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 |

# SES4 income intersection (down)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| goId | description | size | overlap | expect | enrichmentRatio | pValue | FDR |
| <GO:0043122> | regulation of I-kappaB kinase/NF-kappaB signaling | 221 | 7 | 0.2017981 | 34.688131 | 0.0000000 | 0.0000026 |
| <GO:0002224> | toll-like receptor signaling pathway | 124 | 6 | 0.1132261 | 52.991315 | 0.0000000 | 0.0000026 |
| <GO:0051091> | positive regulation of DNA-binding transcription factor activity | 248 | 7 | 0.2264522 | 30.911600 | 0.0000000 | 0.0000026 |
| <GO:0007249> | I-kappaB kinase/NF-kappaB signaling | 251 | 7 | 0.2291915 | 30.542139 | 0.0000000 | 0.0000026 |
| <GO:0070498> | interleukin-1-mediated signaling pathway | 54 | 5 | 0.0493081 | 101.403134 | 0.0000000 | 0.0000026 |
| <GO:0051092> | positive regulation of NF-kappaB transcription factor activity | 144 | 6 | 0.1314884 | 45.631410 | 0.0000000 | 0.0000041 |
| <GO:0002221> | pattern recognition receptor signaling pathway | 164 | 6 | 0.1497506 | 40.066604 | 0.0000000 | 0.0000078 |
| <GO:0043123> | positive regulation of I-kappaB kinase/NF-kappaB signaling | 176 | 6 | 0.1607080 | 37.334790 | 0.0000000 | 0.0000104 |
| <GO:0002758> | innate immune response-activating signal transduction | 209 | 6 | 0.1908408 | 31.439823 | 0.0000000 | 0.0000237 |
| <GO:0051090> | regulation of DNA-binding transcription factor activity | 385 | 7 | 0.3515488 | 19.911888 | 0.0000000 | 0.0000237 |
| <GO:0002218> | activation of innate immune response | 229 | 6 | 0.2091030 | 28.693987 | 0.0000000 | 0.0000365 |
| <GO:0071347> | cellular response to interleukin-1 | 119 | 5 | 0.1086605 | 46.014868 | 0.0000000 | 0.0000599 |
| <GO:0045087> | innate immune response | 734 | 8 | 0.6702255 | 11.936282 | 0.0000000 | 0.0000599 |
| <GO:0045089> | positive regulation of innate immune response | 282 | 6 | 0.2574981 | 23.301146 | 0.0000001 | 0.0000991 |
| <GO:0070555> | response to interleukin-1 | 141 | 5 | 0.1287490 | 38.835243 | 0.0000001 | 0.0001133 |
| <GO:0045088> | regulation of innate immune response | 337 | 6 | 0.3077193 | 19.498288 | 0.0000003 | 0.0002487 |
| <GO:1902533> | positive regulation of intracellular signal transduction | 979 | 8 | 0.8939383 | 8.949163 | 0.0000005 | 0.0004276 |
| <GO:0031349> | positive regulation of defense response | 387 | 6 | 0.3533750 | 16.979129 | 0.0000006 | 0.0004992 |
| <GO:0009967> | positive regulation of signal transduction | 1463 | 9 | 1.3358854 | 6.737105 | 0.0000006 | 0.0005073 |
| <GO:0002757> | immune response-activating signal transduction | 417 | 6 | 0.3807684 | 15.757609 | 0.0000009 | 0.0006961 |
| <GO:0002764> | immune response-regulating signaling pathway | 446 | 6 | 0.4072487 | 14.733011 | 0.0000013 | 0.0009748 |
| <GO:0010647> | positive regulation of cell communication | 1608 | 9 | 1.4682869 | 6.129592 | 0.0000014 | 0.0009748 |
| <GO:0023056> | positive regulation of signaling | 1614 | 9 | 1.4737655 | 6.106806 | 0.0000014 | 0.0009748 |
| <GO:0051707> | response to other organism | 797 | 7 | 0.7277516 | 9.618666 | 0.0000021 | 0.0013805 |
| <GO:0043207> | response to external biotic stimulus | 799 | 7 | 0.7295779 | 9.594589 | 0.0000022 | 0.0013805 |
