRK2/STAT1/TLR2/TLR4 | 6 |
| BP | GO:0016573 | histone acetylation | 26/2221 | 153/18614 | 0.039625688 | 0.219900469 | 0.185841137 | BRCA1/BRCA2/CHEK1/DEK/BAZ1B/DDX21/EPC2/ERCC6/HAT1/ING3/IWS1/JADE1/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA50/OGT/PHF20L1/SDR16C5/SF3B1/SMARCA5/SUPT20H/TAF2/TAF7/ZZZ3 | 26 |
| BP | GO:0030183 | B cell differentiation | 26/2221 | 153/18614 | 0.039625688 | 0.219900469 | 0.185841137 | EZH2/MSH2/ADAM17/ATM/BTK/CR1/DOCK10/DOCK11/FNIP1/INHBA/ITGA4/ITGB1/MALT1/NCKAP1L/PHF14/PIK3R1/PIK3R3/PPP2R3C/PRKDC/PTPN2/PTPRC/RABL3/RBPJ/TOP2B/VCAM1/ZBTB1 | 26 |
| BP | GO:0034101 | erythrocyte homeostasis | 24/2221 | 139/18614 | 0.039687638 | 0.219900469 | 0.185841137 | NCAPG2/ALAS2/ARID4A/BPGM/CASP3/HIF1A/HMGB2/HSPA9/INHBA/IREB2/JAK2/KMT2E/L3MBTL3/LYAR/LYN/NCKAP1L/PRKDC/PTPN2/RACGAP1/RB1/SLC4A1/STAT1/UBA5/UFL1 | 24 |
| BP | GO:0030177 | positive regulation of Wnt signaling pathway | 25/2221 | 146/18614 | 0.039696129 | 0.219900469 | 0.185841137 | ASPM/GSKIP/CAPRIN2/DDX3X/EGF/LRRK2/MACF1/MLLT3/PPM1B/RBPJ/RSPO3/SCEL/SULF1/TBL1XR1/TLR2/TNKS2/TTC21B/UBR5/USP34/USP47/USP8/VCP/VPS35/ZEB2/ZRANB1 | 25 |
| BP | GO:0050714 | positive regulation of protein secretion | 25/2221 | 146/18614 | 0.039696129 | 0.219900469 | 0.185841137 | ACSL4/ADAM9/CD2AP/CD38/CFTR/DNM1L/EXOC1/EXPH5/EZR/HIF1A/IGF1/ITPR1/JAK2/MYOM1/OSBP/OXCT1/PCSK1/PFKFB2/PLCB1/PPARG/RAPGEF4/TLR2/TLR4/TTN/VPS35 | 25 |
| BP | GO:0031668 | cellular response to extracellular stimulus | 41/2221 | 261/18614 | 0.039733687 | 0.219906038 | 0.185845843 | BRIP1/AIFM1/ATP2B1/BECN1/CTSK/DSC2/EIF2AK2/EIF2AK3/EIF2AK4/EIF2S1/ERCC6/FAS/FNIP1/HNRNPA1/HSPA5/HSPA8/IFI16/IMPACT/ITGA4/JMY/LPL/LRRK2/LYN/MIOS/NCOA1/NFE2L2/PHEX/PIK3C3/PIK3R4/PLIN2/POSTN/PRKD1/PTPRC/RICTOR/SESN3/SH3GLB1/SLC38A2/SNW1/VCAM1/VPS41/WRN | 41 |
| BP | GO:0009410 | response to xenobiotic stimulus | 65/2221 | 440/18614 | 0.039982707 | 0.221080851 | 0.186838695 | CDK1/CENPF/HDAC2/RAD54B/ABCB1/ABCC4/ABCD3/ACSL1/ADAM17/AIM2/AOX1/ARG1/ATR/BECN1/CASP3/CCNT1/CD38/CTNNB1/CTPS1/CYBB/FMO1/FMO5/GCLC/GNPAT/HADHA/HSP90AA1/HSPA5/HTR2A/INHBA/ITGA2/ITGB3/LOX/LPL/LRP8/LYN/MAP1B/MEF2C/MIR186/NCEH1/NCKAP1L/NFE2L2/NPC1/OXCT1/OXSR1/PAM/PARP4/PCSK1/PDE4B/PLIN2/PPP1R12A/PTGS2/RB1/RORA/RPN2/SEMA3C/SLC1A3/STAT1/SULT1B1/TFRC/TIMP4/TLR3/TOP1/UMPS/USP47/XRCC5 | 65 |
| BP | GO:0060324 | face development | 11/2221 | 52/18614 | 0.04042718 | 0.222923845 | 0.188396236 | ARID5B/ASPH/CHD7/GRHL2/MKKS/NIPBL/PDGFRA/PTPN11/RAB3GAP1/TIPARP/ZFAND5 | 11 |
| BP | GO:0072599 | establishment of protein localization to endoplasmic reticulum | 11/2221 | 52/18614 | 0.04042718 | 0.222923845 | 0.188396236 | HSPA5/RAB3GAP1/RAB3GAP2/RYR2/SEC62/SEC63/SRP54/SRP72/SRPRB/SSR3/VPS54 | 11 |
| BP | GO:0089718 | amino acid import across plasma membrane | 11/2221 | 52/18614 | 0.04042718 | 0.222923845 | 0.188396236 | ACE2/ARG1/ITGB1/RGS2/SLC1A3/SLC36A4/SLC38A1/SLC38A2/SLC6A14/SLC7A11/SLC7A2 | 11 |
| BP | GO:0045824 | negative regulation of innate immune response | 15/2221 | 78/18614 | 0.04097142 | 0.225718007 | 0.190757625 | ARG1/CD96/CR1/HAVCR2/IFI16/IRAK3/LYAR/MIR181B1/PARP1/PARP14/PPARG/PTPN2/SAMHD1/USP15/YTHDF3 | 15 |
| BP | GO:0046651 | lymphocyte proliferation | 47/2221 | 306/18614 | 0.041357002 | 0.227633782 | 0.192376674 | ATAD5/HELLS/ARG1/ATM/BTK/CASP3/CD180/CD38/CD86/CR1/CTNNB1/CTPS1/DLG1/DOCK2/DOCK8/FCGR3A/GAPT/GPNMB/HAVCR2/HMGB1/HSPD1/IGF1/IL18/IL2RA/IL6ST/IL7R/IMPDH2/JAK2/LYN/MALT1/MEF2C/MIR30B/MNDA/NCK1/NCKAP1L/PDCD1LG2/PIK3CG/PTPRC/RC3H2/RIPK2/SLC39A10/SOS1/SOS2/TFRC/TLR4/TNFSF8/VCAM1 | 47 |
| BP | GO:0030888 | regulation of B cell proliferation | 13/2221 | 65/18614 | 0.041416514 | 0.227752968 | 0.192477399 | ATAD5/ATM/BTK/CASP3/CD38/LYN/MEF2C/MNDA/NCKAP1L/PTPRC/SLC39A10/TFRC/TLR4 | 13 |
| BP | GO:0055010 | ventricular cardiac muscle tissue morphogenesis | 10/2221 | 46/18614 | 0.041811586 | 0.229715526 | 0.194135987 | CHD7/DSP/LRP2/PKP2/PTCD2/RBPJ/RYR2/TGFBR1/TPM1/ZFPM2 | 10 |
| BP | GO:0043473 | pigmentation | 20/2221 | 112/18614 | 0.041917208 | 0.23007599 | 0.19444062 | ADAMTS9/AP3B1/AP3M1/ARCN1/ATP7A/BLOC1S6/ENPP1/FIG4/HPS3/LYST/MEF2C/MKKS/MYO5A/MYSM1/NF1/PIKFYVE/RAB1A/RAB27A/USP13/ZEB2 | 20 |
| BP | GO:0002675 | positive regulation of acute inflammatory response | 7/2221 | 28/18614 | 0.042238036 | 0.23007599 | 0.19444062 | BTK/C3/CNR1/IL6ST/OSMR/PIK3CG/PTGS2 | 7 |
| BP | GO:0021680 | cerebellar Purkinje cell layer development | 7/2221 | 28/18614 | 0.042238036 | 0.23007599 | 0.19444062 | KIF14/ARCN1/ATP7A/HERC1/HSPA5/RORA/TTC21B | 7 |
| BP | GO:0033522 | histone H2A ubiquitination | 7/2221 | 28/18614 | 0.042238036 | 0.23007599 | 0.19444062 | BRCA1/BRCA2/BRCC3/DTX3L/TRIP12/UBR2/UBR5 | 7 |
| BP | GO:0045830 | positive regulation of isotype switching | 7/2221 | 28/18614 | 0.042238036 | 0.23007599 | 0.19444062 | ATAD5/MSH2/MLH1/PTPRC/RIF1/TFRC/TP53BP1 | 7 |
| BP | GO:0051647 | nucleus localization | 7/2221 | 28/18614 | 0.042238036 | 0.23007599 | 0.19444062 | CEP120/DOCK7/DYNC1H1/HOOK3/LMNB1/PCM1/SYNE2 | 7 |
| BP | GO:0070269 | pyroptosis | 7/2221 | 28/18614 | 0.042238036 | 0.23007599 | 0.19444062 | AIM2/CASP1/CASP4/DHX9/NAIP/NLRC4/NLRP3 | 7 |
| BP | GO:1902883 | negative regulation of response to oxidative stress | 7/2221 | 28/18614 | 0.042238036 | 0.23007599 | 0.19444062 | HGF/LRRK2/MCTP1/MET/NCOA7/NFE2L2/OXR1 | 7 |
| BP | GO:0018393 | internal peptidyl-lysine acetylation | 27/2221 | 161/18614 | 0.042246804 | 0.23007599 | 0.19444062 | BRCA1/BRCA2/CHEK1/DEK/BAZ1B/DDX21/EPC2/ERCC6/HAT1/ING3/IWS1/JADE1/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA50/OGT/PHF20L1/SDR16C5/SF3B1/SMARCA5/SMC5/SUPT20H/TAF2/TAF7/ZZZ3 | 27 |
| BP | GO:0018210 | peptidyl-threonine modification | 21/2221 | 119/18614 | 0.04229788 | 0.23007599 | 0.19444062 | CDK1/CHEK1/TTK/CAB39/CDC42BPA/EGF/GALNT1/GALNT3/HIPK3/LRRK2/OXSR1/PRKD1/PRKDC/RIPK2/ROCK1/ROCK2/TAF1/TBK1/TGFBR1/TRIM6/WNK3 | 21 |
| BP | GO:0048675 | axon extension | 21/2221 | 119/18614 | 0.04229788 | 0.23007599 | 0.19444062 | ALCAM/C9orf72/CDKL5/DCLK1/GOLGA4/HSP90AA1/HSP90AB1/IFRD1/ITGB1/MACF1/MAP1B/MAP3K13/NRCAM/RNF6/RUFY3/SEMA3A/SEMA3C/SEMA3D/SPG11/USP9X/VCL | 21 |
| BP | GO:1901292 | nucleoside phosphate catabolic process | 16/2221 | 85/18614 | 0.04238406 | 0.230336501 | 0.194660782 | ACAT1/DPYD/ENPP1/ENTPD1/ENTPD7/MBD4/NT5C2/NT5E/NUDT12/PDE4B/PDE4D/PDE8B/SAMHD1/SUCLA2/SUCLG2/VCP | 16 |
| BP | GO:0010927 | cellular component assembly involved in morphogenesis | 22/2221 | 126/18614 | 0.042539975 | 0.230557234 | 0.194847326 | UGT8/AKAP13/ANK2/CAPN3/CLASP2/CNTN1/DICER1/EPB41L3/FIG4/GNPAT/ITGB1/MTMR2/NEB/PDGFRA/PHLDB2/PIKFYVE/TLR2/TMF1/TMOD2/TPM1/TTN/VPS13B | 22 |
| BP | GO:0032506 | cytokinetic process | 9/2221 | 40/18614 | 0.042777867 | 0.230557234 | 0.194847326 | ANLN/CEP55/ECT2/KIF20A/KIF20B/CHMP2B/RACGAP1/SNX9/SPIRE1 | 9 |
| BP | GO:0051693 | actin filament capping | 9/2221 | 40/18614 | 0.042777867 | 0.230557234 | 0.194847326 | ADD3/CAPZA2/EPS8/RDX/SCIN/SPTAN1/SVIL/TMOD2/TWF1 | 9 |
| BP | GO:0006891 | intra-Golgi vesicle-mediated transport | 8/2221 | 34/18614 | 0.043060983 | 0.230557234 | 0.194847326 | COG5/COG6/COPA/COPB1/COPB2/GOLGA5/NAPG/NSF | 8 |
| BP | GO:0009112 | nucleobase metabolic process | 8/2221 | 34/18614 | 0.043060983 | 0.230557234 | 0.194847326 | ADK/CTPS1/DPYD/GART/GMPS/PAICS/PPAT/UMPS | 8 |
| BP | GO:0009156 | ribonucleoside monophosphate biosynthetic process | 8/2221 | 34/18614 | 0.043060983 | 0.230557234 | 0.194847326 | ADK/ATIC/GART/GMPS/IMPDH2/PAICS/PPAT/UMPS | 8 |
| BP | GO:0036475 | neuron death in response to oxidative stress | 8/2221 | 34/18614 | 0.043060983 | 0.230557234 | 0.194847326 | CTNNB1/HIF1A/NCOA7/OXR1/PARP1/SLC7A11/TLR4/TLR6 | 8 |
| BP | GO:2000780 | negative regulation of double-strand break repair | 8/2221 | 34/18614 | 0.043060983 | 0.230557234 | 0.194847326 | PARPBP/POLQ/ERCC6/RIF1/SMCHD1/TP53BP1/TRIP12/UBR5 | 8 |
| BP | GO:0002822 | regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 31/2221 | 190/18614 | 0.043471844 | 0.230557234 | 0.194847326 | ATAD5/MSH2/ARG1/BTK/C3/CD226/CR1/CR1L/FBXO38/HAVCR2/HMGB1/HSPD1/IL18/IL1R1/IL7R/JAK2/MALT1/MAP3K7/MEF2C/MLH1/NCKAP1L/NLRP3/PLA2G4A/PTPRC/RC3H2/RIF1/RIPK2/TFRC/THOC1/TP53BP1/ZBTB1 | 31 |
| BP | GO:0033143 | regulation of intracellular steroid hormone receptor signaling pathway | 14/2221 | 72/18614 | 0.043527995 | 0.230557234 | 0.194847326 | BRCA1/CLOCK/CNOT1/CYP7B1/DDX5/KDM4C/NCOR1/PARP1/RNF14/RNF6/UBA5/UFL1/UFM1/UFSP2 | 14 |
| BP | GO:0060260 | regulation of transcription initiation by RNA polymerase II | 14/2221 | 72/18614 | 0.043527995 | 0.230557234 | 0.194847326 | ATF7IP/CAND1/DHX36/ERCC6/HMGB1/MED13/MED23/MED6/PSMC6/TAF1/TAF2/TAF4B/TAF7/ZNF451 | 14 |
| BP | GO:0000712 | resolution of meiotic recombination intermediates | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | TOP2A/ERCC4/FANCM/MLH1/TOP2B | 5 |
| BP | GO:0001522 | pseudouridine synthesis | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | DKC1/PUS10/PUS3/PUS7/PUS7L | 5 |
| BP | GO:0002730 | regulation of dendritic cell cytokine production | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | DDX1/DDX21/DHX36/TLR3/TLR4 | 5 |
| BP | GO:0006415 | translational termination | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | ABCE1/ETF1/GFM2/GSPT1/OGFOD1 | 5 |
| BP | GO:0009251 | glucan catabolic process | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | AGL/MGAM/PGM2/PYGL/RB1CC1 | 5 |
| BP | GO:0030889 | negative regulation of B cell proliferation | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | ATM/BTK/CASP3/LYN/MNDA | 5 |
| BP | GO:0033631 | cell-cell adhesion mediated by integrin | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | ADAM9/DPP4/ITGA4/ITGB1/SWAP70 | 5 |
| BP | GO:0034112 | positive regulation of homotypic cell-cell adhesion | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | ANK3/IL6ST/JAK1/JAK2/MMRN1 | 5 |
| BP | GO:0044539 | long-chain fatty acid import into cell | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | ACSL1/ACSL3/CD36/FABP3/SLC27A2 | 5 |
| BP | GO:0048311 | mitochondrion distribution | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | DNM1L/KIF5B/LRRK2/MTM1/TRAK2 | 5 |
| BP | GO:0055119 | relaxation of cardiac muscle | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | ATP1B1/PDE4B/PDE4D/PIK3CA/RGS2 | 5 |
| BP | GO:0060148 | positive regulation of post-transcriptional gene silencing | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | DHX9/FMR1/FXR1/PUM2/XPO5 | 5 |
| BP | GO:0090399 | replicative senescence | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | CHEK1/ATM/ATR/PLA2R1/WRN | 5 |
| BP | GO:1900034 | regulation of cellular response to heat | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | ATM/ATR/CHORDC1/DNAJC2/DNAJC7 | 5 |
| BP | GO:1900370 | positive regulation of post-transcriptional gene silencing by RNA | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | DHX9/FMR1/FXR1/PUM2/XPO5 | 5 |
| BP | GO:1901550 | regulation of endothelial cell development | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | PLCB1/ROCK1/ROCK2/VCL/ZDHHC21 | 5 |
| BP | GO:1902036 | regulation of hematopoietic stem cell differentiation | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | EIF2AK2/HSPA9/NFE2L2/PRKDC/PUS7 | 5 |
| BP | GO:1902570 | protein localization to nucleolus | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | NMD3/NOL8/RPF2/RRS1/WRN | 5 |
| BP | GO:1903140 | regulation of establishment of endothelial barrier | 5/2221 | 17/18614 | 0.043574397 | 0.230557234 | 0.194847326 | PLCB1/ROCK1/ROCK2/VCL/ZDHHC21 | 5 |
| BP | GO:0043409 | negative regulation of MAPK cascade | 30/2221 | 183/18614 | 0.04394904 | 0.232335169 | 0.196349885 | PBK/ACE2/AIDA/ASH1L/CYLD/DLG1/DNAJA1/EIF3A/EPHA4/EZR/FKTN/GBP1/HIPK3/HMGCR/IRAK3/LYN/MECOM/NCOR1/NF1/PDCD4/PIK3CB/PPARG/PTPN2/PTPRC/RGS2/RPS6KA6/TAOK3/TLR4/ZMYND11/ZNF675 | 30 |
| BP | GO:0031331 | positive regulation of cellular catabolic process | 66/2221 | 450/18614 | 0.044004248 | 0.232422786 | 0.196423932 | ADAM9/ANKIB1/ARIH1/ATF6/ATM/BECN1/BNIP3L/C9orf72/CNOT1/CNOT6L/CSDE1/DHX36/DHX9/DIS3/DTX3L/EGF/EXOSC9/GCLC/GIGYF2/GNAI3/HECTD1/HIF1A/HMGB1/HNRNPU/HTR2A/IGF1/L3MBTL3/LRRK2/MAP3K7/MDM2/METTL14/MIR181B1/MLH1/MTDH/NFE2L2/NUB1/PIK3C2A/PIK3CB/PNPT1/PRKD1/RAB3GAP1/RAB3GAP2/RB1CC1/RC3H2/RIPK2/RNF14/RNF19A/RNF217/ROCK1/ROCK2/SESN3/SH3GLB1/SNX30/SNX9/SOCS4/SPTLC1/SYNCRIP/TAF1/TBK1/TRIM22/TRIM38/TRIM6/UFL1/VCP/VPS13D/YTHDF3 | 66 |
| BP | GO:0071824 | protein-DNA complex subunit organization | 41/2221 | 263/18614 | 0.044078857 | 0.232612633 | 0.196584375 | CENPE/CENPF/CENPK/DLGAP5/GMNN/HELLS/KNTC1/ARID2/ATF7IP/ATRX/BAZ1A/BDP1/CAND1/CENPC/CENPN/CENPW/CHD1/CHD2/HAT1/HMGB1/HMGB2/KAT6A/MED23/MED6/MIS12/NAP1L1/NASP/PSMC6/RB1/RSF1/SENP6/SHPRH/SMARCA5/SPTY2D1/SUPT16H/TAF1/TAF1B/TAF2/TAF4B/TAF7/TSPYL2 | 41 |
| BP | GO:0036473 | cell death in response to oxidative stress | 18/2221 | 99/18614 | 0.04435185 | 0.233848142 | 0.197628522 | GSKIP/MELK/CTNNB1/HGF/HIF1A/JAK2/LRRK2/MET/NCOA7/NFE2L2/OXR1/PARP1/RIPK1/SLC7A11/TLR4/TLR6/VNN1/ZNF622 | 18 |
| BP | GO:0000022 | mitotic spindle elongation | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | KIF23/KIF4A/PRC1/RACGAP1 | 4 |
| BP | GO:0032252 | secretory granule localization | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | KIF5B/PIK3CG/TANC2/USO1 | 4 |
| BP | GO:0034086 | maintenance of sister chromatid cohesion | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | ATRX/NIPBL/RB1/SMC5 | 4 |
| BP | GO:0034088 | maintenance of mitotic sister chromatid cohesion | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | ATRX/NIPBL/RB1/SMC5 | 4 |
| BP | GO:0034135 | regulation of toll-like receptor 2 signaling pathway | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | LYN/PJA2/TLR1/TLR6 | 4 |
| BP | GO:0034454 | microtubule anchoring at centrosome | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | HOOK3/KIF3A/NIN/PCM1 | 4 |
| BP | GO:0051095 | regulation of helicase activity | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | MSH2/MSH3/MSH6/POT1 | 4 |
| BP | GO:0051657 | maintenance of organelle location | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | ASPM/AKAP9/ARHGAP21/GPSM2 | 4 |
| BP | GO:0090232 | positive regulation of spindle checkpoint | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | MAD2L1/NDC80/GEN1/TPR | 4 |
| BP | GO:0090267 | positive regulation of mitotic cell cycle spindle assembly checkpoint | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | MAD2L1/NDC80/GEN1/TPR | 4 |
| BP | GO:0090435 | protein localization to nuclear envelope | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | LMNB1/NUP155/OSBPL8/TOR1AIP2 | 4 |
| BP | GO:0098789 | pre-mRNA cleavage required for polyadenylation | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | CPSF2/NCBP1/NCBP2/NUDT21 | 4 |
| BP | GO:0140052 | cellular response to oxidised low-density lipoprotein particle stimulus | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | CD36/MIA3/TLR4/TLR6 | 4 |
| BP | GO:1900152 | negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | CSDE1/DHX9/HNRNPU/SYNCRIP | 4 |
| BP | GO:1901503 | ether biosynthetic process | 4/2221 | 12/18614 | 0.045523808 | 0.236912829 | 0.200218534 | AGPS/FAR1/GNPAT/PLA2G4A | 4 |
| BP | GO:0019724 | B cell mediated immunity | 25/2221 | 148/18614 | 0.045679043 | 0.237347023 | 0.200585477 | ATAD5/MSH2/BTK/C3/C5/C6/C7/CD226/CFI/CR1/CR1L/FCGR3A/GAPT/HSPD1/LIG4/MLH1/MSH6/NBN/PTPRC/RIF1/SWAP70/TFRC/THOC1/TLR8/TP53BP1 | 25 |
| BP | GO:0035065 | regulation of histone acetylation | 11/2221 | 53/18614 | 0.045723463 | 0.237347023 | 0.200585477 | BRCA1/CHEK1/DEK/BAZ1B/DDX21/ERCC6/IWS1/SDR16C5/SF3B1/SMARCA5/TAF7 | 11 |
| BP | GO:0043200 | response to amino acid | 21/2221 | 120/18614 | 0.045725598 | 0.237347023 | 0.200585477 | AIFM1/ARG1/ATP7A/CASP3/COL3A1/COL5A2/CYBB/GCLC/IPO5/LYN/MIR224/PDGFC/PDGFD/PDGFRA/PIK3C3/PIK3CA/SESN3/UBR1/UBR2/UFL1/ZEB1 | 21 |
| BP | GO:0070555 | response to interleukin-1 | 24/2221 | 141/18614 | 0.045837097 | 0.237720667 | 0.20090125 | AKAP12/AQP4/CD38/GBP1/GBP2/GBP3/GCLC/HIF1A/IL1R1/IRAK3/IRAK4/KMO/MAP3K7/MIR142/OTUD4/PCSK1/PLCB1/PRKCI/RIPK2/RORA/RPS6KA5/TANK/VRK2/ZNF675 | 24 |
| BP | GO:0010812 | negative regulation of cell-substrate adhesion | 13/2221 | 66/18614 | 0.046158443 | 0.239101163 | 0.202067927 | ANGPT2/AP1AR/CASK/CLASP2/CORO1C/GBP1/GCNT2/MAP4K4/NF1/PHLDB2/PIK3R1/PTPRO/RASA1 | 13 |
