Significant GO terms accompanying Fig 2 Network Topology analyses

# SES4 (down)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| goId | description | size | overlap | expect | enrichmentRatio | pValue | FDR |
| <GO:0000184> | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 119 | 14 | 0.2256796 | 62.034858 | 0.0000000 | 0.0000000 |
| <GO:0000956> | nuclear-transcribed mRNA catabolic process | 196 | 14 | 0.3717075 | 37.664021 | 0.0000000 | 0.0000000 |
| <GO:0006402> | mRNA catabolic process | 293 | 14 | 0.5556648 | 25.195045 | 0.0000000 | 0.0000000 |
| <GO:0006413> | translational initiation | 185 | 14 | 0.3508464 | 39.903503 | 0.0000000 | 0.0000000 |
| <GO:0006612> | protein targeting to membrane | 179 | 14 | 0.3394676 | 41.241051 | 0.0000000 | 0.0000000 |
| <GO:0006613> | cotranslational protein targeting to membrane | 98 | 14 | 0.1858538 | 75.328042 | 0.0000000 | 0.0000000 |
| <GO:0006614> | SRP-dependent cotranslational protein targeting to membrane | 94 | 14 | 0.1782679 | 78.533491 | 0.0000000 | 0.0000000 |
| <GO:0045047> | protein targeting to ER | 106 | 14 | 0.2010255 | 69.642907 | 0.0000000 | 0.0000000 |
| <GO:0070972> | protein localization to endoplasmic reticulum | 136 | 14 | 0.2579195 | 54.280501 | 0.0000000 | 0.0000000 |
| <GO:0072599> | establishment of protein localization to endoplasmic reticulum | 110 | 14 | 0.2086114 | 67.110438 | 0.0000000 | 0.0000000 |
| <GO:0090150> | establishment of protein localization to membrane | 298 | 14 | 0.5651472 | 24.772309 | 0.0000000 | 0.0000000 |
| <GO:0006401> | RNA catabolic process | 323 | 14 | 0.6125588 | 22.854948 | 0.0000000 | 0.0000000 |
| <GO:0006605> | protein targeting | 397 | 14 | 0.7528974 | 18.594832 | 0.0000000 | 0.0000000 |
| <GO:0006412> | translation | 592 | 15 | 1.1227084 | 13.360548 | 0.0000000 | 0.0000000 |
| <GO:0043043> | peptide biosynthetic process | 614 | 15 | 1.1644307 | 12.881831 | 0.0000000 | 0.0000000 |
| <GO:0034655> | nucleobase-containing compound catabolic process | 520 | 14 | 0.9861628 | 14.196439 | 0.0000000 | 0.0000000 |
| <GO:0072594> | establishment of protein localization to organelle | 520 | 14 | 0.9861628 | 14.196439 | 0.0000000 | 0.0000000 |
| <GO:0046700> | heterocycle catabolic process | 564 | 14 | 1.0696074 | 13.088915 | 0.0000000 | 0.0000000 |
| <GO:0044270> | cellular nitrogen compound catabolic process | 566 | 14 | 1.0734003 | 13.042665 | 0.0000000 | 0.0000000 |
| <GO:0072657> | protein localization to membrane | 567 | 14 | 1.0752968 | 13.019662 | 0.0000000 | 0.0000000 |
| <GO:0019439> | aromatic compound catabolic process | 578 | 14 | 1.0961579 | 12.771883 | 0.0000000 | 0.0000000 |
| <GO:0016071> | mRNA metabolic process | 732 | 15 | 1.3882138 | 10.805252 | 0.0000000 | 0.0000000 |
| <GO:0043604> | amide biosynthetic process | 732 | 15 | 1.3882138 | 10.805252 | 0.0000000 | 0.0000000 |
| <GO:0006518> | peptide metabolic process | 744 | 15 | 1.4109714 | 10.630974 | 0.0000000 | 0.0000000 |
| <GO:1901361> | organic cyclic compound catabolic process | 605 | 14 | 1.1473625 | 12.201898 | 0.0000000 | 0.0000000 |
| <GO:0033365> | protein localization to organelle | 854 | 15 | 1.6195828 | 9.261644 | 0.0000000 | 0.0000000 |
| <GO:0002181> | cytoplasmic translation | 91 | 8 | 0.1725785 | 46.355718 | 0.0000000 | 0.0000000 |
| <GO:0043603> | cellular amide metabolic process | 970 | 15 | 1.8395729 | 8.154066 | 0.0000000 | 0.0000000 |
| <GO:0044265> | cellular macromolecule catabolic process | 1049 | 15 | 1.9893938 | 7.539985 | 0.0000000 | 0.0000000 |
| <GO:0009057> | macromolecule catabolic process | 1263 | 15 | 2.3952378 | 6.262426 | 0.0000000 | 0.0000005 |
| <GO:0006886> | intracellular protein transport | 1059 | 14 | 2.0083585 | 6.970867 | 0.0000000 | 0.0000006 |
| <GO:0044267> | cellular protein metabolic process | 4630 | 24 | 8.7806420 | 2.733285 | 0.0000000 | 0.0000009 |
| <GO:0010629> | negative regulation of gene expression | 1644 | 16 | 3.1177917 | 5.131837 | 0.0000000 | 0.0000017 |
| <GO:0010605> | negative regulation of macromolecule metabolic process | 2399 | 18 | 4.5496242 | 3.956371 | 0.0000000 | 0.0000053 |
| <GO:0019538> | protein metabolic process | 5124 | 24 | 9.7174967 | 2.469772 | 0.0000000 | 0.0000081 |
| <GO:0048519> | negative regulation of biological process | 4669 | 23 | 8.8546042 | 2.597519 | 0.0000000 | 0.0000121 |
| <GO:1901566> | organonitrogen compound biosynthetic process | 1635 | 15 | 3.1007235 | 4.837581 | 0.0000000 | 0.0000145 |
| <GO:0009892> | negative regulation of metabolic process | 2602 | 18 | 4.9346070 | 3.647707 | 0.0000000 | 0.0000177 |
| <GO:0006364> | rRNA processing | 192 | 7 | 0.3641217 | 19.224344 | 0.0000001 | 0.0000209 |
| <GO:0046907> | intracellular transport | 1702 | 15 | 3.2277868 | 4.647147 | 0.0000001 | 0.0000232 |
| <GO:0060255> | regulation of macromolecule metabolic process | 5411 | 24 | 10.2617827 | 2.338775 | 0.0000001 | 0.0000233 |
| <GO:0034613> | cellular protein localization | 1728 | 15 | 3.2770949 | 4.577225 | 0.0000001 | 0.0000271 |
| <GO:0070727> | cellular macromolecule localization | 1738 | 15 | 3.2960596 | 4.550889 | 0.0000001 | 0.0000286 |
| <GO:0051649> | establishment of localization in cell | 2039 | 16 | 3.8668961 | 4.137685 | 0.0000001 | 0.0000289 |
| <GO:0010468> | regulation of gene expression | 3930 | 21 | 7.4531151 | 2.817614 | 0.0000001 | 0.0000295 |
| <GO:0044248> | cellular catabolic process | 2065 | 16 | 3.9162043 | 4.085589 | 0.0000001 | 0.0000332 |
| <GO:0016072> | rRNA metabolic process | 223 | 7 | 0.4229121 | 16.551902 | 0.0000001 | 0.0000483 |
| <GO:0016070> | RNA metabolic process | 4084 | 21 | 7.7451710 | 2.711367 | 0.0000002 | 0.0000572 |
| <GO:1901575> | organic substance catabolic process | 1910 | 15 | 3.6222519 | 4.141070 | 0.0000003 | 0.0000892 |
| <GO:0019222> | regulation of metabolic process | 5854 | 24 | 11.1019175 | 2.161789 | 0.0000003 | 0.0001099 |
| <GO:0034645> | cellular macromolecule biosynthetic process | 4293 | 21 | 8.1415326 | 2.579367 | 0.0000004 | 0.0001369 |
| <GO:0009056> | catabolic process | 2304 | 16 | 4.3694599 | 3.661780 | 0.0000005 | 0.0001374 |
| <GO:0042254> | ribosome biogenesis | 265 | 7 | 0.5025637 | 13.928581 | 0.0000005 | 0.0001374 |
| <GO:0051641> | cellular localization | 2653 | 17 | 5.0313268 | 3.378830 | 0.0000005 | 0.0001374 |
| <GO:0044271> | cellular nitrogen compound biosynthetic process | 4328 | 21 | 8.2079090 | 2.558508 | 0.0000005 | 0.0001477 |
| <GO:1901564> | organonitrogen compound metabolic process | 6041 | 24 | 11.4565569 | 2.094870 | 0.0000007 | 0.0001962 |
| <GO:1902533> | positive regulation of intracellular signal transduction | 979 | 11 | 1.8566411 | 5.924677 | 0.0000007 | 0.0002003 |
| <GO:0009059> | macromolecule biosynthetic process | 4421 | 21 | 8.3842804 | 2.504687 | 0.0000008 | 0.0002079 |
| <GO:0015031> | protein transport | 1824 | 14 | 3.4591557 | 4.047230 | 0.0000012 | 0.0003221 |
| <GO:0090304> | nucleic acid metabolic process | 4544 | 21 | 8.6175458 | 2.436889 | 0.0000013 | 0.0003337 |
| <GO:0015833> | peptide transport | 1855 | 14 | 3.5179462 | 3.979595 | 0.0000015 | 0.0003831 |
| <GO:0042886> | amide transport | 1881 | 14 | 3.5672543 | 3.924587 | 0.0000017 | 0.0004470 |
| <GO:0045184> | establishment of protein localization | 1921 | 14 | 3.6431130 | 3.842867 | 0.0000023 | 0.0005689 |
| <GO:0034470> | ncRNA processing | 340 | 7 | 0.6447988 | 10.856100 | 0.0000025 | 0.0006072 |
| <GO:0010467> | gene expression | 4770 | 21 | 9.0461474 | 2.321430 | 0.0000031 | 0.0007503 |
| <GO:0051092> | positive regulation of NF-kappaB transcription factor activity | 144 | 5 | 0.2730912 | 18.308899 | 0.0000067 | 0.0016007 |
| <GO:1901798> | positive regulation of signal transduction by p53 class mediator | 20 | 3 | 0.0379293 | 79.094444 | 0.0000068 | 0.0016063 |
| <GO:0071705> | nitrogen compound transport | 2130 | 14 | 4.0394746 | 3.465797 | 0.0000079 | 0.0018344 |
| <GO:0042273> | ribosomal large subunit biogenesis | 70 | 4 | 0.1327527 | 30.131217 | 0.0000086 | 0.0019843 |
| <GO:0008104> | protein localization | 2501 | 15 | 4.7430638 | 3.162513 | 0.0000093 | 0.0020997 |
| <GO:0022613> | ribonucleoprotein complex biogenesis | 420 | 7 | 0.7965161 | 8.788272 | 0.0000098 | 0.0021997 |
| <GO:0006139> | nucleobase-containing compound metabolic process | 5102 | 21 | 9.6757744 | 2.170369 | 0.0000104 | 0.0022893 |
| <GO:0046483> | heterocycle metabolic process | 5243 | 21 | 9.9431762 | 2.112001 | 0.0000169 | 0.0036766 |
| <GO:0050789> | regulation of biological process | 9514 | 27 | 18.0429866 | 1.496426 | 0.0000185 | 0.0039735 |
| <GO:0006725> | cellular aromatic compound metabolic process | 5282 | 21 | 10.0171384 | 2.096407 | 0.0000193 | 0.0040831 |
| <GO:0044249> | cellular biosynthetic process | 5314 | 21 | 10.0778254 | 2.083783 | 0.0000215 | 0.0044858 |
| <GO:1901576> | organic substance biosynthetic process | 5388 | 21 | 10.2181639 | 2.055164 | 0.0000275 | 0.0056565 |
| <GO:0034660> | ncRNA metabolic process | 502 | 7 | 0.9520264 | 7.352737 | 0.0000312 | 0.0063480 |
| <GO:0009058> | biosynthetic process | 5446 | 21 | 10.3281590 | 2.033276 | 0.0000332 | 0.0066602 |
| <GO:1901360> | organic cyclic compound metabolic process | 5453 | 21 | 10.3414343 | 2.030666 | 0.0000339 | 0.0067275 |
| <GO:1902255> | positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator | 5 | 2 | 0.0094823 | 210.918519 | 0.0000345 | 0.0067568 |
| <GO:0033036> | macromolecule localization | 2782 | 15 | 5.2759711 | 2.843078 | 0.0000352 | 0.0068071 |
| <GO:0009967> | positive regulation of signal transduction | 1463 | 11 | 2.7745312 | 3.964634 | 0.0000356 | 0.0068071 |
| <GO:0044260> | cellular macromolecule metabolic process | 7260 | 24 | 13.7683501 | 1.743128 | 0.0000368 | 0.0069530 |
| <GO:0071702> | organic substance transport | 2456 | 14 | 4.6577228 | 3.005761 | 0.0000421 | 0.0078450 |
| <GO:0045087> | innate immune response | 734 | 8 | 1.3920067 | 5.747099 | 0.0000444 | 0.0081945 |
| <GO:0034641> | cellular nitrogen compound metabolic process | 5715 | 21 | 10.8383086 | 1.937572 | 0.0000771 | 0.0140534 |
| <GO:0010647> | positive regulation of cell communication | 1608 | 11 | 3.0495189 | 3.607126 | 0.0000858 | 0.0153012 |
| <GO:0065007> | biological regulation | 10069 | 27 | 19.0955257 | 1.413944 | 0.0000859 | 0.0153012 |
| <GO:0043030> | regulation of macrophage activation | 46 | 3 | 0.0872375 | 34.388889 | 0.0000875 | 0.0154080 |
| <GO:0023056> | positive regulation of signaling | 1614 | 11 | 3.0608977 | 3.593717 | 0.0000888 | 0.0154812 |
| <GO:0051091> | positive regulation of DNA-binding transcription factor activity | 248 | 5 | 0.4703238 | 10.630974 | 0.0000909 | 0.0156647 |
| <GO:0006396> | RNA processing | 839 | 8 | 1.5911358 | 5.027855 | 0.0001143 | 0.0194968 |
| <GO:1904667> | negative regulation of ubiquitin protein ligase activity | 9 | 2 | 0.0170682 | 117.176955 | 0.0001237 | 0.0208625 |
| <GO:0051403> | stress-activated MAPK cascade | 266 | 5 | 0.5044602 | 9.911585 | 0.0001264 | 0.0210961 |
| <GO:1902531> | regulation of intracellular signal transduction | 1696 | 11 | 3.2164080 | 3.419964 | 0.0001398 | 0.0230988 |
| <GO:0031098> | stress-activated protein kinase signaling cascade | 291 | 5 | 0.5518719 | 9.060074 | 0.0001924 | 0.0314451 |
| <GO:0042274> | ribosomal small subunit biogenesis | 61 | 3 | 0.1156845 | 25.932605 | 0.0002034 | 0.0329187 |
| <GO:0002376> | immune system process | 2539 | 13 | 4.8151296 | 2.699823 | 0.0002951 | 0.0472674 |
| <GO:0043410> | positive regulation of MAPK cascade | 508 | 6 | 0.9634052 | 6.227909 | 0.0003128 | 0.0496045 |
| <GO:0042116> | macrophage activation | 73 | 3 | 0.1384421 | 21.669711 | 0.0003463 | 0.0543683 |
| <GO:0045088> | regulation of innate immune response | 337 | 5 | 0.6391094 | 7.823387 | 0.0003793 | 0.0589586 |
| <GO:0034134> | toll-like receptor 2 signaling pathway | 16 | 2 | 0.0303435 | 65.912037 | 0.0004089 | 0.0623420 |
| <GO:0051444> | negative regulation of ubiquitin-protein transferase activity | 16 | 2 | 0.0303435 | 65.912037 | 0.0004089 | 0.0623420 |
| <GO:0043170> | macromolecule metabolic process | 8163 | 24 | 15.4808597 | 1.550301 | 0.0004224 | 0.0637849 |
| <GO:0051963> | regulation of synapse assembly | 85 | 3 | 0.1611997 | 18.610457 | 0.0005417 | 0.0810297 |
| <GO:0007254> | JNK cascade | 204 | 4 | 0.3868793 | 10.339143 | 0.0005547 | 0.0822059 |
| <GO:0002758> | innate immune response-activating signal transduction | 209 | 4 | 0.3963616 | 10.091795 | 0.0006076 | 0.0892126 |
| <GO:0007617> | mating behavior | 20 | 2 | 0.0379293 | 52.729630 | 0.0006444 | 0.0937407 |
| <GO:0048584> | positive regulation of response to stimulus | 2027 | 11 | 3.8441385 | 2.861499 | 0.0006829 | 0.0984452 |
| <GO:0051090> | regulation of DNA-binding transcription factor activity | 385 | 5 | 0.7301398 | 6.848004 | 0.0006960 | 0.0994328 |
| <GO:1904666> | regulation of ubiquitin protein ligase activity | 21 | 2 | 0.0398258 | 50.218695 | 0.0007114 | 0.0999898 |
| <GO:0031349> | positive regulation of defense response | 387 | 5 | 0.7339327 | 6.812614 | 0.0007125 | 0.0999898 |
| <GO:0000165> | MAPK cascade | 839 | 7 | 1.5911358 | 4.399373 | 0.0007554 | 0.1050779 |
| <GO:0051234> | establishment of localization | 4500 | 17 | 8.5341013 | 1.992008 | 0.0007765 | 0.1070743 |
| <GO:0023014> | signal transduction by protein phosphorylation | 850 | 7 | 1.6119969 | 4.342440 | 0.0008163 | 0.1115878 |
| <GO:0002218> | activation of innate immune response | 229 | 4 | 0.4342909 | 9.210416 | 0.0008556 | 0.1159527 |
| <GO:0048872> | homeostasis of number of cells | 232 | 4 | 0.4399803 | 9.091316 | 0.0008981 | 0.1206861 |
| <GO:0043032> | positive regulation of macrophage activation | 24 | 2 | 0.0455152 | 43.941358 | 0.0009317 | 0.1241457 |
| <GO:0031347> | regulation of defense response | 642 | 6 | 1.2175318 | 4.928003 | 0.0010789 | 0.1406454 |
| <GO:0051338> | regulation of transferase activity | 893 | 7 | 1.6935450 | 4.133342 | 0.0010930 | 0.1406454 |
| <GO:0048169> | regulation of long-term neuronal synaptic plasticity | 26 | 2 | 0.0493081 | 40.561254 | 0.0010945 | 0.1406454 |
| <GO:1900745> | positive regulation of p38MAPK cascade | 26 | 2 | 0.0493081 | 40.561254 | 0.0010945 | 0.1406454 |
| <GO:0043406> | positive regulation of MAP kinase activity | 245 | 4 | 0.4646344 | 8.608919 | 0.0010998 | 0.1406454 |
| <GO:0051179> | localization | 5656 | 19 | 10.7264171 | 1.771328 | 0.0012328 | 0.1550747 |