| <GO:0002253> | activation of immune response | 492 | 6 | 0.4492519 | 13.355535 | 0.0000023 | 0.0014062 |
| <GO:0051403> | stress-activated MAPK cascade | 266 | 5 | 0.2428882 | 20.585599 | 0.0000025 | 0.0014662 |
| <GO:0009607> | response to biotic stimulus | 820 | 7 | 0.7487532 | 9.348874 | 0.0000026 | 0.0014671 |
| <GO:0070423> | nucleotide-binding oligomerization domain containing signaling pathway | 32 | 3 | 0.0292196 | 102.670673 | 0.0000029 | 0.0015886 |
| <GO:0035872> | nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway | 33 | 3 | 0.0301328 | 99.559441 | 0.0000032 | 0.0016883 |
| <GO:0060255> | regulation of macromolecule metabolic process | 5411 | 13 | 4.9408583 | 2.631122 | 0.0000034 | 0.0017351 |
| <GO:0002755> | MyD88-dependent toll-like receptor signaling pathway | 34 | 3 | 0.0310459 | 96.631222 | 0.0000035 | 0.0017351 |
| <GO:0031098> | stress-activated protein kinase signaling cascade | 291 | 5 | 0.2657161 | 18.817076 | 0.0000039 | 0.0018637 |
| <GO:0002684> | positive regulation of immune system process | 894 | 7 | 0.8163237 | 8.575030 | 0.0000046 | 0.0021542 |
| <GO:0006952> | defense response | 1356 | 8 | 1.2381822 | 6.461085 | 0.0000055 | 0.0024989 |
| <GO:0006950> | response to stress | 3399 | 11 | 3.1036735 | 3.544187 | 0.0000068 | 0.0029800 |
| <GO:0019222> | regulation of metabolic process | 5854 | 13 | 5.3453677 | 2.432012 | 0.0000095 | 0.0040837 |
| <GO:0048584> | positive regulation of response to stimulus | 2027 | 9 | 1.8508815 | 4.862548 | 0.0000098 | 0.0040959 |
| <GO:0031347> | regulation of defense response | 642 | 6 | 0.5862190 | 10.235083 | 0.0000107 | 0.0043671 |
| <GO:0050778> | positive regulation of immune response | 648 | 6 | 0.5916977 | 10.140313 | 0.0000113 | 0.0044915 |
| <GO:0044267> | cellular protein metabolic process | 4630 | 12 | 4.2277165 | 2.838412 | 0.0000126 | 0.0047940 |
| <GO:0019221> | cytokine-mediated signaling pathway | 661 | 6 | 0.6035682 | 9.940882 | 0.0000127 | 0.0047940 |
| <GO:0002753> | cytoplasmic pattern recognition receptor signaling pathway | 53 | 3 | 0.0483950 | 61.989840 | 0.0000136 | 0.0050044 |
| <GO:0051704> | multi-organism process | 2127 | 9 | 1.9421929 | 4.633937 | 0.0000147 | 0.0053050 |
| <GO:0002223> | stimulatory C-type lectin receptor signaling pathway | 56 | 3 | 0.0511344 | 58.668956 | 0.0000160 | 0.0056496 |
| <GO:0002220> | innate immune response activating cell surface receptor signaling pathway | 58 | 3 | 0.0529606 | 56.645889 | 0.0000178 | 0.0061455 |
| <GO:0038095> | Fc-epsilon receptor signaling pathway | 59 | 3 | 0.0538737 | 55.685789 | 0.0000188 | 0.0063337 |
| <GO:0044093> | positive regulation of molecular function | 1607 | 8 | 1.4673737 | 5.451917 | 0.0000198 | 0.0065274 |
| <GO:0007254> | JNK cascade | 204 | 4 | 0.1862752 | 21.473605 | 0.0000264 | 0.0085586 |
| <GO:1902531> | regulation of intracellular signal transduction | 1696 | 8 | 1.5486409 | 5.165820 | 0.0000295 | 0.0093358 |
| <GO:1901224> | positive regulation of NIK/NF-kappaB signaling | 69 | 3 | 0.0630048 | 47.615385 | 0.0000301 | 0.0093358 |
| <GO:0010468> | regulation of gene expression | 3930 | 11 | 3.5885369 | 3.065316 | 0.0000306 | 0.0093358 |
| <GO:0006955> | immune response | 1746 | 8 | 1.5942966 | 5.017887 | 0.0000366 | 0.0109553 |