| BP | GO:0050777 | negative regulation of immune response | 31/2221 | 191/18614 | 0.046182771 | 0.239101163 | 0.202067927 | WDR41/ARG1/CD84/CD96/COL3A1/CR1/CR1L/FER/FGL2/HAVCR2/IFI16/IL7R/IRAK3/LYAR/LYN/MIR181B1/NCKAP1L/PARP1/PARP14/PPARG/PTPN2/PTPRC/RABGEF1/RC3H2/SAMHD1/SAMSN1/SPINK5/THOC1/USP15/YES1/YTHDF3 | 31 |
| BP | GO:0065004 | protein-DNA complex assembly | 38/2221 | 242/18614 | 0.046482144 | 0.240265995 | 0.203052344 | CENPE/CENPF/CENPK/DLGAP5/GMNN/HELLS/KNTC1/ATF7IP/ATRX/BAZ1A/BDP1/CAND1/CENPC/CENPN/CENPW/HAT1/HMGB1/HMGB2/KAT6A/MED23/MED6/MIS12/NAP1L1/NASP/PSMC6/RB1/RSF1/SENP6/SHPRH/SMARCA5/SPTY2D1/SUPT16H/TAF1/TAF1B/TAF2/TAF4B/TAF7/TSPYL2 | 38 |
| BP | GO:0007260 | tyrosine phosphorylation of STAT protein | 16/2221 | 86/18614 | 0.046527574 | 0.240265995 | 0.203052344 | HDAC2/ERBB4/FER/GGNBP2/IGF1/IL18/IL6ST/JAK1/JAK2/LYN/OSBP/PARP14/PARP9/PIBF1/PPP2CA/PTPN2 | 16 |
| BP | GO:0008543 | fibroblast growth factor receptor signaling pathway | 16/2221 | 86/18614 | 0.046527574 | 0.240265995 | 0.203052344 | SHCBP1/CEP57/CHURC1/CTNNB1/FGF7/FLRT2/FLRT3/FRS2/GALNT3/IQGAP1/KIF16B/PTPN11/SETX/SHOC2/SOS1/SULF1 | 16 |
| BP | GO:0046578 | regulation of Ras protein signal transduction | 30/2221 | 184/18614 | 0.046739253 | 0.241152096 | 0.203801201 | KIF14/ABCA1/ABL2/AKAP13/ARFGEF1/ARFGEF2/ARHGAP42/CCDC125/COL3A1/CUL3/DENND4A/DENND4C/EPS8/IGF1/ITGB1/KRAS/MAP4K4/MET/NET1/NF1/OGT/PIK3CB/PIK3CG/PSD3/RABGEF1/RABL3/RASA2/RDX/SHOC2/SSX2IP | 30 |
| BP | GO:0050727 | regulation of inflammatory response | 61/2221 | 414/18614 | 0.047372947 | 0.244212211 | 0.20638735 | FANCD2/PBK/SUCNR1/ACE2/AIM2/ASH1L/ATM/BIRC2/BIRC3/BTK/C3/CASP1/CASP4/CLOCK/CNR1/CYLD/DHX9/HGF/IGF1/IL18/IL1R1/IL2RA/IL6ST/ITGA2/JAK2/LACC1/LPL/LRRK2/LYN/MIR142/MIR15B/MIR181B1/MIR30C2/MMP8/NAIP/NLRC4/NLRP3/NR1D2/NT5E/OSMR/PDCD4/PIK3AP1/PIK3CG/PPARG/PTGS2/PTPN2/PTPRC/RABGEF1/RB1/RICTOR/RIPK1/RORA/STAP1/TLR2/TLR3/TLR4/TNC/TNFAIP6/UFL1/VPS35/YES1 | 61 |
| BP | GO:0045995 | regulation of embryonic development | 17/2221 | 93/18614 | 0.047539068 | 0.244796515 | 0.206881153 | CDK1/ACTR8/CLASP2/CTNNB1/DHX36/LAMA2/LAMA4/NFE2L2/NIPBL/PHLDB2/PLCB1/POGLUT1/RACGAP1/RPS6KA6/TRIP12/UCHL5/ZZZ3 | 17 |
| BP | GO:0001774 | microglial cell activation | 10/2221 | 47/18614 | 0.047649056 | 0.244796515 | 0.206881153 | ATM/IFNGR1/JAK2/LRRK2/MIR142/MMP8/PTPRC/STAP1/TLR2/TLR3 | 10 |
| BP | GO:0010837 | regulation of keratinocyte proliferation | 10/2221 | 47/18614 | 0.047649056 | 0.244796515 | 0.206881153 | CASK/CD109/FGF7/IFT57/IFT74/IFT80/PRKD1/PTPRK/STXBP4/ZEB1 | 10 |
| BP | GO:0035196 | miRNA processing | 10/2221 | 47/18614 | 0.047649056 | 0.244796515 | 0.206881153 | DDX3X/DDX5/DICER1/HNRNPA2B1/NCBP1/NCBP2/NUP155/PUM2/PUS10/ZC3H7A | 10 |
| BP | GO:0043543 | protein acylation | 39/2221 | 250/18614 | 0.048116294 | 0.246739551 | 0.208523242 | BRCA1/BRCA2/CHEK1/DEK/ESCO2/HDAC2/BAZ1B/CLOCK/DDX21/DDX3X/DLD/EPC2/ERCC6/ESCO1/HAT1/ING3/IWS1/JADE1/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA15/NAA25/NAA35/NAA50/OGT/PHF20L1/PPM1B/SDR16C5/SF3B1/SMARCA5/SMC5/SUPT20H/TAF2/TAF7/TAOK1/ZDHHC21/ZZZ3 | 39 |
| BP | GO:0030032 | lamellipodium assembly | 14/2221 | 73/18614 | 0.048174248 | 0.246739551 | 0.208523242 | ACTR2/ACTR3/ATP7A/CCDC88A/FER/HSP90AA1/ITGB1/NCK1/NCKAP1/PIK3CA/PIK3R1/PTPRO/TWF1/VCL | 14 |
| BP | GO:1900076 | regulation of cellular response to insulin stimulus | 14/2221 | 73/18614 | 0.048174248 | 0.246739551 | 0.208523242 | ATP2B1/ENPP1/LPL/MIR15B/NCK1/NCL/NCOA1/NCOA2/NUCKS1/OSBPL8/PPARG/PTPN11/PTPN2/USO1 | 14 |
| BP | GO:0006475 | internal protein amino acid acetylation | 27/2221 | 163/18614 | 0.048191319 | 0.246739551 | 0.208523242 | BRCA1/BRCA2/CHEK1/DEK/BAZ1B/DDX21/EPC2/ERCC6/HAT1/ING3/IWS1/JADE1/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA50/OGT/PHF20L1/SDR16C5/SF3B1/SMARCA5/SMC5/SUPT20H/TAF2/TAF7/ZZZ3 | 27 |
| BP | GO:0031065 | positive regulation of histone deacetylation | 6/2221 | 23/18614 | 0.048363596 | 0.246990994 | 0.20873574 | ING2/LRRK2/NIPBL/PRKD1/SDR16C5/SMARCA5 | 6 |
| BP | GO:0051131 | chaperone-mediated protein complex assembly | 6/2221 | 23/18614 | 0.048363596 | 0.246990994 | 0.20873574 | CCT2/HSP90AA1/HSP90AB1/HSPA4/HSPD1/MKKS | 6 |
| BP | GO:0070076 | histone lysine demethylation | 6/2221 | 23/18614 | 0.048363596 | 0.246990994 | 0.20873574 | JMJD1C/KDM3A/KDM4C/KDM5A/KDM5B/KDM6A | 6 |
| BP | GO:0062207 | regulation of pattern recognition receptor signaling pathway | 19/2221 | 107/18614 | 0.04882197 | 0.248721629 | 0.210198325 | ANKRD17/BIRC2/BIRC3/CD36/DDX3X/DDX60/HMGB1/IRAK3/LYN/OTUD4/PJA2/PUM2/RIOK3/TLR1/TLR2/TLR3/TLR4/TLR6/USP15 | 19 |
| BP | GO:0002886 | regulation of myeloid leukocyte mediated immunity | 12/2221 | 60/18614 | 0.048826503 | 0.248721629 | 0.210198325 | ARG1/BTK/C12orf4/C3/CD84/DDX1/DDX21/DHX36/FER/LYN/RABGEF1/STAP1 | 12 |
| BP | GO:0043407 | negative regulation of MAP kinase activity | 12/2221 | 60/18614 | 0.048826503 | 0.248721629 | 0.210198325 | AIDA/DNAJA1/HIPK3/HMGCR/IRAK3/LYN/NF1/PDCD4/PIK3CB/PPARG/RGS2/ZNF675 | 12 |
| BP | GO:0008064 | regulation of actin polymerization or depolymerization | 25/2221 | 149/18614 | 0.048906108 | 0.248916368 | 0.210362902 | ADD3/ARFGEF1/ARHGAP18/ARHGAP28/CAPZA2/DLG1/EPS8/FER/FMN1/LIMA1/MKKS/NCK1/NCKAP1/NCKAP1L/PIK3CA/RASA1/RDX/RICTOR/SCIN/SNX9/SPTAN1/SVIL/SWAP70/TMOD2/TWF1 | 25 |
| BP | GO:0008154 | actin polymerization or depolymerization | 31/2221 | 192/18614 | 0.049016535 | 0.24926752 | 0.210659665 | DIAPH3/ADD3/ARFGEF1/ARHGAP18/ARHGAP28/CAPZA2/DIAPH2/DLG1/EPS8/FER/FMN1/JAK2/LIMA1/MKKS/NCK1/NCKAP1/NCKAP1L/PIK3CA/PSTPIP2/RASA1/RDX/RICTOR/SCIN/SNX9/SPIRE1/SPTAN1/SVIL/SWAP70/TMOD2/TTC17/TWF1 | 31 |
| BP | GO:0140467 | integrated stress response signaling | 9/2221 | 41/18614 | 0.049226688 | 0.250124795 | 0.211384161 | AGR2/EIF2AK3/EIF2AK4/EIF2S1/HSPA5/IMPACT/NCK1/NFE2L2/PTPN2 | 9 |
| BP | GO:0008033 | tRNA processing | 23/2221 | 135/18614 | 0.049328199 | 0.250429065 | 0.211641305 | ADAT1/ALKBH8/DDX1/DPH3/FAM98A/NSUN2/NSUN6/POP1/PUS10/PUS3/PUS7/RTCB/SSB/THADA/THUMPD1/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TRMT6/TRNT1/TYW3 | 23 |
| BP | GO:0070972 | protein localization to endoplasmic reticulum | 15/2221 | 80/18614 | 0.049746918 | 0.252341869 | 0.213257844 | ANK2/HSPA5/KDELR3/LRRK2/MIA3/RAB3GAP1/RAB3GAP2/RYR2/SEC62/SEC63/SRP54/SRP72/SRPRB/SSR3/VPS54 | 15 |
| CC | GO:0098687 | chromosomal region | 109/2260 | 390/19518 | 4.44E-19 | 3.08E-16 | 2.31E-16 | BLM/BRCA2/BUB1/BUB1B/CDK1/CENPE/CENPF/CENPK/CENPU/CHEK1/ESCO2/EZH2/HDAC2/HELLS/KIF18A/KNTC1/MAD2L1/MCM3/MCM6/MSH2/MTBP/NCAPG/NDC80/NEK2/NUF2/RAD51AP1/SKA3/SPAG5/SPDL1/TOP2A/TTK/XPO1/ZWILCH/AHCTF1/APC/ARID2/ATM/ATR/ATRX/BAZ1A/BAZ1B/BRD7/CBX5/CENPC/CENPL/CENPN/CENPW/CHD4/CHMP2B/CKAP5/CLASP2/CLIP1/DCTN4/DHX36/DNA2/ERCC4/FMR1/GPATCH11/HAT1/HNRNPA2B1/HNRNPU/KDM4C/KNSTRN/LIG4/LRIF1/MIS12/MIS18BP1/NBN/NGDN/NUP107/NUP133/ORC3/ORC4/PARP1/PBRM1/PDS5A/PDS5B/PHF6/POLR2B/POT1/PPP1R12A/PPP2CA/PRKDC/RAD17/RAD21/RAD50/RIF1/SETX/SMARCA5/SMC1A/SMC3/SMC4/SMC5/SMC6/SMCHD1/SP100/SSB/STAG1/STAG2/SUV39H2/THOC1/THOC2/TNKS2/TP53BP1/TPR/WRN/XRCC5/ZNF330/ZW10 | 109 |
| CC | GO:0000793 | condensed chromosome | 79/2260 | 270/19518 | 2.18E-15 | 7.55E-13 | 5.68E-13 | BLM/BRCA1/BRCA2/BUB1/BUB1B/CENPE/CENPF/CENPK/CENPU/CHEK1/FANCD2/KIF18A/KNTC1/MAD2L1/MKI67/MTBP/NCAPG/NCAPG2/NCAPH/NDC80/NEK2/NUF2/SKA3/SPAG5/SPDL1/TOP2A/TTK/XPO1/ZWILCH/ADD3/AHCTF1/APC/ARID2/ATRX/BAZ1B/BRD7/CBX5/CENPC/CENPN/CENPW/CHMP2B/CKAP5/CLASP2/CLIP1/DCTN4/GPATCH11/HMGB1/HMGB2/HNRNPU/KNSTRN/LIG4/LRPPRC/MIS12/MLH1/MLH3/NIFK/NUP107/NUP133/PBRM1/PHF6/PPP1R12A/RAD21/RAD50/RIF1/RRS1/SETMAR/SMARCA5/SMC1A/SMC2/SMC3/SMC4/SMC5/SMC6/SYCP2/TOPBP1/TP53BP1/TPR/TTN/ZW10 | 79 |
| CC | GO:0000775 | chromosome, centromeric region | 71/2260 | 249/19518 | 2.33E-13 | 5.39E-11 | 4.05E-11 | BUB1/BUB1B/CENPE/CENPF/CENPK/CENPU/ESCO2/EZH2/HELLS/KIF18A/KNTC1/MAD2L1/MTBP/NCAPG/NDC80/NEK2/NUF2/SKA3/SPAG5/SPDL1/TOP2A/TTK/XPO1/ZWILCH/AHCTF1/APC/ARID2/ATRX/BAZ1A/BAZ1B/BRD7/CBX5/CENPC/CENPL/CENPN/CENPW/CHMP2B/CKAP5/CLASP2/CLIP1/DCTN4/FMR1/GPATCH11/HNRNPU/KDM4C/KNSTRN/MIS12/MIS18BP1/NGDN/NUP107/NUP133/PBRM1/PDS5A/PDS5B/PHF6/PPP1R12A/PPP2CA/RAD21/SMARCA5/SMC1A/SMC3/SMC4/SMC5/SMC6/STAG1/STAG2/SUV39H2/TP53BP1/TPR/ZNF330/ZW10 | 71 |
| CC | GO:0030684 | preribosome | 34/2260 | 76/19518 | 3.83E-13 | 6.64E-11 | 5.00E-11 | BMS1/EBNA1BP2/HEATR1/KRR1/LTV1/MAK16/MDN1/MPHOSPH10/NGDN/NIP7/NOL10/NOP56/NOP58/NSA2/PRKDC/RIOK1/RIOK2/RIOK3/RRP15/RRS1/RSL1D1/SRFBP1/TSR1/UTP14A/UTP18/UTP20/UTP23/UTP3/UTP6/WDR12/WDR3/WDR36/XRCC5/ZNF622 | 34 |
| CC | GO:0005819 | spindle | 100/2260 | 421/19518 | 1.11E-12 | 1.53E-10 | 1.15E-10 | ASPM/BORA/BUB1B/CDC6/CDK1/CENPE/CENPF/CKAP2L/DLGAP5/ECT2/FBXO5/HMMR/KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF4A/KNTC1/MAD2L1/NEK2/NUSAP1/PRC1/SHCBP1/SKA3/SPAG5/SPDL1/TPX2/TTK/ZWILCH/ALMS1/ALPK1/ATM/BCCIP/BIRC6/BRCC3/CD180/CDC27/CDK5RAP2/CEP128/CEP162/CEP170/CEP350/CHMP2B/CKAP2/CKAP5/CLASP2/CLTC/CNTRL/CTNNB1/CUL3/CYLD/DCTN4/EML4/EPB41/EVI5/FRY/GEM/GPSM2/HAUS6/HNRNPU/INVS/IQCB1/KBTBD8/KIF16B/KIF2A/KIF3A/KNSTRN/MAP7D3/MAP9/MAPRE1/MTUS1/NCOR1/NEDD1/NIN/NSUN2/PARP4/PPP2CA/RACGAP1/RAD21/RB1/RIF1/RMDN2/SMC1A/SMC3/SMC6/SPATA5/SPICE1/STAG1/STAG2/TAF1D/TBL1XR1/TOPBP1/TOPORS/TPR/UBXN2B/ZW10/ZZZ3 | 100 |
| CC | GO:0000228 | nuclear chromosome | 62/2260 | 223/19518 | 2.48E-11 | 2.86E-09 | 2.15E-09 | BLM/BRCA1/BRCA2/CHEK1/HDAC2/MCM3/MCM6/MMS22L/NCAPG/NCAPG2/NCAPH/NEK2/PRIM2/TOP2A/WDHD1/ACTR8/ADD3/ANP32E/ARID4A/ARID4B/ATRX/BAZ1A/BAZ1B/BRMS1L/CHD1/DHX9/ETAA1/EXOSC9/FIGNL1/HNRNPU/ING2/ING3/LRIF1/LRPPRC/MLH1/MLH3/NIFK/NUFIP1/OGT/ORC3/ORC4/PARP1/PBRM1/POLA1/POLD3/RAD21/RAD50/RRS1/SETX/SMARCA5/SMARCAD1/SMC1A/SMC2/SMC3/SMC4/SMCHD1/SYCP2/TOP1/TOPBP1/TTN/UCHL5/ZRANB3 | 62 |
| CC | GO:0016607 | nuclear speck | 91/2260 | 415/19518 | 1.03E-09 | 1.02E-07 | 7.66E-08 | NCAPG2/AAGAB/API5/ARHGAP18/ASCC3/BCLAF1/BNIP3L/CCNL1/CDC40/CDC5L/CIR1/CMYA5/COPS4/CRNKL1/CTR9/CWC22/DDX42/DDX46/DDX5/DHX15/DHX36/EIF4A3/FYTTD1/GPATCH2/HBP1/HEATR5B/HECTD1/HIF1A/HNRNPU/IFI16/JADE1/KAT6A/KMT2E/LUC7L3/MBD4/MECOM/MEF2C/NOC3L/NRIP1/NSRP1/PLAG1/PLCB1/PLRG1/PNISR/PNN/PPIG/PRPF18/PRPF4/PRPF40A/PRPF4B/PSME4/RBBP6/RBM25/RBM27/RBM39/RSRC1/SCAPER/SDE2/SF3A3/SF3B1/SLU7/SMC4/SMC5/SMC6/SMU1/SNRPA1/SNW1/SON/SPRTN/SREK1/SRP54/SRPK1/SRPK2/SRSF10/SRSF11/SYF2/TCF12/THOC1/THOC2/TOPORS/TRIM22/TRIP11/TRIP12/WBP4/WRN/WTAP/YTHDC1/ZC3H13/ZNF106/ZNF217/ZNF638 | 91 |
| CC | GO:0005681 | spliceosomal complex | 52/2260 | 197/19518 | 7.02E-09 | 5.21E-07 | 3.92E-07 | API5/AQR/CDC40/CDC5L/CRNKL1/CWC22/CWC27/CWF19L2/DDX23/DDX46/DDX5/DHX15/DHX32/DHX8/EIF4A3/GCFC2/HNRNPA1/HNRNPA2B1/HNRNPA3/HNRNPH3/HNRNPR/HNRNPU/HSPA8/HTATSF1/IVNS1ABP/LUC7L3/MFAP1/NCL/PLRG1/PNN/PPWD1/PRPF18/PRPF38B/PRPF39/PRPF4/PRPF40A/PRPF4B/PTBP2/RBM41/RNPC3/SF3A3/SF3B1/SLU7/SMU1/SNRNP200/SNRPA1/SNW1/SREK1/SYF2/SYNCRIP/TTF2/WBP4 | 52 |
| CC | GO:0000776 | kinetochore | 45/2260 | 159/19518 | 7.08E-09 | 5.21E-07 | 3.92E-07 | BUB1/BUB1B/CENPE/CENPF/CENPK/CENPU/KIF18A/KNTC1/MAD2L1/MTBP/NDC80/NEK2/NUF2/SKA3/SPAG5/SPDL1/TTK/XPO1/ZWILCH/AHCTF1/APC/ARID2/BRD7/CBX5/CENPC/CENPN/CENPW/CHMP2B/CKAP5/CLASP2/CLIP1/DCTN4/GPATCH11/HNRNPU/KNSTRN/MIS12/NUP107/NUP133/PBRM1/PHF6/PPP1R12A/SMC1A/TP53BP1/TPR/ZW10 | 45 |
| CC | GO:0000779 | condensed chromosome, centromeric region | 47/2260 | 170/19518 | 7.52E-09 | 5.21E-07 | 3.92E-07 | BUB1/BUB1B/CENPE/CENPF/CENPK/CENPU/KIF18A/KNTC1/MAD2L1/MTBP/NCAPG/NDC80/NEK2/NUF2/SKA3/SPAG5/SPDL1/TTK/XPO1/ZWILCH/AHCTF1/APC/ARID2/ATRX/BRD7/CBX5/CENPC/CENPN/CENPW/CHMP2B/CKAP5/CLASP2/CLIP1/DCTN4/GPATCH11/HNRNPU/KNSTRN/MIS12/NUP107/NUP133/PBRM1/PHF6/PPP1R12A/SMC1A/TP53BP1/TPR/ZW10 | 47 |
| CC | GO:0000922 | spindle pole | 47/2260 | 171/19518 | 9.22E-09 | 5.81E-07 | 4.37E-07 | ASPM/CDC6/CENPF/CKAP2L/DLGAP5/KIF11/KIF20B/KNTC1/MAD2L1/NEK2/PRC1/SPAG5/SPDL1/TPX2/ALMS1/ALPK1/BCCIP/BIRC6/BRCC3/CDK5RAP2/CEP128/CKAP2/CKAP5/CNTRL/CTNNB1/CUL3/DCTN4/FRY/GPSM2/HNRNPU/KIF2A/KNSTRN/MAPRE1/NEDD1/NIN/PPP2CA/RAD21/RMDN2/SMC1A/SMC3/SMC6/STAG1/STAG2/TOPBP1/TOPORS/UBXN2B/ZW10 | 47 |
| CC | GO:0072686 | mitotic spindle | 48/2260 | 180/19518 | 1.85E-08 | 1.07E-06 | 8.04E-07 | ASPM/CDC6/CDK1/CENPE/CKAP2L/ECT2/KIF11/KIF18A/KIF20B/KIF23/MAD2L1/NUSAP1/PRC1/SKA3/SPAG5/TPX2/BCCIP/CD180/CDC27/CDK5RAP2/CKAP2/CLASP2/CLTC/CNTRL/CUL3/EML4/EPB41/GEM/GPSM2/HAUS6/HNRNPU/IQCB1/KNSTRN/MAP9/MAPRE1/NCOR1/NIN/RACGAP1/RMDN2/SMC1A/SMC3/SMC6/STAG1/STAG2/TAF1D/TBL1XR1/TPR/ZZZ3 | 48 |
| CC | GO:0005814 | centriole | 42/2260 | 157/19518 | 1.28E-07 | 6.80E-06 | 5.11E-06 | CEP135/CEP55/CEP78/PLK4/SASS6/STIL/TOP2A/AHI1/ALMS1/BCCIP/CCDC102B/CCDC146/CCDC88A/CCP110/CENPJ/CEP120/CEP128/CEP152/CEP162/CEP170/CEP192/CEP290/CEP350/CEP83/CEP97/CNTLN/IQCB1/KIAA0586/KIF2A/KIF3A/LRRCC1/MPHOSPH9/NEDD1/NIN/ODF2L/OFD1/PCM1/ROCK1/RP2/SDCCAG8/SPICE1/TOPORS | 42 |
| CC | GO:0030496 | midbody | 50/2260 | 203/19518 | 1.48E-07 | 6.99E-06 | 5.26E-06 | ANLN/ASPM/CDK1/CENPE/CENPF/CEP55/ECT2/KIF14/KIF20A/KIF20B/KIF23/KIF4A/NEK2/PRC1/SHCBP1/SPAG5/BIRC6/C9orf72/CCDC66/CENPC/CHMP2B/CNTRL/CYLD/EML4/EXOC1/EXOC2/EXOC4/EXOC5/GEM/GNAI3/GNL3/HNRNPU/HSP90B1/HSPA5/IQGAP1/LAP3/PIK3C3/PIK3CB/PKN2/RACGAP1/RAD21/RASGEF1B/RDX/SH3GLB1/SVIL/TACC1/TOPORS/TXNDC9/USP8/ZNF330 | 50 |
| CC | GO:0000781 | chromosome, telomeric region | 44/2260 | 169/19518 | 1.51E-07 | 6.99E-06 | 5.26E-06 | BLM/BRCA2/CDK1/CHEK1/EZH2/HDAC2/MCM3/MCM6/MSH2/RAD51AP1/ATM/ATR/ATRX/CBX5/CHD4/DHX36/DNA2/ERCC4/HAT1/HNRNPA2B1/LIG4/LRIF1/NBN/ORC3/ORC4/PARP1/POLR2B/POT1/PRKDC/RAD17/RAD50/RIF1/SETX/SMC5/SMC6/SMCHD1/SP100/SSB/THOC1/THOC2/TNKS2/TP53BP1/WRN/XRCC5 | 44 |
| CC | GO:0005874 | microtubule | 90/2260 | 461/19518 | 3.92E-07 | 1.63E-05 | 1.23E-05 | ASPM/CDK1/CENPE/KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF4A/KNTC1/NEK2/NUSAP1/PRC1/SKA3/SPAG5/ZWILCH/APC/ARFGEF2/ARHGAP18/CAMSAP2/CASP1/CCDC66/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CDK5RAP2/CENPJ/CEP162/CEP170/CEP57/CEP57L1/CHMP2B/CKAP2/CKAP5/CLASP2/CLIP1/CLMP/CLTC/CUL3/CYLD/DLG1/DNAH14/DNAH5/DNM1L/DST/DYNC1H1/DYNC2H1/EIF3A/EML4/FIGN/GAS2L3/HAUS6/HNRNPU/HOOK1/HOOK3/HSPH1/INVS/IQGAP1/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B/KNSTRN/LRPPRC/MACF1/MAP1B/MAP9/MAPRE1/MNS1/MTUS1/NAV3/NIN/OPA1/PARP4/RACGAP1/RMDN2/RPGRIP1L/SRPRB/SVIL/SYBU/TCP1/TTLL7/WDR47/ZW10 | 90 |
| CC | GO:0031252 | cell leading edge | 84/2260 | 422/19518 | 4.11E-07 | 1.63E-05 | 1.23E-05 | KIF18A/ACAP2/ACTR3/ADAM17/AKAP5/APC/ARHGAP18/ATP2B1/ATP6V1B2/ATP7A/BMX/C2CD5/CAPRIN1/CCDC88A/CD2AP/CDC42BPA/CDH2/CDKL5/CLASP2/CLCN3/CLIP1/CORO1C/CTNNA1/CTNNB1/DDX3X/DOCK8/DPP4/DST/EPB41L3/EPS8/EZR/FAP/FAT1/FER/FERMT2/FGD4/FGD6/FRMD4B/IFIT5/IQGAP1/IQGAP2/ITGAV/ITGB1/ITGB3/ITSN1/JMY/KLHL2/KNSTRN/LCP1/LIMA1/MACF1/MKLN1/MTM1/MTMR6/MYO5A/MYO6/NCKAP1/PHLDB2/PIK3CA/PKN2/PRKCI/PSD3/PTPN13/PTPRK/PTPRO/RAB3IP/RASA1/RDX/ROCK1/RUFY3/SAMSN1/SLC39A6/SLK/SNX2/SNX9/SORBS2/SSX2IP/SWAP70/SYNE2/TLR4/TPM1/TRPM7/TWF1/VEZT | 84 |
| CC | GO:0034399 | nuclear periphery | 39/2260 | 147/19518 | 4.47E-07 | 1.63E-05 | 1.23E-05 | BLM/CENPF/KIF4A/XPOT/AHCTF1/ARFGEF1/ARID2/BRD7/CASK/CENPW/EBNA1BP2/FIGN/HAT1/HLTF/HNRNPA2B1/HNRNPU/LMNB1/LRIF1/MATR3/NUFIP1/NUP107/NUP153/NUP205/PBRM1/POLA1/PPIG/PRPF40A/RAD21/RNASEL/SMC1A/SMC3/SNW1/SRPK1/STAG1/STAG2/THOC1/TPR/ZNF326/ZNF350 | 39 |
| CC | GO:0001726 | ruffle | 45/2260 | 181/19518 | 4.59E-07 | 1.63E-05 | 1.23E-05 | KIF18A/ACAP2/ADAM17/APC/ARHGAP18/ATP6V1B2/BMX/C2CD5/CD2AP/CDKL5/CLASP2/CLCN3/CLIP1/CORO1C/EPS8/EZR/FAP/FGD4/FGD6/FRMD4B/IFIT5/IQGAP1/ITGAV/ITGB1/ITGB3/KLHL2/KNSTRN/LCP1/LIMA1/MACF1/MKLN1/MTM1/MTMR6/MYO5A/MYO6/NCKAP1/PSD3/RASA1/ROCK1/SAMSN1/SNX9/TLR4/TPM1/TRPM7/TWF1 | 45 |
| CC | GO:0032040 | small-subunit processome | 17/2260 | 39/19518 | 4.71E-07 | 1.63E-05 | 1.23E-05 | HEATR1/KRR1/MPHOSPH10/NGDN/NOL10/NOP56/NOP58/PRKDC/UTP14A/UTP18/UTP20/UTP23/UTP3/UTP6/WDR3/WDR36/XRCC5 | 17 |
| CC | GO:1990391 | DNA repair complex | 12/2260 | 22/19518 | 1.19E-06 | 3.94E-05 | 2.96E-05 | BRCA1/BRCA2/FANCD2/FANCI/ASCC3/ATM/LIG4/PALB2/PRKDC/TP53BP1/XRCC4/XRCC5 | 12 |
| CC | GO:0071013 | catalytic step 2 spliceosome | 27/2260 | 88/19518 | 1.25E-06 | 3.94E-05 | 2.96E-05 | AQR/CDC40/CDC5L/CRNKL1/CWC22/CWC27/DDX23/DDX5/DHX8/EIF4A3/HNRNPA1/HNRNPA2B1/HNRNPA3/HNRNPR/HNRNPU/PLRG1/PNN/PPWD1/PRPF4B/SF3A3/SF3B1/SLU7/SNRNP200/SNRPA1/SNW1/SYF2/SYNCRIP | 27 |
| CC | GO:0034451 | centriolar satellite | 32/2260 | 115/19518 | 1.53E-06 | 4.60E-05 | 3.46E-05 | CENPU/DLGAP5/SPAG5/C2CD5/CCDC112/CCDC14/CCDC18/CCDC66/CD2AP/CD86/CEP162/CEP290/CNTRL/FNIP2/HOOK3/KIF5B/KLHL4/KNSTRN/LRIF1/MPP1/NUDT21/ODF2L/OFD1/PCM1/PIBF1/PJA2/RBM39/SDCCAG8/SPAG9/SSX2IP/TAF1D/UPF3B | 32 |