| <GO:0035556> | intracellular signal transduction | 2544 | 12 | 4.8246119 | 2.487247 | 0.0012528 | 0.1550747 |
| <GO:0031647> | regulation of protein stability | 254 | 4 | 0.4817026 | 8.303879 | 0.0012570 | 0.1550747 |
| <GO:0019098> | reproductive behavior | 28 | 2 | 0.0531011 | 37.664021 | 0.0012700 | 0.1550747 |
| <GO:1902253> | regulation of intrinsic apoptotic signaling pathway by p53 class mediator | 28 | 2 | 0.0531011 | 37.664021 | 0.0012700 | 0.1550747 |
| <GO:0034101> | erythrocyte homeostasis | 114 | 3 | 0.2161972 | 13.876218 | 0.0012713 | 0.1550747 |
| <GO:1904646> | cellular response to amyloid-beta | 31 | 2 | 0.0587905 | 34.019116 | 0.0015569 | 0.1884509 |
| <GO:0043408> | regulation of MAPK cascade | 691 | 6 | 1.3104587 | 4.578550 | 0.0015772 | 0.1894612 |
| <GO:0002224> | toll-like receptor signaling pathway | 124 | 3 | 0.2351619 | 12.757169 | 0.0016191 | 0.1915971 |
| <GO:1901796> | regulation of signal transduction by p53 class mediator | 124 | 3 | 0.2351619 | 12.757169 | 0.0016191 | 0.1915971 |
| <GO:0000462> | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 33 | 2 | 0.0625834 | 31.957351 | 0.0017637 | 0.2056349 |
| <GO:0014002> | astrocyte development | 33 | 2 | 0.0625834 | 31.957351 | 0.0017637 | 0.2056349 |
| <GO:0080134> | regulation of response to stress | 1261 | 8 | 2.3914448 | 3.345258 | 0.0017791 | 0.2059226 |
| <GO:0045089> | positive regulation of innate immune response | 282 | 4 | 0.5348037 | 7.479380 | 0.0018462 | 0.2073950 |
| <GO:0007618> | mating | 34 | 2 | 0.0644799 | 31.017429 | 0.0018717 | 0.2073950 |
| <GO:0006807> | nitrogen compound metabolic process | 8795 | 24 | 16.6794268 | 1.438898 | 0.0018861 | 0.2073950 |
| <GO:0038002> | endocrine signaling | 1 | 1 | 0.0018965 | 527.296296 | 0.0018965 | 0.2073950 |
| <GO:0061366> | behavioral response to chemical pain | 1 | 1 | 0.0018965 | 527.296296 | 0.0018965 | 0.2073950 |
| <GO:0061368> | behavioral response to formalin induced pain | 1 | 1 | 0.0018965 | 527.296296 | 0.0018965 | 0.2073950 |
| <GO:1902167> | positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | 1 | 1 | 0.0018965 | 527.296296 | 0.0018965 | 0.2073950 |
| <GO:1904803> | regulation of translation involved in cellular response to UV | 1 | 1 | 0.0018965 | 527.296296 | 0.0018965 | 0.2073950 |
| <GO:0046330> | positive regulation of JNK cascade | 132 | 3 | 0.2503336 | 11.984007 | 0.0019364 | 0.2103116 |
| <GO:0006810> | transport | 4399 | 16 | 8.3425581 | 1.917877 | 0.0021101 | 0.2276195 |
| <GO:1904645> | response to amyloid-beta | 37 | 2 | 0.0701693 | 28.502502 | 0.0022142 | 0.2372387 |
| <GO:0002262> | myeloid cell homeostasis | 139 | 3 | 0.2636089 | 11.380496 | 0.0022438 | 0.2387947 |
| <GO:0007416> | synapse assembly | 140 | 3 | 0.2655054 | 11.299206 | 0.0022901 | 0.2420917 |
| <GO:0032268> | regulation of cellular protein metabolic process | 2353 | 11 | 4.4623867 | 2.465049 | 0.0024126 | 0.2533534 |
| <GO:0045861> | negative regulation of proteolysis | 306 | 4 | 0.5803189 | 6.892762 | 0.0024855 | 0.2592881 |
| <GO:1900744> | regulation of p38MAPK cascade | 40 | 2 | 0.0758587 | 26.364815 | 0.0025842 | 0.2678274 |
| <GO:0071902> | positive regulation of protein serine/threonine kinase activity | 311 | 4 | 0.5898012 | 6.781946 | 0.0026357 | 0.2713873 |
| <GO:0070997> | neuron death | 312 | 4 | 0.5916977 | 6.760209 | 0.0026664 | 0.2727850 |
| <GO:0006952> | defense response | 1356 | 8 | 2.5716092 | 3.110893 | 0.0028262 | 0.2872791 |
| <GO:0043405> | regulation of MAP kinase activity | 321 | 4 | 0.6087659 | 6.570670 | 0.0029547 | 0.2984235 |
| <GO:0030490> | maturation of SSU-rRNA | 43 | 2 | 0.0815481 | 24.525409 | 0.0029812 | 0.2992002 |
| <GO:0032874> | positive regulation of stress-activated MAPK cascade | 157 | 3 | 0.2977453 | 10.075725 | 0.0031687 | 0.3139937 |
| <GO:0070304> | positive regulation of stress-activated protein kinase signaling cascade | 158 | 3 | 0.2996418 | 10.011955 | 0.0032260 | 0.3139937 |
| <GO:0051707> | response to other organism | 797 | 6 | 1.5114842 | 3.969608 | 0.0032463 | 0.3139937 |
| <GO:0008542> | visual learning | 45 | 2 | 0.0853410 | 23.435391 | 0.0032609 | 0.3139937 |
| <GO:0038066> | p38MAPK cascade | 45 | 2 | 0.0853410 | 23.435391 | 0.0032609 | 0.3139937 |
| <GO:2000059> | negative regulation of ubiquitin-dependent protein catabolic process | 45 | 2 | 0.0853410 | 23.435391 | 0.0032609 | 0.3139937 |
| <GO:0050821> | protein stabilization | 159 | 3 | 0.3015382 | 9.948987 | 0.0032839 | 0.3139937 |
| <GO:0043207> | response to external biotic stimulus | 799 | 6 | 1.5152771 | 3.959672 | 0.0032871 | 0.3139937 |
| <GO:0048168> | regulation of neuronal synaptic plasticity | 46 | 2 | 0.0872375 | 22.925926 | 0.0034051 | 0.3233217 |
| <GO:0002221> | pattern recognition receptor signaling pathway | 164 | 3 | 0.3110206 | 9.645664 | 0.0035830 | 0.3381884 |
| <GO:0006955> | immune response | 1746 | 9 | 3.3112313 | 2.718022 | 0.0036437 | 0.3414184 |
| <GO:0009607> | response to biotic stimulus | 820 | 6 | 1.5551029 | 3.858266 | 0.0037393 | 0.3414184 |
| <GO:0000461> | endonucleolytic cleavage to generate mature 3’-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 2 | 1 | 0.0037929 | 263.648148 | 0.0037895 | 0.3414184 |
| <GO:0021896> | forebrain astrocyte differentiation | 2 | 1 | 0.0037929 | 263.648148 | 0.0037895 | 0.3414184 |
| <GO:0021897> | forebrain astrocyte development | 2 | 1 | 0.0037929 | 263.648148 | 0.0037895 | 0.3414184 |
| <GO:0051563> | smooth endoplasmic reticulum calcium ion homeostasis | 2 | 1 | 0.0037929 | 263.648148 | 0.0037895 | 0.3414184 |
| <GO:0071874> | cellular response to norepinephrine stimulus | 2 | 1 | 0.0037929 | 263.648148 | 0.0037895 | 0.3414184 |
| <GO:2000435> | negative regulation of protein neddylation | 2 | 1 | 0.0037929 | 263.648148 | 0.0037895 | 0.3414184 |
| <GO:0007632> | visual behavior | 50 | 2 | 0.0948233 | 21.091852 | 0.0040114 | 0.3573558 |
| <GO:1990090> | cellular response to nerve growth factor stimulus | 50 | 2 | 0.0948233 | 21.091852 | 0.0040114 | 0.3573558 |
| <GO:0051965> | positive regulation of synapse assembly | 51 | 2 | 0.0967198 | 20.678286 | 0.0041703 | 0.3673804 |
| <GO:2001244> | positive regulation of intrinsic apoptotic signaling pathway | 51 | 2 | 0.0967198 | 20.678286 | 0.0041703 | 0.3673804 |
| <GO:0044238> | primary metabolic process | 9173 | 24 | 17.3962914 | 1.379604 | 0.0042809 | 0.3745159 |
| <GO:0046328> | regulation of JNK cascade | 175 | 3 | 0.3318817 | 9.039365 | 0.0042985 | 0.3745159 |
| <GO:0045787> | positive regulation of cell cycle | 358 | 4 | 0.6789352 | 5.891579 | 0.0043660 | 0.3749931 |
| <GO:0043123> | positive regulation of I-kappaB kinase/NF-kappaB signaling | 176 | 3 | 0.3337782 | 8.988005 | 0.0043676 | 0.3749931 |
| <GO:0051246> | regulation of protein metabolic process | 2532 | 11 | 4.8018543 | 2.290782 | 0.0043750 | 0.3749931 |
| <GO:0051438> | regulation of ubiquitin-protein transferase activity | 53 | 2 | 0.1005127 | 19.897973 | 0.0044967 | 0.3813056 |
| <GO:1990089> | response to nerve growth factor | 53 | 2 | 0.1005127 | 19.897973 | 0.0044967 | 0.3813056 |
| <GO:0046579> | positive regulation of Ras protein signal transduction | 54 | 2 | 0.1024092 | 19.529492 | 0.0046642 | 0.3913245 |
| <GO:0070498> | interleukin-1-mediated signaling pathway | 54 | 2 | 0.1024092 | 19.529492 | 0.0046642 | 0.3913245 |
| <GO:0031396> | regulation of protein ubiquitination | 181 | 3 | 0.3432605 | 8.739718 | 0.0047229 | 0.3941666 |
| <GO:0002223> | stimulatory C-type lectin receptor signaling pathway | 56 | 2 | 0.1062021 | 18.832011 | 0.0050078 | 0.4145560 |
| <GO:1901215> | negative regulation of neuron death | 185 | 3 | 0.3508464 | 8.550751 | 0.0050195 | 0.4145560 |
| <GO:0002220> | innate immune response activating cell surface receptor signaling pathway | 58 | 2 | 0.1099951 | 18.182631 | 0.0053627 | 0.4371464 |
| <GO:0042255> | ribosome assembly | 58 | 2 | 0.1099951 | 18.182631 | 0.0053627 | 0.4371464 |
| <GO:0080135> | regulation of cellular response to stress | 617 | 5 | 1.1701201 | 4.273066 | 0.0054941 | 0.4371464 |
| <GO:0050807> | regulation of synapse organization | 192 | 3 | 0.3641217 | 8.239005 | 0.0055653 | 0.4371464 |
| <GO:0044237> | cellular metabolic process | 9305 | 24 | 17.6466250 | 1.360033 | 0.0056276 | 0.4371464 |
| <GO:0002265> | astrocyte activation involved in immune response | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:0021553> | olfactory nerve development | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:0061890> | positive regulation of astrocyte activation | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:0071873> | response to norepinephrine | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:0072717> | cellular response to actinomycin D | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:1902162> | regulation of DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:1902164> | positive regulation of DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:1905598> | negative regulation of low-density lipoprotein receptor activity | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:2000434> | regulation of protein neddylation | 3 | 1 | 0.0056894 | 175.765432 | 0.0056790 | 0.4371464 |
| <GO:0002684> | positive regulation of immune system process | 894 | 6 | 1.6954415 | 3.538901 | 0.0057126 | 0.4376073 |
| <GO:0051057> | positive regulation of small GTPase mediated signal transduction | 61 | 2 | 0.1156845 | 17.288403 | 0.0059163 | 0.4510288 |
| <GO:0050803> | regulation of synapse structure or activity | 198 | 3 | 0.3755005 | 7.989338 | 0.0060605 | 0.4598160 |
| <GO:0001934> | positive regulation of protein phosphorylation | 917 | 6 | 1.7390602 | 3.450139 | 0.0064597 | 0.4877716 |
| <GO:1903320> | regulation of protein modification by small protein conjugation or removal | 205 | 3 | 0.3887757 | 7.716531 | 0.0066708 | 0.5013238 |
| <GO:1903051> | negative regulation of proteolysis involved in cellular protein catabolic process | 66 | 2 | 0.1251668 | 15.978676 | 0.0068944 | 0.5156784 |
| <GO:0031397> | negative regulation of protein ubiquitination | 67 | 2 | 0.1270633 | 15.740188 | 0.0070982 | 0.5261402 |
| <GO:0072331> | signal transduction by p53 class mediator | 211 | 3 | 0.4001545 | 7.497104 | 0.0072222 | 0.5261402 |
| <GO:0009314> | response to radiation | 415 | 4 | 0.7870338 | 5.082374 | 0.0073405 | 0.5261402 |
| <GO:0002757> | immune response-activating signal transduction | 417 | 4 | 0.7908267 | 5.057998 | 0.0074642 | 0.5261402 |
| <GO:0048708> | astrocyte differentiation | 69 | 2 | 0.1308562 | 15.283951 | 0.0075141 | 0.5261402 |
| <GO:1901224> | positive regulation of NIK/NF-kappaB signaling | 69 | 2 | 0.1308562 | 15.283951 | 0.0075141 | 0.5261402 |
| <GO:0014005> | microglia development | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0016199> | axon midline choice point recognition | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0034136> | negative regulation of toll-like receptor 2 signaling pathway | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0035022> | positive regulation of Rac protein signal transduction | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0042270> | protection from natural killer cell mediated cytotoxicity | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0043378> | positive regulation of CD8-positive, alpha-beta T cell differentiation | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0048669> | collateral sprouting in absence of injury | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0072716> | response to actinomycin D | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0150003> | regulation of spontaneous synaptic transmission | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:1905908> | positive regulation of amyloid fibril formation | 4 | 1 | 0.0075859 | 131.824074 | 0.0075651 | 0.5261402 |
| <GO:0070374> | positive regulation of ERK1 and ERK2 cascade | 216 | 3 | 0.4096369 | 7.323560 | 0.0077020 | 0.5333189 |
| <GO:0051402> | neuron apoptotic process | 217 | 3 | 0.4115333 | 7.289810 | 0.0078001 | 0.5377679 |
| <GO:0032872> | regulation of stress-activated MAPK cascade | 218 | 3 | 0.4134298 | 7.256371 | 0.0078990 | 0.5422294 |
| <GO:0070302> | regulation of stress-activated protein kinase signaling cascade | 220 | 3 | 0.4172227 | 7.190404 | 0.0080991 | 0.5531010 |
| <GO:0042327> | positive regulation of phosphorylation | 962 | 6 | 1.8244012 | 3.288750 | 0.0081272 | 0.5531010 |
| <GO:0043122> | regulation of I-kappaB kinase/NF-kappaB signaling | 221 | 3 | 0.4191192 | 7.157868 | 0.0082002 | 0.5546810 |
| <GO:0071704> | organic substance metabolic process | 9494 | 24 | 18.0050572 | 1.332959 | 0.0082323 | 0.5546810 |
| <GO:0002682> | regulation of immune system process | 1278 | 7 | 2.4236848 | 2.888164 | 0.0082553 | 0.5546810 |
| <GO:0008306> | associative learning | 74 | 2 | 0.1403386 | 14.251251 | 0.0086010 | 0.5754663 |
| <GO:0007611> | learning or memory | 226 | 3 | 0.4286015 | 6.999508 | 0.0087172 | 0.5803586 |
| <GO:0070647> | protein modification by small protein conjugation or removal | 977 | 6 | 1.8528482 | 3.238258 | 0.0087473 | 0.5803586 |
| <GO:0072332> | intrinsic apoptotic signaling pathway by p53 class mediator | 75 | 2 | 0.1422350 | 14.061235 | 0.0088263 | 0.5807435 |
| <GO:1903321> | negative regulation of protein modification by small protein conjugation or removal | 75 | 2 | 0.1422350 | 14.061235 | 0.0088263 | 0.5807435 |
| <GO:0002694> | regulation of leukocyte activation | 446 | 4 | 0.8458243 | 4.729115 | 0.0094168 | 0.6040852 |
| <GO:0002764> | immune response-regulating signaling pathway | 446 | 4 | 0.8458243 | 4.729115 | 0.0094168 | 0.6040852 |
| <GO:0014004> | microglia differentiation | 5 | 1 | 0.0094823 | 105.459259 | 0.0094478 | 0.6040852 |
| <GO:0051300> | spindle pole body organization | 5 | 1 | 0.0094823 | 105.459259 | 0.0094478 | 0.6040852 |
| <GO:0051599> | response to hydrostatic pressure | 5 | 1 | 0.0094823 | 105.459259 | 0.0094478 | 0.6040852 |
| <GO:0061888> | regulation of astrocyte activation | 5 | 1 | 0.0094823 | 105.459259 | 0.0094478 | 0.6040852 |
| <GO:1902498> | regulation of protein autoubiquitination | 5 | 1 | 0.0094823 | 105.459259 | 0.0094478 | 0.6040852 |
| <GO:0071158> | positive regulation of cell cycle arrest | 78 | 2 | 0.1479244 | 13.520418 | 0.0095183 | 0.6061483 |