| <GO:0033554> | cellular response to stress | 1771 | 8 | 1.6171244 | 4.947053 | 0.0000407 | 0.0117344 |
| <GO:0019538> | protein metabolic process | 5124 | 12 | 4.6787947 | 2.564763 | 0.0000407 | 0.0117344 |
| <GO:0071900> | regulation of protein serine/threonine kinase activity | 476 | 5 | 0.4346421 | 11.503717 | 0.0000421 | 0.0119345 |
| <GO:0080134> | regulation of response to stress | 1261 | 7 | 1.1514364 | 6.079363 | 0.0000447 | 0.0124435 |
| <GO:0016070> | RNA metabolic process | 4084 | 11 | 3.7291564 | 2.949729 | 0.0000455 | 0.0124455 |
| <GO:0050776> | regulation of immune response | 837 | 6 | 0.7642762 | 7.850565 | 0.0000487 | 0.0128986 |
| <GO:0002682> | regulation of immune system process | 1278 | 7 | 1.1669593 | 5.998495 | 0.0000488 | 0.0128986 |
| <GO:0043406> | positive regulation of MAP kinase activity | 245 | 4 | 0.2237129 | 17.880063 | 0.0000541 | 0.0140762 |
| <GO:0002376> | immune system process | 2539 | 9 | 2.3183957 | 3.881995 | 0.0000643 | 0.0164532 |
| <GO:0035556> | intracellular signal transduction | 2544 | 9 | 2.3229613 | 3.874365 | 0.0000654 | 0.0164571 |
| <GO:0034645> | cellular macromolecule biosynthetic process | 4293 | 11 | 3.9199972 | 2.806125 | 0.0000760 | 0.0188374 |
| <GO:0030522> | intracellular receptor signaling pathway | 270 | 4 | 0.2465407 | 16.224501 | 0.0000790 | 0.0192816 |
| <GO:0044271> | cellular nitrogen compound biosynthetic process | 4328 | 11 | 3.9519562 | 2.783432 | 0.0000826 | 0.0198515 |
| <GO:1901222> | regulation of NIK/NF-kappaB signaling | 98 | 3 | 0.0894851 | 33.525118 | 0.0000860 | 0.0203634 |
| <GO:0051239> | regulation of multicellular organismal process | 2670 | 9 | 2.4380136 | 3.691530 | 0.0000973 | 0.0226973 |
| <GO:0009059> | macromolecule biosynthetic process | 4421 | 11 | 4.0368757 | 2.724880 | 0.0001027 | 0.0236024 |
| <GO:0071345> | cellular response to cytokine stimulus | 959 | 6 | 0.8756761 | 6.851849 | 0.0001046 | 0.0236957 |
| <GO:0032479> | regulation of type I interferon production | 106 | 3 | 0.0967901 | 30.994920 | 0.0001087 | 0.0242713 |
| <GO:0032606> | type I interferon production | 107 | 3 | 0.0977032 | 30.705248 | 0.0001118 | 0.0246116 |
| <GO:0007250> | activation of NF-kappaB-inducing kinase activity | 18 | 2 | 0.0164360 | 121.683761 | 0.0001168 | 0.0250276 |
| <GO:0007252> | I-kappaB phosphorylation | 18 | 2 | 0.0164360 | 121.683761 | 0.0001168 | 0.0250276 |
| <GO:0009605> | response to external stimulus | 2057 | 8 | 1.8782749 | 4.259227 | 0.0001221 | 0.0258188 |
| <GO:0038061> | NIK/NF-kappaB signaling | 113 | 3 | 0.1031819 | 29.074881 | 0.0001314 | 0.0274171 |
| <GO:0090304> | nucleic acid metabolic process | 4544 | 11 | 4.1491887 | 2.651121 | 0.0001359 | 0.0277795 |
| <GO:0071902> | positive regulation of protein serine/threonine kinase activity | 311 | 4 | 0.2839784 | 14.085580 | 0.0001366 | 0.0277795 |
| <GO:0034162> | toll-like receptor 9 signaling pathway | 20 | 2 | 0.0182623 | 109.515385 | 0.0001449 | 0.0288247 |
| <GO:0016310> | phosphorylation | 2107 | 8 | 1.9239306 | 4.158154 | 0.0001454 | 0.0288247 |
| <GO:0043405> | regulation of MAP kinase activity | 321 | 4 | 0.2931095 | 13.646777 | 0.0001544 | 0.0298599 |
| <GO:0044260> | cellular macromolecule metabolic process | 7260 | 13 | 6.6292056 | 1.961019 | 0.0001568 | 0.0298599 |