| CC | GO:0016363 | nuclear matrix | 34/2260 | 127/19518 | 1.91E-06 | 5.52E-05 | 4.15E-05 | BLM/CENPF/KIF4A/XPOT/AHCTF1/ARFGEF1/ARID2/BRD7/CASK/CENPW/FIGN/HAT1/HLTF/HNRNPA2B1/HNRNPU/LMNB1/LRIF1/MATR3/NUFIP1/PBRM1/POLA1/PPIG/PRPF40A/RAD21/RNASEL/SMC1A/SMC3/SNW1/SRPK1/STAG1/STAG2/THOC1/ZNF326/ZNF350 | 34 |
| CC | GO:0005657 | replication fork | 22/2260 | 66/19518 | 2.57E-06 | 7.13E-05 | 5.36E-05 | BLM/CHEK1/MCM3/MMS22L/PRIM2/RAD18/RFC3/RFC4/WDHD1/XRCC2/BAZ1B/ETAA1/NBN/PARP1/POLA1/POLD3/RFC1/SMARCA5/SMARCAD1/TP53BP1/WRN/ZRANB3 | 22 |
| CC | GO:0001650 | fibrillar center | 37/2260 | 146/19518 | 2.87E-06 | 7.66E-05 | 5.76E-05 | ACACA/AFF4/CD2AP/CDCA7L/COIL/DCLRE1A/DDX46/DKC1/EIF3L/EZR/FAM111A/HEATR1/LEO1/LIPA/MALT1/MTDH/NEDD1/NOLC1/NOP56/NOP58/NRIP1/NUFIP1/PLRG1/POLR1B/PTPN13/RAI14/RNMT/RPS6KA6/SMARCA5/STAG2/TAF4B/TOP1/TXNRD1/USO1/UTP15/WDR43/ZNF415 | 37 |
| CC | GO:0005635 | nuclear envelope | 91/2260 | 490/19518 | 3.11E-06 | 7.99E-05 | 6.01E-05 | BRIP1/CENPF/DTL/MAD2L1/XPO1/XPOT/AGPAT5/AHCTF1/AKAP6/ANKRD17/ATF6/ATP11B/BNIP2/BNIP3L/C9orf72/CACYBP/CANX/CBX5/CHMP2B/CSE1L/CYBB/DNAJC2/DST/EPHA3/GTF3C3/GTPBP4/IPO11/IPO5/IPO7/IPO8/ITPR1/ITSN1/KPNA1/KPNA3/KPNA4/KPNB1/LMNB1/LMO7/LRPPRC/LRRC59/MATR3/MNS1/MTDH/MTMR6/MYO6/MYOF/NAV3/NPC1/NUCB2/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/OSBPL3/OSBPL8/PARP1/PARP8/PCM1/PLA2G4A/PLCB1/PLRG1/POLA1/PTGS2/PUM2/RANBP2/RB1CC1/RGPD1/RIF1/RNF6/RTCB/SDCBP/SENP1/SH3BGRL2/SYNE1/SYNE2/TNKS2/TOR1AIP2/TPR/TXLNG/UBXN4/UTP18/VRK2/WDFY3/WDR3/WTAP/XPO4/ZBTB1/ZNF224 | 91 |
| CC | GO:0090734 | site of DNA damage | 30/2260 | 110/19518 | 5.01E-06 | 0.000124026 | 9.33E-05 | ESCO2/MMS22L/RAD18/WDR76/ACTR2/ACTR3/CBX5/CHD1L/CHD4/ERCC6/NBN/PARP1/PARP9/POLK/RAD50/RFWD3/RIF1/SAMHD1/SETMAR/SLFN11/SMARCA5/SMARCAD1/SMC5/SMC6/SMCHD1/TP53BP1/UFL1/VCP/XRCC4/XRCC5 | 30 |
| CC | GO:0014704 | intercalated disc | 18/2260 | 50/19518 | 6.06E-06 | 0.00014488 | 0.000108932 | AKAP6/ANK2/ANK3/ATP1B1/CDH2/CTNNA1/CTNNB1/CXADR/DLG1/DSC2/DSG2/DSP/ITGB1/PIK3CA/PKP2/SCN1A/SLC31A1/VCL | 18 |
| CC | GO:0005938 | cell cortex | 61/2260 | 302/19518 | 9.48E-06 | 0.000218979 | 0.000164646 | ANLN/ECT2/MELK/ACTR2/ADD3/AKAP12/AKAP13/ASPH/BIN2/C2CD5/CALD1/CAPZA2/CDH2/CLASP2/CLIP1/CORO1C/CTNNB1/CTTNBP2/CYTIP/DCTN4/DST/DYNC1H1/EPB41/EPB41L2/EPS8/ERC1/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/EZR/FER/FERMT2/FNBP1L/FRY/FRYL/GPSM2/HMCN1/IQGAP1/ITPR2/MAPRE1/MKLN1/MPP1/MPP7/MYO1E/MYO6/NCL/NEDD4/PHLDB2/PLS1/PPP1R9A/PRKD1/RAI14/RDX/SCIN/SLC4A1/SNX9/SPINK5/SPIRE1/SPTAN1 | 61 |
| CC | GO:0097431 | mitotic spindle pole | 15/2260 | 38/19518 | 9.83E-06 | 0.000219644 | 0.000165146 | ASPM/KIF20B/SPAG5/BCCIP/CDK5RAP2/CNTRL/GPSM2/MAPRE1/NIN/RMDN2/SMC1A/SMC3/SMC6/STAG1/STAG2 | 15 |
| CC | GO:0010494 | cytoplasmic stress granule | 24/2260 | 85/19518 | 2.30E-05 | 0.000497171 | 0.000373812 | C9orf72/CAPRIN1/CSDE1/DDX1/DDX3X/DHX36/EIF2S1/FMR1/G3BP1/G3BP2/GIGYF2/KPNB1/LARP1B/LARP4/NUFIP2/OGFOD1/PRRC2C/PUM2/ROCK1/SSB/VCP/YTHDF3/ZFAND1/ZNFX1 | 24 |
| CC | GO:0000794 | condensed nuclear chromosome | 23/2260 | 80/19518 | 2.45E-05 | 0.000515446 | 0.000387554 | BLM/BRCA1/BRCA2/CHEK1/NCAPG/NCAPG2/NCAPH/NEK2/ADD3/LRPPRC/MLH1/MLH3/NIFK/RAD21/RAD50/RRS1/SMC1A/SMC2/SMC3/SMC4/SYCP2/TOPBP1/TTN | 23 |
| CC | GO:0030175 | filopodium | 28/2260 | 108/19518 | 2.84E-05 | 0.000579591 | 0.000435783 | CXADR/DMD/DYNC1H1/EPHA4/EZR/FAT1/FGD4/FMR1/FXR1/IQGAP2/ITGAV/ITGB1/ITGB3/LCP1/MTM1/MYO1B/MYO5A/MYO6/NGDN/NLGN1/OSBPL3/PPP1R9A/RDX/RUFY3/SYNE2/TWF1/UTRN/VCAM1 | 28 |
| CC | GO:0005684 | U2-type spliceosomal complex | 25/2260 | 92/19518 | 3.20E-05 | 0.000633299 | 0.000476164 | AQR/CDC40/CDC5L/CRNKL1/CWC22/CWC27/DHX8/EIF4A3/GCFC2/HTATSF1/LUC7L3/MFAP1/PLRG1/PRPF18/PRPF39/PRPF4/PRPF40A/SF3A3/SF3B1/SMU1/SNRNP200/SNRPA1/SNW1/SYF2/WBP4 | 25 |
| CC | GO:0005832 | chaperonin-containing T-complex | 7/2260 | 11/19518 | 5.97E-05 | 0.001149645 | 0.000864394 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/TCP1 | 7 |
| CC | GO:1904813 | ficolin-1-rich granule lumen | 30/2260 | 124/19518 | 6.18E-05 | 0.0011568 | 0.000869775 | ACTR2/AGL/BIN2/CAB39/CAND1/CCT8/CTSS/DDX3X/FGL2/HBB/HMGB1/HSP90AA1/HSP90AB1/HSPA8/IDH1/IMPDH2/KPNB1/LTA4H/MNDA/PGM2/PSMC2/PSMD12/PSMD14/PSMD2/PSMD6/PSMD7/PYGL/TNFAIP6/VCL/VCP | 30 |
| CC | GO:0005876 | spindle microtubule | 22/2260 | 81/19518 | 9.40E-05 | 0.001670769 | 0.001256218 | CDK1/CENPE/KIF11/KIF18A/KIF4A/KNTC1/PRC1/SKA3/ZWILCH/CHMP2B/CLASP2/CLTC/CUL3/HAUS6/HNRNPU/KIF2A/KIF3A/MAP9/MAPRE1/PARP4/RMDN2/ZW10 | 22 |
| CC | GO:0015030 | Cajal body | 22/2260 | 81/19518 | 9.40E-05 | 0.001670769 | 0.001256218 | XPO1/ARIH1/COIL/DDX42/DDX46/DKC1/FAM118B/FMR1/HNRNPA2B1/ICE1/ICE2/LSG1/NOLC1/NOP58/NPAT/PHAX/PRPF4/TGS1/TRIM22/USPL1/ZNF473/ZPR1 | 22 |
| CC | GO:0005838 | proteasome regulatory particle | 9/2260 | 19/19518 | 0.000114553 | 0.001921187 | 0.001444502 | PSMC1/PSMC2/PSMC6/PSMD1/PSMD12/PSMD14/PSMD2/PSMD6/PSMD7 | 9 |
| CC | GO:0030687 | preribosome, large subunit precursor | 9/2260 | 19/19518 | 0.000114553 | 0.001921187 | 0.001444502 | EBNA1BP2/MAK16/MDN1/NIP7/NSA2/RRP15/RRS1/WDR12/ZNF622 | 9 |
| CC | GO:0022624 | proteasome accessory complex | 10/2260 | 23/19518 | 0.000116436 | 0.001921187 | 0.001444502 | PSMC1/PSMC2/PSMC6/PSMD1/PSMD12/PSMD14/PSMD2/PSMD5/PSMD6/PSMD7 | 10 |
| CC | GO:0030055 | cell-substrate junction | 76/2260 | 432/19518 | 0.000125713 | 0.002026019 | 0.001523322 | KIF23/ACTR2/ACTR3/ADAM10/ADAM17/ADAM9/AKAP12/ALCAM/ARHGAP26/CASK/CDH2/CLASP2/CLTC/CORO1C/CPNE3/CTNNA1/CTNNB1/DCAF6/DCTN4/DMD/DOCK7/DPP4/DST/EPB41L2/EZR/FAP/FAT1/FERMT2/FLRT2/FLRT3/FLT1/G3BP1/GDI2/HMCN1/HSP90B1/HSPA5/HSPA8/HSPA9/IQGAP1/ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/JAK1/JAK2/KRAS/LAP3/LCP1/LIMA1/LMO7/MAP4K4/MAPRE1/MTF2/NCKAP1/NEXN/PDIA3/PHLDB2/PPFIA1/PPP1R12A/PTPRC/RDX/SDCBP/SENP1/SORBS2/SVIL/SYNE2/TES/TNC/TWF1/VCL/YES1/YWHAB | 76 |
| CC | GO:0045121 | membrane raft | 60/2260 | 323/19518 | 0.000140148 | 0.002207338 | 0.001659653 | KIF18A/ABCA1/ACE2/ADAM17/AKAP5/AKAP6/ANGPT1/ANK2/ATP1B1/ATP2B1/ATP7A/BIRC2/BIRC3/BTK/CASP3/CD226/CD36/CDH2/CNR1/CNTN1/CORO1C/CR1/CTNNA1/CTNNB1/CXADR/DLG1/DMD/DPP4/ERLIN1/EZR/FAS/GNAI3/HTR2A/IL6ST/ITGB1/JAK2/KCND2/KCNMA1/LDHB/LRP6/LRP8/LRRK2/LYN/MFAP3/MYOF/NPC1/PIKFYVE/PPP2CA/PPT1/PRKAR2B/PTGS2/PTPRC/RIPK1/SDCBP/SULF1/TFPI/TGFBR1/TLR1/TLR2/TLR6 | 60 |
| CC | GO:0098857 | membrane microdomain | 60/2260 | 324/19518 | 0.000152967 | 0.002320012 | 0.00174437 | KIF18A/ABCA1/ACE2/ADAM17/AKAP5/AKAP6/ANGPT1/ANK2/ATP1B1/ATP2B1/ATP7A/BIRC2/BIRC3/BTK/CASP3/CD226/CD36/CDH2/CNR1/CNTN1/CORO1C/CR1/CTNNA1/CTNNB1/CXADR/DLG1/DMD/DPP4/ERLIN1/EZR/FAS/GNAI3/HTR2A/IL6ST/ITGB1/JAK2/KCND2/KCNMA1/LDHB/LRP6/LRP8/LRRK2/LYN/MFAP3/MYOF/NPC1/PIKFYVE/PPP2CA/PPT1/PRKAR2B/PTGS2/PTPRC/RIPK1/SDCBP/SULF1/TFPI/TGFBR1/TLR1/TLR2/TLR6 | 60 |
| CC | GO:0035861 | site of double-strand break | 21/2260 | 78/19518 | 0.000153998 | 0.002320012 | 0.00174437 | ESCO2/RAD18/ACTR2/ACTR3/CHD1L/NBN/PARP1/RAD50/RFWD3/RIF1/SAMHD1/SETMAR/SMARCA5/SMARCAD1/SMC5/SMC6/SMCHD1/TP53BP1/UFL1/VCP/XRCC4 | 21 |
| CC | GO:0005925 | focal adhesion | 74/2260 | 422/19518 | 0.000169876 | 0.002504761 | 0.001883279 | KIF23/ACTR2/ACTR3/ADAM10/ADAM17/ADAM9/AKAP12/ALCAM/ARHGAP26/CASK/CDH2/CLASP2/CLTC/CORO1C/CPNE3/CTNNA1/CTNNB1/DCAF6/DCTN4/DOCK7/DPP4/DST/EPB41L2/EZR/FAP/FAT1/FERMT2/FLRT2/FLRT3/FLT1/G3BP1/GDI2/HSP90B1/HSPA5/HSPA8/HSPA9/IQGAP1/ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/JAK1/JAK2/KRAS/LAP3/LCP1/LIMA1/LMO7/MAP4K4/MAPRE1/MTF2/NCKAP1/NEXN/PDIA3/PHLDB2/PPFIA1/PPP1R12A/PTPRC/RDX/SDCBP/SENP1/SORBS2/SVIL/SYNE2/TES/TNC/TWF1/VCL/YES1/YWHAB | 74 |
| CC | GO:0061695 | transferase complex, transferring phosphorus-containing groups | 57/2260 | 306/19518 | 0.000188257 | 0.002717961 | 0.002043579 | CCNA2/CCNB2/CDK1/GTF2H3/MCM3/PRIM2/AZI2/BCCIP/BECN1/CAB39/CCNC/CCNE2/CCNG1/CCNH/CCNL1/CCNT1/CCNT2/CHUK/CTR9/DBF4/ERC1/GTF2H1/LEO1/MYO6/PHKA1/PHKB/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/POLA1/POLD3/POLR1B/POLR2B/POLR3B/POLR3C/PRKACB/PRKCI/PRKDC/RB1CC1/REV3L/RTF1/SOCS4/TAF1/TAF2/TAF4B/TAF7/TANK/TBK1/TCEA1/TGFBR1/XRCC5/ZNFX1 | 57 |
| CC | GO:0030686 | 90S preribosome | 11/2260 | 29/19518 | 0.000230999 | 0.00326699 | 0.002456384 | BMS1/HEATR1/MPHOSPH10/RSL1D1/SRFBP1/UTP18/UTP20/UTP6/WDR12/WDR3/WDR36 | 11 |
| CC | GO:1902554 | serine/threonine protein kinase complex | 28/2260 | 121/19518 | 0.000239948 | 0.003325673 | 0.002500506 | CCNA2/CCNB2/CDK1/GTF2H3/AZI2/BCCIP/CAB39/CCNC/CCNE2/CCNG1/CCNH/CCNL1/CCNT1/CCNT2/CHUK/DBF4/ERC1/GTF2H1/PHKA1/PHKB/PRKACB/PRKCI/PRKDC/RB1CC1/TANK/TBK1/TGFBR1/XRCC5 | 28 |
| CC | GO:0000502 | proteasome complex | 17/2260 | 60/19518 | 0.000330231 | 0.004410797 | 0.003316389 | PSMA4/PSMA3/PSMC1/PSMC2/PSMC6/PSMD1/PSMD12/PSMD14/PSMD2/PSMD5/PSMD6/PSMD7/PSME4/UBR1/UCHL5/USP14/VCP | 17 |
| CC | GO:0098858 | actin-based cell projection | 44/2260 | 225/19518 | 0.000330969 | 0.004410797 | 0.003316389 | ANGPT1/ATP6V1A/ATP6V1B2/ATP7A/ATP8B1/CTNNB1/CXADR/DMD/DYNC1H1/EPHA4/EPS8/EXOC4/EZR/FAT1/FGD4/FMR1/FXR1/IQGAP2/ITGAV/ITGB1/ITGB3/LCP1/LRRK2/MPP1/MTM1/MYO1B/MYO1E/MYO5A/MYO6/NGDN/NLGN1/OSBPL3/PDGFRA/PKHD1L1/PLS1/PPP1R9A/RDX/RUFY3/SLC4A7/SYNE2/TWF1/UTRN/VCAM1/VEZT | 44 |
| CC | GO:0043596 | nuclear replication fork | 12/2260 | 35/19518 | 0.000363439 | 0.004752131 | 0.003573031 | MCM3/MMS22L/PRIM2/WDHD1/BAZ1B/ETAA1/PARP1/POLA1/POLD3/SMARCA5/SMARCAD1/ZRANB3 | 12 |
| CC | GO:0044291 | cell-cell contact zone | 19/2260 | 72/19518 | 0.000411498 | 0.005280893 | 0.003970596 | AKAP6/ANK2/ANK3/ATP1B1/CDH2/CTNNA1/CTNNB1/CXADR/DLG1/DSC2/DSG2/DSP/ITGB1/PCDH9/PIK3CA/PKP2/SCN1A/SLC31A1/VCL | 19 |
| CC | GO:0000242 | pericentriolar material | 9/2260 | 22/19518 | 0.000446021 | 0.005519509 | 0.004150007 | CDK5RAP2/CEP152/CEP192/HOOK3/NEDD1/NIN/PCM1/TCP1/TNKS2 | 9 |
| CC | GO:0031258 | lamellipodium membrane | 9/2260 | 22/19518 | 0.000446021 | 0.005519509 | 0.004150007 | DOCK8/DPP4/FAP/FERMT2/ITGAV/ITGB3/NCKAP1/SLC39A6/SYNE2 | 9 |
| CC | GO:0070993 | translation preinitiation complex | 8/2260 | 18/19518 | 0.000477284 | 0.005759632 | 0.00433055 | EIF3M/DHX29/EIF2S1/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L | 8 |
| CC | GO:0051233 | spindle midzone | 12/2260 | 36/19518 | 0.000488219 | 0.005759632 | 0.00433055 | CDC6/CENPE/KIF14/KIF18A/KIF20B/PRC1/GEM/HNRNPU/MAP9/MAPRE1/RACGAP1/RIF1 | 12 |
| CC | GO:0008023 | transcription elongation factor complex | 14/2260 | 46/19518 | 0.000490358 | 0.005759632 | 0.00433055 | AFF4/CCNT1/CCNT2/CTR9/ELL2/ERCC6/ICE1/ICE2/LEO1/MLLT3/NUFIP1/RTF1/SUPT16H/TTF2 | 14 |
| CC | GO:0101002 | ficolin-1-rich granule | 37/2260 | 185/19518 | 0.000609826 | 0.007043486 | 0.005295854 | ACTR2/AGL/BIN2/CAB39/CAND1/CCT8/CLEC4D/COPB1/CR1/CTSS/DDX3X/DSP/FGL2/HBB/HMGB1/HSP90AA1/HSP90AB1/HSPA8/IDH1/IMPDH2/KPNB1/LTA4H/MGAM/MNDA/NCKAP1L/PGM2/PSMC2/PSMD12/PSMD14/PSMD2/PSMD6/PSMD7/PYGL/TNFAIP6/UBR4/VCL/VCP | 37 |
| CC | GO:0101031 | chaperone complex | 13/2260 | 42/19518 | 0.000645954 | 0.007338457 | 0.005517637 | CCDC47/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/HSP90AB1/HSPA8/RPAP3/SPAG1/STIP1/TCP1 | 13 |
| CC | GO:0034708 | methyltransferase complex | 22/2260 | 92/19518 | 0.000665791 | 0.007441825 | 0.005595357 | EZH2/HDAC2/BOD1L1/CBX5/CHD8/E2F6/HCFC2/KDM6A/KMT2C/METTL14/MGA/RBBP5/RIOK1/RNMT/SUZ12/TAF1/TAF7/TEX10/TRMT10C/TRMT6/WTAP/ZC3H13 | 22 |
| CC | GO:0036064 | ciliary basal body | 34/2260 | 167/19518 | 0.000714688 | 0.007861569 | 0.005910954 | CENPF/CEP78/SPAG5/AHI1/CAMSAP2/CCDC66/CCDC88A/CDKL5/CENPJ/CEP290/CYLD/DAAM1/ERC1/EZR/IFT57/IFT80/JADE1/KIAA0586/LCA5/MAPRE1/MKKS/NEDD1/ODF2L/OFD1/PCM1/RP2/RPGR/RPGRIP1L/SDCCAG8/SSX2IP/TBC1D30/TOPORS/WDR11/WDR35 | 34 |
| CC | GO:0033290 | eukaryotic 48S preinitiation complex | 7/2260 | 15/19518 | 0.000763987 | 0.008272547 | 0.00621996 | EIF3M/EIF2S1/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L | 7 |
| CC | GO:0005777 | peroxisome | 30/2260 | 143/19518 | 0.000860318 | 0.008893998 | 0.006687217 | ABCD3/ACBD5/ACSL1/ACSL3/ACSL4/AGPS/ATM/BAAT/DNM1L/ECI2/FAR1/FAR2/GNPAT/HMGCR/HSD17B4/HSDL2/IDE/IDH1/IDI1/IMPDH2/LACC1/MGAT4A/MYO5A/NUDT12/PEX1/PIK3C3/PNPLA8/RAB8B/SCP2/SLC27A2 | 30 |
| CC | GO:0042579 | microbody | 30/2260 | 143/19518 | 0.000860318 | 0.008893998 | 0.006687217 | ABCD3/ACBD5/ACSL1/ACSL3/ACSL4/AGPS/ATM/BAAT/DNM1L/ECI2/FAR1/FAR2/GNPAT/HMGCR/HSD17B4/HSDL2/IDE/IDH1/IDI1/IMPDH2/LACC1/MGAT4A/MYO5A/NUDT12/PEX1/PIK3C3/PNPLA8/RAB8B/SCP2/SLC27A2 | 30 |
| CC | GO:0015629 | actin cytoskeleton | 80/2260 | 489/19518 | 0.000870321 | 0.008893998 | 0.006687217 | ANLN/DIAPH3/KNTC1/ABL2/ACACA/ACTR2/ACTR3/ADAM17/AKAP13/ARHGAP21/BIN2/CALD1/CAPZA2/CASK/CD2AP/CDC42BPA/CDH2/CGNL1/CNR1/CORO1C/CTNNA1/CTTNBP2/DAAM1/DCTN4/DGKH/DHX9/DIAPH2/DOCK5/EPB41L2/EPHA3/EZR/FER/FERMT2/FILIP1/FLT1/FMN1/GAS2L3/GBP1/IFIT5/INTS6/IQGAP1/IQGAP2/KLHL2/LCP1/LIMA1/MACF1/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/MYO9A/NCKAP1/NEB/NEXN/PLS1/PLS3/POF1B/PPP1R12A/PPP1R9A/PSTPIP2/RDX/SCIN/SH3PXD2B/SIPA1L1/SNX9/SORBS2/SPTAN1/STK38L/SVIL/SWAP70/TJP1/TMOD2/TOPBP1/TPM1/TTC17/TWF1/VCAM1/VCL/YES1 | 80 |
| CC | GO:0042470 | melanosome | 25/2260 | 112/19518 | 0.00088555 | 0.008893998 | 0.006687217 | ATP6V1B2/ATP7A/CALU/CANX/CCT4/CLTC/GPNMB/HSP90AA1/HSP90AB1/HSP90B1/HSPA5/HSPA8/ITGB1/ITGB3/MYO5A/NAP1L1/PDIA3/PDIA6/RAB1A/RAB27A/RAB27B/SDCBP/SYTL2/TFRC/YWHAB | 25 |
| CC | GO:0048770 | pigment granule | 25/2260 | 112/19518 | 0.00088555 | 0.008893998 | 0.006687217 | ATP6V1B2/ATP7A/CALU/CANX/CCT4/CLTC/GPNMB/HSP90AA1/HSP90AB1/HSP90B1/HSPA5/HSPA8/ITGB1/ITGB3/MYO5A/NAP1L1/PDIA3/PDIA6/RAB1A/RAB27A/RAB27B/SDCBP/SYTL2/TFRC/YWHAB | 25 |
| CC | GO:0005942 | phosphatidylinositol 3-kinase complex | 10/2260 | 29/19518 | 0.001060916 | 0.010503064 | 0.007897041 | BECN1/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/SOCS4 | 10 |
| CC | GO:0090543 | Flemming body | 11/2260 | 34/19518 | 0.001104673 | 0.010632475 | 0.007994342 | CEP55/KIF14/KIF23/BIRC6/C9orf72/CCDC66/CNTRL/EXOC1/EXOC2/EXOC4/RACGAP1 | 11 |
| CC | GO:1990752 | microtubule end | 11/2260 | 34/19518 | 0.001104673 | 0.010632475 | 0.007994342 | ASPM/SPAG5/CAMSAP2/CDK5RAP2/CKAP5/CLIP1/DST/KNSTRN/MAPRE1/NAV3/SVIL | 11 |
| CC | GO:0031074 | nucleocytoplasmic transport complex | 6/2260 | 12/19518 | 0.001188813 | 0.011166144 | 0.008395597 | KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/XPO5 | 6 |
| CC | GO:0034774 | secretory granule lumen | 56/2260 | 322/19518 | 0.001206614 | 0.011166144 | 0.008395597 | OLA1/ACTR2/AGA/AGL/APOOL/ARG1/ARMC8/BIN2/C3/CAB39/CAND1/CCT2/CCT8/CEP290/CRISP3/DDX3X/DNAJC3/DOCK2/DYNC1H1/EGF/F13A1/FRK/GCA/GDI2/HGF/HMGB1/HP/HSP90AA1/HSP90AB1/HSPA8/IDH1/IGF1/IMPDH2/KPNB1/MMP8/MMRN1/MNDA/PCSK1/PGM2/PROS1/PSMC2/PSMD1/PSMD12/PSMD14/PSMD2/PSMD6/PSMD7/PYGL/RAB27A/ROCK1/SDCBP/SPTAN1/VCL/VCP/VPS13A/XRCC5 | 56 |
| CC | GO:0061702 | inflammasome complex | 7/2260 | 16/19518 | 0.001223013 | 0.011166144 | 0.008395597 | AIM2/CASP1/CASP5/DDX3X/NAIP/NLRC4/NLRP3 | 7 |
| CC | GO:0030427 | site of polarized growth | 34/2260 | 172/19518 | 0.00122457 | 0.011166144 | 0.008395597 | KIF20B/C9orf72/CDKL5/CNR1/COPA/CXADR/DOCK7/EPHA4/EPS8/EXOC4/FLRT3/FMR1/FRY/FRYL/FXR1/HSP90AA1/HSP90AB1/IQGAP1/ITGA4/LRRK2/MAP1B/MYO5A/MYO9A/NIN/PCDH9/PTBP2/PTPRO/RUFY3/SETX/SNAP25/SYAP1/USP9X/WDR47/ZPR1 | 34 |
| CC | GO:0009295 | nucleoid | 13/2260 | 45/19518 | 0.001326281 | 0.011783495 | 0.008859771 | CLPX/DBT/DNA2/FASTKD2/HADHA/HSPA9/LRPPRC/LRRC59/MTERF1/MTERF2/TFAM/TFB2M/TRMT10C | 13 |
| CC | GO:0042645 | mitochondrial nucleoid | 13/2260 | 45/19518 | 0.001326281 | 0.011783495 | 0.008859771 | CLPX/DBT/DNA2/FASTKD2/HADHA/HSPA9/LRPPRC/LRRC59/MTERF1/MTERF2/TFAM/TFB2M/TRMT10C | 13 |
| CC | GO:0005721 | pericentric heterochromatin | 10/2260 | 30/19518 | 0.001427967 | 0.012369763 | 0.009300574 | ESCO2/EZH2/HELLS/ATRX/BAZ1A/BAZ1B/CBX5/CENPC/KDM4C/SMARCA5 | 10 |
| CC | GO:0071007 | U2-type catalytic step 2 spliceosome | 10/2260 | 30/19518 | 0.001427967 | 0.012369763 | 0.009300574 | AQR/CDC40/CDC5L/CRNKL1/CWC22/DHX8/PLRG1/SNRPA1/SNW1/SYF2 | 10 |
| CC | GO:0060205 | cytoplasmic vesicle lumen | 56/2260 | 325/19518 | 0.001502004 | 0.012850475 | 0.009662011 | OLA1/ACTR2/AGA/AGL/APOOL/ARG1/ARMC8/BIN2/C3/CAB39/CAND1/CCT2/CCT8/CEP290/CRISP3/DDX3X/DNAJC3/DOCK2/DYNC1H1/EGF/F13A1/FRK/GCA/GDI2/HGF/HMGB1/HP/HSP90AA1/HSP90AB1/HSPA8/IDH1/IGF1/IMPDH2/KPNB1/MMP8/MMRN1/MNDA/PCSK1/PGM2/PROS1/PSMC2/PSMD1/PSMD12/PSMD14/PSMD2/PSMD6/PSMD7/PYGL/RAB27A/ROCK1/SDCBP/SPTAN1/VCL/VCP/VPS13A/XRCC5 | 56 |
| CC | GO:0098636 | protein complex involved in cell adhesion | 15/2260 | 57/19518 | 0.001664899 | 0.013900906 | 0.010451809 | ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/LAMA2/LAMB1/LAMC1/LYN/MMRN1/NLGN1/TNC | 15 |