| <GO:1903363> | negative regulation of cellular protein catabolic process | 79 | 2 | 0.1498209 | 13.349273 | 0.0097541 | 0.6186850 |
| <GO:0031399> | regulation of protein modification process | 1667 | 8 | 3.1614104 | 2.530516 | 0.0099655 | 0.6295732 |
| <GO:0009966> | regulation of signal transduction | 2831 | 11 | 5.3688979 | 2.048838 | 0.0104366 | 0.6567220 |
| <GO:0045859> | regulation of protein kinase activity | 724 | 5 | 1.3730421 | 3.641549 | 0.0106559 | 0.6678653 |
| <GO:0009605> | response to external stimulus | 2057 | 9 | 3.9010325 | 2.307081 | 0.0108206 | 0.6755236 |
| <GO:0010562> | positive regulation of phosphorus metabolic process | 1026 | 6 | 1.9457751 | 3.083604 | 0.0110145 | 0.6822515 |
| <GO:0045937> | positive regulation of phosphate metabolic process | 1026 | 6 | 1.9457751 | 3.083604 | 0.0110145 | 0.6822515 |
| <GO:0016198> | axon choice point recognition | 6 | 1 | 0.0113788 | 87.882716 | 0.0113270 | 0.6829344 |
| <GO:0035900> | response to isolation stress | 6 | 1 | 0.0113788 | 87.882716 | 0.0113270 | 0.6829344 |
| <GO:0043376> | regulation of CD8-positive, alpha-beta T cell differentiation | 6 | 1 | 0.0113788 | 87.882716 | 0.0113270 | 0.6829344 |
| <GO:0060385> | axonogenesis involved in innervation | 6 | 1 | 0.0113788 | 87.882716 | 0.0113270 | 0.6829344 |
| <GO:0098814> | spontaneous synaptic transmission | 6 | 1 | 0.0113788 | 87.882716 | 0.0113270 | 0.6829344 |
| <GO:1902231> | positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage | 6 | 1 | 0.0113788 | 87.882716 | 0.0113270 | 0.6829344 |
| <GO:2001187> | positive regulation of CD8-positive, alpha-beta T cell activation | 6 | 1 | 0.0113788 | 87.882716 | 0.0113270 | 0.6829344 |
| <GO:0032092> | positive regulation of protein binding | 86 | 2 | 0.1630962 | 12.262705 | 0.0114776 | 0.6893938 |
| <GO:0007249> | I-kappaB kinase/NF-kappaB signaling | 251 | 3 | 0.4760132 | 6.302346 | 0.0115883 | 0.6934193 |
| <GO:0050790> | regulation of catalytic activity | 2083 | 9 | 3.9503407 | 2.278284 | 0.0117266 | 0.6965349 |
| <GO:0071900> | regulation of protein serine/threonine kinase activity | 476 | 4 | 0.9027183 | 4.431061 | 0.0117630 | 0.6965349 |
| <GO:0030097> | hemopoiesis | 742 | 5 | 1.4071785 | 3.553209 | 0.0117722 | 0.6965349 |
| <GO:0050865> | regulation of cell activation | 479 | 4 | 0.9084077 | 4.403309 | 0.0120167 | 0.7083574 |
| <GO:0034504> | protein localization to nucleus | 258 | 3 | 0.4892885 | 6.131352 | 0.0124792 | 0.7328976 |
| <GO:0050890> | cognition | 259 | 3 | 0.4911849 | 6.107679 | 0.0126096 | 0.7331526 |
| <GO:0090068> | positive regulation of cell cycle process | 259 | 3 | 0.4911849 | 6.107679 | 0.0126096 | 0.7331526 |
| <GO:0045860> | positive regulation of protein kinase activity | 486 | 4 | 0.9216829 | 4.339887 | 0.0126222 | 0.7331526 |
| <GO:0002253> | activation of immune response | 492 | 4 | 0.9330617 | 4.286962 | 0.0131568 | 0.7530789 |
| <GO:0023035> | CD40 signaling pathway | 7 | 1 | 0.0132753 | 75.328042 | 0.0132027 | 0.7530789 |
| <GO:0034137> | positive regulation of toll-like receptor 2 signaling pathway | 7 | 1 | 0.0132753 | 75.328042 | 0.0132027 | 0.7530789 |
| <GO:0034144> | negative regulation of toll-like receptor 4 signaling pathway | 7 | 1 | 0.0132753 | 75.328042 | 0.0132027 | 0.7530789 |
| <GO:0090647> | modulation of age-related behavioral decline | 7 | 1 | 0.0132753 | 75.328042 | 0.0132027 | 0.7530789 |
| <GO:0021782> | glial cell development | 93 | 2 | 0.1763714 | 11.339705 | 0.0133252 | 0.7557149 |
| <GO:0006468> | protein phosphorylation | 1753 | 8 | 3.3245066 | 2.406372 | 0.0133579 | 0.7557149 |
| <GO:0051704> | multi-organism process | 2127 | 9 | 4.0337852 | 2.231155 | 0.0133919 | 0.7557149 |
| <GO:0033554> | cellular response to stress | 1771 | 8 | 3.3586430 | 2.381914 | 0.0141663 | 0.7965773 |
| <GO:0048534> | hematopoietic or lymphoid organ development | 782 | 5 | 1.4830372 | 3.371460 | 0.0145374 | 0.8145595 |
| <GO:1901222> | regulation of NIK/NF-kappaB signaling | 98 | 2 | 0.1858538 | 10.761149 | 0.0147190 | 0.8218280 |
| <GO:0000447> | endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 8 | 1 | 0.0151717 | 65.912037 | 0.0150751 | 0.8271480 |
| <GO:0006610> | ribosomal protein import into nucleus | 8 | 1 | 0.0151717 | 65.912037 | 0.0150751 | 0.8271480 |
| <GO:0031666> | positive regulation of lipopolysaccharide-mediated signaling pathway | 8 | 1 | 0.0151717 | 65.912037 | 0.0150751 | 0.8271480 |
| <GO:0071316> | cellular response to nicotine | 8 | 1 | 0.0151717 | 65.912037 | 0.0150751 | 0.8271480 |
| <GO:1905906> | regulation of amyloid fibril formation | 8 | 1 | 0.0151717 | 65.912037 | 0.0150751 | 0.8271480 |
| <GO:0043549> | regulation of kinase activity | 791 | 5 | 1.5001054 | 3.333099 | 0.0152158 | 0.8319906 |
| <GO:1901214> | regulation of neuron death | 280 | 3 | 0.5310107 | 5.649603 | 0.0155317 | 0.8463072 |
| <GO:0071156> | regulation of cell cycle arrest | 101 | 2 | 0.1915432 | 10.441511 | 0.0155844 | 0.8463072 |
| <GO:0002696> | positive regulation of leukocyte activation | 281 | 3 | 0.5329072 | 5.629498 | 0.0156796 | 0.8485735 |
| <GO:0032270> | positive regulation of cellular protein metabolic process | 1447 | 7 | 2.7441877 | 2.550846 | 0.0158486 | 0.8548012 |
| <GO:0031401> | positive regulation of protein modification process | 1113 | 6 | 2.1107677 | 2.842568 | 0.0160401 | 0.8592851 |
| <GO:0045321> | leukocyte activation | 1113 | 6 | 2.1107677 | 2.842568 | 0.0160401 | 0.8592851 |
| <GO:0033674> | positive regulation of kinase activity | 523 | 4 | 0.9918522 | 4.032859 | 0.0161515 | 0.8623381 |
| <GO:0009416> | response to light stimulus | 286 | 3 | 0.5423895 | 5.531080 | 0.0164314 | 0.8724202 |
| <GO:0010628> | positive regulation of gene expression | 1818 | 8 | 3.4477769 | 2.320336 | 0.0164504 | 0.8724202 |
| <GO:0070372> | regulation of ERK1 and ERK2 cascade | 287 | 3 | 0.5442860 | 5.511808 | 0.0165842 | 0.8765858 |
| <GO:0030218> | erythrocyte differentiation | 105 | 2 | 0.1991290 | 10.043739 | 0.0167717 | 0.8780436 |
| <GO:0007610> | behavior | 530 | 4 | 1.0051275 | 3.979595 | 0.0168829 | 0.8780436 |
| <GO:0016322> | neuron remodeling | 9 | 1 | 0.0170682 | 58.588477 | 0.0169440 | 0.8780436 |
| <GO:0031125> | rRNA 3’-end processing | 9 | 1 | 0.0170682 | 58.588477 | 0.0169440 | 0.8780436 |
| <GO:0048266> | behavioral response to pain | 9 | 1 | 0.0170682 | 58.588477 | 0.0169440 | 0.8780436 |
| <GO:1903980> | positive regulation of microglial cell activation | 9 | 1 | 0.0170682 | 58.588477 | 0.0169440 | 0.8780436 |
| <GO:0050867> | positive regulation of cell activation | 290 | 3 | 0.5499754 | 5.454789 | 0.0170474 | 0.8805222 |
| <GO:0007568> | aging | 292 | 3 | 0.5537684 | 5.417428 | 0.0173602 | 0.8917421 |
| <GO:0010604> | positive regulation of macromolecule metabolic process | 3032 | 11 | 5.7500878 | 1.913014 | 0.0173771 | 0.8917421 |
| <GO:0008152> | metabolic process | 9888 | 24 | 18.7522652 | 1.279845 | 0.0174463 | 0.8924066 |
| <GO:0002520> | immune system development | 824 | 5 | 1.5626888 | 3.199613 | 0.0178874 | 0.9120293 |
| <GO:0009615> | response to virus | 297 | 3 | 0.5632507 | 5.326225 | 0.0181565 | 0.9227785 |
| <GO:0034135> | regulation of toll-like receptor 2 signaling pathway | 10 | 1 | 0.0189647 | 52.729630 | 0.0188095 | 0.9379333 |
| <GO:0051124> | synaptic growth at neuromuscular junction | 10 | 1 | 0.0189647 | 52.729630 | 0.0188095 | 0.9379333 |
| <GO:0071287> | cellular response to manganese ion | 10 | 1 | 0.0189647 | 52.729630 | 0.0188095 | 0.9379333 |
| <GO:1900044> | regulation of protein K63-linked ubiquitination | 10 | 1 | 0.0189647 | 52.729630 | 0.0188095 | 0.9379333 |
| <GO:1900272> | negative regulation of long-term synaptic potentiation | 10 | 1 | 0.0189647 | 52.729630 | 0.0188095 | 0.9379333 |
| <GO:1990535> | neuron projection maintenance | 10 | 1 | 0.0189647 | 52.729630 | 0.0188095 | 0.9379333 |
| <GO:0050776> | regulation of immune response | 837 | 5 | 1.5873428 | 3.149918 | 0.0190215 | 0.9455300 |
| <GO:0038061> | NIK/NF-kappaB signaling | 113 | 2 | 0.2143008 | 9.332678 | 0.0192585 | 0.9536580 |
| <GO:0070371> | ERK1 and ERK2 cascade | 304 | 3 | 0.5765260 | 5.203582 | 0.0193053 | 0.9536580 |
| <GO:0000478> | endonucleolytic cleavage involved in rRNA processing | 11 | 1 | 0.0208611 | 47.936027 | 0.0206716 | 1.0000000 |
| <GO:0000479> | endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 11 | 1 | 0.0208611 | 47.936027 | 0.0206716 | 1.0000000 |
| <GO:0010623> | programmed cell death involved in cell development | 11 | 1 | 0.0208611 | 47.936027 | 0.0206716 | 1.0000000 |
| <GO:0050966> | detection of mechanical stimulus involved in sensory perception of pain | 11 | 1 | 0.0208611 | 47.936027 | 0.0206716 | 1.0000000 |
| <GO:1902004> | positive regulation of amyloid-beta formation | 11 | 1 | 0.0208611 | 47.936027 | 0.0206716 | 1.0000000 |
| <GO:2000774> | positive regulation of cellular senescence | 11 | 1 | 0.0208611 | 47.936027 | 0.0206716 | 1.0000000 |
| <GO:0071347> | cellular response to interleukin-1 | 119 | 2 | 0.2256796 | 8.862123 | 0.0212195 | 1.0000000 |
| <GO:0006417> | regulation of translation | 316 | 3 | 0.5992836 | 5.005978 | 0.0213676 | 1.0000000 |
| <GO:0051247> | positive regulation of protein metabolic process | 1543 | 7 | 2.9262485 | 2.392141 | 0.0219480 | 1.0000000 |
| <GO:0042177> | negative regulation of protein catabolic process | 122 | 2 | 0.2313690 | 8.644202 | 0.0222302 | 1.0000000 |
| <GO:0001967> | suckling behavior | 12 | 1 | 0.0227576 | 43.941358 | 0.0225303 | 1.0000000 |
| <GO:0038180> | nerve growth factor signaling pathway | 12 | 1 | 0.0227576 | 43.941358 | 0.0225303 | 1.0000000 |
| <GO:0045953> | negative regulation of natural killer cell mediated cytotoxicity | 12 | 1 | 0.0227576 | 43.941358 | 0.0225303 | 1.0000000 |
| <GO:0048934> | peripheral nervous system neuron differentiation | 12 | 1 | 0.0227576 | 43.941358 | 0.0225303 | 1.0000000 |
| <GO:0048935> | peripheral nervous system neuron development | 12 | 1 | 0.0227576 | 43.941358 | 0.0225303 | 1.0000000 |
| <GO:0090343> | positive regulation of cell aging | 12 | 1 | 0.0227576 | 43.941358 | 0.0225303 | 1.0000000 |
| <GO:0010646> | regulation of cell communication | 3150 | 11 | 5.9738709 | 1.841352 | 0.0228762 | 1.0000000 |
| <GO:0006508> | proteolysis | 1567 | 7 | 2.9717637 | 2.355504 | 0.0237036 | 1.0000000 |
| <GO:0051094> | positive regulation of developmental process | 1215 | 6 | 2.3042073 | 2.603932 | 0.0237806 | 1.0000000 |
| <GO:0031123> | RNA 3’-end processing | 127 | 2 | 0.2408513 | 8.303879 | 0.0239584 | 1.0000000 |
| <GO:0023051> | regulation of signaling | 3178 | 11 | 6.0269720 | 1.825129 | 0.0243584 | 1.0000000 |
| <GO:0000463> | maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0002716> | negative regulation of natural killer cell mediated immunity | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0006878> | cellular copper ion homeostasis | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0035020> | regulation of Rac protein signal transduction | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0043374> | CD8-positive, alpha-beta T cell differentiation | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0043517> | positive regulation of DNA damage response, signal transduction by p53 class mediator | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0050961> | detection of temperature stimulus involved in sensory perception | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0050965> | detection of temperature stimulus involved in sensory perception of pain | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:1902993> | positive regulation of amyloid precursor protein catabolic process | 13 | 1 | 0.0246541 | 40.561254 | 0.0243856 | 1.0000000 |
| <GO:0051347> | positive regulation of transferase activity | 595 | 4 | 1.1283978 | 3.544849 | 0.0246884 | 1.0000000 |
| <GO:0034250> | positive regulation of cellular amide metabolic process | 131 | 2 | 0.2484372 | 8.050325 | 0.0253798 | 1.0000000 |
| <GO:0002274> | myeloid leukocyte activation | 603 | 4 | 1.1435696 | 3.497819 | 0.0257791 | 1.0000000 |
| <GO:0007612> | learning | 133 | 2 | 0.2522301 | 7.929268 | 0.0261033 | 1.0000000 |
| <GO:0007635> | chemosensory behavior | 14 | 1 | 0.0265505 | 37.664021 | 0.0262376 | 1.0000000 |
| <GO:0009415> | response to water | 14 | 1 | 0.0265505 | 37.664021 | 0.0262376 | 1.0000000 |
| <GO:0048711> | positive regulation of astrocyte differentiation | 14 | 1 | 0.0265505 | 37.664021 | 0.0262376 | 1.0000000 |
| <GO:0060009> | Sertoli cell development | 14 | 1 | 0.0265505 | 37.664021 | 0.0262376 | 1.0000000 |
| <GO:0150078> | positive regulation of neuroinflammatory response | 14 | 1 | 0.0265505 | 37.664021 | 0.0262376 | 1.0000000 |
| <GO:2001185> | regulation of CD8-positive, alpha-beta T cell activation | 14 | 1 | 0.0265505 | 37.664021 | 0.0262376 | 1.0000000 |
| <GO:1901653> | cellular response to peptide | 343 | 3 | 0.6504882 | 4.611921 | 0.0264385 | 1.0000000 |
| <GO:0044093> | positive regulation of molecular function | 1607 | 7 | 3.0476224 | 2.296873 | 0.0268480 | 1.0000000 |
| <GO:0048583> | regulation of response to stimulus | 3667 | 12 | 6.9543443 | 1.725540 | 0.0270075 | 1.0000000 |
| <GO:0043524> | negative regulation of neuron apoptotic process | 136 | 2 | 0.2579195 | 7.754357 | 0.0272042 | 1.0000000 |
| <GO:0001775> | cell activation | 1254 | 6 | 2.3781696 | 2.522949 | 0.0273226 | 1.0000000 |
| <GO:0000028> | ribosomal small subunit assembly | 15 | 1 | 0.0284470 | 35.153086 | 0.0280861 | 1.0000000 |
| <GO:0045116> | protein neddylation | 15 | 1 | 0.0284470 | 35.153086 | 0.0280861 | 1.0000000 |
| <GO:0048143> | astrocyte activation | 15 | 1 | 0.0284470 | 35.153086 | 0.0280861 | 1.0000000 |
| <GO:1902187> | negative regulation of viral release from host cell | 15 | 1 | 0.0284470 | 35.153086 | 0.0280861 | 1.0000000 |
| <GO:1903978> | regulation of microglial cell activation | 15 | 1 | 0.0284470 | 35.153086 | 0.0280861 | 1.0000000 |
| <GO:1990000> | amyloid fibril formation | 15 | 1 | 0.0284470 | 35.153086 | 0.0280861 | 1.0000000 |
| <GO:0032269> | negative regulation of cellular protein metabolic process | 926 | 5 | 1.7561284 | 2.847172 | 0.0280965 | 1.0000000 |
| <GO:0050808> | synapse organization | 352 | 3 | 0.6675564 | 4.494002 | 0.0282614 | 1.0000000 |