| <GO:0009966> | regulation of signal transduction | 2831 | 9 | 2.5850249 | 3.481591 | 0.0001571 | 0.0298599 |
| <GO:0070887> | cellular response to chemical stimulus | 2837 | 9 | 2.5905036 | 3.474228 | 0.0001598 | 0.0298599 |
| <GO:0002479> | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 21 | 2 | 0.0191754 | 104.300366 | 0.0001601 | 0.0298599 |
| <GO:0034097> | response to cytokine | 1040 | 6 | 0.9496383 | 6.318195 | 0.0001643 | 0.0303003 |
| <GO:0038093> | Fc receptor signaling pathway | 123 | 3 | 0.1123130 | 26.711069 | 0.0001689 | 0.0305860 |
| <GO:0065009> | regulation of molecular function | 2858 | 9 | 2.6096790 | 3.448700 | 0.0001697 | 0.0305860 |
| <GO:0006464> | cellular protein modification process | 3699 | 10 | 3.3776076 | 2.960675 | 0.0001778 | 0.0312074 |
| <GO:0036211> | protein modification process | 3699 | 10 | 3.3776076 | 2.960675 | 0.0001778 | 0.0312074 |
| <GO:0048519> | negative regulation of biological process | 4669 | 11 | 4.2633279 | 2.580144 | 0.0001791 | 0.0312074 |
| <GO:0010033> | response to organic substance | 2893 | 9 | 2.6416380 | 3.406977 | 0.0001874 | 0.0322999 |
| <GO:0035666> | TRIF-dependent toll-like receptor signaling pathway | 24 | 2 | 0.0219147 | 91.262821 | 0.0002100 | 0.0358132 |
| <GO:0050852> | T cell receptor signaling pathway | 133 | 3 | 0.1214441 | 24.702718 | 0.0002129 | 0.0359084 |
| <GO:0010467> | gene expression | 4770 | 11 | 4.3555524 | 2.525512 | 0.0002225 | 0.0371401 |
| <GO:0016032> | viral process | 679 | 5 | 0.6200042 | 8.064461 | 0.0002272 | 0.0373029 |
| <GO:0042590> | antigen processing and presentation of exogenous peptide antigen via MHC class I | 25 | 2 | 0.0228278 | 87.612308 | 0.0002282 | 0.0373029 |
| <GO:0042221> | response to chemical | 3820 | 10 | 3.4880944 | 2.866895 | 0.0002381 | 0.0385195 |
| <GO:0000187> | activation of MAPK activity | 142 | 3 | 0.1296621 | 23.137053 | 0.0002582 | 0.0413582 |
| <GO:0002756> | MyD88-independent toll-like receptor signaling pathway | 27 | 2 | 0.0246541 | 81.122507 | 0.0002667 | 0.0417064 |
| <GO:1901564> | organonitrogen compound metabolic process | 6041 | 12 | 5.5161200 | 2.175442 | 0.0002679 | 0.0417064 |
| <GO:0001959> | regulation of cytokine-mediated signaling pathway | 144 | 3 | 0.1314884 | 22.815705 | 0.0002691 | 0.0417064 |
| <GO:0043412> | macromolecule modification | 3875 | 10 | 3.5383157 | 2.826204 | 0.0002709 | 0.0417064 |
| <GO:0006355> | regulation of transcription, DNA-templated | 3057 | 9 | 2.7913886 | 3.224202 | 0.0002928 | 0.0446458 |
| <GO:0045859> | regulation of protein kinase activity | 724 | 5 | 0.6610943 | 7.563217 | 0.0003067 | 0.0463146 |
| <GO:0060759> | regulation of response to cytokine stimulus | 154 | 3 | 0.1406195 | 21.334166 | 0.0003278 | 0.0487277 |
| <GO:1903506> | regulation of nucleic acid-templated transcription | 3106 | 9 | 2.8361312 | 3.173337 | 0.0003328 | 0.0487277 |
| <GO:0071310> | cellular response to organic substance | 2367 | 8 | 2.1613402 | 3.701407 | 0.0003365 | 0.0487277 |
| <GO:0044403> | symbiont process | 739 | 5 | 0.6747910 | 7.409701 | 0.0003374 | 0.0487277 |
| <GO:2001141> | regulation of RNA biosynthetic process | 3112 | 9 | 2.8416099 | 3.167219 | 0.0003380 | 0.0487277 |