| CC | GO:0099023 | vesicle tethering complex | 15/2260 | 57/19518 | 0.001664899 | 0.013900906 | 0.010451809 | COG5/COG6/EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B/NBAS/TRAPPC11/TRAPPC13/TRAPPC8/VPS41/VPS54/VPS8/ZW10 | 15 |
| CC | GO:0030027 | lamellipodium | 38/2260 | 202/19518 | 0.00170561 | 0.014071279 | 0.010579909 | ACTR3/APC/CAPRIN1/CCDC88A/CDC42BPA/CDH2/CORO1C/CTNNA1/CTNNB1/DDX3X/DOCK8/DPP4/FAP/FAT1/FER/FERMT2/FGD4/FGD6/IQGAP2/ITGAV/ITGB1/ITGB3/ITSN1/KLHL2/NCKAP1/PIK3CA/PKN2/PTPN13/PTPRO/RAB3IP/RDX/ROCK1/RUFY3/SLC39A6/SNX2/SORBS2/SWAP70/SYNE2 | 38 |
| CC | GO:0031983 | vesicle lumen | 56/2260 | 327/19518 | 0.001732684 | 0.014126473 | 0.010621408 | OLA1/ACTR2/AGA/AGL/APOOL/ARG1/ARMC8/BIN2/C3/CAB39/CAND1/CCT2/CCT8/CEP290/CRISP3/DDX3X/DNAJC3/DOCK2/DYNC1H1/EGF/F13A1/FRK/GCA/GDI2/HGF/HMGB1/HP/HSP90AA1/HSP90AB1/HSPA8/IDH1/IGF1/IMPDH2/KPNB1/MMP8/MMRN1/MNDA/PCSK1/PGM2/PROS1/PSMC2/PSMD1/PSMD12/PSMD14/PSMD2/PSMD6/PSMD7/PYGL/RAB27A/ROCK1/SDCBP/SPTAN1/VCL/VCP/VPS13A/XRCC5 | 56 |
| CC | GO:0016282 | eukaryotic 43S preinitiation complex | 7/2260 | 17/19518 | 0.001872608 | 0.015069051 | 0.011330114 | EIF3M/DHX29/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L | 7 |
| CC | GO:0000803 | sex chromosome | 10/2260 | 31/19518 | 0.001891786 | 0.015069051 | 0.011330114 | BRCA1/ESCO2/PLK4/BIRC2/HNRNPU/LRIF1/SMC5/SMC6/SMCHD1/SUZ12 | 10 |
| CC | GO:0000940 | outer kinetochore | 6/2260 | 13/19518 | 0.001992288 | 0.015689271 | 0.011796445 | BUB1B/CENPF/NDC80/NUF2/SKA3/SPDL1 | 6 |
| CC | GO:0031965 | nuclear membrane | 53/2260 | 308/19518 | 0.002034564 | 0.015842163 | 0.011911401 | BRIP1/DTL/XPO1/AHCTF1/AKAP6/ANKRD17/ATP11B/C9orf72/CANX/DNAJC2/EPHA3/GTF3C3/GTPBP4/ITPR1/KPNA4/KPNB1/LMNB1/LRPPRC/MATR3/MTDH/MYO6/MYOF/NAV3/NUP107/NUP133/NUP153/NUP155/NUP205/OSBPL3/OSBPL8/PCM1/PLCB1/PLRG1/PTGS2/PUM2/RANBP2/RB1CC1/RIF1/RNF6/SDCBP/SENP1/SH3BGRL2/SYNE1/SYNE2/TOR1AIP2/TPR/TXLNG/UTP18/WDFY3/WDR3/WTAP/ZBTB1/ZNF224 | 53 |
| CC | GO:0036464 | cytoplasmic ribonucleoprotein granule | 45/2260 | 253/19518 | 0.002212978 | 0.016877504 | 0.012689853 | PSMA4/C9orf72/CAPRIN1/CLOCK/CNOT1/CSDE1/DDX1/DDX3X/DHX36/DHX9/EIF2S1/FMR1/FXR1/G3BP1/G3BP2/GABPB1/GIGYF2/HELZ/HNRNPU/IQGAP1/KPNB1/LARP1B/LARP4/LIG4/NCL/NSUN2/NUFIP2/OGFOD1/PNRC2/PRRC2C/PSMC2/PUM2/RC3H2/ROCK1/ROCK2/SSB/SYNE1/TOP1/UPF2/VCP/XRN1/YTHDF3/ZC3H12C/ZFAND1/ZNFX1 | 45 |
| CC | GO:0019898 | extrinsic component of membrane | 50/2260 | 288/19518 | 0.002216238 | 0.016877504 | 0.012689853 | AKAP9/APC/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/BECN1/BLOC1S6/CDH2/CDH6/CTNNA1/CTNNB1/CYLD/EEA1/EFCAB7/EMC2/EZR/FER/FERMT2/FMR1/FRK/GNAI3/IQGAP1/KRAS/LYN/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R1/PIK3R3/PIK3R4/RACGAP1/RB1CC1/RGS1/SEC23A/SNAP25/SNX10/SNX16/SOCS4/SYAP1/SYTL2/TPR/TRIO/USP8/VPS13A/VPS13C/VPS13D/YES1 | 50 |
| CC | GO:0005912 | adherens junction | 35/2260 | 185/19518 | 0.002295869 | 0.01729388 | 0.013002917 | ADAM10/AHI1/APC/CDH2/CDH6/CTNNA1/CTNNB1/CXADR/DLG1/DLG2/DSC2/DSP/EIF4G2/EPHA4/EZR/FERMT2/FMN1/FRMD4B/FRS2/HMCN1/KLHL24/LYN/MPP7/MYO1E/NEXN/PKP2/POF1B/PTPRK/RDX/SDCBP/SSX2IP/TJP1/VCL/VEZT/WNK3 | 35 |
| CC | GO:0032587 | ruffle membrane | 22/2260 | 101/19518 | 0.002431014 | 0.018114975 | 0.013620282 | ADAM17/APC/BMX/C2CD5/CDKL5/CLASP2/CLCN3/CORO1C/EPS8/EZR/FAP/IFIT5/ITGAV/ITGB1/ITGB3/LCP1/MACF1/MTMR6/MYO6/PSD3/TPM1/TWF1 | 22 |
| CC | GO:0005778 | peroxisomal membrane | 16/2260 | 65/19518 | 0.00251145 | 0.018320366 | 0.013774712 | ABCD3/ACBD5/ACSL1/ACSL3/ACSL4/AGPS/FAR1/FAR2/GNPAT/HMGCR/HSD17B4/IMPDH2/PEX1/PNPLA8/RAB8B/SLC27A2 | 16 |
| CC | GO:0031903 | microbody membrane | 16/2260 | 65/19518 | 0.00251145 | 0.018320366 | 0.013774712 | ABCD3/ACBD5/ACSL1/ACSL3/ACSL4/AGPS/FAR1/FAR2/GNPAT/HMGCR/HSD17B4/IMPDH2/PEX1/PNPLA8/RAB8B/SLC27A2 | 16 |
| CC | GO:0030426 | growth cone | 32/2260 | 167/19518 | 0.002805373 | 0.020251287 | 0.015226532 | KIF20B/C9orf72/CDKL5/CNR1/COPA/CXADR/DOCK7/EPHA4/EPS8/EXOC4/FLRT3/FMR1/FXR1/HSP90AA1/HSP90AB1/IQGAP1/ITGA4/LRRK2/MAP1B/MYO5A/MYO9A/NIN/PCDH9/PTBP2/PTPRO/RUFY3/SETX/SNAP25/SYAP1/USP9X/WDR47/ZPR1 | 32 |
| CC | GO:0035097 | histone methyltransferase complex | 15/2260 | 60/19518 | 0.002876566 | 0.020551134 | 0.015451981 | EZH2/HDAC2/BOD1L1/CBX5/CHD8/E2F6/HCFC2/KDM6A/KMT2C/MGA/RBBP5/SUZ12/TAF1/TAF7/TEX10 | 15 |
| CC | GO:0035770 | ribonucleoprotein granule | 47/2260 | 271/19518 | 0.003007588 | 0.021256582 | 0.015982393 | PSMA4/C9orf72/CAPRIN1/CLOCK/CNOT1/CSDE1/DDX1/DDX3X/DHX36/DHX9/EIF2S1/FASTKD2/FMR1/FXR1/G3BP1/G3BP2/GABPB1/GIGYF2/HELZ/HNRNPA3/HNRNPU/IQGAP1/KPNB1/LARP1B/LARP4/LIG4/NCL/NSUN2/NUFIP2/OGFOD1/PNRC2/PRRC2C/PSMC2/PUM2/RC3H2/ROCK1/ROCK2/SSB/SYNE1/TOP1/UPF2/VCP/XRN1/YTHDF3/ZC3H12C/ZFAND1/ZNFX1 | 47 |
| CC | GO:1990023 | mitotic spindle midzone | 6/2260 | 14/19518 | 0.003147055 | 0.021256582 | 0.015982393 | CENPE/KIF18A/KIF20B/PRC1/HNRNPU/MAP9 | 6 |
| CC | GO:1990531 | phospholipid-translocating ATPase complex | 6/2260 | 14/19518 | 0.003147055 | 0.021256582 | 0.015982393 | ATP10D/ATP11B/ATP11C/ATP8A1/ATP8B1/ATP8B4 | 6 |
| CC | GO:0008278 | cohesin complex | 5/2260 | 10/19518 | 0.003159348 | 0.021256582 | 0.015982393 | RAD21/SMC1A/SMC3/STAG1/STAG2 | 5 |
| CC | GO:0042564 | NLS-dependent protein nuclear import complex | 5/2260 | 10/19518 | 0.003159348 | 0.021256582 | 0.015982393 | KPNA1/KPNA2/KPNA3/KPNA4/KPNB1 | 5 |
| CC | GO:0120103 | centriolar subdistal appendage | 5/2260 | 10/19518 | 0.003159348 | 0.021256582 | 0.015982393 | CEP128/CEP170/CNTRL/KIF2A/NIN | 5 |
| CC | GO:1902911 | protein kinase complex | 28/2260 | 142/19518 | 0.00326635 | 0.021765194 | 0.016364808 | CCNA2/CCNB2/CDK1/GTF2H3/AZI2/BCCIP/CAB39/CCNC/CCNE2/CCNG1/CCNH/CCNL1/CCNT1/CCNT2/CHUK/DBF4/ERC1/GTF2H1/PHKA1/PHKB/PRKACB/PRKCI/PRKDC/RB1CC1/TANK/TBK1/TGFBR1/XRCC5 | 28 |
| CC | GO:0044232 | organelle membrane contact site | 13/2260 | 50/19518 | 0.003716909 | 0.024531601 | 0.018444813 | ACSL4/AHCYL1/APOOL/CANX/CHCHD3/GRAMD1C/IMMT/MOSPD2/PDZD8/PIK3R4/SACM1L/STX17/VPS13A | 13 |
| CC | GO:0016605 | PML body | 22/2260 | 105/19518 | 0.004021365 | 0.026290624 | 0.019767387 | BLM/ATR/ATRX/CASP8AP2/CBX5/EIF3E/HIPK3/KAT6A/NBN/RB1/RFWD3/RNF6/SMC5/SMC6/SP100/TDP2/TOPBP1/TOPORS/USP7/WDFY3/ZMYM2/ZNF451 | 22 |
| CC | GO:0070603 | SWI/SNF superfamily-type complex | 20/2260 | 93/19518 | 0.004355805 | 0.02821096 | 0.021211248 | DEK/HDAC2/ACTR8/ANP32E/ARID2/BAZ1A/BAZ1B/BRD7/CHD4/DDX21/ERCC6/ING3/PBRM1/RB1/RSF1/SF3B1/SMARCA1/SMARCA5/SUZ12/UCHL5 | 20 |
| CC | GO:0005852 | eukaryotic translation initiation factor 3 complex | 6/2260 | 15/19518 | 0.004735767 | 0.030109052 | 0.022638385 | EIF3M/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L | 6 |
| CC | GO:0030688 | preribosome, small subunit precursor | 6/2260 | 15/19518 | 0.004735767 | 0.030109052 | 0.022638385 | LTV1/RIOK1/RIOK2/RIOK3/TSR1/UTP20 | 6 |
| CC | GO:0005769 | early endosome | 67/2260 | 423/19518 | 0.004787858 | 0.030163506 | 0.022679328 | ANK2/AP1AR/AP3B1/AP3M1/ARRDC3/ARRDC4/ATP11B/ATP11C/ATP13A3/ATP13A4/ATP7A/CCDC93/CFTR/CLCN3/CLCN5/CYTIP/DIAPH2/DNAJC13/DTX3L/EEA1/EPHA3/EPHA4/EPS15/FIG4/GPNMB/HAVCR2/HPS3/HSPD1/KIF16B/LRP6/MON2/MTMR2/MTMR4/MYO1B/MYO5A/PIKFYVE/RAB1A/RABEP1/RABGAP1L/RABGEF1/RASGEF1B/REP15/RPS6KC1/SAMD9L/SGK3/SLC9A9/SNX13/SNX16/SNX2/SNX30/SNX6/STAM2/STEAP2/STEAP4/TFRC/TLR3/TLR4/TRAK2/USP8/VCAM1/VPS13B/VPS26A/VPS35/VPS41/VPS8/ZFYVE16/ZFYVE9 | 67 |
| CC | GO:0031256 | leading edge membrane | 33/2260 | 180/19518 | 0.004982013 | 0.030886504 | 0.023222935 | ADAM17/AKAP5/APC/ATP2B1/BMX/C2CD5/CDKL5/CLASP2/CLCN3/CORO1C/DOCK8/DPP4/EPB41L3/EPS8/EZR/FAP/FERMT2/IFIT5/ITGAV/ITGB1/ITGB3/LCP1/MACF1/MTMR6/MYO6/NCKAP1/PSD3/PTPRK/SLC39A6/SYNE2/TPM1/TWF1/VEZT | 33 |
| CC | GO:0045177 | apical part of cell | 70/2260 | 446/19518 | 0.004991758 | 0.030886504 | 0.023222935 | ASPM/ABCB1/ABCC4/ACE2/ADAM17/AHCYL1/ANK2/ATP1B1/ATP2B1/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP7A/ATP8B1/CD36/CDH2/CFTR/CHL1/CLCN3/CLCN5/CLDN1/CTNNB1/CTSK/CTSL/DLG1/DPP4/DYNC2H1/ENPEP/EXOC1/EZR/FAP/FAT1/HSP90AA1/IFIT5/IQGAP1/ITGB3/KCNMA1/LMO7/LRP2/MGAM/MPDZ/MTDH/MYO1B/NEDD1/NIN/OSMR/PCM1/PDE4D/PLD1/PRKCI/PTPRO/RAB18/RAB27A/RAB27B/RAPGEF2/RAPGEF6/RDX/SLC16A1/SLC38A1/SLC4A7/SLC5A3/SLC5A8/SLC6A14/SLC7A11/SNX10/SORBS2/STXBP3/TJP1/TNIK/VCAM1 | 70 |
| CC | GO:0031901 | early endosome membrane | 34/2260 | 187/19518 | 0.005044174 | 0.030934624 | 0.023259116 | ATP11B/ATP11C/ATP13A3/ATP13A4/ATP7A/CFTR/CLCN3/DNAJC13/DTX3L/EEA1/EPHA4/EPS15/FIG4/GPNMB/KIF16B/LRP6/MON2/MTMR2/MTMR4/PIKFYVE/RABEP1/RABGEF1/REP15/SNX13/SNX16/SNX2/SNX30/SNX6/STAM2/STEAP4/VPS13B/VPS41/ZFYVE16/ZFYVE9 | 34 |
| CC | GO:0031838 | haptoglobin-hemoglobin complex | 5/2260 | 11/19518 | 0.005243068 | 0.031872334 | 0.023964161 | HBA2/HBB/HBD/HBG2/HP | 5 |
| CC | GO:0002102 | podosome | 9/2260 | 30/19518 | 0.005443471 | 0.032802832 | 0.024663784 | BIN2/DOCK5/LCP1/SCIN/SH3PXD2B/SVIL/TJP1/VCAM1/VCL | 9 |
| CC | GO:0120111 | neuron projection cytoplasm | 19/2260 | 89/19518 | 0.005831325 | 0.034837138 | 0.026193337 | KIF4A/AP3B1/AP3M1/BLOC1S6/CANX/CDKL5/DLG2/DST/DYNC1H1/FMR1/HIF1A/HNRNPU/KIF3A/KIF5B/LRRK2/OPA1/RAB27B/SYBU/TRAK2 | 19 |
| CC | GO:0005871 | kinesin complex | 12/2260 | 47/19518 | 0.006104696 | 0.036158586 | 0.027186907 | KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B | 12 |
| CC | GO:0008305 | integrin complex | 9/2260 | 31/19518 | 0.006896434 | 0.040501937 | 0.030452584 | ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/LYN | 9 |
| CC | GO:0005643 | nuclear pore | 20/2260 | 97/19518 | 0.007115143 | 0.041435242 | 0.031154318 | MAD2L1/XPOT/AHCTF1/CHMP2B/IPO5/IPO7/KPNA1/KPNA3/KPNB1/NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/NXT2/RANBP2/RGPD1/TPR/XPO4 | 20 |
| CC | GO:0005828 | kinetochore microtubule | 7/2260 | 21/19518 | 0.007385368 | 0.042650499 | 0.032068044 | CENPE/KIF18A/KNTC1/ZWILCH/CHMP2B/CLASP2/ZW10 | 7 |
| CC | GO:0000800 | lateral element | 5/2260 | 12/19518 | 0.008138964 | 0.045856116 | 0.034478283 | BLM/BRCA1/BRCA2/SMC3/SYCP2 | 5 |
| CC | GO:0030904 | retromer complex | 5/2260 | 12/19518 | 0.008138964 | 0.045856116 | 0.034478283 | DENND4C/SNX2/SNX6/VPS26A/VPS35 | 5 |
| CC | GO:0042405 | nuclear inclusion body | 5/2260 | 12/19518 | 0.008138964 | 0.045856116 | 0.034478283 | RAD18/NBN/NUP153/RANBP2/TPR | 5 |
| CC | GO:0030057 | desmosome | 8/2260 | 27/19518 | 0.009349357 | 0.052250844 | 0.039286349 | CDH2/DSC2/DSG2/DSP/KLHL24/PKP2/PNN/POF1B | 8 |
| CC | GO:0005923 | bicellular tight junction | 24/2260 | 126/19518 | 0.009490257 | 0.052613986 | 0.039559388 | ECT2/ANK3/APC/ASH1L/CGNL1/CLDN1/CLMP/CTNNB1/CXADR/DLG1/FRMD4B/MAGI3/MPDZ/MPP7/MTDH/POF1B/PRKCI/RAPGEF2/RPGRIP1L/STRN/TGFBR1/TJP1/USP53/WNK3 | 24 |
| CC | GO:0030139 | endocytic vesicle | 55/2260 | 347/19518 | 0.009719983 | 0.053459909 | 0.04019542 | ABCA1/ACE2/ATP7A/BECN1/CD163/CD2AP/CD36/CFTR/CLCN3/CLTC/COLEC12/CTSL/CTSS/CYBB/DPP4/EGF/ENTPD7/GAPVD1/GOLIM4/HBA2/HBB/HEATR5A/HEATR5B/HP/HSP90AA1/HSP90B1/HSPH1/IL7R/ITGAV/KIF5B/LRP2/LYN/MDM2/MSR1/MYO1E/MYO6/NOSTRIN/PDIA3/PIK3C3/PIK3R4/PIKFYVE/PLD1/RAB8B/RABEP1/RABGEF1/RAPGEF2/RAPGEF6/SLC9A9/STAM2/STXBP3/STXBP4/TFRC/TLR1/TLR2/TLR6 | 55 |
| CC | GO:0030016 | myofibril | 39/2260 | 233/19518 | 0.011488833 | 0.062691031 | 0.047136114 | ABCC9/ANK2/ANK3/CAB39/CALD1/CAPN3/CMYA5/CORO1C/CTNNB1/DCTN4/DMD/DST/FBXO32/FERMT2/FHL5/FXR1/LMAN1/LRRC39/MTM1/MYOM1/NEB/NEXN/PDE4B/PPP1R12A/PPP1R12B/PYROXD1/RYR2/SCN1A/SLC4A1/SORBS2/SVIL/SYNE1/SYNE2/TIMP4/TMOD2/TPM1/TTN/TWF1/VCL | 39 |
| CC | GO:1904115 | axon cytoplasm | 14/2260 | 63/19518 | 0.011681572 | 0.06324476 | 0.047552451 | KIF4A/AP3B1/AP3M1/BLOC1S6/DLG2/DST/DYNC1H1/HIF1A/KIF3A/KIF5B/OPA1/RAB27B/SYBU/TRAK2 | 14 |
| CC | GO:0000145 | exocyst | 5/2260 | 13/19518 | 0.011980637 | 0.06386601 | 0.048019556 | EXOC1/EXOC2/EXOC4/EXOC5/EXOC6B | 5 |
| CC | GO:0000974 | Prp19 complex | 5/2260 | 13/19518 | 0.011980637 | 0.06386601 | 0.048019556 | CDC5L/CRNKL1/HSPA8/PLRG1/SYF2 | 5 |
| CC | GO:0071682 | endocytic vesicle lumen | 7/2260 | 23/19518 | 0.012664957 | 0.066998591 | 0.05037488 | CTSL/HBA2/HBB/HP/HSP90AA1/HSP90B1/HSPH1 | 7 |
| CC | GO:0043034 | costamere | 6/2260 | 18/19518 | 0.012951886 | 0.067997401 | 0.051125866 | ANK2/ANK3/DMD/FXR1/SVIL/VCL | 6 |
| CC | GO:0043292 | contractile fiber | 40/2260 | 243/19518 | 0.013812428 | 0.071970021 | 0.054112798 | DEK/ABCC9/ANK2/ANK3/CAB39/CALD1/CAPN3/CMYA5/CORO1C/CTNNB1/DCTN4/DMD/DST/FBXO32/FERMT2/FHL5/FXR1/LMAN1/LRRC39/MTM1/MYOM1/NEB/NEXN/PDE4B/PPP1R12A/PPP1R12B/PYROXD1/RYR2/SCN1A/SLC4A1/SORBS2/SVIL/SYNE1/SYNE2/TIMP4/TMOD2/TPM1/TTN/TWF1/VCL | 40 |
| CC | GO:1905369 | endopeptidase complex | 18/2260 | 90/19518 | 0.014056776 | 0.072696609 | 0.054659104 | PSMA4/CFH/PSMA3/PSMC1/PSMC2/PSMC6/PSMD1/PSMD12/PSMD14/PSMD2/PSMD5/PSMD6/PSMD7/PSME4/UBR1/UCHL5/USP14/VCP | 18 |
| CC | GO:0070160 | tight junction | 24/2260 | 131/19518 | 0.015113448 | 0.077582368 | 0.058332607 | ECT2/ANK3/APC/ASH1L/CGNL1/CLDN1/CLMP/CTNNB1/CXADR/DLG1/FRMD4B/MAGI3/MPDZ/MPP7/MTDH/POF1B/PRKCI/RAPGEF2/RPGRIP1L/STRN/TGFBR1/TJP1/USP53/WNK3 | 24 |
| CC | GO:0030863 | cortical cytoskeleton | 20/2260 | 104/19518 | 0.015243927 | 0.077676774 | 0.058403589 | ANLN/ACTR2/AKAP13/CALD1/CAPZA2/CDH2/EPB41/EPB41L2/ERC1/EZR/IQGAP1/MAPRE1/MPP1/MYO1E/PLS1/PPP1R9A/RDX/SLC4A1/SNX9/SPTAN1 | 20 |
| CC | GO:0035371 | microtubule plus-end | 7/2260 | 24/19518 | 0.016131717 | 0.081009274 | 0.060909229 | SPAG5/CDK5RAP2/CKAP5/CLIP1/DST/KNSTRN/MAPRE1 | 7 |
| CC | GO:0044295 | axonal growth cone | 7/2260 | 24/19518 | 0.016131717 | 0.081009274 | 0.060909229 | C9orf72/EPHA4/FLRT3/HSP90AA1/HSP90AB1/MYO9A/NIN | 7 |
| CC | GO:0005788 | endoplasmic reticulum lumen | 49/2260 | 312/19518 | 0.016438439 | 0.08195567 | 0.061620804 | ACE2/ADAM10/ADAM17/ADAMTS5/ARSK/C3/CALU/CANX/CDH2/COL12A1/COL14A1/COL3A1/COL5A2/COL6A3/COL8A1/CP/DNAJC10/DNAJC3/EDEM3/ERAP2/FBN1/FKBP14/FMO1/FSTL1/GOLM1/GPX8/HSP90B1/HSPA5/KTN1/LAMB1/LAMC1/LTBP1/MGAT4A/MIA3/P4HA1/PDGFC/PDGFD/PDIA3/PDIA6/POGLUT1/PTGS2/RCN1/SLC27A2/SPARCL1/SPP1/TNC/UGGT1/UGGT2/VCAN | 49 |
| CC | GO:0042581 | specific granule | 28/2260 | 160/19518 | 0.016751104 | 0.082419085 | 0.061969237 | ADAM10/ARG1/ARMC8/ATP6V1D/ATP8A1/ATP8B4/CD36/CEP290/CLCN3/CLEC4D/CRISP3/CYBB/DOCK2/FRK/HP/ITGAV/KPNB1/MMP8/MOSPD2/PLD1/RAB27A/SLC27A2/SLCO4C1/SNAP25/SPTAN1/STXBP3/UBR4/VCL | 28 |
| CC | GO:0005903 | brush border | 20/2260 | 105/19518 | 0.016842211 | 0.082419085 | 0.061969237 | ACE2/ACTR3/ADD3/ATP7A/CAPZA2/CD36/DNM1L/ENPEP/EPS8/EZR/HSP90AA1/LIMA1/LRP2/MYO1B/MYO1E/PLS1/PRKCI/SCIN/SLC38A2/SLC7A11 | 20 |
| CC | GO:0031010 | ISWI-type complex | 5/2260 | 14/19518 | 0.016888182 | 0.082419085 | 0.061969237 | BAZ1A/BAZ1B/RSF1/SMARCA1/SMARCA5 | 5 |
| CC | GO:0000178 | exosome (RNase complex) | 6/2260 | 19/19518 | 0.017111884 | 0.082926823 | 0.062350995 | DIS3/DIS3L/EXOSC9/MPHOSPH6/PNPT1/ZFC3H1 | 6 |
| CC | GO:0000118 | histone deacetylase complex | 16/2260 | 79/19518 | 0.017712764 | 0.085242679 | 0.06409224 | HDAC2/ANP32E/ARID4A/ARID4B/BRMS1L/CBX5/CHD4/ING2/ING3/JMJD1C/KDM3A/NCOR1/NRIP1/OGT/TBL1XR1/ZNF217 | 16 |
| CC | GO:0032154 | cleavage furrow | 12/2260 | 54/19518 | 0.018764008 | 0.089141755 | 0.067023876 | CEP55/ECT2/PLK4/HMCN1/ITGB1/LIMA1/MASTL/PKN2/RACGAP1/RDX/SPIRE1/SVIL | 12 |
| CC | GO:0000151 | ubiquitin ligase complex | 48/2260 | 307/19518 | 0.018780225 | 0.089141755 | 0.067023876 | BRCA1/BRCA2/BUB1B/DTL/RAD18/UBXN8/ANAPC1/ANKIB1/ARIH1/ARMC8/ATG3/BRCC3/CACYBP/CAND1/CDC27/CUL1/CUL2/CUL3/DCAF6/DCUN1D3/FBXL3/FBXL5/FBXO11/FBXO32/FBXO38/FBXO45/FEM1C/KBTBD8/KLHL13/KLHL2/KLHL24/KLHL8/LMO7/MKLN1/NEDD4/RNF14/RNF19A/RNF20/RNF217/SEL1L/SPOPL/TOPORS/UBE4A/UBR1/UBR2/UBR3/USP47/WWP1 | 48 |
| CC | GO:0045178 | basal part of cell | 45/2260 | 285/19518 | 0.019071234 | 0.089907247 | 0.067599434 | ABCA8/ABCC4/ANK2/ANK3/AQP4/AQP9/ATP1B1/ATP2B1/ATP7A/CASK/CD38/CDH2/CLASP2/CLDN1/CTNNB1/CXADR/DLG1/DOCK7/DSP/DST/ENPP1/EPB41/ERBB4/EZR/FAP/HSP90AA1/IDE/IQGAP1/ITGA2/LRRK2/MET/NAIP/PHLDB2/SLC16A1/SLC16A7/SLC1A3/SLC38A1/SLC4A1/SLC4A7/SLC5A3/SLCO4C1/STXBP3/TFRC/TJP1/VSIG1 | 45 |
| CC | GO:0019908 | nuclear cyclin-dependent protein kinase holoenzyme complex | 4/2260 | 10/19518 | 0.021177616 | 0.097192636 | 0.07307717 | BCCIP/CCNH/CCNT1/CCNT2 | 4 |
| CC | GO:0031414 | N-terminal protein acetyltransferase complex | 4/2260 | 10/19518 | 0.021177616 | 0.097192636 | 0.07307717 | NAA15/NAA25/NAA35/NAA50 | 4 |
| CC | GO:0070938 | contractile ring | 4/2260 | 10/19518 | 0.021177616 | 0.097192636 | 0.07307717 | ANLN/KIF20B/PRC1/UTRN | 4 |