| <GO:0009893> | positive regulation of metabolic process | 3257 | 11 | 6.1767929 | 1.780860 | 0.0289377 | 1.0000000 |
| <GO:0070555> | response to interleukin-1 | 141 | 2 | 0.2674018 | 7.479380 | 0.0290804 | 1.0000000 |
| <GO:2000058> | regulation of ubiquitin-dependent protein catabolic process | 143 | 2 | 0.2711948 | 7.374773 | 0.0298452 | 1.0000000 |
| <GO:0001911> | negative regulation of leukocyte mediated cytotoxicity | 16 | 1 | 0.0303435 | 32.956018 | 0.0299312 | 1.0000000 |
| <GO:0002227> | innate immune response in mucosa | 16 | 1 | 0.0303435 | 32.956018 | 0.0299312 | 1.0000000 |
| <GO:0006978> | DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator | 16 | 1 | 0.0303435 | 32.956018 | 0.0299312 | 1.0000000 |
| <GO:0010042> | response to manganese ion | 16 | 1 | 0.0303435 | 32.956018 | 0.0299312 | 1.0000000 |
| <GO:0016048> | detection of temperature stimulus | 16 | 1 | 0.0303435 | 32.956018 | 0.0299312 | 1.0000000 |
| <GO:0055070> | copper ion homeostasis | 16 | 1 | 0.0303435 | 32.956018 | 0.0299312 | 1.0000000 |
| <GO:0030099> | myeloid cell differentiation | 361 | 3 | 0.6846246 | 4.381964 | 0.0301507 | 1.0000000 |
| <GO:0065009> | regulation of molecular function | 2858 | 10 | 5.4201025 | 1.844984 | 0.0310242 | 1.0000000 |
| <GO:0034248> | regulation of cellular amide metabolic process | 366 | 3 | 0.6941069 | 4.322101 | 0.0312289 | 1.0000000 |
| <GO:0042772> | DNA damage response, signal transduction resulting in transcription | 17 | 1 | 0.0322399 | 31.017429 | 0.0317730 | 1.0000000 |
| <GO:0001932> | regulation of protein phosphorylation | 1303 | 6 | 2.4710964 | 2.428072 | 0.0322619 | 1.0000000 |
| <GO:0050778> | positive regulation of immune response | 648 | 4 | 1.2289106 | 3.254915 | 0.0324622 | 1.0000000 |
| <GO:0050806> | positive regulation of synaptic transmission | 150 | 2 | 0.2844700 | 7.030617 | 0.0325849 | 1.0000000 |
| <GO:2001242> | regulation of intrinsic apoptotic signaling pathway | 152 | 2 | 0.2882630 | 6.938109 | 0.0333854 | 1.0000000 |
| <GO:0034143> | regulation of toll-like receptor 4 signaling pathway | 18 | 1 | 0.0341364 | 29.294239 | 0.0336114 | 1.0000000 |
| <GO:0046597> | negative regulation of viral entry into host cell | 18 | 1 | 0.0341364 | 29.294239 | 0.0336114 | 1.0000000 |
| <GO:1902165> | regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | 18 | 1 | 0.0341364 | 29.294239 | 0.0336114 | 1.0000000 |
| <GO:0006954> | inflammatory response | 656 | 4 | 1.2440823 | 3.215221 | 0.0337490 | 1.0000000 |
| <GO:0002683> | negative regulation of immune system process | 379 | 3 | 0.7187610 | 4.173849 | 0.0341275 | 1.0000000 |
| <GO:0048522> | positive regulation of cellular process | 4719 | 14 | 8.9494275 | 1.564346 | 0.0341284 | 1.0000000 |
| <GO:0019221> | cytokine-mediated signaling pathway | 661 | 4 | 1.2535647 | 3.190900 | 0.0345684 | 1.0000000 |
| <GO:0050804> | modulation of chemical synaptic transmission | 384 | 3 | 0.7282433 | 4.119502 | 0.0352789 | 1.0000000 |
| <GO:0051248> | negative regulation of protein metabolic process | 984 | 5 | 1.8661235 | 2.679351 | 0.0353111 | 1.0000000 |
| <GO:0031342> | negative regulation of cell killing | 19 | 1 | 0.0360329 | 27.752437 | 0.0354464 | 1.0000000 |
| <GO:0043371> | negative regulation of CD4-positive, alpha-beta T cell differentiation | 19 | 1 | 0.0360329 | 27.752437 | 0.0354464 | 1.0000000 |
| <GO:0050951> | sensory perception of temperature stimulus | 19 | 1 | 0.0360329 | 27.752437 | 0.0354464 | 1.0000000 |
| <GO:1900273> | positive regulation of long-term synaptic potentiation | 19 | 1 | 0.0360329 | 27.752437 | 0.0354464 | 1.0000000 |
| <GO:2000310> | regulation of NMDA receptor activity | 19 | 1 | 0.0360329 | 27.752437 | 0.0354464 | 1.0000000 |
| <GO:0099177> | regulation of trans-synaptic signaling | 385 | 3 | 0.7301398 | 4.108802 | 0.0355116 | 1.0000000 |
| <GO:0030162> | regulation of proteolysis | 673 | 4 | 1.2763223 | 3.134005 | 0.0365833 | 1.0000000 |
| <GO:0016310> | phosphorylation | 2107 | 8 | 3.9958559 | 2.002074 | 0.0369107 | 1.0000000 |
| <GO:0000470> | maturation of LSU-rRNA | 20 | 1 | 0.0379293 | 26.364815 | 0.0372781 | 1.0000000 |
| <GO:0034162> | toll-like receptor 9 signaling pathway | 20 | 1 | 0.0379293 | 26.364815 | 0.0372781 | 1.0000000 |
| <GO:0050974> | detection of mechanical stimulus involved in sensory perception | 20 | 1 | 0.0379293 | 26.364815 | 0.0372781 | 1.0000000 |
| <GO:0060008> | Sertoli cell differentiation | 20 | 1 | 0.0379293 | 26.364815 | 0.0372781 | 1.0000000 |
| <GO:0071157> | negative regulation of cell cycle arrest | 20 | 1 | 0.0379293 | 26.364815 | 0.0372781 | 1.0000000 |
| <GO:1902003> | regulation of amyloid-beta formation | 20 | 1 | 0.0379293 | 26.364815 | 0.0372781 | 1.0000000 |
| <GO:1902914> | regulation of protein polyubiquitination | 20 | 1 | 0.0379293 | 26.364815 | 0.0372781 | 1.0000000 |
| <GO:2001235> | positive regulation of apoptotic signaling pathway | 162 | 2 | 0.3072276 | 6.509831 | 0.0375031 | 1.0000000 |
| <GO:0048167> | regulation of synaptic plasticity | 163 | 2 | 0.3091241 | 6.469893 | 0.0379252 | 1.0000000 |
| <GO:0044085> | cellular component biogenesis | 2953 | 10 | 5.6002669 | 1.785629 | 0.0381492 | 1.0000000 |
| <GO:1901701> | cellular response to oxygen-containing compound | 1009 | 5 | 1.9135352 | 2.612965 | 0.0387526 | 1.0000000 |
| <GO:0006950> | response to stress | 3399 | 11 | 6.4460912 | 1.706460 | 0.0387677 | 1.0000000 |
| <GO:0000466> | maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0000469> | cleavage involved in rRNA processing | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0002479> | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0031664> | regulation of lipopolysaccharide-mediated signaling pathway | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0032469> | endoplasmic reticulum calcium ion homeostasis | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0032986> | protein-DNA complex disassembly | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0034123> | positive regulation of toll-like receptor signaling pathway | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0034138> | toll-like receptor 3 signaling pathway | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0036037> | CD8-positive, alpha-beta T cell activation | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0048261> | negative regulation of receptor-mediated endocytosis | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0048485> | sympathetic nervous system development | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0051000> | positive regulation of nitric-oxide synthase activity | 21 | 1 | 0.0398258 | 25.109347 | 0.0391065 | 1.0000000 |
| <GO:0043086> | negative regulation of catalytic activity | 697 | 4 | 1.3218375 | 3.026091 | 0.0408176 | 1.0000000 |
| <GO:0051099> | positive regulation of binding | 170 | 2 | 0.3223994 | 6.203486 | 0.0409315 | 1.0000000 |
| <GO:0031348> | negative regulation of defense response | 172 | 2 | 0.3261923 | 6.131352 | 0.0418067 | 1.0000000 |
| <GO:0046639> | negative regulation of alpha-beta T cell differentiation | 23 | 1 | 0.0436187 | 22.925926 | 0.0427531 | 1.0000000 |
| <GO:0071280> | cellular response to copper ion | 23 | 1 | 0.0436187 | 22.925926 | 0.0427531 | 1.0000000 |
| <GO:0150077> | regulation of neuroinflammatory response | 23 | 1 | 0.0436187 | 22.925926 | 0.0427531 | 1.0000000 |
| <GO:0016567> | protein ubiquitination | 711 | 4 | 1.3483880 | 2.966505 | 0.0434141 | 1.0000000 |
| <GO:0006915> | apoptotic process | 1782 | 7 | 3.3795041 | 2.071310 | 0.0440761 | 1.0000000 |
| <GO:0071222> | cellular response to lipopolysaccharide | 178 | 2 | 0.3375711 | 5.924677 | 0.0444748 | 1.0000000 |
| <GO:0010288> | response to lead ion | 24 | 1 | 0.0455152 | 21.970679 | 0.0445715 | 1.0000000 |
| <GO:0035666> | TRIF-dependent toll-like receptor signaling pathway | 24 | 1 | 0.0455152 | 21.970679 | 0.0445715 | 1.0000000 |
| <GO:2000515> | negative regulation of CD4-positive, alpha-beta T cell activation | 24 | 1 | 0.0455152 | 21.970679 | 0.0445715 | 1.0000000 |
| <GO:0042325> | regulation of phosphorylation | 1408 | 6 | 2.6702255 | 2.247001 | 0.0447843 | 1.0000000 |
| <GO:0007623> | circadian rhythm | 180 | 2 | 0.3413641 | 5.858848 | 0.0453782 | 1.0000000 |
| <GO:0002385> | mucosal immune response | 25 | 1 | 0.0474117 | 21.091852 | 0.0463864 | 1.0000000 |
| <GO:0035235> | ionotropic glutamate receptor signaling pathway | 25 | 1 | 0.0474117 | 21.091852 | 0.0463864 | 1.0000000 |
| <GO:0042590> | antigen processing and presentation of exogenous peptide antigen via MHC class I | 25 | 1 | 0.0474117 | 21.091852 | 0.0463864 | 1.0000000 |
| <GO:0048668> | collateral sprouting | 25 | 1 | 0.0474117 | 21.091852 | 0.0463864 | 1.0000000 |
| <GO:1902991> | regulation of amyloid precursor protein catabolic process | 25 | 1 | 0.0474117 | 21.091852 | 0.0463864 | 1.0000000 |
| <GO:1905606> | regulation of presynapse assembly | 25 | 1 | 0.0474117 | 21.091852 | 0.0463864 | 1.0000000 |
| <GO:0051726> | regulation of cell cycle | 1064 | 5 | 2.0178408 | 2.477896 | 0.0470469 | 1.0000000 |
| <GO:0071219> | cellular response to molecule of bacterial origin | 184 | 2 | 0.3489499 | 5.731482 | 0.0472054 | 1.0000000 |
| <GO:0010001> | glial cell differentiation | 185 | 2 | 0.3508464 | 5.700501 | 0.0476664 | 1.0000000 |
| <GO:0000460> | maturation of 5.8S rRNA | 26 | 1 | 0.0493081 | 20.280627 | 0.0481981 | 1.0000000 |
| <GO:0007176> | regulation of epidermal growth factor-activated receptor activity | 26 | 1 | 0.0493081 | 20.280627 | 0.0481981 | 1.0000000 |
| <GO:0032228> | regulation of synaptic transmission, GABAergic | 26 | 1 | 0.0493081 | 20.280627 | 0.0481981 | 1.0000000 |
| <GO:0034205> | amyloid-beta formation | 26 | 1 | 0.0493081 | 20.280627 | 0.0481981 | 1.0000000 |
| <GO:0048265> | response to pain | 26 | 1 | 0.0493081 | 20.280627 | 0.0481981 | 1.0000000 |
| <GO:0060384> | innervation | 26 | 1 | 0.0493081 | 20.280627 | 0.0481981 | 1.0000000 |
| <GO:0099174> | regulation of presynapse organization | 26 | 1 | 0.0493081 | 20.280627 | 0.0481981 | 1.0000000 |
| <GO:0002756> | MyD88-independent toll-like receptor signaling pathway | 27 | 1 | 0.0512046 | 19.529492 | 0.0500065 | 1.0000000 |
| <GO:0010800> | positive regulation of peptidyl-threonine phosphorylation | 27 | 1 | 0.0512046 | 19.529492 | 0.0500065 | 1.0000000 |
| <GO:0032770> | positive regulation of monooxygenase activity | 27 | 1 | 0.0512046 | 19.529492 | 0.0500065 | 1.0000000 |
| <GO:0046596> | regulation of viral entry into host cell | 27 | 1 | 0.0512046 | 19.529492 | 0.0500065 | 1.0000000 |
| <GO:0048710> | regulation of astrocyte differentiation | 27 | 1 | 0.0512046 | 19.529492 | 0.0500065 | 1.0000000 |
| <GO:0051968> | positive regulation of synaptic transmission, glutamatergic | 27 | 1 | 0.0512046 | 19.529492 | 0.0500065 | 1.0000000 |
| <GO:0042127> | regulation of cell proliferation | 1448 | 6 | 2.7460841 | 2.184929 | 0.0502814 | 1.0000000 |
| <GO:0043523> | regulation of neuron apoptotic process | 191 | 2 | 0.3622252 | 5.521427 | 0.0504678 | 1.0000000 |
| <GO:0002251> | organ or tissue specific immune response | 28 | 1 | 0.0531011 | 18.832011 | 0.0518115 | 1.0000000 |
| <GO:0010971> | positive regulation of G2/M transition of mitotic cell cycle | 28 | 1 | 0.0531011 | 18.832011 | 0.0518115 | 1.0000000 |
| <GO:0071480> | cellular response to gamma radiation | 28 | 1 | 0.0531011 | 18.832011 | 0.0518115 | 1.0000000 |
| <GO:2000352> | negative regulation of endothelial cell apoptotic process | 28 | 1 | 0.0531011 | 18.832011 | 0.0518115 | 1.0000000 |
| <GO:1901700> | response to oxygen-containing compound | 1461 | 6 | 2.7707382 | 2.165488 | 0.0521567 | 1.0000000 |
| <GO:0032446> | protein modification by small protein conjugation | 761 | 4 | 1.4432114 | 2.771597 | 0.0534510 | 1.0000000 |
| <GO:0043516> | regulation of DNA damage response, signal transduction by p53 class mediator | 29 | 1 | 0.0549975 | 18.182631 | 0.0536133 | 1.0000000 |
| <GO:0060441> | epithelial tube branching involved in lung morphogenesis | 29 | 1 | 0.0549975 | 18.182631 | 0.0536133 | 1.0000000 |
| <GO:1900181> | negative regulation of protein localization to nucleus | 29 | 1 | 0.0549975 | 18.182631 | 0.0536133 | 1.0000000 |
| <GO:2000406> | positive regulation of T cell migration | 29 | 1 | 0.0549975 | 18.182631 | 0.0536133 | 1.0000000 |
| <GO:1903050> | regulation of proteolysis involved in cellular protein catabolic process | 199 | 2 | 0.3773969 | 5.299460 | 0.0542942 | 1.0000000 |
| <GO:0001774> | microglial cell activation | 30 | 1 | 0.0568940 | 17.576543 | 0.0554118 | 1.0000000 |
| <GO:0002269> | leukocyte activation involved in inflammatory response | 30 | 1 | 0.0568940 | 17.576543 | 0.0554118 | 1.0000000 |
| <GO:0048873> | homeostasis of number of cells within a tissue | 30 | 1 | 0.0568940 | 17.576543 | 0.0554118 | 1.0000000 |
| <GO:0010608> | posttranscriptional regulation of gene expression | 461 | 3 | 0.8742713 | 3.431429 | 0.0555315 | 1.0000000 |
| <GO:0071216> | cellular response to biotic stimulus | 203 | 2 | 0.3849828 | 5.195037 | 0.0562456 | 1.0000000 |
| <GO:1901652> | response to peptide | 464 | 3 | 0.8799607 | 3.409243 | 0.0564143 | 1.0000000 |
| <GO:0002521> | leukocyte differentiation | 465 | 3 | 0.8818571 | 3.401912 | 0.0567101 | 1.0000000 |
| <GO:0043393> | regulation of protein binding | 204 | 2 | 0.3868793 | 5.169571 | 0.0567373 | 1.0000000 |
| <GO:0000027> | ribosomal large subunit assembly | 31 | 1 | 0.0587905 | 17.009558 | 0.0572069 | 1.0000000 |
| <GO:0048011> | neurotrophin TRK receptor signaling pathway | 31 | 1 | 0.0587905 | 17.009558 | 0.0572069 | 1.0000000 |
| <GO:1902186> | regulation of viral release from host cell | 31 | 1 | 0.0587905 | 17.009558 | 0.0572069 | 1.0000000 |
| <GO:1902751> | positive regulation of cell cycle G2/M phase transition | 31 | 1 | 0.0587905 | 17.009558 | 0.0572069 | 1.0000000 |
| <GO:0051962> | positive regulation of nervous system development | 467 | 3 | 0.8856501 | 3.387342 | 0.0573040 | 1.0000000 |
| <GO:0010951> | negative regulation of endopeptidase activity | 208 | 2 | 0.3944651 | 5.070157 | 0.0587195 | 1.0000000 |
| <GO:0016601> | Rac protein signal transduction | 32 | 1 | 0.0606869 | 16.478009 | 0.0589988 | 1.0000000 |
| <GO:0032435> | negative regulation of proteasomal ubiquitin-dependent protein catabolic process | 32 | 1 | 0.0606869 | 16.478009 | 0.0589988 | 1.0000000 |
| <GO:0034142> | toll-like receptor 4 signaling pathway | 32 | 1 | 0.0606869 | 16.478009 | 0.0589988 | 1.0000000 |
| <GO:0051385> | response to mineralocorticoid | 32 | 1 | 0.0606869 | 16.478009 | 0.0589988 | 1.0000000 |
| <GO:0070423> | nucleotide-binding oligomerization domain containing signaling pathway | 32 | 1 | 0.0606869 | 16.478009 | 0.0589988 | 1.0000000 |
| <GO:0012501> | programmed cell death | 1901 | 7 | 3.6051837 | 1.941649 | 0.0593077 | 1.0000000 |
| <GO:0033280> | response to vitamin D | 33 | 1 | 0.0625834 | 15.978676 | 0.0607874 | 1.0000000 |
| <GO:0035872> | nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway | 33 | 1 | 0.0625834 | 15.978676 | 0.0607874 | 1.0000000 |
| <GO:0043276> | anoikis | 33 | 1 | 0.0625834 | 15.978676 | 0.0607874 | 1.0000000 |
| <GO:0043628> | ncRNA 3’-end processing | 33 | 1 | 0.0625834 | 15.978676 | 0.0607874 | 1.0000000 |
| <GO:0071868> | cellular response to monoamine stimulus | 33 | 1 | 0.0625834 | 15.978676 | 0.0607874 | 1.0000000 |
| <GO:0071870> | cellular response to catecholamine stimulus | 33 | 1 | 0.0625834 | 15.978676 | 0.0607874 | 1.0000000 |
| <GO:0010466> | negative regulation of peptidase activity | 214 | 2 | 0.4058439 | 4.928003 | 0.0617382 | 1.0000000 |
| <GO:0010941> | regulation of cell death | 1528 | 6 | 2.8978015 | 2.070535 | 0.0625239 | 1.0000000 |
| <GO:0034122> | negative regulation of toll-like receptor signaling pathway | 34 | 1 | 0.0644799 | 15.508715 | 0.0625727 | 1.0000000 |
| <GO:0042987> | amyloid precursor protein catabolic process | 34 | 1 | 0.0644799 | 15.508715 | 0.0625727 | 1.0000000 |
| <GO:0046636> | negative regulation of alpha-beta T cell activation | 34 | 1 | 0.0644799 | 15.508715 | 0.0625727 | 1.0000000 |
| <GO:2000403> | positive regulation of lymphocyte migration | 34 | 1 | 0.0644799 | 15.508715 | 0.0625727 | 1.0000000 |
| <GO:0046578> | regulation of Ras protein signal transduction | 216 | 2 | 0.4096369 | 4.882373 | 0.0627562 | 1.0000000 |
| <GO:0042113> | B cell activation | 219 | 2 | 0.4153263 | 4.815491 | 0.0642942 | 1.0000000 |
| <GO:0019076> | viral release from host cell | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0035890> | exit from host | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0035891> | exit from host cell | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0038083> | peptidyl-tyrosine autophosphorylation | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0042269> | regulation of natural killer cell mediated cytotoxicity | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0045687> | positive regulation of glial cell differentiation | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0050982> | detection of mechanical stimulus | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0052126> | movement in host environment | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0052192> | movement in environment of other organism involved in symbiotic interaction | 35 | 1 | 0.0663763 | 15.065608 | 0.0643548 | 1.0000000 |
| <GO:0022618> | ribonucleoprotein complex assembly | 222 | 2 | 0.4210157 | 4.750417 | 0.0658452 | 1.0000000 |
| <GO:0002707> | negative regulation of lymphocyte mediated immunity | 36 | 1 | 0.0682728 | 14.647119 | 0.0661336 | 1.0000000 |
| <GO:0019731> | antibacterial humoral response | 36 | 1 | 0.0682728 | 14.647119 | 0.0661336 | 1.0000000 |
| <GO:1900271> | regulation of long-term synaptic potentiation | 36 | 1 | 0.0682728 | 14.647119 | 0.0661336 | 1.0000000 |
| <GO:2000273> | positive regulation of signaling receptor activity | 36 | 1 | 0.0682728 | 14.647119 | 0.0661336 | 1.0000000 |
| <GO:0071310> | cellular response to organic substance | 2367 | 8 | 4.4889373 | 1.782159 | 0.0667445 | 1.0000000 |
| <GO:0006464> | cellular protein modification process | 3699 | 11 | 7.0150313 | 1.568061 | 0.0673129 | 1.0000000 |
| <GO:0036211> | protein modification process | 3699 | 11 | 7.0150313 | 1.568061 | 0.0673129 | 1.0000000 |
| <GO:0048523> | negative regulation of cellular process | 4167 | 12 | 7.9025778 | 1.518492 | 0.0674967 | 1.0000000 |
| <GO:0002715> | regulation of natural killer cell mediated immunity | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0002833> | positive regulation of response to biotic stimulus | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0019985> | translesion synthesis | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0042551> | neuron maturation | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0045581> | negative regulation of T cell differentiation | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0061900> | glial cell activation | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0071867> | response to monoamine | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0071869> | response to catecholamine | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0098815> | modulation of excitatory postsynaptic potential | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0099054> | presynapse assembly | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:2000772> | regulation of cellular senescence | 37 | 1 | 0.0701693 | 14.251251 | 0.0679091 | 1.0000000 |
| <GO:0031330> | negative regulation of cellular catabolic process | 227 | 2 | 0.4304980 | 4.645782 | 0.0684583 | 1.0000000 |
| <GO:0046688> | response to copper ion | 38 | 1 | 0.0720657 | 13.876218 | 0.0696814 | 1.0000000 |
| <GO:1902229> | regulation of intrinsic apoptotic signaling pathway in response to DNA damage | 38 | 1 | 0.0720657 | 13.876218 | 0.0696814 | 1.0000000 |
| <GO:1904036> | negative regulation of epithelial cell apoptotic process | 38 | 1 | 0.0720657 | 13.876218 | 0.0696814 | 1.0000000 |
| <GO:1903362> | regulation of cellular protein catabolic process | 230 | 2 | 0.4361874 | 4.585185 | 0.0700429 | 1.0000000 |
| <GO:0007050> | cell cycle arrest | 232 | 2 | 0.4399803 | 4.545658 | 0.0711060 | 1.0000000 |
| <GO:0038179> | neurotrophin signaling pathway | 39 | 1 | 0.0739622 | 13.520418 | 0.0714504 | 1.0000000 |
| <GO:0050435> | amyloid-beta metabolic process | 39 | 1 | 0.0739622 | 13.520418 | 0.0714504 | 1.0000000 |
| <GO:0051932> | synaptic transmission, GABAergic | 39 | 1 | 0.0739622 | 13.520418 | 0.0714504 | 1.0000000 |
| <GO:0099172> | presynapse organization | 39 | 1 | 0.0739622 | 13.520418 | 0.0714504 | 1.0000000 |
| <GO:2000404> | regulation of T cell migration | 39 | 1 | 0.0739622 | 13.520418 | 0.0714504 | 1.0000000 |
| <GO:0051171> | regulation of nitrogen compound metabolic process | 5172 | 14 | 9.8085271 | 1.427329 | 0.0716668 | 1.0000000 |
| <GO:0019220> | regulation of phosphate metabolic process | 1585 | 6 | 3.0059001 | 1.996074 | 0.0722811 | 1.0000000 |
| <GO:0051174> | regulation of phosphorus metabolic process | 1587 | 6 | 3.0096931 | 1.993559 | 0.0726392 | 1.0000000 |
| <GO:0009617> | response to bacterium | 517 | 3 | 0.9804734 | 3.059746 | 0.0731174 | 1.0000000 |
| <GO:0010799> | regulation of peptidyl-threonine phosphorylation | 40 | 1 | 0.0758587 | 13.182407 | 0.0732162 | 1.0000000 |
| <GO:0030225> | macrophage differentiation | 40 | 1 | 0.0758587 | 13.182407 | 0.0732162 | 1.0000000 |
| <GO:0032480> | negative regulation of type I interferon production | 40 | 1 | 0.0758587 | 13.182407 | 0.0732162 | 1.0000000 |
| <GO:0071826> | ribonucleoprotein complex subunit organization | 236 | 2 | 0.4475662 | 4.468613 | 0.0732486 | 1.0000000 |
| <GO:0033993> | response to lipid | 849 | 4 | 1.6101004 | 2.484317 | 0.0739992 | 1.0000000 |
| <GO:0051602> | response to electrical stimulus | 41 | 1 | 0.0777551 | 12.860885 | 0.0749788 | 1.0000000 |
| <GO:0007411> | axon guidance | 240 | 2 | 0.4551521 | 4.394136 | 0.0754123 | 1.0000000 |
| <GO:0071417> | cellular response to organonitrogen compound | 525 | 3 | 0.9956451 | 3.013122 | 0.0758157 | 1.0000000 |
| <GO:0097485> | neuron projection guidance | 241 | 2 | 0.4570485 | 4.375903 | 0.0759564 | 1.0000000 |
| <GO:0002474> | antigen processing and presentation of peptide antigen via MHC class I | 42 | 1 | 0.0796516 | 12.554674 | 0.0767381 | 1.0000000 |
| <GO:0050999> | regulation of nitric-oxide synthase activity | 42 | 1 | 0.0796516 | 12.554674 | 0.0767381 | 1.0000000 |
| <GO:1900449> | regulation of glutamate receptor signaling pathway | 42 | 1 | 0.0796516 | 12.554674 | 0.0767381 | 1.0000000 |
| <GO:0008219> | cell death | 2018 | 7 | 3.8270703 | 1.829075 | 0.0772639 | 1.0000000 |
| <GO:0051251> | positive regulation of lymphocyte activation | 244 | 2 | 0.4627379 | 4.322101 | 0.0775967 | 1.0000000 |
| <GO:0021545> | cranial nerve development | 43 | 1 | 0.0815481 | 12.262705 | 0.0784942 | 1.0000000 |
| <GO:0048483> | autonomic nervous system development | 43 | 1 | 0.0815481 | 12.262705 | 0.0784942 | 1.0000000 |
| <GO:0016579> | protein deubiquitination | 248 | 2 | 0.4703238 | 4.252389 | 0.0798015 | 1.0000000 |
| <GO:0010033> | response to organic substance | 2893 | 9 | 5.4864789 | 1.640396 | 0.0798631 | 1.0000000 |
| <GO:0006378> | mRNA polyadenylation | 44 | 1 | 0.0834445 | 11.984007 | 0.0802471 | 1.0000000 |
| <GO:0035094> | response to nicotine | 44 | 1 | 0.0834445 | 11.984007 | 0.0802471 | 1.0000000 |
| <GO:0042771> | intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | 44 | 1 | 0.0834445 | 11.984007 | 0.0802471 | 1.0000000 |
| <GO:0043631> | RNA polyadenylation | 44 | 1 | 0.0834445 | 11.984007 | 0.0802471 | 1.0000000 |
| <GO:0090342> | regulation of cell aging | 44 | 1 | 0.0834445 | 11.984007 | 0.0802471 | 1.0000000 |
| <GO:0031400> | negative regulation of protein modification process | 538 | 3 | 1.0202992 | 2.940314 | 0.0802961 | 1.0000000 |
| <GO:0045786> | negative regulation of cell cycle | 540 | 3 | 1.0240922 | 2.929424 | 0.0809957 | 1.0000000 |
| <GO:0051173> | positive regulation of nitrogen compound metabolic process | 2901 | 9 | 5.5016506 | 1.635873 | 0.0810226 | 1.0000000 |
| <GO:0007528> | neuromuscular junction development | 45 | 1 | 0.0853410 | 11.717695 | 0.0819968 | 1.0000000 |
| <GO:0008038> | neuron recognition | 45 | 1 | 0.0853410 | 11.717695 | 0.0819968 | 1.0000000 |
| <GO:0043370> | regulation of CD4-positive, alpha-beta T cell differentiation | 45 | 1 | 0.0853410 | 11.717695 | 0.0819968 | 1.0000000 |
| <GO:0045620> | negative regulation of lymphocyte differentiation | 45 | 1 | 0.0853410 | 11.717695 | 0.0819968 | 1.0000000 |
| <GO:0046638> | positive regulation of alpha-beta T cell differentiation | 45 | 1 | 0.0853410 | 11.717695 | 0.0819968 | 1.0000000 |
| <GO:0042063> | gliogenesis | 252 | 2 | 0.4779097 | 4.184891 | 0.0820263 | 1.0000000 |
| <GO:0007049> | cell cycle | 1642 | 6 | 3.1139987 | 1.926783 | 0.0829081 | 1.0000000 |
| <GO:0002704> | negative regulation of leukocyte mediated immunity | 46 | 1 | 0.0872375 | 11.462963 | 0.0837433 | 1.0000000 |
| <GO:0045824> | negative regulation of innate immune response | 46 | 1 | 0.0872375 | 11.462963 | 0.0837433 | 1.0000000 |
| <GO:0050885> | neuromuscular process controlling balance | 46 | 1 | 0.0872375 | 11.462963 | 0.0837433 | 1.0000000 |
| <GO:0099601> | regulation of neurotransmitter receptor activity | 46 | 1 | 0.0872375 | 11.462963 | 0.0837433 | 1.0000000 |
| <GO:0150076> | neuroinflammatory response | 46 | 1 | 0.0872375 | 11.462963 | 0.0837433 | 1.0000000 |
| <GO:0051348> | negative regulation of transferase activity | 256 | 2 | 0.4854955 | 4.119502 | 0.0842706 | 1.0000000 |
| <GO:0010243> | response to organonitrogen compound | 892 | 4 | 1.6916485 | 2.364557 | 0.0853506 | 1.0000000 |
| <GO:0000731> | DNA synthesis involved in DNA repair | 47 | 1 | 0.0891339 | 11.219070 | 0.0854866 | 1.0000000 |
| <GO:0051353> | positive regulation of oxidoreductase activity | 47 | 1 | 0.0891339 | 11.219070 | 0.0854866 | 1.0000000 |
| <GO:0070534> | protein K63-linked ubiquitination | 47 | 1 | 0.0891339 | 11.219070 | 0.0854866 | 1.0000000 |
| <GO:0048511> | rhythmic process | 259 | 2 | 0.4911849 | 4.071786 | 0.0859665 | 1.0000000 |
| <GO:0006511> | ubiquitin-dependent protein catabolic process | 556 | 3 | 1.0544356 | 2.845124 | 0.0866911 | 1.0000000 |
| <GO:0048518> | positive regulation of biological process | 5307 | 14 | 10.0645501 | 1.391021 | 0.0871756 | 1.0000000 |
| <GO:0006301> | postreplication repair | 48 | 1 | 0.0910304 | 10.985340 | 0.0872267 | 1.0000000 |
| <GO:2000351> | regulation of endothelial cell apoptotic process | 48 | 1 | 0.0910304 | 10.985340 | 0.0872267 | 1.0000000 |
| <GO:0080090> | regulation of primary metabolic process | 5313 | 14 | 10.0759289 | 1.389450 | 0.0879158 | 1.0000000 |
| <GO:0070646> | protein modification by small protein removal | 264 | 2 | 0.5006673 | 3.994669 | 0.0888163 | 1.0000000 |
| <GO:0019941> | modification-dependent protein catabolic process | 562 | 3 | 1.0658144 | 2.814749 | 0.0888712 | 1.0000000 |
| <GO:0000186> | activation of MAPKK activity | 49 | 1 | 0.0929269 | 10.761149 | 0.0889636 | 1.0000000 |
| <GO:0043412> | macromolecule modification | 3875 | 11 | 7.3488094 | 1.496841 | 0.0896228 | 1.0000000 |
| <GO:0009895> | negative regulation of catabolic process | 266 | 2 | 0.5044602 | 3.964634 | 0.0899643 | 1.0000000 |
| <GO:0010948> | negative regulation of cell cycle process | 266 | 2 | 0.5044602 | 3.964634 | 0.0899643 | 1.0000000 |
| <GO:0042267> | natural killer cell mediated cytotoxicity | 50 | 1 | 0.0948233 | 10.545926 | 0.0906973 | 1.0000000 |
| <GO:0042982> | amyloid precursor protein metabolic process | 50 | 1 | 0.0948233 | 10.545926 | 0.0906973 | 1.0000000 |
| <GO:0060425> | lung morphogenesis | 50 | 1 | 0.0948233 | 10.545926 | 0.0906973 | 1.0000000 |
| <GO:0007165> | signal transduction | 4848 | 13 | 9.1940718 | 1.413955 | 0.0915579 | 1.0000000 |
| <GO:0032103> | positive regulation of response to external stimulus | 269 | 2 | 0.5101496 | 3.920419 | 0.0916949 | 1.0000000 |
| <GO:0043632> | modification-dependent macromolecule catabolic process | 570 | 3 | 1.0809862 | 2.775244 | 0.0918149 | 1.0000000 |
| <GO:0043085> | positive regulation of catalytic activity | 1292 | 5 | 2.4502353 | 2.040620 | 0.0923238 | 1.0000000 |
| <GO:0032768> | regulation of monooxygenase activity | 51 | 1 | 0.0967198 | 10.339143 | 0.0924278 | 1.0000000 |
| <GO:0042490> | mechanoreceptor differentiation | 51 | 1 | 0.0967198 | 10.339143 | 0.0924278 | 1.0000000 |
| <GO:0045806> | negative regulation of endocytosis | 51 | 1 | 0.0967198 | 10.339143 | 0.0924278 | 1.0000000 |