| CC | GO:0071014 | post-mRNA release spliceosomal complex | 4/2260 | 10/19518 | 0.021177616 | 0.097192636 | 0.07307717 | CRNKL1/CWF19L2/GCFC2/SYF2 | 4 |
| CC | GO:0071339 | MLL1 complex | 8/2260 | 31/19518 | 0.02188487 | 0.099777729 | 0.075020849 | CHD8/E2F6/HCFC2/MGA/RBBP5/TAF1/TAF7/TEX10 | 8 |
| CC | GO:1905354 | exoribonuclease complex | 6/2260 | 20/19518 | 0.022104976 | 0.100086669 | 0.075253134 | DIS3/DIS3L/EXOSC9/MPHOSPH6/PNPT1/ZFC3H1 | 6 |
| CC | GO:0098791 | Golgi apparatus subcompartment | 57/2260 | 378/19518 | 0.022241482 | 0.100086669 | 0.075253134 | VRK1/AKAP9/AP4E1/ARFGEF1/ARFGEF2/ATL1/ATP2C1/ATP7A/ATP8A1/ATP8B1/ATP8B4/BECN1/BIRC6/CCDC186/CLASP2/CLTC/CNST/COG5/COG6/CSGALNACT1/FAM91A1/FUT8/GALNT1/GALNT3/GCC2/GCNT1/GOLGA4/GOLGA5/GOLGB1/GOLIM4/GSAP/LRRK2/MGAT4A/MS4A6A/MYO1B/NBEA/NSF/OSBP/PAM/PCSK1/PIK3C2A/POSTN/PREPL/PRKD1/RAB27B/RHOBTB3/SAR1B/SCFD1/SNAP25/SNX9/SULF1/TBC1D23/TMEM87A/TOM1L1/USO1/VPS54/WDR11 | 57 |
| CC | GO:0030127 | COPII vesicle coat | 5/2260 | 15/19518 | 0.022964389 | 0.10217358 | 0.076822241 | SAR1B/SEC23A/SEC23B/SEC24D/SEC31A | 5 |
| CC | GO:0043296 | apical junction complex | 26/2260 | 150/19518 | 0.023000113 | 0.10217358 | 0.076822241 | ECT2/ANK3/APC/ASH1L/CGNL1/CLDN1/CLMP/CTNNA1/CTNNB1/CXADR/DLG1/FRMD4B/MAGI3/MPDZ/MPP7/MTDH/PKN2/POF1B/PRKCI/RAPGEF2/RPGRIP1L/STRN/TGFBR1/TJP1/USP53/WNK3 | 26 |
| CC | GO:0000307 | cyclin-dependent protein kinase holoenzyme complex | 11/2260 | 50/19518 | 0.025598276 | 0.112991117 | 0.084955727 | CCNA2/CCNB2/CDK1/BCCIP/CCNC/CCNE2/CCNG1/CCNH/CCNL1/CCNT1/CCNT2 | 11 |
| CC | GO:0044665 | MLL1/2 complex | 8/2260 | 32/19518 | 0.02630364 | 0.115369761 | 0.086744181 | CHD8/E2F6/HCFC2/MGA/RBBP5/TAF1/TAF7/TEX10 | 8 |
| CC | GO:0009898 | cytoplasmic side of plasma membrane | 27/2260 | 159/19518 | 0.02651114 | 0.115548555 | 0.086878612 | AKAP5/ATP2B1/BIRC2/CHUK/CYLD/DLG1/EXOC1/EZR/FER/FERMT2/FRK/GEM/GNAI3/IQGAP1/KRAS/LYN/PTPN3/PTPN4/PTPRC/RACGAP1/RGS1/RGS2/SLC4A1/SNAP25/SYAP1/TRAF5/YES1 | 27 |
| CC | GO:0005901 | caveola | 16/2260 | 83/19518 | 0.027362894 | 0.118515535 | 0.089109425 | KIF18A/AKAP6/ATP1B1/CD36/CORO1C/CTNNA1/CTNNB1/HTR2A/JAK2/KCNMA1/LRP6/LRP8/LRRK2/MYOF/PTGS2/TFPI | 16 |
| CC | GO:0044233 | mitochondria-associated endoplasmic reticulum membrane | 6/2260 | 21/19518 | 0.027992819 | 0.120142893 | 0.090333002 | ACSL4/AHCYL1/CANX/PDZD8/STX17/VPS13A | 6 |
| CC | GO:0016528 | sarcoplasm | 17/2260 | 90/19518 | 0.028128426 | 0.120142893 | 0.090333002 | AGL/AKAP6/ANK3/ASPH/ATP2A2/CACNA2D1/CALU/CMYA5/HK2/HSP90B1/IFRD1/ITPR1/ITPR2/MEF2C/RYR2/SCN3A/SYNE2 | 17 |
| CC | GO:0005774 | vacuolar membrane | 67/2260 | 460/19518 | 0.028258718 | 0.120142893 | 0.090333002 | WDR41/ABCA5/AP3B1/AP3M1/ATP11B/ATP11C/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/ATP8A1/CFTR/CHMP2B/CLCN3/CLCN5/CLTC/CP/CPNE3/DNAJC13/DPP4/DTX3L/EGF/ENPEP/ENPP1/FNIP1/FNIP2/GDAP2/GLIPR1/GNAI3/GOPC/HSPA8/JMY/KIF5B/LRBA/LRP2/LYN/MIOS/MTMR2/MYO6/NAPG/NPC1/NSF/PLD1/PRKD1/RB1CC1/RPN2/SBF2/SH3GLB1/SLC36A4/SLCO4C1/SPAG9/SPG11/STX17/TAB2/TLR3/TLR8/TRIM23/VLDLR/VNN1/VPS13A/VPS13B/VPS13C/VPS35/VPS41/WDFY3/WDR11/YWHAB | 67 |
| CC | GO:1902493 | acetyltransferase complex | 19/2260 | 104/19518 | 0.029090016 | 0.122048996 | 0.091766162 | DLD/EPC2/ING3/JADE1/KANSL1L/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA15/NAA25/NAA35/NAA50/OGT/PHF20L1/SUPT20H/TAF2/TAF7/ZZZ3 | 19 |
| CC | GO:0005782 | peroxisomal matrix | 11/2260 | 51/19518 | 0.029334584 | 0.122048996 | 0.091766162 | ABCD3/AGPS/ATM/BAAT/ECI2/GNPAT/HSD17B4/IDE/IDH1/NUDT12/SCP2 | 11 |
| CC | GO:0031907 | microbody lumen | 11/2260 | 51/19518 | 0.029334584 | 0.122048996 | 0.091766162 | ABCD3/AGPS/ATM/BAAT/ECI2/GNPAT/HSD17B4/IDE/IDH1/NUDT12/SCP2 | 11 |
| CC | GO:0000221 | vacuolar proton-transporting V-type ATPase, V1 domain | 4/2260 | 11/19518 | 0.030283073 | 0.122048996 | 0.091766162 | ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D | 4 |
| CC | GO:0005614 | interstitial matrix | 4/2260 | 11/19518 | 0.030283073 | 0.122048996 | 0.091766162 | CCDC80/COL14A1/ECM2/TNC | 4 |
| CC | GO:0033180 | proton-transporting V-type ATPase, V1 domain | 4/2260 | 11/19518 | 0.030283073 | 0.122048996 | 0.091766162 | ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D | 4 |
| CC | GO:0034663 | endoplasmic reticulum chaperone complex | 4/2260 | 11/19518 | 0.030283073 | 0.122048996 | 0.091766162 | DNAJC10/HSP90B1/HSPA5/PDIA6 | 4 |
| CC | GO:0098850 | extrinsic component of synaptic vesicle membrane | 4/2260 | 11/19518 | 0.030283073 | 0.122048996 | 0.091766162 | ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D | 4 |
| CC | GO:0045239 | tricarboxylic acid cycle enzyme complex | 5/2260 | 16/19518 | 0.030292103 | 0.122048996 | 0.091766162 | DBT/DLD/FH/SUCLA2/SUCLG2 | 5 |
| CC | GO:0016323 | basolateral plasma membrane | 37/2260 | 234/19518 | 0.030504948 | 0.12219612 | 0.091876782 | ABCA8/ABCC4/ANK2/ANK3/AQP4/AQP9/ATP1B1/ATP2B1/ATP7A/CASK/CD38/CDH2/CLDN1/CTNNB1/CXADR/DLG1/DSP/ENPP1/EPB41/ERBB4/EZR/HSP90AA1/IDE/IQGAP1/LRRK2/NAIP/SLC16A1/SLC16A7/SLC38A1/SLC4A1/SLC4A7/SLC5A3/SLCO4C1/STXBP3/TFRC/TJP1/VSIG1 | 37 |
| CC | GO:1904949 | ATPase complex | 25/2260 | 147/19518 | 0.031303608 | 0.124674715 | 0.093740388 | DEK/HDAC2/ACTR8/ANP32E/ARID2/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/BAZ1A/BAZ1B/BRD7/CHD4/DDX21/ERCC6/ING3/PBRM1/RB1/RSF1/SF3B1/SMARCA1/SMARCA5/SUZ12/UCHL5/VCP | 25 |
| CC | GO:0005884 | actin filament | 19/2260 | 105/19518 | 0.031795926 | 0.125911869 | 0.094670578 | DIAPH3/CD2AP/DIAPH2/EZR/FMN1/GAS2L3/IQGAP1/LCP1/MYO1B/MYO5A/MYO6/NCKAP1/PLS1/PLS3/POF1B/PSTPIP2/TPM1/TWF1/YES1 | 19 |
| CC | GO:0017053 | transcription repressor complex | 15/2260 | 78/19518 | 0.032590358 | 0.127874857 | 0.096146509 | DEPDC1/GMNN/ARID4A/CBX5/CTNNB1/DDX20/HMGB1/MDM2/NCOR1/RBBP8/RBPJ/SDR16C5/TBL1XR1/ZNF224/ZNF350 | 15 |
| CC | GO:0030017 | sarcomere | 34/2260 | 213/19518 | 0.032660678 | 0.127874857 | 0.096146509 | ABCC9/ANK2/ANK3/CAB39/CAPN3/CMYA5/CORO1C/CTNNB1/DCTN4/DMD/DST/FBXO32/FERMT2/FHL5/LMAN1/LRRC39/MTM1/MYOM1/NEB/NEXN/PDE4B/PPP1R12A/PPP1R12B/PYROXD1/RYR2/SCN1A/SLC4A1/SORBS2/SYNE1/SYNE2/TIMP4/TMOD2/TPM1/TTN | 34 |
| CC | GO:0098978 | glutamatergic synapse | 60/2260 | 410/19518 | 0.033374347 | 0.129934956 | 0.097695456 | ADAM10/ADAM23/AKAP9/ARFGEF2/ATP2B1/CADPS2/CANX/CAPRIN1/CDH6/CDKL5/CHD4/CLCN3/CNR1/CPSF2/CTNNB1/CTTNBP2/CUL3/DLG1/EEA1/EIF4A3/EPHA4/EPS8/ERBB4/FBXO45/FLRT3/FXR1/HNRNPA3/HSPA8/HTR2A/IL1RAP/ITGB1/ITGB3/JAK2/KCND2/KPNA1/LRRK2/LRRTM2/LYN/NF1/NGDN/NLGN1/NRCAM/OGT/PLCB1/PLEKHA5/PLXNC1/PRKAR2B/PRKCI/PTPRD/PTPRO/RNF19A/SNAP25/SNX6/SPARCL1/STK38L/TNIK/TRIO/USP8/VCP/VPS35 | 60 |
| CC | GO:0016328 | lateral plasma membrane | 13/2260 | 65/19518 | 0.033589587 | 0.130042367 | 0.097776216 | ANK3/APC/ATP1B1/CLDN1/CORO1C/CTNNB1/DLG1/DMD/GPSM2/IQGAP1/MPP7/PTPRO/SLC16A1 | 13 |
| CC | GO:0016580 | Sin3 complex | 6/2260 | 22/19518 | 0.034827223 | 0.133344007 | 0.100258652 | HDAC2/ARID4A/ARID4B/BRMS1L/ING2/OGT | 6 |
| CC | GO:0070822 | Sin3-type complex | 6/2260 | 22/19518 | 0.034827223 | 0.133344007 | 0.100258652 | HDAC2/ARID4A/ARID4B/BRMS1L/ING2/OGT | 6 |
| CC | GO:0098562 | cytoplasmic side of membrane | 31/2260 | 193/19518 | 0.037045739 | 0.141058775 | 0.10605923 | AKAP5/ATP2B1/BIRC2/CHUK/CYLD/DLG1/DNAJA1/EPM2AIP1/EXOC1/EZR/FER/FERMT2/FRK/GEM/GNAI3/IQGAP1/KRAS/LRRK2/LYN/PTPN3/PTPN4/PTPRC/RACGAP1/RGS1/RGS2/SLC4A1/SNAP25/SYAP1/THADA/TRAF5/YES1 | 31 |
| CC | GO:0044853 | plasma membrane raft | 20/2260 | 114/19518 | 0.037739699 | 0.142915911 | 0.107455572 | KIF18A/AKAP6/ATP1B1/CD36/CDH2/CORO1C/CR1/CTNNA1/CTNNB1/EZR/HTR2A/JAK2/KCND2/KCNMA1/LRP6/LRP8/LRRK2/MYOF/PTGS2/TFPI | 20 |
| CC | GO:0071011 | precatalytic spliceosome | 11/2260 | 53/19518 | 0.037946652 | 0.142918639 | 0.107457623 | CWC22/CWC27/MFAP1/PRPF38B/PRPF4/SF3A3/SF3B1/SMU1/SNRNP200/SNRPA1/WBP4 | 11 |
| CC | GO:0016529 | sarcoplasmic reticulum | 14/2260 | 73/19518 | 0.038877502 | 0.143512403 | 0.107904063 | AGL/AKAP6/ANK3/ASPH/ATP2A2/CACNA2D1/CALU/CMYA5/HK2/HSP90B1/ITPR1/ITPR2/RYR2/SYNE2 | 14 |
| CC | GO:0031092 | platelet alpha granule membrane | 5/2260 | 17/19518 | 0.038932658 | 0.143512403 | 0.107904063 | CD109/CD36/ITGB3/LHFPL2/TMX3 | 5 |
| CC | GO:0032045 | guanyl-nucleotide exchange factor complex | 5/2260 | 17/19518 | 0.038932658 | 0.143512403 | 0.107904063 | WDR41/C9orf72/EIF2B3/PDE3B/RASGRP3 | 5 |
| CC | GO:0098637 | protein complex involved in cell-matrix adhesion | 5/2260 | 17/19518 | 0.038932658 | 0.143512403 | 0.107904063 | LAMA2/LAMB1/LAMC1/MMRN1/TNC | 5 |
| CC | GO:0005833 | hemoglobin complex | 4/2260 | 12/19518 | 0.041355127 | 0.14926616 | 0.112230196 | HBA2/HBB/HBD/HBG2 | 4 |
| CC | GO:0005845 | mRNA cap binding complex | 4/2260 | 12/19518 | 0.041355127 | 0.14926616 | 0.112230196 | FMR1/NCBP1/NCBP2/RNMT | 4 |
| CC | GO:0044615 | nuclear pore nuclear basket | 4/2260 | 12/19518 | 0.041355127 | 0.14926616 | 0.112230196 | MAD2L1/NUP153/RANBP2/TPR | 4 |
| CC | GO:0097504 | Gemini of coiled bodies | 4/2260 | 12/19518 | 0.041355127 | 0.14926616 | 0.112230196 | DDX20/GEMIN5/NPAT/ZPR1 | 4 |
| CC | GO:0000792 | heterochromatin | 15/2260 | 81/19518 | 0.043844718 | 0.157432071 | 0.118369978 | ESCO2/EZH2/HELLS/WDR76/ATRX/BAZ1A/BAZ1B/CBX5/CENPC/KDM4C/SMARCA5/SMARCAD1/SUZ12/TCP1/TOP2B | 15 |
| CC | GO:0097542 | ciliary tip | 10/2260 | 48/19518 | 0.045493074 | 0.162508766 | 0.122187042 | CDKL5/CYLD/DYNC2H1/IFT57/IFT74/IFT80/KIF3A/TTC21B/WDR19/WDR35 | 10 |
| CC | GO:0031248 | protein acetyltransferase complex | 18/2260 | 103/19518 | 0.04846574 | 0.172107649 | 0.129404247 | EPC2/ING3/JADE1/KANSL1L/KAT6A/MAP3K7/MORF4L2/MSL3P1/NAA15/NAA25/NAA35/NAA50/OGT/PHF20L1/SUPT20H/TAF2/TAF7/ZZZ3 | 18 |
| CC | GO:0030663 | COPI-coated vesicle membrane | 5/2260 | 18/19518 | 0.048925262 | 0.172107649 | 0.129404247 | ARCN1/COPA/COPB1/COPB2/KDELR3 | 5 |
| CC | GO:0031527 | filopodium membrane | 5/2260 | 18/19518 | 0.048925262 | 0.172107649 | 0.129404247 | DMD/ITGAV/ITGB3/SYNE2/UTRN | 5 |
| CC | GO:0016324 | apical plasma membrane | 55/2260 | 381/19518 | 0.049773639 | 0.174207736 | 0.13098326 | ASPM/ABCB1/ABCC4/ACE2/ADAM17/AHCYL1/ANK2/ATP1B1/ATP2B1/ATP6V1A/ATP6V1B2/ATP7A/ATP8B1/CD36/CDH2/CFTR/CLCN3/CLDN1/CTSK/CTSL/DLG1/DPP4/ENPEP/EXOC1/EZR/FAT1/HSP90AA1/IQGAP1/ITGB3/KCNMA1/LMO7/LRP2/MGAM/MPDZ/MTDH/OSMR/PDE4D/PLD1/PRKCI/PTPRO/RAB18/RAB27A/RAB27B/RAPGEF2/RAPGEF6/RDX/SLC16A1/SLC38A1/SLC4A7/SLC5A3/SLC5A8/SLC6A14/SORBS2/STXBP3/TNIK | 55 |
| MF | GO:0016887 | ATP hydrolysis activity | 135/2263 | 376/18369 | 8.96E-33 | 9.89E-30 | 8.34E-30 | ATAD5/BLM/BRIP1/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/MCM3/MCM6/MCM8/MSH2/OLA1/RFC4/ABCA1/ABCA5/ABCA8/ABCB1/ABCB7/ABCC4/ABCC9/ABCD3/ABCE1/ABCF2/AQR/ASCC3/ATAD2/ATF7IP/ATP10D/ATP11B/ATP11C/ATP13A3/ATP13A4/ATP2A2/ATP2B1/ATP2C1/ATP7A/ATP8A1/ATP8B1/ATP8B4/ATRX/BTAF1/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CFTR/CHD1/CHD1L/CHD2/CHD4/CHD6/CHD7/CHD8/CHD9/CLPX/DDX1/DDX10/DDX18/DDX20/DDX21/DDX23/DDX24/DDX3X/DDX42/DDX46/DDX47/DDX5/DDX52/DDX60/DDX60L/DHX15/DHX29/DHX32/DHX36/DHX57/DHX8/DHX9/DNA2/EIF4A3/ERCC6/FANCM/FIGN/FIGNL1/G3BP1/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSP90B1/HSPA13/HSPA5/HSPA8/HSPA9/HSPD1/IFIH1/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B/MDN1/MLH1/MLH3/MYO1E/NAV3/NLRP3/NSF/PEX1/PSMC1/PSMC2/PSMC6/RAD50/RECQL/RFC1/RHOBTB3/SLFN11/SMARCA5/SMARCAD1/SMC1A/SMC2/SMC3/SMC4/SMC5/SMCHD1/SNRNP200/SPATA5/TCP1/VCP/WRN/XRCC5/YME1L1 | 135 |
| MF | GO:0004386 | helicase activity | 66/2263 | 153/18369 | 1.25E-21 | 6.92E-19 | 5.83E-19 | BLM/BRIP1/HELLS/MCM3/MCM6/MCM8/POLQ/RAD54B/RFC3/RFC4/AQR/ASCC3/ATRX/BTAF1/CHD1/CHD1L/CHD2/CHD4/CHD6/CHD7/CHD8/CHD9/DDX1/DDX10/DDX18/DDX20/DDX21/DDX23/DDX24/DDX3X/DDX42/DDX46/DDX47/DDX5/DDX52/DDX60/DDX60L/DHX15/DHX29/DHX32/DHX36/DHX57/DHX8/DHX9/DICER1/DNA2/EIF4A3/ERCC6L2/FANCM/G3BP1/HELZ/HLTF/IFIH1/RAD50/RECQL/SETX/SHPRH/SLFN11/SMARCA1/SMARCA5/SMARCAD1/SNRNP200/TTF2/WRN/XRCC5/ZNFX1 | 66 |
| MF | GO:0008094 | ATP-dependent activity, acting on DNA | 56/2263 | 126/18369 | 2.66E-19 | 9.79E-17 | 8.25E-17 | ATAD5/BLM/BRIP1/HELLS/MCM3/MCM6/MCM8/MSH2/POLQ/RAD54B/RFC3/RFC4/TOP2A/XRCC2/ASCC3/ATRX/BTAF1/CHD1/CHD1L/CHD2/CHD4/CHD6/CHD7/CHD8/CHD9/DDX1/DDX3X/DHX36/DHX9/DNA2/ERCC6/ERCC6L2/FANCM/G3BP1/HLTF/MLH1/MLH3/MSH3/MSH6/NIPBL/RAD17/RAD50/RECQL/RFC1/RSF1/SETX/SHPRH/SMARCA1/SMARCA5/SMARCAD1/SMC3/TOP2B/TTF2/WRN/XRCC5/ZRANB3 | 56 |
| MF | GO:0140097 | catalytic activity, acting on DNA | 76/2263 | 245/18369 | 6.23E-15 | 1.72E-12 | 1.45E-12 | ATAD5/BLM/BRIP1/HELLS/MCM3/MCM6/MCM8/MGME1/MSH2/NEIL3/POLQ/RAD54B/RFC3/RFC4/TOP2A/XRCC2/ASCC3/ATRX/BTAF1/CHD1/CHD1L/CHD2/CHD4/CHD6/CHD7/CHD8/CHD9/DCLRE1A/DDX1/DDX3X/DHX36/DHX9/DICER1/DKC1/DNA2/ERCC4/ERCC5/ERCC6/ERCC6L2/FANCM/G3BP1/GEN1/HLTF/LIG4/MBD4/MLH1/MLH3/MSH3/MSH6/N4BP2/NIPBL/POLA1/POLD3/POLK/RAD17/RAD50/RBBP8/RECQL/REV1/REV3L/RFC1/RSF1/SETMAR/SETX/SHPRH/SMARCA1/SMARCA5/SMARCAD1/SMC3/TDP2/TOP1/TOP2B/TTF2/WRN/XRCC5/ZRANB3 | 76 |
| MF | GO:0003697 | single-stranded DNA binding | 44/2263 | 119/18369 | 4.49E-12 | 9.02E-10 | 7.60E-10 | BLM/BRCA2/MCM3/MCM6/MCM8/MMS22L/MSH2/NEIL3/RAD18/RAD51AP1/DHX36/DHX9/ERCC4/ERCC5/FAM111A/HMGB1/HMGB2/HNRNPA1/HNRNPA2B1/HNRNPU/HSPD1/LRPPRC/MLH1/MSH3/NUCKS1/POLA1/POLR3C/POT1/RAD50/RECQL/RTF1/SAMHD1/SETMAR/SMARCA1/SMC2/SMC4/SMC5/SMC6/SPRTN/TDP2/TOP1/TSNAX/WDR48/ZRANB3 | 44 |
| MF | GO:0140658 | ATP-dependent chromatin remodeler activity | 22/2263 | 36/18369 | 6.01E-12 | 9.02E-10 | 7.60E-10 | HELLS/RAD54B/ATRX/BTAF1/CHD1/CHD1L/CHD2/CHD4/CHD6/CHD7/CHD8/CHD9/ERCC6/ERCC6L2/HLTF/RSF1/SHPRH/SMARCA1/SMARCA5/SMARCAD1/TTF2/ZRANB3 | 22 |
| MF | GO:0030695 | GTPase regulator activity | 115/2263 | 495/18369 | 6.54E-12 | 9.02E-10 | 7.60E-10 | ARHGAP11A/ARHGAP11B/DEPDC1/ECT2/WDR41/ACAP2/AKAP13/ARAP2/ARFGAP3/ARFGEF1/ARFGEF2/ARHGAP10/ARHGAP12/ARHGAP15/ARHGAP18/ARHGAP21/ARHGAP26/ARHGAP28/ARHGAP29/ARHGAP42/ARHGEF12/ARHGEF38/BNIP2/C9orf72/CCDC88A/CHM/CHML/DENND4A/DENND4C/DIS3/DNM1L/DOCK10/DOCK11/DOCK2/DOCK5/DOCK7/DOCK8/DOCK9/EGF/EIF2B3/EIF5/ELMOD2/EVI5/FAM13A/FAM13B/FGD4/FGD6/FNIP1/GAPVD1/GDI2/GPSM2/HERC1/IPO5/IPO7/IQGAP1/IQGAP2/ITSN1/ITSN2/KRIT1/LRRK2/MYCBP2/MYO9A/NCKAP1L/NET1/NF1/NUCB2/PLCB1/PLEKHG1/PREX2/PSD3/RAB3GAP1/RAB3GAP2/RAB3IP/RABEP1/RABGAP1/RABGAP1L/RABGEF1/RACGAP1/RALGAPA1/RALGAPA2/RALGPS2/RANBP2/RAP1GDS1/RAPGEF2/RAPGEF4/RAPGEF5/RAPGEF6/RASA1/RASA2/RASAL2/RASGEF1B/RASGRF2/RASGRP3/RCBTB2/RGL1/RGPD1/RGS1/RGS18/RGS2/RGS5/RP2/RPGR/SBF2/SEC23A/SEC23B/SIPA1L1/SOS1/SOS2/SRGAP1/SWAP70/TBC1D15/TBC1D30/TBC1D4/TBC1D8B/TRIO | 115 |
| MF | GO:0060589 | nucleoside-triphosphatase regulator activity | 115/2263 | 495/18369 | 6.54E-12 | 9.02E-10 | 7.60E-10 | ARHGAP11A/ARHGAP11B/DEPDC1/ECT2/WDR41/ACAP2/AKAP13/ARAP2/ARFGAP3/ARFGEF1/ARFGEF2/ARHGAP10/ARHGAP12/ARHGAP15/ARHGAP18/ARHGAP21/ARHGAP26/ARHGAP28/ARHGAP29/ARHGAP42/ARHGEF12/ARHGEF38/BNIP2/C9orf72/CCDC88A/CHM/CHML/DENND4A/DENND4C/DIS3/DNM1L/DOCK10/DOCK11/DOCK2/DOCK5/DOCK7/DOCK8/DOCK9/EGF/EIF2B3/EIF5/ELMOD2/EVI5/FAM13A/FAM13B/FGD4/FGD6/FNIP1/GAPVD1/GDI2/GPSM2/HERC1/IPO5/IPO7/IQGAP1/IQGAP2/ITSN1/ITSN2/KRIT1/LRRK2/MYCBP2/MYO9A/NCKAP1L/NET1/NF1/NUCB2/PLCB1/PLEKHG1/PREX2/PSD3/RAB3GAP1/RAB3GAP2/RAB3IP/RABEP1/RABGAP1/RABGAP1L/RABGEF1/RACGAP1/RALGAPA1/RALGAPA2/RALGPS2/RANBP2/RAP1GDS1/RAPGEF2/RAPGEF4/RAPGEF5/RAPGEF6/RASA1/RASA2/RASAL2/RASGEF1B/RASGRF2/RASGRP3/RCBTB2/RGL1/RGPD1/RGS1/RGS18/RGS2/RGS5/RP2/RPGR/SBF2/SEC23A/SEC23B/SIPA1L1/SOS1/SOS2/SRGAP1/SWAP70/TBC1D15/TBC1D30/TBC1D4/TBC1D8B/TRIO | 115 |
| MF | GO:0051020 | GTPase binding | 80/2263 | 304/18369 | 1.88E-11 | 2.30E-09 | 1.94E-09 | DIAPH3/ECT2/KNTC1/XPO1/XPOT/ABCA1/AKAP13/AP3M1/ATP7A/BECN1/C9orf72/CCDC186/CDKL5/CHM/CHML/CORO1C/CSE1L/DAAM1/DIAPH2/DMXL2/DNM1L/DOCK11/DOCK2/DOCK5/DOCK7/EPS8/ERC1/EVI5/EXOC2/EXOC4/EXOC5/EXPH5/FER/FGD4/FGD6/FMNL2/FNBP1L/GAPVD1/GCC2/GDI2/GOLGA4/GOLGA5/HSP90AA1/IPO11/IPO5/IPO7/IPO8/IQGAP1/IQGAP2/KIF3A/KPNB1/LCP1/LRRK2/MYCBP2/MYO5A/NCKAP1/PKN2/RAB11FIP2/RAB3GAP1/RAB3GAP2/RAB3IP/RABGAP1/RABGAP1L/RABGEF1/RABGGTB/RANBP2/RAPGEF4/RAPGEF6/RASA1/RASGRP3/RHOBTB3/ROCK1/ROCK2/SIKE1/SYTL2/SYTL5/TBC1D30/TNPO1/TRIP11/XPO5 | 80 |
| MF | GO:0031267 | small GTPase binding | 74/2263 | 273/18369 | 2.36E-11 | 2.61E-09 | 2.20E-09 | DIAPH3/ECT2/KNTC1/XPO1/XPOT/ABCA1/AKAP13/AP3M1/ATP7A/C9orf72/CCDC186/CDKL5/CHM/CHML/CORO1C/CSE1L/DAAM1/DIAPH2/DMXL2/DNM1L/DOCK11/DOCK2/DOCK5/DOCK7/EPS8/ERC1/EVI5/EXOC2/EXOC4/EXOC5/EXPH5/FER/FGD4/FGD6/FMNL2/GAPVD1/GCC2/GDI2/GOLGA4/GOLGA5/IPO11/IPO5/IPO7/IPO8/IQGAP1/IQGAP2/KIF3A/KPNB1/LRRK2/MYCBP2/MYO5A/NCKAP1/PKN2/RAB11FIP2/RAB3GAP1/RAB3GAP2/RABGAP1/RABGAP1L/RABGEF1/RABGGTB/RANBP2/RAPGEF4/RAPGEF6/RASGRP3/RHOBTB3/ROCK1/ROCK2/SIKE1/SYTL2/SYTL5/TBC1D30/TNPO1/TRIP11/XPO5 | 74 |