| <GO:0071320> | cellular response to cAMP | 51 | 1 | 0.0967198 | 10.339143 | 0.0924278 | 1.0000000 |
| <GO:1901799> | negative regulation of proteasomal protein catabolic process | 51 | 1 | 0.0967198 | 10.339143 | 0.0924278 | 1.0000000 |
| <GO:1901699> | cellular response to nitrogen compound | 575 | 3 | 1.0904685 | 2.751111 | 0.0936759 | 1.0000000 |
| <GO:0010803> | regulation of tumor necrosis factor-mediated signaling pathway | 52 | 1 | 0.0986163 | 10.140313 | 0.0941552 | 1.0000000 |
| <GO:2000112> | regulation of cellular macromolecule biosynthetic process | 3447 | 10 | 6.5371216 | 1.529725 | 0.0949761 | 1.0000000 |
| <GO:0097193> | intrinsic apoptotic signaling pathway | 275 | 2 | 0.5215284 | 3.834882 | 0.0951860 | 1.0000000 |
| <GO:0060548> | negative regulation of cell death | 927 | 4 | 1.7580249 | 2.275281 | 0.0952053 | 1.0000000 |
| <GO:0043068> | positive regulation of programmed cell death | 580 | 3 | 1.0999508 | 2.727395 | 0.0955531 | 1.0000000 |
| <GO:0002753> | cytoplasmic pattern recognition receptor signaling pathway | 53 | 1 | 0.1005127 | 9.948987 | 0.0958794 | 1.0000000 |
| <GO:0010332> | response to gamma radiation | 53 | 1 | 0.1005127 | 9.948987 | 0.0958794 | 1.0000000 |
| <GO:0031663> | lipopolysaccharide-mediated signaling pathway | 53 | 1 | 0.1005127 | 9.948987 | 0.0958794 | 1.0000000 |
| <GO:0072577> | endothelial cell apoptotic process | 53 | 1 | 0.1005127 | 9.948987 | 0.0958794 | 1.0000000 |
| <GO:2000401> | regulation of lymphocyte migration | 53 | 1 | 0.1005127 | 9.948987 | 0.0958794 | 1.0000000 |
| <GO:2000514> | regulation of CD4-positive, alpha-beta T cell activation | 53 | 1 | 0.1005127 | 9.948987 | 0.0958794 | 1.0000000 |
| <GO:0002429> | immune response-activating cell surface receptor signaling pathway | 277 | 2 | 0.5253213 | 3.807193 | 0.0963585 | 1.0000000 |
| <GO:0051172> | negative regulation of nitrogen compound metabolic process | 2128 | 7 | 4.0356817 | 1.734527 | 0.0969222 | 1.0000000 |
| <GO:0031325> | positive regulation of cellular metabolic process | 3007 | 9 | 5.7026761 | 1.578206 | 0.0974231 | 1.0000000 |
| <GO:0002228> | natural killer cell mediated immunity | 54 | 1 | 0.1024092 | 9.764746 | 0.0976005 | 1.0000000 |
| <GO:0065008> | regulation of biological quality | 3471 | 10 | 6.5826368 | 1.519148 | 0.0986707 | 1.0000000 |
| <GO:0006977> | DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest | 55 | 1 | 0.1043057 | 9.587205 | 0.0993183 | 1.0000000 |
| <GO:0072431> | signal transduction involved in mitotic G1 DNA damage checkpoint | 56 | 1 | 0.1062021 | 9.416005 | 0.1010331 | 1.0000000 |
| <GO:1902400> | intracellular signal transduction involved in G1 DNA damage checkpoint | 56 | 1 | 0.1062021 | 9.416005 | 0.1010331 | 1.0000000 |
| <GO:0031323> | regulation of cellular metabolic process | 5417 | 14 | 10.2731615 | 1.362774 | 0.1014562 | 1.0000000 |
| <GO:0061844> | antimicrobial humoral immune response mediated by antimicrobial peptide | 57 | 1 | 0.1080986 | 9.250812 | 0.1027447 | 1.0000000 |
| <GO:0072413> | signal transduction involved in mitotic cell cycle checkpoint | 57 | 1 | 0.1080986 | 9.250812 | 0.1027447 | 1.0000000 |
| <GO:0072678> | T cell migration | 57 | 1 | 0.1080986 | 9.250812 | 0.1027447 | 1.0000000 |
| <GO:1902402> | signal transduction involved in mitotic DNA damage checkpoint | 57 | 1 | 0.1080986 | 9.250812 | 0.1027447 | 1.0000000 |
| <GO:1902403> | signal transduction involved in mitotic DNA integrity checkpoint | 57 | 1 | 0.1080986 | 9.250812 | 0.1027447 | 1.0000000 |
| <GO:0046649> | lymphocyte activation | 601 | 3 | 1.1397766 | 2.632095 | 0.1036099 | 1.0000000 |
| <GO:0035308> | negative regulation of protein dephosphorylation | 58 | 1 | 0.1099951 | 9.091316 | 0.1044531 | 1.0000000 |
| <GO:0045685> | regulation of glial cell differentiation | 58 | 1 | 0.1099951 | 9.091316 | 0.1044531 | 1.0000000 |
| <GO:0071345> | cellular response to cytokine stimulus | 959 | 4 | 1.8187118 | 2.199359 | 0.1046845 | 1.0000000 |
| <GO:0006355> | regulation of transcription, DNA-templated | 3057 | 9 | 5.7974995 | 1.552393 | 0.1058348 | 1.0000000 |
| <GO:0034121> | regulation of toll-like receptor signaling pathway | 59 | 1 | 0.1118916 | 8.937225 | 0.1061585 | 1.0000000 |
| <GO:0038095> | Fc-epsilon receptor signaling pathway | 59 | 1 | 0.1118916 | 8.937225 | 0.1061585 | 1.0000000 |
| <GO:0046635> | positive regulation of alpha-beta T cell activation | 59 | 1 | 0.1118916 | 8.937225 | 0.1061585 | 1.0000000 |
| <GO:0032496> | response to lipopolysaccharide | 294 | 2 | 0.5575613 | 3.587050 | 0.1064926 | 1.0000000 |
| <GO:0007268> | chemical synaptic transmission | 611 | 3 | 1.1587413 | 2.589016 | 0.1075422 | 1.0000000 |
| <GO:0098916> | anterograde trans-synaptic signaling | 611 | 3 | 1.1587413 | 2.589016 | 0.1075422 | 1.0000000 |
| <GO:0046637> | regulation of alpha-beta T cell differentiation | 60 | 1 | 0.1137880 | 8.788272 | 0.1078606 | 1.0000000 |
| <GO:0061515> | myeloid cell development | 60 | 1 | 0.1137880 | 8.788272 | 0.1078606 | 1.0000000 |
| <GO:1901698> | response to nitrogen compound | 970 | 4 | 1.8395729 | 2.174418 | 0.1080440 | 1.0000000 |
| <GO:0045596> | negative regulation of cell differentiation | 615 | 3 | 1.1663272 | 2.572177 | 0.1091320 | 1.0000000 |
| <GO:0014015> | positive regulation of gliogenesis | 61 | 1 | 0.1156845 | 8.644202 | 0.1095597 | 1.0000000 |
| <GO:0051966> | regulation of synaptic transmission, glutamatergic | 61 | 1 | 0.1156845 | 8.644202 | 0.1095597 | 1.0000000 |
| <GO:0099537> | trans-synaptic signaling | 619 | 3 | 1.1739130 | 2.555556 | 0.1107314 | 1.0000000 |
| <GO:0044092> | negative regulation of molecular function | 979 | 4 | 1.8566411 | 2.154428 | 0.1108304 | 1.0000000 |
| <GO:0001910> | regulation of leukocyte mediated cytotoxicity | 62 | 1 | 0.1175810 | 8.504779 | 0.1112557 | 1.0000000 |
| <GO:0031571> | mitotic G1 DNA damage checkpoint | 62 | 1 | 0.1175810 | 8.504779 | 0.1112557 | 1.0000000 |
| <GO:0044819> | mitotic G1/S transition checkpoint | 62 | 1 | 0.1175810 | 8.504779 | 0.1112557 | 1.0000000 |
| <GO:0090398> | cellular senescence | 62 | 1 | 0.1175810 | 8.504779 | 0.1112557 | 1.0000000 |
| <GO:0002768> | immune response-regulating cell surface receptor signaling pathway | 304 | 2 | 0.5765260 | 3.469055 | 0.1125872 | 1.0000000 |
| <GO:0099536> | synaptic signaling | 624 | 3 | 1.1833954 | 2.535078 | 0.1127439 | 1.0000000 |
| <GO:0008088> | axo-dendritic transport | 63 | 1 | 0.1194774 | 8.369782 | 0.1129485 | 1.0000000 |
| <GO:0044783> | G1 DNA damage checkpoint | 63 | 1 | 0.1194774 | 8.369782 | 0.1129485 | 1.0000000 |
| <GO:0051865> | protein autoubiquitination | 63 | 1 | 0.1194774 | 8.369782 | 0.1129485 | 1.0000000 |
| <GO:0009987> | cellular process | 13134 | 27 | 24.9081970 | 1.083981 | 0.1131149 | 1.0000000 |
| <GO:0010556> | regulation of macromolecule biosynthetic process | 3560 | 10 | 6.7514224 | 1.481169 | 0.1131695 | 1.0000000 |
| <GO:0002237> | response to molecule of bacterial origin | 305 | 2 | 0.5784224 | 3.457681 | 0.1132018 | 1.0000000 |
| <GO:0032147> | activation of protein kinase activity | 305 | 2 | 0.5784224 | 3.457681 | 0.1132018 | 1.0000000 |
| <GO:1903506> | regulation of nucleic acid-templated transcription | 3106 | 9 | 5.8904264 | 1.527903 | 0.1145006 | 1.0000000 |
| <GO:0016239> | positive regulation of macroautophagy | 64 | 1 | 0.1213739 | 8.239005 | 0.1146383 | 1.0000000 |
| <GO:0051705> | multi-organism behavior | 64 | 1 | 0.1213739 | 8.239005 | 0.1146383 | 1.0000000 |
| <GO:0010942> | positive regulation of cell death | 629 | 3 | 1.1928777 | 2.514927 | 0.1147709 | 1.0000000 |
| <GO:0051056> | regulation of small GTPase mediated signal transduction | 308 | 2 | 0.5841118 | 3.424002 | 0.1150511 | 1.0000000 |
| <GO:0008285> | negative regulation of cell proliferation | 630 | 3 | 1.1947742 | 2.510935 | 0.1151781 | 1.0000000 |
| <GO:2001141> | regulation of RNA biosynthetic process | 3112 | 9 | 5.9018052 | 1.524957 | 0.1155904 | 1.0000000 |
| <GO:0048678> | response to axon injury | 65 | 1 | 0.1232704 | 8.112251 | 0.1163249 | 1.0000000 |
| <GO:0006513> | protein monoubiquitination | 66 | 1 | 0.1251668 | 7.989338 | 0.1180085 | 1.0000000 |
| <GO:0040014> | regulation of multicellular organism growth | 66 | 1 | 0.1251668 | 7.989338 | 0.1180085 | 1.0000000 |
| <GO:0007422> | peripheral nervous system development | 67 | 1 | 0.1270633 | 7.870094 | 0.1196889 | 1.0000000 |
| <GO:0043507> | positive regulation of JUN kinase activity | 67 | 1 | 0.1270633 | 7.870094 | 0.1196889 | 1.0000000 |
| <GO:0090502> | RNA phosphodiester bond hydrolysis, endonucleolytic | 67 | 1 | 0.1270633 | 7.870094 | 0.1196889 | 1.0000000 |
| <GO:0042981> | regulation of apoptotic process | 1405 | 5 | 2.6645361 | 1.876499 | 0.1211936 | 1.0000000 |
| <GO:0030433> | ubiquitin-dependent ERAD pathway | 68 | 1 | 0.1289598 | 7.754357 | 0.1213663 | 1.0000000 |
| <GO:0051603> | proteolysis involved in cellular protein catabolic process | 648 | 3 | 1.2289106 | 2.441187 | 0.1226041 | 1.0000000 |
| <GO:0050871> | positive regulation of B cell activation | 69 | 1 | 0.1308562 | 7.641975 | 0.1230406 | 1.0000000 |
| <GO:0030098> | lymphocyte differentiation | 321 | 2 | 0.6087659 | 3.285335 | 0.1231566 | 1.0000000 |
| <GO:0070848> | response to growth factor | 651 | 3 | 1.2346000 | 2.429937 | 0.1238593 | 1.0000000 |
| <GO:0033555> | multicellular organismal response to stress | 70 | 1 | 0.1327527 | 7.532804 | 0.1247118 | 1.0000000 |
| <GO:0050830> | defense response to Gram-positive bacterium | 70 | 1 | 0.1327527 | 7.532804 | 0.1247118 | 1.0000000 |
| <GO:0071479> | cellular response to ionizing radiation | 70 | 1 | 0.1327527 | 7.532804 | 0.1247118 | 1.0000000 |
| <GO:0072401> | signal transduction involved in DNA integrity checkpoint | 70 | 1 | 0.1327527 | 7.532804 | 0.1247118 | 1.0000000 |
| <GO:0072422> | signal transduction involved in DNA damage checkpoint | 70 | 1 | 0.1327527 | 7.532804 | 0.1247118 | 1.0000000 |
| <GO:1903901> | negative regulation of viral life cycle | 70 | 1 | 0.1327527 | 7.532804 | 0.1247118 | 1.0000000 |
| <GO:0043067> | regulation of programmed cell death | 1419 | 5 | 2.6910866 | 1.857986 | 0.1250527 | 1.0000000 |
| <GO:0031324> | negative regulation of cellular metabolic process | 2265 | 7 | 4.2954976 | 1.629613 | 0.1251762 | 1.0000000 |
| <GO:0021675> | nerve development | 71 | 1 | 0.1346492 | 7.426708 | 0.1263800 | 1.0000000 |
| <GO:0043367> | CD4-positive, alpha-beta T cell differentiation | 71 | 1 | 0.1346492 | 7.426708 | 0.1263800 | 1.0000000 |
| <GO:0043627> | response to estrogen | 71 | 1 | 0.1346492 | 7.426708 | 0.1263800 | 1.0000000 |
| <GO:0072395> | signal transduction involved in cell cycle checkpoint | 71 | 1 | 0.1346492 | 7.426708 | 0.1263800 | 1.0000000 |
| <GO:0008283> | cell proliferation | 1844 | 6 | 3.4970851 | 1.715715 | 0.1275132 | 1.0000000 |
| <GO:0010564> | regulation of cell cycle process | 660 | 3 | 1.2516682 | 2.396801 | 0.1276547 | 1.0000000 |
| <GO:0007193> | adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway | 72 | 1 | 0.1365456 | 7.323560 | 0.1280451 | 1.0000000 |
| <GO:0008344> | adult locomotory behavior | 72 | 1 | 0.1365456 | 7.323560 | 0.1280451 | 1.0000000 |
| <GO:0050886> | endocrine process | 73 | 1 | 0.1384421 | 7.223237 | 0.1297071 | 1.0000000 |
| <GO:1904035> | regulation of epithelial cell apoptotic process | 73 | 1 | 0.1384421 | 7.223237 | 0.1297071 | 1.0000000 |
| <GO:0034097> | response to cytokine | 1040 | 4 | 1.9723256 | 2.028063 | 0.1305845 | 1.0000000 |
| <GO:1901992> | positive regulation of mitotic cell cycle phase transition | 74 | 1 | 0.1403386 | 7.125626 | 0.1313661 | 1.0000000 |
| <GO:0050727> | regulation of inflammatory response | 334 | 2 | 0.6334200 | 3.157463 | 0.1314026 | 1.0000000 |
| <GO:0043900> | regulation of multi-organism process | 336 | 2 | 0.6372129 | 3.138668 | 0.1326830 | 1.0000000 |
| <GO:0006351> | transcription, DNA-templated | 3202 | 9 | 6.0724872 | 1.482095 | 0.1326872 | 1.0000000 |
| <GO:0009628> | response to abiotic stimulus | 1047 | 4 | 1.9856009 | 2.014504 | 0.1329451 | 1.0000000 |
| <GO:0031341> | regulation of cell killing | 76 | 1 | 0.1441315 | 6.938109 | 0.1346749 | 1.0000000 |
| <GO:0060291> | long-term synaptic potentiation | 76 | 1 | 0.1441315 | 6.938109 | 0.1346749 | 1.0000000 |
| <GO:0031326> | regulation of cellular biosynthetic process | 3683 | 10 | 6.9846878 | 1.431703 | 0.1352833 | 1.0000000 |
| <GO:0045582> | positive regulation of T cell differentiation | 77 | 1 | 0.1460280 | 6.848004 | 0.1363248 | 1.0000000 |
| <GO:0034644> | cellular response to UV | 78 | 1 | 0.1479244 | 6.760209 | 0.1379716 | 1.0000000 |
| <GO:0042058> | regulation of epidermal growth factor receptor signaling pathway | 78 | 1 | 0.1479244 | 6.760209 | 0.1379716 | 1.0000000 |
| <GO:0035249> | synaptic transmission, glutamatergic | 79 | 1 | 0.1498209 | 6.674637 | 0.1396155 | 1.0000000 |
| <GO:0030900> | forebrain development | 347 | 2 | 0.6580740 | 3.039172 | 0.1397782 | 1.0000000 |
| <GO:1901990> | regulation of mitotic cell cycle phase transition | 347 | 2 | 0.6580740 | 3.039172 | 0.1397782 | 1.0000000 |
| <GO:0097659> | nucleic acid-templated transcription | 3238 | 9 | 6.1407600 | 1.465617 | 0.1399168 | 1.0000000 |
| <GO:0002252> | immune effector process | 1071 | 4 | 2.0311161 | 1.969361 | 0.1411790 | 1.0000000 |
| <GO:0048013> | ephrin receptor signaling pathway | 80 | 1 | 0.1517174 | 6.591204 | 0.1412563 | 1.0000000 |
| <GO:0051098> | regulation of binding | 351 | 2 | 0.6656599 | 3.004537 | 0.1423797 | 1.0000000 |
| <GO:0032774> | RNA biosynthetic process | 3251 | 9 | 6.1654141 | 1.459756 | 0.1425818 | 1.0000000 |
| <GO:0043506> | regulation of JUN kinase activity | 81 | 1 | 0.1536138 | 6.509831 | 0.1428940 | 1.0000000 |
| <GO:0051341> | regulation of oxidoreductase activity | 81 | 1 | 0.1536138 | 6.509831 | 0.1428940 | 1.0000000 |
| <GO:2001022> | positive regulation of response to DNA damage stimulus | 81 | 1 | 0.1536138 | 6.509831 | 0.1428940 | 1.0000000 |
| <GO:0035710> | CD4-positive, alpha-beta T cell activation | 82 | 1 | 0.1555103 | 6.430443 | 0.1445288 | 1.0000000 |
| <GO:0060333> | interferon-gamma-mediated signaling pathway | 82 | 1 | 0.1555103 | 6.430443 | 0.1445288 | 1.0000000 |
| <GO:0061097> | regulation of protein tyrosine kinase activity | 82 | 1 | 0.1555103 | 6.430443 | 0.1445288 | 1.0000000 |
| <GO:0106027> | neuron projection organization | 82 | 1 | 0.1555103 | 6.430443 | 0.1445288 | 1.0000000 |
| <GO:0044257> | cellular protein catabolic process | 700 | 3 | 1.3275269 | 2.259841 | 0.1450353 | 1.0000000 |
| <GO:0007215> | glutamate receptor signaling pathway | 83 | 1 | 0.1574068 | 6.352967 | 0.1461606 | 1.0000000 |
| <GO:0048525> | negative regulation of viral process | 83 | 1 | 0.1574068 | 6.352967 | 0.1461606 | 1.0000000 |
| <GO:1901184> | regulation of ERBB signaling pathway | 83 | 1 | 0.1574068 | 6.352967 | 0.1461606 | 1.0000000 |
| <GO:0052548> | regulation of endopeptidase activity | 357 | 2 | 0.6770387 | 2.954041 | 0.1463024 | 1.0000000 |
| <GO:0042176> | regulation of protein catabolic process | 359 | 2 | 0.6808316 | 2.937584 | 0.1476153 | 1.0000000 |
| <GO:0009719> | response to endogenous stimulus | 1497 | 5 | 2.8390110 | 1.761177 | 0.1476342 | 1.0000000 |
| <GO:0009889> | regulation of biosynthetic process | 3747 | 10 | 7.1060617 | 1.407249 | 0.1477379 | 1.0000000 |
| <GO:0032101> | regulation of response to external stimulus | 712 | 3 | 1.3502845 | 2.221754 | 0.1504042 | 1.0000000 |
| <GO:0033273> | response to vitamin | 86 | 1 | 0.1630962 | 6.131352 | 0.1510379 | 1.0000000 |
| <GO:0046634> | regulation of alpha-beta T cell activation | 86 | 1 | 0.1630962 | 6.131352 | 0.1510379 | 1.0000000 |
| <GO:0019233> | sensory perception of pain | 87 | 1 | 0.1649926 | 6.060877 | 0.1526577 | 1.0000000 |
| <GO:0070887> | cellular response to chemical stimulus | 2837 | 8 | 5.3802767 | 1.486912 | 0.1529685 | 1.0000000 |
| <GO:0007631> | feeding behavior | 88 | 1 | 0.1668891 | 5.992003 | 0.1542746 | 1.0000000 |
| <GO:0010595> | positive regulation of endothelial cell migration | 88 | 1 | 0.1668891 | 5.992003 | 0.1542746 | 1.0000000 |
| <GO:0036503> | ERAD pathway | 88 | 1 | 0.1668891 | 5.992003 | 0.1542746 | 1.0000000 |
| <GO:0045621> | positive regulation of lymphocyte differentiation | 88 | 1 | 0.1668891 | 5.992003 | 0.1542746 | 1.0000000 |
| <GO:1901989> | positive regulation of cell cycle phase transition | 88 | 1 | 0.1668891 | 5.992003 | 0.1542746 | 1.0000000 |
| <GO:1902106> | negative regulation of leukocyte differentiation | 88 | 1 | 0.1668891 | 5.992003 | 0.1542746 | 1.0000000 |
| <GO:0060079> | excitatory postsynaptic potential | 89 | 1 | 0.1687856 | 5.924677 | 0.1558884 | 1.0000000 |
| <GO:0072676> | lymphocyte migration | 89 | 1 | 0.1687856 | 5.924677 | 0.1558884 | 1.0000000 |
| <GO:0018108> | peptidyl-tyrosine phosphorylation | 372 | 2 | 0.7054857 | 2.834926 | 0.1562107 | 1.0000000 |
| <GO:2001233> | regulation of apoptotic signaling pathway | 372 | 2 | 0.7054857 | 2.834926 | 0.1562107 | 1.0000000 |
| <GO:0023052> | signaling | 5257 | 13 | 9.9697268 | 1.303948 | 0.1562222 | 1.0000000 |
| <GO:0001909> | leukocyte mediated cytotoxicity | 90 | 1 | 0.1706820 | 5.858848 | 0.1574993 | 1.0000000 |
| <GO:0043161> | proteasome-mediated ubiquitin-dependent protein catabolic process | 374 | 2 | 0.7092786 | 2.819766 | 0.1575421 | 1.0000000 |
| <GO:0018212> | peptidyl-tyrosine modification | 375 | 2 | 0.7111751 | 2.812247 | 0.1582087 | 1.0000000 |
| <GO:1901987> | regulation of cell cycle phase transition | 375 | 2 | 0.7111751 | 2.812247 | 0.1582087 | 1.0000000 |
| <GO:0051249> | regulation of lymphocyte activation | 376 | 2 | 0.7130716 | 2.804768 | 0.1588759 | 1.0000000 |
| <GO:0051240> | positive regulation of multicellular organismal process | 1534 | 5 | 2.9091803 | 1.718697 | 0.1589609 | 1.0000000 |
| <GO:0051252> | regulation of RNA metabolic process | 3332 | 9 | 6.3190279 | 1.424270 | 0.1598292 | 1.0000000 |
| <GO:0019730> | antimicrobial humoral response | 92 | 1 | 0.1744750 | 5.731482 | 0.1607123 | 1.0000000 |
| <GO:0031124> | mRNA 3’-end processing | 92 | 1 | 0.1744750 | 5.731482 | 0.1607123 | 1.0000000 |
| <GO:0031329> | regulation of cellular catabolic process | 735 | 3 | 1.3939032 | 2.152230 | 0.1608804 | 1.0000000 |
| <GO:0052547> | regulation of peptidase activity | 379 | 2 | 0.7187610 | 2.782566 | 0.1608809 | 1.0000000 |
| <GO:0044773> | mitotic DNA damage checkpoint | 93 | 1 | 0.1763714 | 5.669853 | 0.1623143 | 1.0000000 |
| <GO:0048259> | regulation of receptor-mediated endocytosis | 93 | 1 | 0.1763714 | 5.669853 | 0.1623143 | 1.0000000 |
| <GO:2000134> | negative regulation of G1/S transition of mitotic cell cycle | 93 | 1 | 0.1763714 | 5.669853 | 0.1623143 | 1.0000000 |
| <GO:0051591> | response to cAMP | 94 | 1 | 0.1782679 | 5.609535 | 0.1639134 | 1.0000000 |
| <GO:1990823> | response to leukemia inhibitory factor | 94 | 1 | 0.1782679 | 5.609535 | 0.1639134 | 1.0000000 |
| <GO:1990830> | cellular response to leukemia inhibitory factor | 94 | 1 | 0.1782679 | 5.609535 | 0.1639134 | 1.0000000 |
| <GO:0007154> | cell communication | 5304 | 13 | 10.0588607 | 1.292393 | 0.1650958 | 1.0000000 |
| <GO:0099565> | chemical synaptic transmission, postsynaptic | 95 | 1 | 0.1801644 | 5.550487 | 0.1655095 | 1.0000000 |
| <GO:1904019> | epithelial cell apoptotic process | 95 | 1 | 0.1801644 | 5.550487 | 0.1655095 | 1.0000000 |
| <GO:0046632> | alpha-beta T cell differentiation | 96 | 1 | 0.1820608 | 5.492670 | 0.1671028 | 1.0000000 |
| <GO:0050905> | neuromuscular process | 96 | 1 | 0.1820608 | 5.492670 | 0.1671028 | 1.0000000 |
| <GO:1902807> | negative regulation of cell cycle G1/S phase transition | 96 | 1 | 0.1820608 | 5.492670 | 0.1671028 | 1.0000000 |
| <GO:0046916> | cellular transition metal ion homeostasis | 97 | 1 | 0.1839573 | 5.436044 | 0.1686930 | 1.0000000 |
| <GO:0050868> | negative regulation of T cell activation | 97 | 1 | 0.1839573 | 5.436044 | 0.1686930 | 1.0000000 |
| <GO:0006796> | phosphate-containing compound metabolic process | 2911 | 8 | 5.5206153 | 1.449114 | 0.1703557 | 1.0000000 |
| <GO:0051346> | negative regulation of hydrolase activity | 395 | 2 | 0.7491044 | 2.669855 | 0.1716562 | 1.0000000 |
| <GO:0035305> | negative regulation of dephosphorylation | 99 | 1 | 0.1877502 | 5.326225 | 0.1718648 | 1.0000000 |
| <GO:0006974> | cellular response to DNA damage stimulus | 759 | 3 | 1.4394184 | 2.084175 | 0.1720575 | 1.0000000 |
| <GO:0050896> | response to stimulus | 7411 | 17 | 14.0547166 | 1.209558 | 0.1730720 | 1.0000000 |
| <GO:0007569> | cell aging | 100 | 1 | 0.1896467 | 5.272963 | 0.1734464 | 1.0000000 |
| <GO:0033138> | positive regulation of peptidyl-serine phosphorylation | 100 | 1 | 0.1896467 | 5.272963 | 0.1734464 | 1.0000000 |
| <GO:0030330> | DNA damage response, signal transduction by p53 class mediator | 101 | 1 | 0.1915432 | 5.220755 | 0.1750250 | 1.0000000 |
| <GO:0008630> | intrinsic apoptotic signaling pathway in response to DNA damage | 102 | 1 | 0.1934396 | 5.169571 | 0.1766007 | 1.0000000 |
| <GO:0018107> | peptidyl-threonine phosphorylation | 102 | 1 | 0.1934396 | 5.169571 | 0.1766007 | 1.0000000 |
| <GO:0044774> | mitotic DNA integrity checkpoint | 102 | 1 | 0.1934396 | 5.169571 | 0.1766007 | 1.0000000 |
| <GO:0050906> | detection of stimulus involved in sensory perception | 102 | 1 | 0.1934396 | 5.169571 | 0.1766007 | 1.0000000 |
| <GO:0006793> | phosphorus metabolic process | 2937 | 8 | 5.5699234 | 1.436286 | 0.1766956 | 1.0000000 |
| <GO:0098542> | defense response to other organism | 407 | 2 | 0.7718620 | 2.591137 | 0.1798215 | 1.0000000 |
| <GO:0009581> | detection of external stimulus | 105 | 1 | 0.1991290 | 5.021870 | 0.1813105 | 1.0000000 |
| <GO:0014013> | regulation of gliogenesis | 105 | 1 | 0.1991290 | 5.021870 | 0.1813105 | 1.0000000 |
| <GO:0032479> | regulation of type I interferon production | 106 | 1 | 0.2010255 | 4.974493 | 0.1828746 | 1.0000000 |
| <GO:0007265> | Ras protein signal transduction | 412 | 2 | 0.7813444 | 2.559691 | 0.1832429 | 1.0000000 |
| <GO:0002062> | chondrocyte differentiation | 107 | 1 | 0.2029220 | 4.928003 | 0.1844359 | 1.0000000 |
| <GO:0009582> | detection of abiotic stimulus | 107 | 1 | 0.2029220 | 4.928003 | 0.1844359 | 1.0000000 |
| <GO:0032606> | type I interferon production | 107 | 1 | 0.2029220 | 4.928003 | 0.1844359 | 1.0000000 |
| <GO:0002698> | negative regulation of immune effector process | 108 | 1 | 0.2048184 | 4.882373 | 0.1859943 | 1.0000000 |
| <GO:0050864> | regulation of B cell activation | 108 | 1 | 0.2048184 | 4.882373 | 0.1859943 | 1.0000000 |
| <GO:1903038> | negative regulation of leukocyte cell-cell adhesion | 108 | 1 | 0.2048184 | 4.882373 | 0.1859943 | 1.0000000 |
| <GO:1903828> | negative regulation of cellular protein localization | 108 | 1 | 0.2048184 | 4.882373 | 0.1859943 | 1.0000000 |
| <GO:0022402> | cell cycle process | 1194 | 4 | 2.2643815 | 1.766487 | 0.1865194 | 1.0000000 |
| <GO:0002687> | positive regulation of leukocyte migration | 109 | 1 | 0.2067149 | 4.837581 | 0.1875499 | 1.0000000 |
| <GO:0010508> | positive regulation of autophagy | 109 | 1 | 0.2067149 | 4.837581 | 0.1875499 | 1.0000000 |
| <GO:0018210> | peptidyl-threonine modification | 109 | 1 | 0.2067149 | 4.837581 | 0.1875499 | 1.0000000 |
| <GO:0033209> | tumor necrosis factor-mediated signaling pathway | 109 | 1 | 0.2067149 | 4.837581 | 0.1875499 | 1.0000000 |
| <GO:0050769> | positive regulation of neurogenesis | 419 | 2 | 0.7946197 | 2.516927 | 0.1880507 | 1.0000000 |
| <GO:0007409> | axonogenesis | 422 | 2 | 0.8003091 | 2.499035 | 0.1901173 | 1.0000000 |
| <GO:0000122> | negative regulation of transcription by RNA polymerase II | 801 | 3 | 1.5190700 | 1.974892 | 0.1921648 | 1.0000000 |
| <GO:0045727> | positive regulation of translation | 112 | 1 | 0.2124043 | 4.708003 | 0.1921993 | 1.0000000 |
| <GO:0046718> | viral entry into host cell | 112 | 1 | 0.2124043 | 4.708003 | 0.1921993 | 1.0000000 |
| <GO:0051960> | regulation of nervous system development | 804 | 3 | 1.5247594 | 1.967523 | 0.1936256 | 1.0000000 |
| <GO:0007173> | epidermal growth factor receptor signaling pathway | 113 | 1 | 0.2143008 | 4.666339 | 0.1937434 | 1.0000000 |
| <GO:0031644> | regulation of neurological system process | 113 | 1 | 0.2143008 | 4.666339 | 0.1937434 | 1.0000000 |
| <GO:0050680> | negative regulation of epithelial cell proliferation | 113 | 1 | 0.2143008 | 4.666339 | 0.1937434 | 1.0000000 |
| <GO:0071482> | cellular response to light stimulus | 113 | 1 | 0.2143008 | 4.666339 | 0.1937434 | 1.0000000 |
| <GO:0007166> | cell surface receptor signaling pathway | 2546 | 7 | 4.8284049 | 1.449754 | 0.1955346 | 1.0000000 |
| <GO:0050728> | negative regulation of inflammatory response | 115 | 1 | 0.2180937 | 4.585185 | 0.1968231 | 1.0000000 |
| <GO:0010498> | proteasomal protein catabolic process | 433 | 2 | 0.8211702 | 2.435549 | 0.1977236 | 1.0000000 |
| <GO:0002478> | antigen processing and presentation of exogenous peptide antigen | 116 | 1 | 0.2199902 | 4.545658 | 0.1983587 | 1.0000000 |
| <GO:0002831> | regulation of response to biotic stimulus | 116 | 1 | 0.2199902 | 4.545658 | 0.1983587 | 1.0000000 |
| <GO:0030335> | positive regulation of cell migration | 435 | 2 | 0.8249631 | 2.424351 | 0.1991112 | 1.0000000 |
| <GO:0032434> | regulation of proteasomal ubiquitin-dependent protein catabolic process | 117 | 1 | 0.2218866 | 4.506806 | 0.1998915 | 1.0000000 |
| <GO:0030183> | B cell differentiation | 118 | 1 | 0.2237831 | 4.468613 | 0.2014215 | 1.0000000 |
| <GO:0022414> | reproductive process | 1236 | 4 | 2.3440332 | 1.706460 | 0.2030705 | 1.0000000 |
| <GO:0000003> | reproduction | 1239 | 4 | 2.3497226 | 1.702329 | 0.2042711 | 1.0000000 |
| <GO:0050729> | positive regulation of inflammatory response | 120 | 1 | 0.2275760 | 4.394136 | 0.2044729 | 1.0000000 |
| <GO:1900180> | regulation of protein localization to nucleus | 120 | 1 | 0.2275760 | 4.394136 | 0.2044729 | 1.0000000 |
| <GO:0008284> | positive regulation of cell proliferation | 827 | 3 | 1.5683782 | 1.912804 | 0.2049248 | 1.0000000 |
| <GO:0051093> | negative regulation of developmental process | 827 | 3 | 1.5683782 | 1.912804 | 0.2049248 | 1.0000000 |
| <GO:0042592> | homeostatic process | 1674 | 5 | 3.1746857 | 1.574959 | 0.2050519 | 1.0000000 |
| <GO:0002576> | platelet degranulation | 122 | 1 | 0.2313690 | 4.322101 | 0.2075131 | 1.0000000 |
| <GO:0055076> | transition metal ion homeostasis | 122 | 1 | 0.2313690 | 4.322101 | 0.2075131 | 1.0000000 |
| <GO:0019884> | antigen processing and presentation of exogenous antigen | 123 | 1 | 0.2332654 | 4.286962 | 0.2090291 | 1.0000000 |
| <GO:0032640> | tumor necrosis factor production | 123 | 1 | 0.2332654 | 4.286962 | 0.2090291 | 1.0000000 |
| <GO:0038093> | Fc receptor signaling pathway | 123 | 1 | 0.2332654 | 4.286962 | 0.2090291 | 1.0000000 |
| <GO:1903707> | negative regulation of hemopoiesis | 123 | 1 | 0.2332654 | 4.286962 | 0.2090291 | 1.0000000 |
| <GO:2000147> | positive regulation of cell motility | 451 | 2 | 0.8553066 | 2.338343 | 0.2102586 | 1.0000000 |
| <GO:0060078> | regulation of postsynaptic membrane potential | 124 | 1 | 0.2351619 | 4.252389 | 0.2105422 | 1.0000000 |
| <GO:0009894> | regulation of catabolic process | 840 | 3 | 1.5930322 | 1.883201 | 0.2113853 | 1.0000000 |
| <GO:0030260> | entry into host cell | 125 | 1 | 0.2370584 | 4.218370 | 0.2120525 | 1.0000000 |
| <GO:0030534> | adult behavior | 125 | 1 | 0.2370584 | 4.218370 | 0.2120525 | 1.0000000 |
| <GO:0042770> | signal transduction in response to DNA damage | 125 | 1 | 0.2370584 | 4.218370 | 0.2120525 | 1.0000000 |
| <GO:0044409> | entry into host | 125 | 1 | 0.2370584 | 4.218370 | 0.2120525 | 1.0000000 |
| <GO:0051806> | entry into cell of other organism involved in symbiotic interaction | 125 | 1 | 0.2370584 | 4.218370 | 0.2120525 | 1.0000000 |
| <GO:0051828> | entry into other organism involved in symbiotic interaction | 125 | 1 | 0.2370584 | 4.218370 | 0.2120525 | 1.0000000 |
| <GO:0043066> | negative regulation of apoptotic process | 842 | 3 | 1.5968252 | 1.878728 | 0.2123837 | 1.0000000 |
| <GO:0035304> | regulation of protein dephosphorylation | 126 | 1 | 0.2389548 | 4.184891 | 0.2135601 | 1.0000000 |
| <GO:0045580> | regulation of T cell differentiation | 126 | 1 | 0.2389548 | 4.184891 | 0.2135601 | 1.0000000 |
| <GO:0050777> | negative regulation of immune response | 126 | 1 | 0.2389548 | 4.184891 | 0.2135601 | 1.0000000 |
| <GO:0051250> | negative regulation of lymphocyte activation | 126 | 1 | 0.2389548 | 4.184891 | 0.2135601 | 1.0000000 |
| <GO:0030163> | protein catabolic process | 845 | 3 | 1.6025146 | 1.872058 | 0.2138835 | 1.0000000 |