| MF | GO:0045296 | cadherin binding | 82/2263 | 333/18369 | 3.76E-10 | 3.77E-08 | 3.18E-08 | ANLN/CCNB2/DIAPH3/OLA1/ANK3/ARHGAP18/ATIC/BZW1/BZW2/CALD1/CAST/CCT8/CD2AP/CDH2/CDH6/CHMP2B/CKAP5/CLINT1/COBLL1/CTNNA1/CTNNAL1/CTNNB1/DDX3X/DHX29/DLG1/DOCK9/EIF2A/EIF3E/EIF4G2/EIF5/EPS15/ERC1/EZR/FER/FMNL2/FNBP1L/GAPVD1/GIGYF2/HDLBP/HSP90AB1/HSPA5/HSPA8/IDH1/IQGAP1/ITGA6/ITGB1/KIF5B/KTN1/LIMA1/LRRC59/MACF1/MAPRE1/MPP7/MYO1B/NCK1/NOP56/PAICS/PHLDB2/PKN2/PKP2/PTPN11/PTPRO/RAB1A/RDX/RSL1D1/SERBP1/SH3GLB1/SLK/SNX2/SNX9/SPTAN1/STAT1/SWAP70/TES/TJP1/TWF1/TXNDC9/USO1/USP8/VCL/YWHAB/ZC3H15 | 82 |
| MF | GO:0140662 | ATP-dependent protein folding chaperone | 21/2263 | 41/18369 | 1.67E-09 | 1.54E-07 | 1.29E-07 | CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CLPX/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSP90B1/HSPA13/HSPA4/HSPA4L/HSPA5/HSPA8/HSPA9/HSPD1/HSPH1/TCP1 | 21 |
| MF | GO:0003724 | RNA helicase activity | 30/2263 | 76/18369 | 1.81E-09 | 1.54E-07 | 1.29E-07 | BRIP1/RAD54B/AQR/DDX1/DDX10/DDX18/DDX20/DDX21/DDX23/DDX24/DDX3X/DDX42/DDX46/DDX47/DDX5/DDX52/DDX60/DDX60L/DHX15/DHX29/DHX32/DHX36/DHX57/DHX8/DHX9/EIF4A3/FANCM/G3BP1/IFIH1/SNRNP200 | 30 |
| MF | GO:0008186 | ATP-dependent activity, acting on RNA | 30/2263 | 78/18369 | 3.75E-09 | 2.96E-07 | 2.49E-07 | BRIP1/RAD54B/AQR/DDX1/DDX10/DDX18/DDX20/DDX21/DDX23/DDX24/DDX3X/DDX42/DDX46/DDX47/DDX5/DDX52/DDX60/DDX60L/DHX15/DHX29/DHX32/DHX36/DHX57/DHX8/DHX9/EIF4A3/FANCM/G3BP1/IFIH1/SNRNP200 | 30 |
| MF | GO:0043021 | ribonucleoprotein complex binding | 47/2263 | 161/18369 | 8.02E-09 | 5.90E-07 | 4.97E-07 | EZH2/GUF1/OLA1/PRMT3/ABCE1/CBX5/CCDC47/CKAP5/DDX3X/DDX5/DHX29/DHX9/DNAJC2/EIF2A/EIF2S1/EIF4A3/ERI1/ETF1/FMR1/GEMIN5/GTPBP4/HNRNPU/HSPA5/IFIH1/IMPACT/LTN1/MDM2/MTIF2/NAA15/NEMF/NMD3/NOLC1/PHF6/PTCD3/RBM39/RICTOR/RNASEL/RPN2/SECISBP2L/SERBP1/SPATA5/SRP54/SRP72/WDR12/XPO5/YTHDF3/ZNF622 | 47 |
| MF | GO:0005096 | GTPase activator activity | 67/2263 | 280/18369 | 4.98E-08 | 3.44E-06 | 2.90E-06 | ARHGAP11A/ARHGAP11B/DEPDC1/ECT2/ACAP2/ARAP2/ARFGAP3/ARHGAP10/ARHGAP12/ARHGAP15/ARHGAP18/ARHGAP21/ARHGAP26/ARHGAP28/ARHGAP29/ARHGAP42/ARHGEF12/BNIP2/CHM/CHML/DNM1L/DOCK2/DOCK5/ELMOD2/EVI5/FAM13A/FAM13B/GAPVD1/GDI2/IQGAP1/IQGAP2/LRRK2/MYO9A/NCKAP1L/NF1/PLCB1/PREX2/RAB3GAP1/RAB3GAP2/RABEP1/RABGAP1/RABGAP1L/RACGAP1/RALGAPA1/RALGAPA2/RANBP2/RAPGEF2/RAPGEF4/RASA1/RASA2/RASAL2/RASGRP3/RGPD1/RGS1/RGS18/RGS2/RGS5/RP2/SEC23A/SEC23B/SIPA1L1/SOS1/SRGAP1/TBC1D15/TBC1D30/TBC1D4/TBC1D8B | 67 |
| MF | GO:0042393 | histone binding | 60/2263 | 241/18369 | 5.50E-08 | 3.57E-06 | 3.01E-06 | DEK/NCAPG2/VRK1/AASS/ANP32E/ATAD2/ATRX/BAZ1B/BRD7/CBX5/CHD1/CHD2/CHD4/CHD6/CHD7/CHD8/CTSL/DNAJC2/DTX3L/FMR1/HAT1/ING2/ING3/IPO7/JAK2/KAT6A/KDM5A/KDM5B/KDM7A/KMT2C/KMT2E/MLLT3/MSH6/MTF2/MYSM1/NAP1L1/NASP/PARP9/PHF14/PHF6/PHIP/PSME4/PWP1/RBBP5/RNF20/RSF1/SBNO1/SMARCA5/SPTY2D1/STAT1/SUZ12/TAF1/TAF7/TBL1XR1/TP53BP1/TSPYL2/USP15/USP16/ZMYND11/ZZZ3 | 60 |
| MF | GO:0015631 | tubulin binding | 82/2263 | 374/18369 | 1.07E-07 | 6.55E-06 | 5.52E-06 | BRCA1/BRCA2/CENPE/CENPF/DLGAP5/KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF4A/NUSAP1/PRC1/SPAG5/VBP1/ALMS1/APC/CACYBP/CAMSAP2/CCDC66/CCDC88A/CCSER2/CCT5/CDK5RAP2/CENPJ/CEP350/CEP57/CEP57L1/CEP70/CKAP5/CLASP2/CLIP1/DDX3X/DNM1L/DST/EML4/EZR/FMN1/FMR1/GAS2L3/HAUS6/HOOK1/HOOK3/HSPH1/IFT74/JMY/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B/KNSTRN/KRIT1/LRPPRC/LRRK2/LYN/MACF1/MAP1B/MAP4K4/MAP7D3/MAP9/MAPRE1/MTUS1/NAV3/NEDD1/NIN/OFD1/OPA1/PDE4B/PHF6/RABGAP1/RACGAP1/RGS2/RMDN2/SMC3/STRBP/TAOK1/TPR/TTLL7/VPS41 | 82 |
| MF | GO:0003678 | DNA helicase activity | 23/2263 | 58/18369 | 1.26E-07 | 7.33E-06 | 6.18E-06 | BLM/BRIP1/MCM3/MCM6/MCM8/POLQ/RAD54B/RFC3/RFC4/ASCC3/CHD1L/CHD8/DDX3X/DHX36/DHX9/DNA2/FANCM/G3BP1/RAD50/RECQL/SETX/WRN/XRCC5 | 23 |
| MF | GO:0005085 | guanyl-nucleotide exchange factor activity | 55/2263 | 227/18369 | 5.00E-07 | 2.76E-05 | 2.32E-05 | ECT2/WDR41/AKAP13/ARFGEF1/ARFGEF2/ARHGEF12/ARHGEF38/C9orf72/CCDC88A/DENND4A/DENND4C/DIS3/DOCK10/DOCK11/DOCK2/DOCK5/DOCK7/DOCK8/DOCK9/EGF/EIF2B3/FGD4/FGD6/FNIP1/GAPVD1/HERC1/ITSN1/ITSN2/MYCBP2/NET1/NUCB2/PLEKHG1/PREX2/PSD3/RAB3GAP1/RAB3GAP2/RAB3IP/RABGEF1/RALGPS2/RAP1GDS1/RAPGEF2/RAPGEF4/RAPGEF5/RAPGEF6/RASGEF1B/RASGRF2/RASGRP3/RCBTB2/RGL1/RPGR/SBF2/SOS1/SOS2/SWAP70/TRIO | 55 |
| MF | GO:0140030 | modification-dependent protein binding | 45/2263 | 175/18369 | 9.36E-07 | 4.92E-05 | 4.15E-05 | NCAPG2/RAD18/AGL/ANK2/ATRX/BRCC3/BRD7/CBX5/CHD1/CHD1L/CHD8/DNAJC2/DZIP3/EPS15/FMR1/IDE/ING2/ING3/KDM5A/KDM7A/KMT2E/L3MBTL3/LYN/MLLT3/MSH6/MTF2/PEX1/PHF20L1/PHIP/PSME4/PWP1/SPRTN/SUZ12/TAB2/TAB3/TAF1/TAF7/TP53BP1/USP15/VCP/ZBTB1/ZMYND11/ZRANB1/ZRANB3/ZZZ3 | 45 |
| MF | GO:0106310 | protein serine kinase activity | 77/2263 | 363/18369 | 1.03E-06 | 5.15E-05 | 4.34E-05 | BUB1/BUB1B/CDK1/CHEK1/MELK/NEK2/NRK/PBK/PLK4/TTK/VRK1/ALPK1/ATM/ATR/CASK/CDC42BPA/CDKL2/CDKL5/CLK4/DCLK1/EIF2AK2/EIF2AK3/EIF2AK4/HIPK3/IRAK4/LRRK2/MAP3K1/MAP3K13/MAP3K2/MAP3K4/MAP3K7/MAP4K4/MAPK10/MAPK6/MASTL/NEK11/OXSR1/PIK3CA/PIK3CB/PIK3CG/PIK3R4/PIKFYVE/PKN2/PRKACB/PRKCI/PRKD1/PRKDC/PRPF4B/RIOK1/RIOK2/RIOK3/RIPK1/RIPK2/ROCK1/ROCK2/RPS6KA3/RPS6KA5/RPS6KA6/RPS6KC1/SGK3/SLK/SRPK1/SRPK2/STK32A/STK33/STK38L/TAF1/TAOK1/TAOK3/TBK1/TLK1/TNIK/TRIO/TRPM7/TTN/VRK2/WNK3 | 77 |
| MF | GO:0008017 | microtubule binding | 61/2263 | 268/18369 | 1.21E-06 | 5.79E-05 | 4.88E-05 | CENPE/CENPF/DLGAP5/KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF4A/NUSAP1/PRC1/SPAG5/ALMS1/APC/CAMSAP2/CCDC66/CCDC88A/CCSER2/CDK5RAP2/CEP350/CEP57/CEP57L1/CKAP5/CLASP2/CLIP1/DNM1L/DST/EML4/EZR/FMN1/FMR1/GAS2L3/HAUS6/HOOK1/HOOK3/JMY/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B/KNSTRN/KRIT1/LRPPRC/LRRK2/MACF1/MAP1B/MAP4K4/MAP7D3/MAP9/MAPRE1/MTUS1/NAV3/NIN/OPA1/RACGAP1/RMDN2/STRBP/VPS41 | 61 |
| MF | GO:0019783 | ubiquitin-like protein peptidase activity | 36/2263 | 130/18369 | 1.75E-06 | 8.03E-05 | 6.77E-05 | ATG4A/BRCC3/COPS4/CYLD/MYSM1/OTUD4/OTUD6B/PSMD14/SENP1/SENP5/SENP6/SENP7/TANK/UCHL3/UCHL5/UFSP2/USP1/USP13/USP14/USP15/USP16/USP24/USP25/USP27X/USP32/USP34/USP37/USP38/USP44/USP47/USP7/USP8/USP9X/USPL1/YOD1/ZRANB1 | 36 |
| MF | GO:0044183 | protein folding chaperone | 23/2263 | 67/18369 | 2.51E-06 | 0.000110847 | 9.34E-05 | ANP32E/CCDC47/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CLPX/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSP90B1/HSPA13/HSPA4/HSPA4L/HSPA5/HSPA8/HSPA9/HSPD1/HSPH1/TCP1 | 23 |
| MF | GO:0008234 | cysteine-type peptidase activity | 45/2263 | 185/18369 | 4.71E-06 | 0.000200194 | 0.000168737 | ATG4A/BRCC3/CAPN3/CAPN7/CASP1/CASP3/CASP4/CASP5/CTSK/CTSL/CTSS/CYLD/MALT1/OTUD4/OTUD6B/PDIA3/SCRN3/SENP1/SENP5/SENP6/SENP7/TANK/UCHL3/UCHL5/UFSP2/USP1/USP13/USP14/USP15/USP16/USP24/USP25/USP27X/USP32/USP34/USP37/USP38/USP44/USP47/USP7/USP8/USP9X/USPL1/YOD1/ZRANB1 | 45 |
| MF | GO:0000217 | DNA secondary structure binding | 15/2263 | 35/18369 | 6.29E-06 | 0.000257306 | 0.000216875 | BLM/MSH2/NEIL3/RAD18/RAD51AP1/XRCC2/ERCC5/FANCM/GEN1/HMGB1/HMGB2/MEF2C/MSH6/POT1/WRN | 15 |
| MF | GO:0003684 | damaged DNA binding | 23/2263 | 71/18369 | 7.66E-06 | 0.000302179 | 0.000254697 | BLM/BRCA1/MSH2/NEIL3/POLQ/RAD18/DCLRE1A/ERCC4/ERCC5/HMGB1/HMGB2/MSH6/NBN/PARP1/POLK/POT1/RBBP8/REV1/SDE2/SMC6/TP53BP1/WRN/XRCC5 | 23 |
| MF | GO:0140098 | catalytic activity, acting on RNA | 79/2263 | 396/18369 | 8.65E-06 | 0.000329133 | 0.000277416 | BRIP1/LACTB2/PRIM2/RAD54B/ALKBH8/AQR/CNOT1/CNOT6L/CPSF3/DDX1/DDX10/DDX18/DDX20/DDX21/DDX23/DDX24/DDX3X/DDX42/DDX46/DDX47/DDX5/DDX52/DDX60/DDX60L/DHX15/DHX29/DHX32/DHX36/DHX57/DHX8/DHX9/DICER1/DIS3/DIS3L/EIF4A3/ERI1/ERI2/EXOSC9/FANCM/FARSB/G3BP1/IARS2/IFIH1/METTL14/METTL15/NSUN2/NSUN6/NUDT12/PNPT1/POLR1B/POLR2B/POLR3B/POLR3C/POP1/PRPF18/PUS10/PUS3/RNASEL/RNMT/RTCB/SAMHD1/SLFN13/SLU7/SNRNP200/TDP2/TFB2M/TGS1/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TRNT1/TSNAX/TYW3/WARS2/XRN1/XRN2/ZC3H12C | 79 |
| MF | GO:0140104 | molecular carrier activity | 26/2263 | 88/18369 | 1.32E-05 | 0.000485503 | 0.000409215 | XPO1/ANP32E/ATP7A/CSE1L/DPH3/EMC2/HBA2/HBB/HBD/HBG2/HSPA8/IPCEF1/IPO11/IPO5/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/NAP1L1/PWP1/RANBP6/SPTY2D1/TNPO1/XPO4/XPO5 | 26 |
| MF | GO:0030515 | snoRNA binding | 14/2263 | 33/18369 | 1.48E-05 | 0.000513607 | 0.000432903 | BMS1/DDX21/DKC1/HEATR1/NOLC1/NOP56/NOP58/NUFIP1/PRKDC/SDE2/TSR1/UTP6/WDR3/XRCC5 | 14 |
| MF | GO:0004674 | protein serine/threonine kinase activity | 82/2263 | 421/18369 | 1.49E-05 | 0.000513607 | 0.000432903 | BUB1/BUB1B/CDK1/CHEK1/MELK/NEK2/PBK/PLK4/TTK/VRK1/ALPK1/ATM/ATR/CASK/CDC42BPA/CDKL2/CDKL5/CHUK/CLK4/CPNE3/DCLK1/EIF2AK2/EIF2AK3/EIF2AK4/HIPK3/IRAK3/IRAK4/LRRK2/LTBP1/MAP3K1/MAP3K13/MAP3K2/MAP3K4/MAP3K7/MAP4K4/MAPK10/MAPK6/MASTL/NEK11/OXSR1/PHKA1/PIK3CA/PIK3CG/PIK3R4/PIKFYVE/PKN2/PRKACB/PRKCI/PRKD1/PRKDC/PRPF4B/RIOK1/RIOK2/RIOK3/RIPK1/RIPK2/ROCK1/ROCK2/RPS6KA3/RPS6KA5/RPS6KA6/RPS6KC1/SGK3/SLK/SRPK1/SRPK2/STK32A/STK33/STK38L/TAF1/TAOK1/TAOK3/TBK1/TGFBR1/TLK1/TNIK/TOP1/TRIO/TRPM7/TTN/VRK2/WNK3 | 82 |
| MF | GO:0140142 | nucleocytoplasmic carrier activity | 13/2263 | 30/18369 | 2.27E-05 | 0.000759073 | 0.000639798 | XPO1/CSE1L/IPO11/IPO5/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/RANBP6/TNPO1/XPO4/XPO5 | 13 |
| MF | GO:0016303 | 1-phosphatidylinositol-3-kinase activity | 7/2263 | 10/18369 | 3.65E-05 | 0.00118424 | 0.000998158 | ATM/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R3 | 7 |
| MF | GO:0000400 | four-way junction DNA binding | 9/2263 | 17/18369 | 6.17E-05 | 0.001891798 | 0.001594536 | BLM/MSH2/XRCC2/FANCM/GEN1/HMGB1/HMGB2/MSH6/WRN | 9 |
| MF | GO:0052742 | phosphatidylinositol kinase activity | 9/2263 | 17/18369 | 6.17E-05 | 0.001891798 | 0.001594536 | ATM/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R3/PIKFYVE/PIP5K1B | 9 |
| MF | GO:0003725 | double-stranded RNA binding | 21/2263 | 70/18369 | 6.80E-05 | 0.002028804 | 0.001710014 | CLTC/DDX1/DDX21/DDX60/DDX60L/DHX15/DHX36/DHX9/DICER1/EIF2AK2/HNRNPU/HSP90AB1/HSPD1/IFIH1/MTDH/RC3H2/STRBP/TFRC/TLR3/TLR8/ZFR | 21 |
| MF | GO:0004197 | cysteine-type endopeptidase activity | 30/2263 | 118/18369 | 7.25E-05 | 0.002076535 | 0.001750245 | CAPN3/CAPN7/CASP1/CASP3/CASP4/CASP5/CTSK/CTSL/CTSS/MALT1/PDIA3/SENP1/SENP5/SENP6/SENP7/USP1/USP13/USP14/USP15/USP16/USP24/USP25/USP27X/USP34/USP37/USP38/USP47/USP7/USP8/USP9X | 30 |
| MF | GO:0003743 | translation initiation factor activity | 17/2263 | 51/18369 | 7.69E-05 | 0.002076535 | 0.001750245 | EIF3M/DHX29/EIF1AX/EIF2A/EIF2B3/EIF2S1/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF4B/EIF4G2/EIF5/EIF5B/MTIF2 | 17 |
| MF | GO:0051018 | protein kinase A binding | 17/2263 | 51/18369 | 7.69E-05 | 0.002076535 | 0.001750245 | GSKIP/ACBD3/AKAP11/AKAP12/AKAP13/AKAP5/AKAP6/AKAP9/ARFGEF1/ARFGEF2/CRYBG3/EZR/LRRK2/PJA2/PRKAR2B/RDX/RYR2 | 17 |
| MF | GO:0005545 | 1-phosphatidylinositol binding | 8/2263 | 14/18369 | 7.90E-05 | 0.002076535 | 0.001750245 | EEA1/EPB41/SCIN/SNX10/SNX9/WDFY3/ZFYVE16/ZFYVE9 | 8 |
| MF | GO:0061578 | K63-linked deubiquitinase activity | 8/2263 | 14/18369 | 7.90E-05 | 0.002076535 | 0.001750245 | BRCC3/CYLD/OTUD4/PSMD14/USP14/USP27X/USP9X/YOD1 | 8 |
| MF | GO:0034237 | protein kinase A regulatory subunit binding | 11/2263 | 25/18369 | 8.23E-05 | 0.002113995 | 0.001781819 | GSKIP/ACBD3/AKAP11/AKAP5/AKAP6/AKAP9/ARFGEF1/ARFGEF2/EZR/PJA2/RYR2 | 11 |
| MF | GO:0140666 | annealing activity | 7/2263 | 11/18369 | 8.96E-05 | 0.002247519 | 0.001894362 | BLM/DDX3X/FMR1/FXR1/RECQL/SMARCA1/ZRANB3 | 7 |
| MF | GO:0035091 | phosphatidylinositol binding | 56/2263 | 275/18369 | 9.47E-05 | 0.002323154 | 0.001958113 | AIDA/ARAP2/BTK/CCDC88A/DAPP1/EEA1/EPB41/EXOC1/FCHO2/FERMT2/ING2/IQGAP1/IQGAP2/ITPR1/ITPR2/KIF16B/KRIT1/MTM1/MYO1B/MYO1E/NLRP3/OGT/OSBP/OSBPL8/PIK3C2A/PITPNB/PLA2G4A/PLCB1/PLD1/PLEKHA5/RACGAP1/RPS6KC1/SBF2/SCIN/SDCBP/SESTD1/SGK3/SH3PXD2B/SNX10/SNX13/SNX16/SNX2/SNX25/SNX30/SNX6/SNX9/STAM2/SVIL/SYTL2/TOM1L1/TWF1/VEPH1/VPS13B/WDFY3/ZFYVE16/ZFYVE9 | 56 |
| MF | GO:0004715 | non-membrane spanning protein tyrosine kinase activity | 15/2263 | 43/18369 | 0.000112142 | 0.002691419 | 0.002268511 | MELK/ABL2/BAZ1B/BMX/BTK/EIF2AK2/FER/FRK/ITK/JAK1/JAK2/LYN/RIPK2/TEC/YES1 | 15 |
| MF | GO:0061608 | nuclear import signal receptor activity | 9/2263 | 19/18369 | 0.000185987 | 0.004326927 | 0.003647028 | IPO11/IPO5/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/RANBP6/TNPO1 | 9 |
| MF | GO:0140034 | methylation-dependent protein binding | 22/2263 | 80/18369 | 0.000191377 | 0.004326927 | 0.003647028 | NCAPG2/ATRX/CBX5/CHD1/CHD8/FMR1/ING2/ING3/KDM5A/KDM7A/KMT2E/L3MBTL3/MSH6/MTF2/PHF20L1/PWP1/SUZ12/TAF1/TAF7/TP53BP1/ZMYND11/ZZZ3 | 22 |
| MF | GO:0035004 | phosphatidylinositol 3-kinase activity | 7/2263 | 12/18369 | 0.000192047 | 0.004326927 | 0.003647028 | ATM/PIK3C2A/PIK3C3/PIK3CA/PIK3CB/PIK3CG/PIK3R3 | 7 |
| MF | GO:0003953 | NAD+ nucleosidase activity | 8/2263 | 16/18369 | 0.000269351 | 0.005678514 | 0.004786238 | CD38/IL18RAP/IL1R1/IL1RAP/TLR1/TLR2/TLR4/TLR6 | 8 |
| MF | GO:0050135 | NAD(P)+ nucleosidase activity | 8/2263 | 16/18369 | 0.000269351 | 0.005678514 | 0.004786238 | CD38/IL18RAP/IL1R1/IL1RAP/TLR1/TLR2/TLR4/TLR6 | 8 |
| MF | GO:0061809 | NAD+ nucleotidase, cyclic ADP-ribose generating | 8/2263 | 16/18369 | 0.000269351 | 0.005678514 | 0.004786238 | CD38/IL18RAP/IL1R1/IL1RAP/TLR1/TLR2/TLR4/TLR6 | 8 |
| MF | GO:0101005 | deubiquitinase activity | 28/2263 | 115/18369 | 0.00027261 | 0.005678514 | 0.004786238 | BRCC3/CYLD/MYSM1/OTUD4/OTUD6B/PSMD14/TANK/UCHL3/UCHL5/USP1/USP13/USP14/USP15/USP16/USP24/USP25/USP27X/USP32/USP34/USP37/USP38/USP44/USP47/USP7/USP8/USP9X/YOD1/ZRANB1 | 28 |
| MF | GO:0000287 | magnesium ion binding | 46/2263 | 223/18369 | 0.000282096 | 0.005767302 | 0.004861075 | ME1/MSH2/TOP2A/AASDHPPT/ABL2/ATP10D/ATP11B/ATP11C/ATP8A1/ATP8B1/ATP8B4/CDC42BPA/DHX36/FARSB/FIGNL1/GCLC/GEM/GEN1/IDH1/IMPA1/IRAK3/IRAK4/LRRK2/MAP3K7/MSH6/MTHFD2/NLRC4/NUDT12/OPA1/OXSR1/PAPOLA/PGM2/PGM3/PPM1B/PRKACB/RP2/RPS6KA3/RPS6KA5/RPS6KA6/SRPK1/SRPK2/STK38L/SUCLA2/SUCLG2/TDP2/WRN | 46 |
| MF | GO:0003779 | actin binding | 77/2263 | 434/18369 | 0.000582524 | 0.011692836 | 0.009855518 | ANLN/DIAPH3/KIF18A/ABL2/ACTR2/ACTR3/ADD3/BLOC1S6/CALD1/CAPZA2/CCDC88A/COBLL1/CORO1C/CTNNA1/CTNNAL1/DAAM1/DIAPH2/DMD/DST/EPB41/EPB41L2/EPB41L3/EPS8/EZR/FER/FERMT2/FGD4/FMN1/FMNL2/GAS2L3/GBP1/HNRNPU/HOOK1/IMPACT/IQGAP1/IQGAP2/ITGB1/JMY/KCNMA1/KLHL2/KLHL4/LCP1/LIMA1/LRRK2/MACF1/MAP1B/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/MYO9A/NEB/NEXN/PANX1/PLS1/PLS3/POF1B/PPP1R9A/PSTPIP2/RAI14/RDX/SCIN/SPIRE1/SPTAN1/STK38L/SVIL/SYNE1/SYNE2/TMOD2/TPM1/TRPM7/TTN/TWF1/UACA/UTRN/VCL | 77 |
| MF | GO:0004843 | cysteine-type deubiquitinase activity | 26/2263 | 109/18369 | 0.000620299 | 0.012228754 | 0.010307226 | BRCC3/CYLD/OTUD4/OTUD6B/TANK/UCHL3/UCHL5/USP1/USP13/USP14/USP15/USP16/USP24/USP25/USP27X/USP32/USP34/USP37/USP38/USP44/USP47/USP7/USP8/USP9X/YOD1/ZRANB1 | 26 |
| MF | GO:0008139 | nuclear localization sequence binding | 10/2263 | 26/18369 | 0.000643851 | 0.012255556 | 0.010329817 | IPO5/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/NOLC1/NUP153/RANBP6/TNPO1 | 10 |
| MF | GO:0043015 | gamma-tubulin binding | 12/2263 | 35/18369 | 0.000643861 | 0.012255556 | 0.010329817 | BRCA2/CDK5RAP2/CENPJ/CEP57/CEP57L1/CEP70/DDX3X/LYN/NEDD1/OFD1/PDE4B/RACGAP1 | 12 |
| MF | GO:0043138 | 3'-5' DNA helicase activity | 7/2263 | 14/18369 | 0.000664607 | 0.012436042 | 0.010481942 | BLM/MCM6/ASCC3/DHX9/FANCM/RECQL/WRN | 7 |
| MF | GO:0051082 | unfolded protein binding | 28/2263 | 122/18369 | 0.000755089 | 0.013893634 | 0.0117105 | VBP1/CANX/CCT2/CCT3/CCT4/CCT5/CCT6A/CCT8/CLPX/DNAJA1/GRPEL1/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/HSP90B1/HSPA13/HSPA5/HSPA8/HSPA9/HSPD1/LMAN1/MKKS/RP2/SRSF10/TCP1/UGGT1/UGGT2 | 28 |
| MF | GO:0032404 | mismatch repair complex binding | 6/2263 | 11/18369 | 0.000923059 | 0.016705847 | 0.014080825 | MCM8/MSH2/ATR/MLH1/MSH6/WRN | 6 |
| MF | GO:0035064 | methylated histone binding | 20/2263 | 78/18369 | 0.000976364 | 0.017385582 | 0.014653752 | NCAPG2/ATRX/CBX5/CHD1/CHD8/FMR1/ING2/ING3/KDM5A/KDM7A/KMT2E/MSH6/MTF2/PWP1/SUZ12/TAF1/TAF7/TP53BP1/ZMYND11/ZZZ3 | 20 |
| MF | GO:0008135 | translation factor activity, RNA binding | 21/2263 | 84/18369 | 0.001051603 | 0.018096221 | 0.015252726 | EIF3M/DHX29/EIF1AX/EIF2A/EIF2B3/EIF2S1/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF4B/EIF4G2/EIF5/EIF5B/ETF1/GFM1/GSPT1/HBS1L/MTIF2 | 21 |