| <GO:0031667> | response to nutrient levels | 457 | 2 | 0.8666854 | 2.307642 | 0.2144583 | 1.0000000 |
| <GO:0002706> | regulation of lymphocyte mediated immunity | 127 | 1 | 0.2408513 | 4.151939 | 0.2150648 | 1.0000000 |
| <GO:0046631> | alpha-beta T cell activation | 127 | 1 | 0.2408513 | 4.151939 | 0.2150648 | 1.0000000 |
| <GO:0044703> | multi-organism reproductive process | 848 | 3 | 1.6082040 | 1.865435 | 0.2153859 | 1.0000000 |
| <GO:0031023> | microtubule organizing center organization | 128 | 1 | 0.2427478 | 4.119502 | 0.2165668 | 1.0000000 |
| <GO:0048002> | antigen processing and presentation of peptide antigen | 128 | 1 | 0.2427478 | 4.119502 | 0.2165668 | 1.0000000 |
| <GO:1903900> | regulation of viral life cycle | 128 | 1 | 0.2427478 | 4.119502 | 0.2165668 | 1.0000000 |
| <GO:0019219> | regulation of nucleobase-containing compound metabolic process | 3572 | 9 | 6.7741800 | 1.328574 | 0.2171217 | 1.0000000 |
| <GO:0061564> | axon development | 462 | 2 | 0.8761677 | 2.282668 | 0.2179653 | 1.0000000 |
| <GO:0008037> | cell recognition | 129 | 1 | 0.2446442 | 4.087568 | 0.2180661 | 1.0000000 |
| <GO:0008203> | cholesterol metabolic process | 129 | 1 | 0.2446442 | 4.087568 | 0.2180661 | 1.0000000 |
| <GO:0033135> | regulation of peptidyl-serine phosphorylation | 129 | 1 | 0.2446442 | 4.087568 | 0.2180661 | 1.0000000 |
| <GO:0071236> | cellular response to antibiotic | 129 | 1 | 0.2446442 | 4.087568 | 0.2180661 | 1.0000000 |
| <GO:0071706> | tumor necrosis factor superfamily cytokine production | 129 | 1 | 0.2446442 | 4.087568 | 0.2180661 | 1.0000000 |
| <GO:0050877> | nervous system process | 854 | 3 | 1.6195828 | 1.852329 | 0.2183983 | 1.0000000 |
| <GO:0051272> | positive regulation of cellular component movement | 463 | 2 | 0.8780642 | 2.277738 | 0.2186675 | 1.0000000 |
| <GO:0043069> | negative regulation of programmed cell death | 855 | 3 | 1.6214792 | 1.850162 | 0.2189014 | 1.0000000 |
| <GO:0008584> | male gonad development | 130 | 1 | 0.2465407 | 4.056125 | 0.2195625 | 1.0000000 |
| <GO:0010634> | positive regulation of epithelial cell migration | 130 | 1 | 0.2465407 | 4.056125 | 0.2195625 | 1.0000000 |
| <GO:0046546> | development of primary male sexual characteristics | 130 | 1 | 0.2465407 | 4.056125 | 0.2195625 | 1.0000000 |
| <GO:0046683> | response to organophosphorus | 131 | 1 | 0.2484372 | 4.025163 | 0.2210563 | 1.0000000 |
| <GO:0040012> | regulation of locomotion | 861 | 3 | 1.6328580 | 1.837269 | 0.2219254 | 1.0000000 |
| <GO:1902652> | secondary alcohol metabolic process | 132 | 1 | 0.2503336 | 3.994669 | 0.2225472 | 1.0000000 |
| <GO:2001257> | regulation of cation channel activity | 132 | 1 | 0.2503336 | 3.994669 | 0.2225472 | 1.0000000 |
| <GO:0014070> | response to organic cyclic compound | 863 | 3 | 1.6366510 | 1.833012 | 0.2229356 | 1.0000000 |
| <GO:0044087> | regulation of cellular component biogenesis | 864 | 3 | 1.6385474 | 1.830890 | 0.2234411 | 1.0000000 |
| <GO:0001906> | cell killing | 133 | 1 | 0.2522301 | 3.964634 | 0.2240354 | 1.0000000 |
| <GO:0050852> | T cell receptor signaling pathway | 133 | 1 | 0.2522301 | 3.964634 | 0.2240354 | 1.0000000 |
| <GO:1902107> | positive regulation of leukocyte differentiation | 133 | 1 | 0.2522301 | 3.964634 | 0.2240354 | 1.0000000 |
| <GO:0038127> | ERBB signaling pathway | 134 | 1 | 0.2541266 | 3.935047 | 0.2255209 | 1.0000000 |
| <GO:0050954> | sensory perception of mechanical stimulus | 134 | 1 | 0.2541266 | 3.935047 | 0.2255209 | 1.0000000 |
| <GO:0044089> | positive regulation of cellular component biogenesis | 473 | 2 | 0.8970289 | 2.229583 | 0.2257018 | 1.0000000 |
| <GO:0001889> | liver development | 135 | 1 | 0.2560230 | 3.905899 | 0.2270036 | 1.0000000 |
| <GO:0009411> | response to UV | 135 | 1 | 0.2560230 | 3.905899 | 0.2270036 | 1.0000000 |
| <GO:2000045> | regulation of G1/S transition of mitotic cell cycle | 135 | 1 | 0.2560230 | 3.905899 | 0.2270036 | 1.0000000 |
| <GO:0045597> | positive regulation of cell differentiation | 874 | 3 | 1.6575121 | 1.809942 | 0.2285101 | 1.0000000 |
| <GO:0044772> | mitotic cell cycle phase transition | 479 | 2 | 0.9084077 | 2.201655 | 0.2299327 | 1.0000000 |
| <GO:0010557> | positive regulation of macromolecule biosynthetic process | 1747 | 5 | 3.3131278 | 1.509148 | 0.2308714 | 1.0000000 |
| <GO:0010594> | regulation of endothelial cell migration | 138 | 1 | 0.2617124 | 3.820988 | 0.2314354 | 1.0000000 |
| <GO:0061008> | hepaticobiliary system development | 138 | 1 | 0.2617124 | 3.820988 | 0.2314354 | 1.0000000 |
| <GO:0040017> | positive regulation of locomotion | 482 | 2 | 0.9140971 | 2.187951 | 0.2320508 | 1.0000000 |
| <GO:2000026> | regulation of multicellular organismal development | 1751 | 5 | 3.3207136 | 1.505700 | 0.2323171 | 1.0000000 |
| <GO:0000077> | DNA damage checkpoint | 139 | 1 | 0.2636089 | 3.793499 | 0.2329073 | 1.0000000 |
| <GO:0035264> | multicellular organism growth | 139 | 1 | 0.2636089 | 3.793499 | 0.2329073 | 1.0000000 |
| <GO:0010720> | positive regulation of cell development | 484 | 2 | 0.9178900 | 2.178910 | 0.2334637 | 1.0000000 |
| <GO:0090501> | RNA phosphodiester bond hydrolysis | 140 | 1 | 0.2655054 | 3.766402 | 0.2343764 | 1.0000000 |
| <GO:0009991> | response to extracellular stimulus | 486 | 2 | 0.9216829 | 2.169944 | 0.2348774 | 1.0000000 |
| <GO:0000187> | activation of MAPK activity | 142 | 1 | 0.2692983 | 3.713354 | 0.2373065 | 1.0000000 |
| <GO:0051384> | response to glucocorticoid | 142 | 1 | 0.2692983 | 3.713354 | 0.2373065 | 1.0000000 |
| <GO:0071695> | anatomical structure maturation | 142 | 1 | 0.2692983 | 3.713354 | 0.2373065 | 1.0000000 |
| <GO:0010212> | response to ionizing radiation | 143 | 1 | 0.2711948 | 3.687387 | 0.2387675 | 1.0000000 |
| <GO:0001959> | regulation of cytokine-mediated signaling pathway | 144 | 1 | 0.2730912 | 3.661780 | 0.2402258 | 1.0000000 |
| <GO:0014074> | response to purine-containing compound | 144 | 1 | 0.2730912 | 3.661780 | 0.2402258 | 1.0000000 |
| <GO:0016125> | sterol metabolic process | 144 | 1 | 0.2730912 | 3.661780 | 0.2402258 | 1.0000000 |
| <GO:0045931> | positive regulation of mitotic cell cycle | 144 | 1 | 0.2730912 | 3.661780 | 0.2402258 | 1.0000000 |
| <GO:0048754> | branching morphogenesis of an epithelial tube | 144 | 1 | 0.2730912 | 3.661780 | 0.2402258 | 1.0000000 |
| <GO:0010389> | regulation of G2/M transition of mitotic cell cycle | 145 | 1 | 0.2749877 | 3.636526 | 0.2416814 | 1.0000000 |
| <GO:0050793> | regulation of developmental process | 2238 | 6 | 4.2442930 | 1.413663 | 0.2424234 | 1.0000000 |
| <GO:0002695> | negative regulation of leukocyte activation | 146 | 1 | 0.2768842 | 3.611619 | 0.2431343 | 1.0000000 |
| <GO:0045766> | positive regulation of angiogenesis | 147 | 1 | 0.2787806 | 3.587050 | 0.2445845 | 1.0000000 |
| <GO:0006606> | protein import into nucleus | 148 | 1 | 0.2806771 | 3.562813 | 0.2460321 | 1.0000000 |
| <GO:0043902> | positive regulation of multi-organism process | 148 | 1 | 0.2806771 | 3.562813 | 0.2460321 | 1.0000000 |
| <GO:1902806> | regulation of cell cycle G1/S phase transition | 148 | 1 | 0.2806771 | 3.562813 | 0.2460321 | 1.0000000 |
| <GO:0010035> | response to inorganic substance | 503 | 2 | 0.9539229 | 2.096606 | 0.2469185 | 1.0000000 |
| <GO:0010970> | transport along microtubule | 149 | 1 | 0.2825736 | 3.538901 | 0.2474770 | 1.0000000 |
| <GO:0099111> | microtubule-based transport | 149 | 1 | 0.2825736 | 3.538901 | 0.2474770 | 1.0000000 |
| <GO:0051897> | positive regulation of protein kinase B signaling | 150 | 1 | 0.2844700 | 3.515309 | 0.2489192 | 1.0000000 |
| <GO:0031570> | DNA integrity checkpoint | 151 | 1 | 0.2863665 | 3.492028 | 0.2503588 | 1.0000000 |
| <GO:0043901> | negative regulation of multi-organism process | 151 | 1 | 0.2863665 | 3.492028 | 0.2503588 | 1.0000000 |
| <GO:0046661> | male sex differentiation | 151 | 1 | 0.2863665 | 3.492028 | 0.2503588 | 1.0000000 |
| <GO:0034654> | nucleobase-containing compound biosynthetic process | 3701 | 9 | 7.0188242 | 1.282266 | 0.2513865 | 1.0000000 |
| <GO:0022408> | negative regulation of cell-cell adhesion | 152 | 1 | 0.2882630 | 3.469055 | 0.2517957 | 1.0000000 |
| <GO:0045619> | regulation of lymphocyte differentiation | 154 | 1 | 0.2920559 | 3.424002 | 0.2546616 | 1.0000000 |
| <GO:0048469> | cell maturation | 154 | 1 | 0.2920559 | 3.424002 | 0.2546616 | 1.0000000 |
| <GO:0060759> | regulation of response to cytokine stimulus | 154 | 1 | 0.2920559 | 3.424002 | 0.2546616 | 1.0000000 |
| <GO:0044770> | cell cycle phase transition | 514 | 2 | 0.9747840 | 2.051737 | 0.2547292 | 1.0000000 |
| <GO:0048015> | phosphatidylinositol-mediated signaling | 155 | 1 | 0.2939524 | 3.401912 | 0.2560905 | 1.0000000 |
| <GO:0016241> | regulation of macroautophagy | 156 | 1 | 0.2958488 | 3.380104 | 0.2575169 | 1.0000000 |
| <GO:0048017> | inositol lipid-mediated signaling | 157 | 1 | 0.2977453 | 3.358575 | 0.2589406 | 1.0000000 |
| <GO:0007264> | small GTPase mediated signal transduction | 521 | 2 | 0.9880593 | 2.024170 | 0.2597053 | 1.0000000 |
| <GO:0031960> | response to corticosteroid | 158 | 1 | 0.2996418 | 3.337318 | 0.2603616 | 1.0000000 |
| <GO:0031328> | positive regulation of cellular biosynthetic process | 1828 | 5 | 3.4667416 | 1.442276 | 0.2607046 | 1.0000000 |
| <GO:0007093> | mitotic cell cycle checkpoint | 159 | 1 | 0.3015382 | 3.316329 | 0.2617801 | 1.0000000 |
| <GO:0030324> | lung development | 159 | 1 | 0.3015382 | 3.316329 | 0.2617801 | 1.0000000 |
| <GO:0071346> | cellular response to interferon-gamma | 159 | 1 | 0.3015382 | 3.316329 | 0.2617801 | 1.0000000 |
| <GO:1902749> | regulation of cell cycle G2/M phase transition | 160 | 1 | 0.3034347 | 3.295602 | 0.2631959 | 1.0000000 |
| <GO:0048667> | cell morphogenesis involved in neuron differentiation | 526 | 2 | 0.9975416 | 2.004929 | 0.2632619 | 1.0000000 |
| <GO:0002685> | regulation of leukocyte migration | 161 | 1 | 0.3053312 | 3.275132 | 0.2646091 | 1.0000000 |
| <GO:0050792> | regulation of viral process | 162 | 1 | 0.3072276 | 3.254915 | 0.2660197 | 1.0000000 |
| <GO:0019882> | antigen processing and presentation | 163 | 1 | 0.3091241 | 3.234947 | 0.2674277 | 1.0000000 |
| <GO:0030323> | respiratory tube development | 163 | 1 | 0.3091241 | 3.234947 | 0.2674277 | 1.0000000 |
| <GO:0018130> | heterocycle biosynthetic process | 3759 | 9 | 7.1288193 | 1.262481 | 0.2674852 | 1.0000000 |
| <GO:0009891> | positive regulation of biosynthetic process | 1852 | 5 | 3.5122568 | 1.423586 | 0.2697511 | 1.0000000 |
| <GO:0019438> | aromatic compound biosynthetic process | 3768 | 9 | 7.1458875 | 1.259466 | 0.2700189 | 1.0000000 |
| <GO:1901991> | negative regulation of mitotic cell cycle phase transition | 165 | 1 | 0.3129170 | 3.195735 | 0.2702359 | 1.0000000 |
| <GO:1904018> | positive regulation of vasculature development | 165 | 1 | 0.3129170 | 3.195735 | 0.2702359 | 1.0000000 |
| <GO:0050866> | negative regulation of cell activation | 166 | 1 | 0.3148135 | 3.176484 | 0.2716361 | 1.0000000 |
| <GO:0030705> | cytoskeleton-dependent intracellular transport | 167 | 1 | 0.3167100 | 3.157463 | 0.2730337 | 1.0000000 |
| <GO:0007219> | Notch signaling pathway | 168 | 1 | 0.3186064 | 3.138668 | 0.2744287 | 1.0000000 |
| <GO:0051170> | import into nucleus | 168 | 1 | 0.3186064 | 3.138668 | 0.2744287 | 1.0000000 |
| <GO:0071840> | cellular component organization or biogenesis | 5803 | 13 | 11.0051977 | 1.181260 | 0.2766560 | 1.0000000 |
| <GO:0061136> | regulation of proteasomal protein catabolic process | 170 | 1 | 0.3223994 | 3.101743 | 0.2772110 | 1.0000000 |
| <GO:1903708> | positive regulation of hemopoiesis | 170 | 1 | 0.3223994 | 3.101743 | 0.2772110 | 1.0000000 |
| <GO:0010952> | positive regulation of peptidase activity | 171 | 1 | 0.3242958 | 3.083604 | 0.2785984 | 1.0000000 |
| <GO:0071248> | cellular response to metal ion | 172 | 1 | 0.3261923 | 3.065676 | 0.2799831 | 1.0000000 |
| <GO:0006935> | chemotaxis | 551 | 2 | 1.0449533 | 1.913961 | 0.2810588 | 1.0000000 |
| <GO:0050851> | antigen receptor-mediated signaling pathway | 173 | 1 | 0.3280888 | 3.047956 | 0.2813653 | 1.0000000 |
| <GO:0042330> | taxis | 553 | 2 | 1.0487462 | 1.907039 | 0.2824829 | 1.0000000 |
| <GO:0022008> | neurogenesis | 1425 | 4 | 2.7024654 | 1.480130 | 0.2825831 | 1.0000000 |
| <GO:0007565> | female pregnancy | 174 | 1 | 0.3299852 | 3.030438 | 0.2827449 | 1.0000000 |
| <GO:0071478> | cellular response to radiation | 174 | 1 | 0.3299852 | 3.030438 | 0.2827449 | 1.0000000 |
| <GO:0006357> | regulation of transcription by RNA polymerase II | 2361 | 6 | 4.4775585 | 1.340016 | 0.2841569 | 1.0000000 |
| <GO:0045893> | positive regulation of transcription, DNA-templated | 1429 | 4 | 2.7100513 | 1.475987 | 0.2843345 | 1.0000000 |
| <GO:0042221> | response to chemical | 3820 | 9 | 7.2445038 | 1.242321 | 0.2848351 | 1.0000000 |
| <GO:0007188> | adenylate cyclase-modulating G protein-coupled receptor signaling pathway | 176 | 1 | 0.3337782 | 2.996002 | 0.2854965 | 1.0000000 |
| <GO:0061138> | morphogenesis of a branching epithelium | 176 | 1 | 0.3337782 | 2.996002 | 0.2854965 | 1.0000000 |
| <GO:0097190> | apoptotic signaling pathway | 558 | 2 | 1.0582286 | 1.889951 | 0.2860427 | 1.0000000 |
| <GO:0002703> | regulation of leukocyte mediated immunity | 177 | 1 | 0.3356747 | 2.979075 | 0.2868685 | 1.0000000 |
| <GO:0034341> | response to interferon-gamma | 177 | 1 | 0.3356747 | 2.979075 | 0.2868685 | 1.0000000 |
| <GO:0071897> | DNA biosynthetic process | 177 | 1 | 0.3356747 | 2.979075 | 0.2868685 | 1.0000000 |
| <GO:0007346> | regulation of mitotic cell cycle | 561 | 2 | 1.0639180 | 1.879844 | 0.2881783 | 1.0000000 |
| <GO:0071396> | cellular response to lipid | 561 | 2 | 1.0639180 | 1.879844 | 0.2881783 | 1.0000000 |
| <GO:1902905> | positive regulation of supramolecular fiber organization | 178 | 1 | 0.3375711 | 2.962339 | 0.2882380 | 1.0000000 |
| <GO:0043542> | endothelial cell migration | 179 | 1 | 0.3394676 | 2.945789 | 0.2896049 | 1.0000000 |
| <GO:1901988> | negative regulation of cell cycle phase transition | 179 | 1 | 0.3394676 | 2.945789 | 0.2896049 | 1.0000000 |
| <GO:0048666> | neuron development | 993 | 3 | 1.8831917 | 1.593040 | 0.2904095 | 1.0000000 |
| <GO:0007626> | locomotory behavior | 181 | 1 | 0.3432605 | 2.913239 | 0.2923312 | 1.0000000 |