| MF | GO:0003777 | microtubule motor activity | 19/2263 | 73/18369 | 0.001065448 | 0.018096221 | 0.015252726 | CENPE/KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF4A/DNAH14/DNAH5/DYNC1H1/DYNC2H1/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B/SMC3 | 19 |
| MF | GO:0043022 | ribosome binding | 19/2263 | 73/18369 | 0.001065448 | 0.018096221 | 0.015252726 | GUF1/OLA1/PRMT3/CCDC47/DNAJC2/EIF2A/EIF2S1/ERI1/ETF1/FMR1/GEMIN5/HSPA5/IMPACT/NAA15/RICTOR/RPN2/SERBP1/SRP72/YTHDF3 | 19 |
| MF | GO:0005178 | integrin binding | 32/2263 | 151/18369 | 0.001402119 | 0.023453623 | 0.019768309 | ADAM10/ADAM17/ADAM23/ADAM9/ADAMTS5/CD226/COL3A1/CXADR/DST/ECM2/EGFL6/FAP/FBN1/FERMT2/GPNMB/HMGB1/IGF1/ITGA2/ITGA4/ITGA6/ITGAV/ITGB1/ITGB3/ITGB6/ITGB8/LCP1/LGALS8/LYN/PTPN2/SPP1/UTRN/VCAM1 | 32 |
| MF | GO:0086080 | protein binding involved in heterotypic cell-cell adhesion | 6/2263 | 12/18369 | 0.001654071 | 0.027255134 | 0.022972482 | CXADR/DSC2/DSG2/DSP/NRCAM/PKP2 | 6 |
| MF | GO:0016853 | isomerase activity | 32/2263 | 154/18369 | 0.001960421 | 0.031544147 | 0.026587553 | TOP2A/BPGM/CFTR/DHRS9/DKC1/DSE/DSEL/FKBP14/FKBP5/GLCE/GNPDA2/HSD17B4/HSPD1/IDI1/ITGB3/NKTR/PDIA3/PDIA6/PGM2/PGM2L1/PGM3/PPIG/PPIL4/PPWD1/PUS10/PUS3/PUS7/PUS7L/RPE/TMX3/TOP1/TOP2B | 32 |
| MF | GO:0003727 | single-stranded RNA binding | 21/2263 | 88/18369 | 0.001971509 | 0.031544147 | 0.026587553 | LACTB2/AQR/DDX1/DDX3X/DDX60/DDX60L/DHX9/EIF4A3/FMR1/FXR1/HNRNPA1/HNRNPU/IFIH1/IFIT5/LARP4/PNPT1/SSB/STRBP/SYNCRIP/TLR8/ZFR | 21 |
| MF | GO:0004713 | protein tyrosine kinase activity | 29/2263 | 137/18369 | 0.002327199 | 0.035609159 | 0.030013822 | MELK/PBK/TTK/ABL2/BAZ1B/BMX/BTK/CLK4/EIF2AK2/EPHA3/EPHA4/ERBB4/FER/FLT1/FRK/HIPK3/ITK/JAK1/JAK2/LYN/MERTK/MET/PDGFRA/RIPK2/ROS1/RPS6KA5/TEC/TTN/YES1 | 29 |
| MF | GO:0005516 | calmodulin binding | 39/2263 | 200/18369 | 0.002335203 | 0.035609159 | 0.030013822 | ASPM/ADD3/AKAP12/AKAP5/ATP2B1/CALD1/CAMSAP2/CASK/CDK5RAP2/CEP97/EEA1/EPB41/FAS/GEM/INVS/IQCB1/IQCG/IQGAP1/IQGAP2/KCNQ3/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/PDE1A/PHKA1/PHKB/PLCB1/RASGRF2/RGS1/RGS2/RIT1/RYR2/SPTAN1/STRN/TJP1/TTN/UBR4 | 39 |
| MF | GO:0001098 | basal transcription machinery binding | 16/2263 | 61/18369 | 0.002354591 | 0.035609159 | 0.030013822 | CTR9/DHX9/ERCC4/ERCC5/HNRNPU/LEO1/LLPH/NCOA3/NOLC1/NOP58/PCF11/TAF1/TAF7/WDR43/ZNF326/ZNHIT6 | 16 |
| MF | GO:0001099 | basal RNA polymerase II transcription machinery binding | 16/2263 | 61/18369 | 0.002354591 | 0.035609159 | 0.030013822 | CTR9/DHX9/ERCC4/ERCC5/HNRNPU/LEO1/LLPH/NCOA3/NOLC1/NOP58/PCF11/TAF1/TAF7/WDR43/ZNF326/ZNHIT6 | 16 |
| MF | GO:0051010 | microtubule plus-end binding | 8/2263 | 21/18369 | 0.002413179 | 0.036002023 | 0.030344955 | KIF18A/APC/CKAP5/CLASP2/CLIP1/DST/KNSTRN/MAPRE1 | 8 |
| MF | GO:0016922 | nuclear receptor binding | 29/2263 | 138/18369 | 0.002607013 | 0.037894658 | 0.031940196 | CNOT1/CTNNB1/DDX5/GTF2H1/HIF1A/JMJD1C/KDM3A/KDM4C/LRIF1/MED13/NCOA1/NCOA2/NCOA3/NCOA7/NCOR1/NRIP1/PARP1/PPARG/RNF14/RNF6/SLC30A9/SNW1/STAT1/STRN/TACC1/TAF1/TAF7/TMF1/TRIP12 | 29 |
| MF | GO:0030674 | protein-macromolecule adaptor activity | 63/2263 | 361/18369 | 0.002619818 | 0.037894658 | 0.031940196 | DTL/NDC80/UBXN8/AKAP13/AKAP6/ANK2/ANK3/AP4E1/ARRDC4/ATP1B1/BANK1/CBX5/CCNT1/CHD1L/CNTLN/COL14A1/CUL1/CUL2/DDX20/DTX3L/EPB41L3/FEM1C/FLRT2/FLRT3/FMR1/FRS2/G3BP2/GAS2L3/HNRNPA1/HNRNPA2B1/HSPA8/ICE1/IQGAP1/KRAS/LPL/LRRK2/MPP7/NAPG/NCK1/NLRP3/NMD3/NOLC1/NUFIP1/NUP153/PHF14/PIK3R1/POLD3/PPP4R2/PSMC6/PTPN11/RAD50/RAPGEF4/SDCBP/SLC4A1/SNAP25/SORBS2/SPAG9/STAP1/STX17/SYNE1/SYNE2/TRIM22/TRIM6 | 63 |
| MF | GO:0070628 | proteasome binding | 7/2263 | 17/18369 | 0.002692963 | 0.037894658 | 0.031940196 | PSMD14/PSME4/SACS/UCHL5/USP13/USP14/ZFAND1 | 7 |
| MF | GO:0032182 | ubiquitin-like protein binding | 25/2263 | 114/18369 | 0.002738254 | 0.037894658 | 0.031940196 | TOP2A/UBXN8/BIRC2/CASP8AP2/DCUN1D3/MDM2/N4BP2/NEDD4/PLAA/SERBP1/SMARCAD1/SPRTN/STAM2/TAB2/TAB3/TOM1L1/UBR5/UBXN2B/UCHL3/UEVLD/USP13/USP16/USP25/USPL1/WDR48 | 25 |
| MF | GO:0004438 | phosphatidylinositol-3-phosphate phosphatase activity | 6/2263 | 13/18369 | 0.002753157 | 0.037894658 | 0.031940196 | FIG4/MTM1/MTMR2/MTMR4/MTMR6/SACM1L | 6 |
| MF | GO:0051015 | actin filament binding | 39/2263 | 202/18369 | 0.002804789 | 0.037894658 | 0.031940196 | ABL2/ACTR2/ACTR3/ADD3/BLOC1S6/CAPZA2/CORO1C/CTNNA1/CTNNAL1/EZR/FERMT2/FMNL2/GAS2L3/IQGAP1/IQGAP2/LCP1/LIMA1/MACF1/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/MYO9A/NEB/NEXN/PANX1/PLS1/PLS3/POF1B/PPP1R9A/PSTPIP2/SCIN/SPTAN1/SVIL/SYNE1/TPM1/TTN/TWF1 | 39 |
| MF | GO:0016866 | intramolecular transferase activity | 9/2263 | 26/18369 | 0.002814639 | 0.037894658 | 0.031940196 | BPGM/DKC1/PGM2/PGM2L1/PGM3/PUS10/PUS3/PUS7/PUS7L | 9 |
| MF | GO:0048027 | mRNA 5'-UTR binding | 9/2263 | 26/18369 | 0.002814639 | 0.037894658 | 0.031940196 | CCT5/DDX3X/DHX36/FMR1/GNL3/NCL/RSL1D1/SYNCRIP/UTP23 | 9 |
| MF | GO:0004520 | DNA endonuclease activity | 11/2263 | 36/18369 | 0.003067236 | 0.039916539 | 0.033644375 | DICER1/DNA2/ERCC4/ERCC5/GEN1/MBD4/N4BP2/RAD50/RBBP8/SETMAR/ZRANB3 | 11 |
| MF | GO:0097718 | disordered domain specific binding | 11/2263 | 36/18369 | 0.003067236 | 0.039916539 | 0.033644375 | CLTC/CTNNB1/EZR/HSP90AA1/HSP90AA4P/HSP90AB1/HSP90AB3P/MDM2/NCOA3/RB1/RRM1 | 11 |
| MF | GO:0070063 | RNA polymerase binding | 15/2263 | 57/18369 | 0.003073284 | 0.039916539 | 0.033644375 | BRCA1/CCNT1/CCNT2/CTR9/DHX9/ERCC5/HNRNPU/LEO1/NCOA3/NEDD4/PCF11/PKN2/SPTY2D1/WDR43/ZNF326 | 15 |
| MF | GO:0008237 | metallopeptidase activity | 38/2263 | 197/18369 | 0.003201544 | 0.041098896 | 0.034640946 | ACE2/ADAM10/ADAM12/ADAM17/ADAM23/ADAM28/ADAM9/ADAMDEC1/ADAMTS3/ADAMTS5/ADAMTS6/ADAMTS9/BRCC3/CNDP2/CPD/CPM/CPXM1/ENPEP/ERAP2/IDE/LAP3/LTA4H/METAP1/METAP2/MMP1/MMP16/MMP8/MYSM1/NLN/PAPPA/PHEX/PMPCB/PSMD14/RAPGEF2/SDCBP/SPRTN/UQCRC2/YME1L1 | 38 |
| MF | GO:0004709 | MAP kinase kinase kinase activity | 8/2263 | 22/18369 | 0.003387176 | 0.042982095 | 0.036228234 | LRRK2/MAP3K1/MAP3K13/MAP3K2/MAP3K4/MAP3K7/RIPK1/RIPK2 | 8 |
| MF | GO:0044389 | ubiquitin-like protein ligase binding | 56/2263 | 320/18369 | 0.004110134 | 0.049481716 | 0.041706557 | BRCA1/RAD18/ABCB1/APC/ARIH1/ATF6/BECN1/BLZF1/CACYBP/CCT2/CUL1/CUL2/CUL3/DBT/DNAJA1/DNM1L/DTX3L/ERLIN1/HIF1A/HLTF/HSP90AA1/HSP90AB1/HSPA5/HSPA8/HSPA9/HSPD1/JAK1/LRPPRC/LYN/MDM2/NAE1/PARP9/PRKACB/PRKAR2B/PSMA3/PSMD1/RB1/RHOBTB3/RIPK1/RNF20/SHPRH/SMC6/SNX9/SPOPL/STAT1/TANK/TCP1/TRAF5/USP13/USP25/USP7/VCL/VCP/XRCC5/YOD1/ZNF675 | 56 |
| MF | GO:0032356 | oxidized DNA binding | 5/2263 | 10/18369 | 0.004164846 | 0.049481716 | 0.041706557 | BLM/MSH2/MSH6/POT1/WRN | 5 |
| MF | GO:0051880 | G-quadruplex DNA binding | 5/2263 | 10/18369 | 0.004164846 | 0.049481716 | 0.041706557 | BLM/DHX36/RAD50/WRN/XRN1 | 5 |
| MF | GO:0052813 | phosphatidylinositol bisphosphate kinase activity | 5/2263 | 10/18369 | 0.004164846 | 0.049481716 | 0.041706557 | PIK3C2A/PIK3CA/PIK3CB/PIK3CG/PIP5K1B | 5 |
| MF | GO:0005161 | platelet-derived growth factor receptor binding | 6/2263 | 14/18369 | 0.00431957 | 0.049481716 | 0.041706557 | IL1R1/ITGB3/LYN/PDGFC/PDGFD/PDGFRA | 6 |
| MF | GO:0016307 | phosphatidylinositol phosphate kinase activity | 6/2263 | 14/18369 | 0.00431957 | 0.049481716 | 0.041706557 | PIK3C2A/PIK3CA/PIK3CB/PIK3CG/PIKFYVE/PIP5K1B | 6 |
| MF | GO:0042043 | neurexin family protein binding | 6/2263 | 14/18369 | 0.00431957 | 0.049481716 | 0.041706557 | CASK/LRRTM2/NLGN1/SDCBP/SYTL2/SYTL5 | 6 |
| MF | GO:0052744 | phosphatidylinositol monophosphate phosphatase activity | 6/2263 | 14/18369 | 0.00431957 | 0.049481716 | 0.041706557 | FIG4/MTM1/MTMR2/MTMR4/MTMR6/SACM1L | 6 |
| MF | GO:0106018 | phosphatidylinositol-3,5-bisphosphate phosphatase activity | 6/2263 | 14/18369 | 0.00431957 | 0.049481716 | 0.041706557 | FIG4/MTM1/MTMR2/MTMR4/MTMR6/PIKFYVE | 6 |
| MF | GO:0004518 | nuclease activity | 39/2263 | 207/18369 | 0.004347578 | 0.049481716 | 0.041706557 | LACTB2/MGME1/CNOT1/CNOT6L/CPSF3/DCLRE1A/DDX1/DICER1/DIS3/DIS3L/DNA2/ENDOD1/ENPP1/ERCC4/ERCC5/ERI1/ERI2/EXOSC9/FANCM/G3BP1/GEN1/MBD4/N4BP2/NUDT12/PNPT1/POP1/RAD50/RBBP8/RNASEL/SAMHD1/SETMAR/SLFN13/TDP2/TSNAX/WRN/XRN1/XRN2/ZC3H12C/ZRANB3 | 39 |
| MF | GO:0031625 | ubiquitin protein ligase binding | 53/2263 | 301/18369 | 0.00452243 | 0.050222546 | 0.042330979 | BRCA1/RAD18/ABCB1/APC/ARIH1/ATF6/BECN1/BLZF1/CACYBP/CCT2/CUL1/CUL2/CUL3/DBT/DNAJA1/DNM1L/ERLIN1/HIF1A/HLTF/HSP90AA1/HSP90AB1/HSPA5/HSPA8/HSPA9/HSPD1/JAK1/LRPPRC/LYN/MDM2/NAE1/PRKACB/PRKAR2B/PSMA3/PSMD1/RB1/RHOBTB3/RIPK1/RNF20/SHPRH/SMC6/SNX9/SPOPL/TANK/TCP1/TRAF5/USP13/USP25/USP7/VCL/VCP/XRCC5/YOD1/ZNF675 | 53 |
| MF | GO:0043130 | ubiquitin binding | 21/2263 | 94/18369 | 0.004571495 | 0.050222546 | 0.042330979 | TOP2A/UBXN8/BIRC2/MDM2/N4BP2/NEDD4/PLAA/SMARCAD1/SPRTN/STAM2/TAB2/TAB3/TOM1L1/UBR5/UBXN2B/UCHL3/UEVLD/USP13/USP16/USP25/WDR48 | 21 |
| MF | GO:0003950 | NAD+ ADP-ribosyltransferase activity | 8/2263 | 23/18369 | 0.004640127 | 0.050222546 | 0.042330979 | PARP1/PARP14/PARP15/PARP4/PARP8/PARP9/TIPARP/TNKS2 | 8 |
| MF | GO:0017116 | single-stranded DNA helicase activity | 8/2263 | 23/18369 | 0.004640127 | 0.050222546 | 0.042330979 | MCM3/MCM6/MCM8/POLQ/RFC3/RFC4/DHX9/DNA2 | 8 |
| MF | GO:1990404 | NAD+-protein ADP-ribosyltransferase activity | 8/2263 | 23/18369 | 0.004640127 | 0.050222546 | 0.042330979 | PARP1/PARP14/PARP15/PARP4/PARP8/PARP9/TIPARP/TNKS2 | 8 |
| MF | GO:0016799 | hydrolase activity, hydrolyzing N-glycosyl compounds | 11/2263 | 38/18369 | 0.004872077 | 0.052221092 | 0.04401549 | NEIL3/CD38/IL18RAP/IL1R1/IL1RAP/MACROD2/MBD4/TLR1/TLR2/TLR4/TLR6 | 11 |
| MF | GO:0001618 | virus receptor activity | 18/2263 | 77/18369 | 0.00504488 | 0.053553339 | 0.045138398 | CDK1/ACE2/CD86/CLDN1/CR1/CXADR/DPP4/GYPA/HTR2A/IDE/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/MRC1/NPC1/TFRC | 18 |
| MF | GO:0140272 | exogenous protein binding | 18/2263 | 78/18369 | 0.005820164 | 0.061194863 | 0.051579194 | CDK1/ACE2/CD86/CLDN1/CR1/CXADR/DPP4/GYPA/HTR2A/IDE/ITGA2/ITGAV/ITGB1/ITGB3/ITGB6/MRC1/NPC1/TFRC | 18 |
| MF | GO:0016896 | RNA exonuclease activity, producing 5'-phosphomonoesters | 11/2263 | 39/18369 | 0.006044889 | 0.062958094 | 0.053065365 | CNOT1/CNOT6L/CPSF3/DIS3/DIS3L/ERI1/ERI2/EXOSC9/PNPT1/XRN1/XRN2 | 11 |
| MF | GO:0016504 | peptidase activator activity | 13/2263 | 50/18369 | 0.006318254 | 0.063643556 | 0.053643119 | CASP1/CASP8AP2/CLPX/CTSK/CTSL/CTSS/NLRC4/PCOLCE2/PSMD14/PSME4/TANK/VCP/WDR48 | 13 |
| MF | GO:0003774 | cytoskeletal motor activity | 24/2263 | 115/18369 | 0.006352523 | 0.063643556 | 0.053643119 | CENPE/KIF11/KIF14/KIF15/KIF18A/KIF20A/KIF20B/KIF23/KIF4A/DNAH14/DNAH5/DYNC1H1/DYNC2H1/KIF16B/KIF21A/KIF2A/KIF3A/KIF5B/MYO1B/MYO1E/MYO5A/MYO5C/MYO6/SMC3 | 24 |
| MF | GO:0002039 | p53 binding | 16/2263 | 67/18369 | 0.006395443 | 0.063643556 | 0.053643119 | BLM/BRCA1/BRD7/CDKN2AIP/CHD8/HIF1A/HSPD1/MDM2/RFWD3/RNF20/SETD7/TAF1/TP53BP1/TP53BP2/USP7/ZNF385B | 16 |
| MF | GO:0005041 | low-density lipoprotein particle receptor activity | 6/2263 | 15/18369 | 0.006456593 | 0.063643556 | 0.053643119 | CD36/LRP12/LRP2/LRP6/LRP8/VLDLR | 6 |
| MF | GO:0140036 | ubiquitin-dependent protein binding | 6/2263 | 15/18369 | 0.006456593 | 0.063643556 | 0.053643119 | DNAJC2/IDE/PEX1/TP53BP1/USP15/VCP | 6 |
| MF | GO:1990380 | K48-linked deubiquitinase activity | 6/2263 | 15/18369 | 0.006456593 | 0.063643556 | 0.053643119 | USP13/USP15/USP27X/USP7/USP9X/YOD1 | 6 |
| MF | GO:0002162 | dystroglycan binding | 5/2263 | 11/18369 | 0.006866335 | 0.066725893 | 0.056241123 | AGR2/AGR3/CLASP2/DMD/VCL | 5 |
| MF | GO:0005543 | phospholipid binding | 77/2263 | 475/18369 | 0.006890174 | 0.066725893 | 0.056241123 | ABCA1/AIDA/ARAP2/ARHGAP26/ATP8B1/BIN2/BTK/C2CD5/CCDC88A/CLINT1/CPNE3/DAPP1/EEA1/EPB41/EXOC1/FCHO2/FERMT2/HMGB1/HSPA8/ING2/IQGAP1/IQGAP2/ITPR1/ITPR2/KIF16B/KRIT1/MAP1B/MTM1/MYO1B/MYO1E/MYOF/NF1/NLRP3/OGT/OPA1/OSBP/OSBPL8/PIK3C2A/PITPNB/PLA2G4A/PLCB1/PLD1/PLEKHA5/PPT1/PRKCI/RACGAP1/RAPGEF2/RAPGEF6/RASA2/RPS6KC1/SBF2/SCIN/SDCBP/SESTD1/SGK3/SH3PXD2B/SNX10/SNX13/SNX16/SNX2/SNX25/SNX30/SNX6/SNX9/STAM2/STAP1/SVIL/SYTL2/SYTL5/TEC/TOM1L1/TWF1/VEPH1/VPS13B/WDFY3/ZFYVE16/ZFYVE9 | 77 |
| MF | GO:0005547 | phosphatidylinositol-3,4,5-trisphosphate binding | 11/2263 | 40/18369 | 0.007428344 | 0.071312102 | 0.060106691 | ARAP2/BTK/DAPP1/FERMT2/IQGAP1/IQGAP2/KIF16B/MYO1B/OGT/RACGAP1/ZFYVE16 | 11 |
| MF | GO:0016408 | C-acyltransferase activity | 7/2263 | 20/18369 | 0.007694176 | 0.073227332 | 0.061720978 | ACAT1/ACAT2/ACSM3/HADHA/SCP2/SPTLC1/SPTLC3 | 7 |
| MF | GO:0061733 | peptide-lysine-N-acetyltransferase activity | 12/2263 | 46/18369 | 0.008298626 | 0.078304982 | 0.066000767 | BRCA2/ESCO2/CLOCK/ESCO1/HAT1/ING3/JADE1/KAT6A/NAA50/NCOA1/NCOA3/TAF1 | 12 |
| MF | GO:0042626 | ATPase-coupled transmembrane transporter activity | 21/2263 | 99/18369 | 0.008489665 | 0.079428735 | 0.066947942 | ABCA1/ABCA5/ABCA8/ABCB1/ABCB7/ABCC4/ABCC9/ABCD3/ATP13A3/ATP13A4/ATP1B1/ATP2A2/ATP2B1/ATP2C1/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/ATP7A/ATP8A1/CFTR | 21 |
| MF | GO:0000049 | tRNA binding | 17/2263 | 75/18369 | 0.008710384 | 0.080808937 | 0.06811127 | XPOT/ALKBH8/EIF2A/EIF2AK4/IARS2/IFIT5/NEMF/NSUN2/NSUN6/SLFN11/SLFN13/SSB/THUMPD3/TRMT10C/TRMT1L/TRNT1/XPO5 | 17 |
| MF | GO:0004532 | exoribonuclease activity | 11/2263 | 41/18369 | 0.009046312 | 0.081854454 | 0.068992503 | CNOT1/CNOT6L/CPSF3/DIS3/DIS3L/ERI1/ERI2/EXOSC9/PNPT1/XRN1/XRN2 | 11 |
| MF | GO:0016877 | ligase activity, forming carbon-sulfur bonds | 11/2263 | 41/18369 | 0.009046312 | 0.081854454 | 0.068992503 | ACSL1/ACSL3/ACSL4/ACSM3/ACSS3/NAE1/SLC27A2/SUCLA2/SUCLG2/UBA5/UBA6 | 11 |
| MF | GO:0003688 | DNA replication origin binding | 6/2263 | 16/18369 | 0.009267941 | 0.081854454 | 0.068992503 | CDC6/DHX9/HSPD1/ORC3/ORC4/POLA1 | 6 |
| MF | GO:0005092 | GDP-dissociation inhibitor activity | 6/2263 | 16/18369 | 0.009267941 | 0.081854454 | 0.068992503 | CCDC88A/CHM/CHML/EIF5/GDI2/GPSM2 | 6 |
| MF | GO:0140327 | flippase activity | 6/2263 | 16/18369 | 0.009267941 | 0.081854454 | 0.068992503 | ABCB1/ATP10D/ATP11B/ATP11C/ATP8A1/ATP8B1 | 6 |
| MF | GO:0140328 | floppase activity | 6/2263 | 16/18369 | 0.009267941 | 0.081854454 | 0.068992503 | ABCA1/ABCB1/ATP11B/ATP11C/ATP8A1/ATP8B1 | 6 |
| MF | GO:0043394 | proteoglycan binding | 10/2263 | 36/18369 | 0.009736663 | 0.085311711 | 0.071906514 | CFH/CTSK/CTSL/CTSS/GPNMB/ITGA2/LPL/PTPRC/SDCBP/TNC | 10 |
| MF | GO:0001968 | fibronectin binding | 9/2263 | 31/18369 | 0.010286162 | 0.088565738 | 0.07464923 | CCDC80/CTSK/CTSL/CTSS/ITGA4/ITGAV/ITGB1/ITGB3/TNFAIP6 | 9 |
| MF | GO:0140664 | ATP-dependent DNA damage sensor activity | 7/2263 | 21/18369 | 0.010334675 | 0.088565738 | 0.07464923 | MSH2/XRCC2/MLH1/MLH3/MSH3/MSH6/RAD50 | 7 |
| MF | GO:0019829 | ATPase-coupled monoatomic cation transmembrane transporter activity | 13/2263 | 53/18369 | 0.010554206 | 0.088565738 | 0.07464923 | ABCC9/ATP13A3/ATP13A4/ATP1B1/ATP2A2/ATP2B1/ATP2C1/ATP6V1A/ATP6V1B2/ATP6V1C1/ATP6V1D/ATP7A/ATP8A1 | 13 |
| MF | GO:0140296 | general transcription initiation factor binding | 13/2263 | 53/18369 | 0.010554206 | 0.088565738 | 0.07464923 | BDP1/BTAF1/CAND1/ERCC4/HNRNPU/NOLC1/NOP58/PSMC1/TAF1/TAF1B/TAF7/ZBTB43/ZNHIT6 | 13 |
| MF | GO:0030507 | spectrin binding | 8/2263 | 26/18369 | 0.010558722 | 0.088565738 | 0.07464923 | ANK2/ANK3/CAMSAP2/EPB41/EPB41L2/GBP1/KIF3A/PTPRC | 8 |
| MF | GO:0009982 | pseudouridine synthase activity | 5/2263 | 12/18369 | 0.010589382 | 0.088565738 | 0.07464923 | DKC1/PUS10/PUS3/PUS7/PUS7L | 5 |
| MF | GO:0005048 | signal sequence binding | 12/2263 | 48/18369 | 0.011783938 | 0.097815547 | 0.082445599 | IPO5/KDELR3/KPNA1/KPNA2/KPNA3/KPNA4/KPNB1/NOLC1/NUP153/RANBP6/SRP54/TNPO1 | 12 |
| MF | GO:0042162 | telomeric DNA binding | 10/2263 | 37/18369 | 0.011903255 | 0.098068608 | 0.082658896 | BLM/HNRNPA1/HNRNPA2B1/NCL/POT1/RAD50/TP53BP1/UPF2/WRN/XRCC5 | 10 |
| MF | GO:0019902 | phosphatase binding | 34/2263 | 187/18369 | 0.012591991 | 0.102834339 | 0.086675778 | NEK2/SH2D4A/AKAP11/AKAP5/AP3B1/CDC27/CDH2/CEP192/CHCHD3/CNST/CTNNB1/DLG1/DZIP3/EIF2AK3/FER/HSP90AA1/HSP90B1/IQGAP1/JAK1/KIF3A/MASTL/MET/MTMR4/PIK3R1/PPP6R3/ROS1/SBF2/SHOC2/STAT1/STRN/STX17/SYTL2/TBK1/VCP | 34 |
| MF | GO:0031072 | heat shock protein binding | 25/2263 | 128/18369 | 0.012684961 | 0.102834339 | 0.086675778 | CDK1/HDAC2/CHORDC1/DNAJA1/DNAJC10/DNAJC2/DNAJC7/EIF2AK3/FKBP5/GBP1/HIF1A/HSP90AB1/HSPA13/HSPA5/HSPA8/HSPA9/IQCG/KPNB1/METTL18/SACS/STIP1/TFAM/TFRC/TOMM34/TPR | 25 |
| MF | GO:0004115 | 3',5'-cyclic-AMP phosphodiesterase activity | 6/2263 | 17/18369 | 0.012854292 | 0.102834339 | 0.086675778 | ENPP1/PDE1A/PDE3B/PDE4B/PDE4D/PDE8B | 6 |
| MF | GO:0140035 | ubiquitination-like modification-dependent protein binding | 6/2263 | 17/18369 | 0.012854292 | 0.102834339 | 0.086675778 | DNAJC2/IDE/PEX1/TP53BP1/USP15/VCP | 6 |
| MF | GO:0043539 | protein serine/threonine kinase activator activity | 16/2263 | 72/18369 | 0.012971025 | 0.103021669 | 0.086833672 | CAB39/CCNT1/CCNT2/DBF4/DDX3X/ETAA1/IQGAP1/KRAS/MAP3K13/PARP8/PIK3CA/PIK3R1/PLCB1/RICTOR/SOS1/TAOK1 | 16 |
| MF | GO:0004222 | metalloendopeptidase activity | 24/2263 | 122/18369 | 0.013211865 | 0.10418499 | 0.087814198 | ADAM10/ADAM12/ADAM17/ADAM23/ADAM28/ADAM9/ADAMDEC1/ADAMTS3/ADAMTS5/ADAMTS6/ADAMTS9/IDE/MMP1/MMP16/MMP8/NLN/PAPPA/PHEX/PMPCB/RAPGEF2/SDCBP/SPRTN/UQCRC2/YME1L1 | 24 |
| MF | GO:0140326 | ATPase-coupled intramembrane lipid transporter activity | 8/2263 | 27/18369 | 0.013418537 | 0.105064293 | 0.088555335 | ABCA1/ABCB1/ATP10D/ATP11B/ATP11C/ATP8A1/ATP8B1/ATP8B4 | 8 |
| MF | GO:0005158 | insulin receptor binding | 7/2263 | 22/18369 | 0.013576841 | 0.105555158 | 0.088969069 | CCDC88A/ENPP1/IGF1/PHIP/PIK3R1/PTPN11/SNX2 | 7 |
| MF | GO:0016763 | pentosyltransferase activity | 12/2263 | 49/18369 | 0.0139011 | 0.10732038 | 0.090456918 | LACC1/PARP1/PARP14/PARP15/PARP4/PARP8/PARP9/POGLUT1/PPAT/TIPARP/TNKS2/UMPS | 12 |
| MF | GO:0050660 | flavin adenine dinucleotide binding | 18/2263 | 85/18369 | 0.014359844 | 0.110092136 | 0.092793142 | ACADL/ACADM/ACADSB/AGPS/AIFM1/AOX1/CYBB/DLD/DPYD/ETFDH/FMO1/FMO5/KMO/MTRR/PYROXD1/SQLE/STEAP4/TXNRD1 | 18 |
| MF | GO:0043560 | insulin receptor substrate binding | 5/2263 | 13/18369 | 0.015487022 | 0.116310696 | 0.098034568 | JAK2/NCL/PIK3CA/PIK3CB/PIK3R1 | 5 |
| MF | GO:0045295 | gamma-catenin binding | 5/2263 | 13/18369 | 0.015487022 | 0.116310696 | 0.098034568 | APC/CDH2/CTNNA1/FER/PTPRK | 5 |
| MF | GO:0140333 | glycerophospholipid flippase activity | 5/2263 | 13/18369 | 0.015487022 | 0.116310696 | 0.098034568 | ABCB1/ATP11B/ATP11C/ATP8A1/ATP8B1 | 5 |
| MF | GO:0008175 | tRNA methyltransferase activity | 9/2263 | 33/18369 | 0.015699767 | 0.117111776 | 0.098709773 | ALKBH8/NSUN2/NSUN6/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TYW3 | 9 |
| MF | GO:0070851 | growth factor receptor binding | 26/2263 | 137/18369 | 0.015996693 | 0.118525832 | 0.099901636 | AGR2/ADAM17/CCDC88A/CD2AP/EGF/ERBB4/FAM83B/FER/FGF7/FLRT2/FLRT3/FRS2/IL1R1/IL1RAP/IL6ST/IRAK4/ITGB3/JAK2/LYN/PDGFC/PDGFD/PDGFRA/PIBF1/SDCBP/SLA/SNX2 | 26 |
| MF | GO:0004527 | exonuclease activity | 17/2263 | 80/18369 | 0.016479916 | 0.121292179 | 0.102233301 | MGME1/CNOT1/CNOT6L/CPSF3/DCLRE1A/DDX1/DIS3/DIS3L/ENPP1/ERI1/ERI2/EXOSC9/PNPT1/RAD50/WRN/XRN1/XRN2 | 17 |
| MF | GO:0019207 | kinase regulator activity | 37/2263 | 211/18369 | 0.016625823 | 0.121555686 | 0.102455403 | GSKIP/NCAPG2/APC/BCCIP/CAB39/CCNT1/CCNT2/DBF4/DDX3X/DNAJC3/EGF/ERBB4/ERCC6/ETAA1/HSP90AB1/IBTK/IQGAP1/KIDINS220/KRAS/LRP6/MALT1/MAP3K13/NCK1/NCKAP1L/PARP8/PIK3CA/PIK3R1/PIK3R3/PLCB1/RICTOR/SOCS4/SOS1/STAP1/TAOK1/TAOK3/TOM1L1/YWHAB | 37 |
| MF | GO:0030228 | lipoprotein particle receptor activity | 6/2263 | 18/18369 | 0.017310117 | 0.124904376 | 0.105277906 | CD36/LRP12/LRP2/LRP6/LRP8/VLDLR | 6 |
| MF | GO:0034185 | apolipoprotein binding | 6/2263 | 18/18369 | 0.017310117 | 0.124904376 | 0.105277906 | ABCA1/CANX/HSPD1/LPL/LRP8/VLDLR | 6 |
| MF | GO:0034212 | peptide N-acetyltransferase activity | 12/2263 | 51/18369 | 0.018988429 | 0.13612484 | 0.114735277 | BRCA2/ESCO2/CLOCK/ESCO1/HAT1/ING3/JADE1/KAT6A/NAA50/NCOA1/NCOA3/TAF1 | 12 |
| MF | GO:0042826 | histone deacetylase binding | 24/2263 | 126/18369 | 0.019232144 | 0.13652994 | 0.115076723 | GMNN/HDAC2/TOP2A/BRMS1L/CBX5/CHD4/CIR1/DDX20/DHX36/HIF1A/HSP90AA1/HSP90AB1/KPNA2/MEF2C/MIER3/NCOR1/NIPBL/NRIP1/NUDT21/PARP1/PHF6/PKN2/TOP2B/YWHAB | 24 |
| MF | GO:0004536 | deoxyribonuclease activity | 13/2263 | 57/18369 | 0.019292274 | 0.13652994 | 0.115076723 | MGME1/DCLRE1A/DICER1/DNA2/ERCC4/ERCC5/GEN1/MBD4/N4BP2/RAD50/RBBP8/SETMAR/ZRANB3 | 13 |
| MF | GO:0016407 | acetyltransferase activity | 19/2263 | 94/18369 | 0.019520822 | 0.137267439 | 0.115698337 | BRCA2/ESCO2/ACAT1/ACAT2/CLOCK/DBT/ESCO1/GNPAT/GNPNAT1/HADHA/HAT1/ING3/JADE1/KAT6A/NAA15/NAA50/NCOA1/NCOA3/TAF1 | 19 |
| MF | GO:0004177 | aminopeptidase activity | 10/2263 | 40/18369 | 0.020591119 | 0.143274056 | 0.120761123 | DPP4/DPP8/ENPEP/ERAP2/LAP3/LTA4H/METAP1/METAP2/MMP16/TPP2 | 10 |
| MF | GO:0019903 | protein phosphatase binding | 26/2263 | 140/18369 | 0.020734306 | 0.143274056 | 0.120761123 | NEK2/AKAP11/AKAP5/AP3B1/CDC27/CDH2/CTNNB1/EIF2AK3/FER/HSP90AA1/HSP90B1/IQGAP1/JAK1/KIF3A/MASTL/MET/MTMR4/PIK3R1/PPP6R3/ROS1/SHOC2/STAT1/STRN/STX17/TBK1/VCP | 26 |
| MF | GO:0046966 | nuclear thyroid hormone receptor binding | 8/2263 | 29/18369 | 0.020764356 | 0.143274056 | 0.120761123 | GTF2H1/JMJD1C/MED13/NCOA3/NCOR1/TACC1/TAF7/TRIP12 | 8 |
| MF | GO:0005344 | oxygen carrier activity | 5/2263 | 14/18369 | 0.021691162 | 0.143817625 | 0.12121928 | HBA2/HBB/HBD/HBG2/IPCEF1 | 5 |
| MF | GO:0030983 | mismatched DNA binding | 5/2263 | 14/18369 | 0.021691162 | 0.143817625 | 0.12121928 | MSH2/MLH1/MLH3/MSH3/MSH6 | 5 |
| MF | GO:0016779 | nucleotidyltransferase activity | 28/2263 | 154/18369 | 0.021958116 | 0.143817625 | 0.12121928 | POLQ/PRIM2/DKC1/EIF2B3/PAPOLA/PAPOLG/PARP1/PARP14/PARP15/PARP4/PARP8/PARP9/PNPT1/POLA1/POLD3/POLK/POLR1B/POLR2B/POLR3B/POLR3C/REV1/REV3L/TIPARP/TNKS2/TRNT1/UAP1/UBA6/UGP2 | 28 |
| MF | GO:0008173 | RNA methyltransferase activity | 14/2263 | 64/18369 | 0.022039941 | 0.143817625 | 0.12121928 | ALKBH8/METTL14/METTL15/NSUN2/NSUN6/RNMT/TFB2M/TGS1/THUMPD3/TRMT10C/TRMT12/TRMT1L/TRMT5/TYW3 | 14 |
| MF | GO:0008093 | cytoskeletal anchor activity | 7/2263 | 24/18369 | 0.022125922 | 0.143817625 | 0.12121928 | ANK2/ANK3/EPB41L3/GAS2L3/NCK1/SDCBP/SORBS2 | 7 |
| MF | GO:0017056 | structural constituent of nuclear pore | 7/2263 | 24/18369 | 0.022125922 | 0.143817625 | 0.12121928 | NUP107/NUP133/NUP153/NUP155/NUP205/NUP88/TPR | 7 |
| MF | GO:0140358 | P-type transmembrane transporter activity | 7/2263 | 24/18369 | 0.022125922 | 0.143817625 | 0.12121928 | ATP13A3/ATP13A4/ATP1B1/ATP2A2/ATP2B1/ATP2C1/ATP7A | 7 |
| MF | GO:0140612 | DNA damage sensor activity | 7/2263 | 24/18369 | 0.022125922 | 0.143817625 | 0.12121928 | MSH2/XRCC2/MLH1/MLH3/MSH3/MSH6/RAD50 | 7 |
| MF | GO:0016796 | exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | 13/2263 | 58/18369 | 0.02214583 | 0.143817625 | 0.12121928 | MGME1/CNOT1/CNOT6L/CPSF3/DCLRE1A/DIS3/DIS3L/ERI1/ERI2/EXOSC9/PNPT1/XRN1/XRN2 | 13 |
| MF | GO:0045309 | protein phosphorylated amino acid binding | 13/2263 | 58/18369 | 0.02214583 | 0.143817625 | 0.12121928 | ABL2/LEO1/NEDD4/PIK3R1/PIK3R3/PTPN11/PTPN3/RASA1/SAMSN1/SLA/STAP1/YES1/YWHAB | 13 |
| MF | GO:0000993 | RNA polymerase II complex binding | 9/2263 | 35/18369 | 0.022953213 | 0.148189162 | 0.124903908 | CTR9/DHX9/ERCC5/HNRNPU/LEO1/NCOA3/PCF11/WDR43/ZNF326 | 9 |
| MF | GO:0090079 | translation regulator activity, nucleic acid binding | 21/2263 | 109/18369 | 0.024250715 | 0.154276068 | 0.130034367 | EIF3M/DHX29/EIF1AX/EIF2A/EIF2B3/EIF2S1/EIF2S2/EIF3A/EIF3D/EIF3E/EIF3J/EIF3L/EIF4B/EIF4G2/EIF5/EIF5B/ETF1/GFM1/GSPT1/HBS1L/MTIF2 | 21 |
| MF | GO:0043175 | RNA polymerase core enzyme binding | 10/2263 | 41/18369 | 0.02431525 | 0.154276068 | 0.130034367 | CTR9/DHX9/ERCC5/HNRNPU/LEO1/NCOA3/PCF11/SPTY2D1/WDR43/ZNF326 | 10 |
| MF | GO:0051539 | 4 iron, 4 sulfur cluster binding | 10/2263 | 41/18369 | 0.02431525 | 0.154276068 | 0.130034367 | BRIP1/PRIM2/ABCE1/ACO1/DNA2/DPYD/ETFDH/IREB2/PPAT/REV3L | 10 |
| MF | GO:0052866 | phosphatidylinositol phosphate phosphatase activity | 8/2263 | 30/18369 | 0.0253422 | 0.159873081 | 0.13475191 | FIG4/INPP4B/MTM1/MTMR2/MTMR4/MTMR6/PIKFYVE/SACM1L | 8 |
| MF | GO:0000014 | single-stranded DNA endodeoxyribonuclease activity | 4/2263 | 10/18369 | 0.026119979 | 0.160202537 | 0.135029598 | ERCC4/RAD50/RBBP8/SETMAR | 4 |
| MF | GO:0016868 | intramolecular transferase activity, phosphotransferases | 4/2263 | 10/18369 | 0.026119979 | 0.160202537 | 0.135029598 | BPGM/PGM2/PGM2L1/PGM3 | 4 |
| MF | GO:0031720 | haptoglobin binding | 4/2263 | 10/18369 | 0.026119979 | 0.160202537 | 0.135029598 | HBA2/HBB/HBD/HBG2 | 4 |
| MF | GO:0045294 | alpha-catenin binding | 4/2263 | 10/18369 | 0.026119979 | 0.160202537 | 0.135029598 | CDH2/CTNNB1/PKP2/VCL | 4 |
| MF | GO:0070878 | primary miRNA binding | 4/2263 | 10/18369 | 0.026119979 | 0.160202537 | 0.135029598 | EZH2/DDX3X/DDX5/PUS10 | 4 |
| MF | GO:0019887 | protein kinase regulator activity | 32/2263 | 184/18369 | 0.027280897 | 0.165049383 | 0.13911485 | GSKIP/NCAPG2/APC/CAB39/CCNT1/CCNT2/DBF4/DDX3X/DNAJC3/EGF/ERBB4/ERCC6/ETAA1/HSP90AB1/IBTK/IQGAP1/KIDINS220/KRAS/MAP3K13/NCK1/NCKAP1L/PARP8/PIK3CA/PIK3R1/PLCB1/RICTOR/SOS1/STAP1/TAOK1/TAOK3/TOM1L1/YWHAB | 32 |
| MF | GO:0000175 | 3'-5'-RNA exonuclease activity | 9/2263 | 36/18369 | 0.027358729 | 0.165049383 | 0.13911485 | CNOT1/CNOT6L/DIS3/DIS3L/ERI1/ERI2/EXOSC9/PNPT1/XRN2 | 9 |
| MF | GO:0015248 | sterol transporter activity | 9/2263 | 36/18369 | 0.027358729 | 0.165049383 | 0.13911485 | ABCA1/GRAMD1C/NPC1/OSBP/OSBPL11/OSBPL3/OSBPL8/OSBPL9/STARD4 | 9 |
| MF | GO:0017069 | snRNA binding | 12/2263 | 54/18369 | 0.029057474 | 0.174344844 | 0.146949697 | CCNT1/CCNT2/COIL/DDX21/GEMIN5/HNRNPU/LARP7/NCBP2/PRPF4/RBM41/RNPC3/SNRPA1 | 12 |
| MF | GO:0043024 | ribosomal small subunit binding | 5/2263 | 15/18369 | 0.029308447 | 0.174900138 | 0.147417736 | ABCE1/DDX3X/DHX29/MTIF2/PTCD3 | 5 |
| MF | GO:0051219 | phosphoprotein binding | 18/2263 | 92/18369 | 0.030548514 | 0.178620676 | 0.150553659 | ABL2/EPB41/LEO1/LYN/NEDD4/PHF6/PIK3R1/PIK3R3/PTPN11/PTPN3/RASA1/RB1/SAMSN1/SLA/STAP1/TBK1/YES1/YWHAB | 18 |
| MF | GO:0005154 | epidermal growth factor receptor binding | 8/2263 | 31/18369 | 0.030579083 | 0.178620676 | 0.150553659 | AGR2/CCDC88A/EGF/ERBB4/FAM83B/FER/SLA/SNX2 | 8 |
| MF | GO:0016878 | acid-thiol ligase activity | 8/2263 | 31/18369 | 0.030579083 | 0.178620676 | 0.150553659 | ACSL1/ACSL3/ACSL4/ACSM3/ACSS3/SLC27A2/SUCLA2/SUCLG2 | 8 |
| MF | GO:0043495 | protein-membrane adaptor activity | 8/2263 | 31/18369 | 0.030579083 | 0.178620676 | 0.150553659 | AKAP6/EPB41L3/KRAS/LPL/NUP153/SLC4A1/SYNE1/SYNE2 | 8 |
| MF | GO:1901981 | phosphatidylinositol phosphate binding | 31/2263 | 179/18369 | 0.030986039 | 0.180045197 | 0.151754342 | ARAP2/BTK/DAPP1/EXOC1/FCHO2/FERMT2/IQGAP1/IQGAP2/KIF16B/KRIT1/MYO1B/NLRP3/OGT/OSBP/OSBPL8/PLA2G4A/PLCB1/PLEKHA5/RACGAP1/SCIN/SDCBP/SESTD1/SH3PXD2B/SNX10/SNX13/SVIL/SYTL2/TWF1/VEPH1/VPS13B/ZFYVE16 | 31 |
| MF | GO:0031593 | polyubiquitin modification-dependent protein binding | 12/2263 | 55/18369 | 0.033141457 | 0.188523074 | 0.158900074 | RAD18/AGL/BRCC3/DZIP3/EPS15/SPRTN/TAB2/TAB3/VCP/ZBTB1/ZRANB1/ZRANB3 | 12 |
| MF | GO:0004402 | histone acetyltransferase activity | 10/2263 | 43/18369 | 0.033171811 | 0.188523074 | 0.158900074 | BRCA2/CLOCK/HAT1/ING3/JADE1/KAT6A/NAA50/NCOA1/NCOA3/TAF1 | 10 |
| MF | GO:0043028 | cysteine-type endopeptidase regulator activity involved in apoptotic process | 10/2263 | 43/18369 | 0.033171811 | 0.188523074 | 0.158900074 | BIRC2/BIRC3/CASP1/CASP8AP2/CTSK/CTSL/CTSS/NAIP/RPS6KA3/TNFAIP8 | 10 |
| MF | GO:0001091 | RNA polymerase II general transcription initiation factor binding | 7/2263 | 26/18369 | 0.033811203 | 0.188523074 | 0.158900074 | ERCC4/HNRNPU/NOLC1/NOP58/TAF1/TAF7/ZNHIT6 | 7 |
| MF | GO:0008574 | plus-end-directed microtubule motor activity | 7/2263 | 26/18369 | 0.033811203 | 0.188523074 | 0.158900074 | KIF11/KIF14/KIF18A/KIF20B/KIF16B/KIF3A/KIF5B | 7 |
| MF | GO:0034593 | phosphatidylinositol bisphosphate phosphatase activity | 7/2263 | 26/18369 | 0.033811203 | 0.188523074 | 0.158900074 | FIG4/INPP4B/MTM1/MTMR2/MTMR4/MTMR6/PIKFYVE | 7 |
| MF | GO:0050681 | nuclear androgen receptor binding | 7/2263 | 26/18369 | 0.033811203 | 0.188523074 | 0.158900074 | DDX5/KDM3A/KDM4C/RNF14/RNF6/SNW1/TMF1 | 7 |
| MF | GO:0070006 | metalloaminopeptidase activity | 7/2263 | 26/18369 | 0.033811203 | 0.188523074 | 0.158900074 | ENPEP/ERAP2/LAP3/LTA4H/METAP1/METAP2/MMP16 | 7 |
| MF | GO:0070717 | poly-purine tract binding | 8/2263 | 32/18369 | 0.036511592 | 0.196089737 | 0.165277772 | DDX1/DDX3X/EIF4A3/FMR1/HNRNPU/LARP4/PNPT1/SYNCRIP | 8 |
| MF | GO:0035173 | histone kinase activity | 6/2263 | 21/18369 | 0.03669146 | 0.196089737 | 0.165277772 | CDK1/CHEK1/VRK1/BAZ1B/JAK2/RPS6KA5 | 6 |
| MF | GO:0035613 | RNA stem-loop binding | 6/2263 | 21/18369 | 0.03669146 | 0.196089737 | 0.165277772 | CSDE1/DDX3X/DHX9/EIF4A3/FMR1/RC3H2 | 6 |
| MF | GO:0001851 | complement component C3b binding | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | CFH/CFHR1/CFHR3/CR1 | 4 |
| MF | GO:0004706 | JUN kinase kinase kinase activity | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | LRRK2/MAP3K13/RIPK1/RIPK2 | 4 |
| MF | GO:0005049 | nuclear export signal receptor activity | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | XPO1/CSE1L/XPO4/XPO5 | 4 |
| MF | GO:0016857 | racemase and epimerase activity, acting on carbohydrates and derivatives | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | DSE/DSEL/GLCE/RPE | 4 |
| MF | GO:0034511 | U3 snoRNA binding | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | BMS1/PRKDC/TSR1/XRCC5 | 4 |
| MF | GO:0036312 | phosphatidylinositol 3-kinase regulatory subunit binding | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | FAM83B/PIK3AP1/PIK3R1/PTPN13 | 4 |
| MF | GO:0047676 | arachidonate-CoA ligase activity | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | ACSL1/ACSL3/ACSL4/SLC27A2 | 4 |
| MF | GO:0052629 | phosphatidylinositol-3,5-bisphosphate 3-phosphatase activity | 4/2263 | 11/18369 | 0.037122061 | 0.196089737 | 0.165277772 | MTM1/MTMR2/MTMR4/MTMR6 | 4 |
| MF | GO:0050664 | oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor | 5/2263 | 16/18369 | 0.038417768 | 0.201967694 | 0.170232115 | AIFM1/CYB5R4/CYBB/FMO5/KMO | 5 |
| MF | GO:0051959 | dynein light intermediate chain binding | 7/2263 | 27/18369 | 0.040948637 | 0.214252582 | 0.180586653 | CCDC88A/DNAH14/DNAH5/DYNC1H1/DYNC2H1/HOOK1/HOOK3 | 7 |
| MF | GO:0004519 | endonuclease activity | 22/2263 | 122/18369 | 0.042072826 | 0.219096228 | 0.184669208 | LACTB2/CPSF3/DICER1/DIS3/DNA2/ENDOD1/ERCC4/ERCC5/G3BP1/GEN1/MBD4/N4BP2/NUDT12/POP1/RAD50/RBBP8/RNASEL/SETMAR/SLFN13/TSNAX/ZC3H12C/ZRANB3 | 22 |
| MF | GO:0061629 | RNA polymerase II-specific DNA-binding transcription factor binding | 54/2263 | 348/18369 | 0.043275718 | 0.224302315 | 0.189057253 | HDAC2/CHD4/CNOT1/CTNNB1/DDX5/DHX9/DNAJA1/DTX3L/EXOSC9/GTF2H1/GTF2I/HIF1A/HMGB1/JMJD1C/KDM3A/KDM4C/LRIF1/MED13/MEF2C/MKKS/MTDH/NCOA1/NCOA2/NCOA3/NCOA7/NCOR1/NFE2L2/NRIP1/PARP1/PARP9/PPARG/PRKDC/PRRX1/PTPN2/RB1/RBBP8/RBPJ/RNF14/RNF6/SDR16C5/SLC30A9/SMARCA1/SNW1/STAT1/STRN/TACC1/TAF1/TAF4B/TAF7/TMF1/TP53BP1/TP53BP2/TRIP12/ZFPM2 | 54 |
| MF | GO:0038024 | cargo receptor activity | 16/2263 | 83/18369 | 0.044873316 | 0.231495985 | 0.195120567 | HMMR/ABCA1/CD163/CD36/CFI/COLEC12/ENPP1/LRP12/LRP2/LRP6/LRP8/MIA3/MRC1/MSR1/TFRC/VLDLR | 16 |
| MF | GO:0010485 | histone H4 acetyltransferase activity | 6/2263 | 22/18369 | 0.045359442 | 0.232915461 | 0.196316998 | BRCA2/HAT1/ING3/JADE1/KAT6A/NAA50 | 6 |
| MF | GO:0046332 | SMAD binding | 15/2263 | 77/18369 | 0.047070436 | 0.240582228 | 0.202779071 | COL3A1/COL5A2/CTNNB1/DDX5/FERMT2/IPO7/PARP1/PPARG/SKIL/SNW1/TCF12/TGFBR1/TRIM33/USP15/USP9X | 15 |
| MF | GO:0016706 | 2-oxoglutarate-dependent dioxygenase activity | 12/2263 | 58/18369 | 0.04781747 | 0.24081729 | 0.202977197 | ALKBH8/ASPH/KDM3A/KDM4C/KDM5A/KDM5B/KDM6A/KDM7A/OGFOD1/P4HA1/PLOD2/TET2 | 12 |
| MF | GO:0016874 | ligase activity | 28/2263 | 165/18369 | 0.048485538 | 0.24081729 | 0.202977197 | ACACA/ACSL1/ACSL3/ACSL4/ACSM3/ACSS3/ATP6V1A/CTPS1/FARSB/GART/GCLC/GMPS/IARS2/LIG4/MCCC1/MDM2/MTHFD1/MTHFD1L/NAE1/PAICS/RTCB/SLC27A2/SUCLA2/SUCLG2/TTLL7/UBA5/UBA6/WARS2 | 28 |
| MF | GO:0016854 | racemase and epimerase activity | 5/2263 | 17/18369 | 0.049069216 | 0.24081729 | 0.202977197 | DHRS9/DSE/DSEL/GLCE/RPE | 5 |
| MF | GO:0070064 | proline-rich region binding | 5/2263 | 17/18369 | 0.049069216 | 0.24081729 | 0.202977197 | CYLD/GIGYF2/ITSN1/NEDD4/WBP4 | 5 |