|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| ID | setSize | enrichmentScore | NES | pvalue | qvalue | Description |
| R-HSA-156902 | 84 | -0.28146453 | -3.439549063 | 0.002369668 | 0.017364006 | Peptide chain elongation |
| R-HSA-192823 | 84 | -0.28110297 | -3.43513073 | 0.002369668 | 0.017364006 | Viral mRNA Translation |
| R-HSA-156842 | 88 | -0.264410931 | -3.248876872 | 0.002666667 | 0.017364006 | Eukaryotic Translation Elongation |
| R-HSA-2408557 | 87 | -0.262391012 | -3.227042321 | 0.00255102 | 0.017364006 | Selenocysteine synthesis |
| R-HSA-72764 | 88 | -0.251633167 | -3.091873593 | 0.002666667 | 0.017364006 | Eukaryotic Translation Termination |
| R-HSA-176814 | 70 | -0.265665598 | -2.89932914 | 0.001655629 | 0.017364006 | Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins |
| R-HSA-73886 | 80 | -0.242525968 | -2.885833307 | 0.00212766 | 0.017364006 | Chromosome Maintenance |
| R-HSA-68867 | 79 | -0.24519564 | -2.885131973 | 0.002123142 | 0.017364006 | Assembly of the pre-replicative complex |
| R-HSA-176409 | 69 | -0.265047013 | -2.882099387 | 0.001626016 | 0.017364006 | APC/C:Cdc20 mediated degradation of mitotic proteins |
| R-HSA-69052 | 85 | -0.232982573 | -2.845709157 | 0.002457002 | 0.017364006 | Switching of origins to a post-replicative state |
| R-HSA-6784531 | 51 | -0.308535106 | -2.839510688 | 0.001057082 | 0.017364006 | tRNA processing in the nucleus |
| R-HSA-68949 | 65 | -0.269381467 | -2.830468994 | 0.00149925 | 0.017364006 | Orc1 removal from chromatin |
| R-HSA-174178 | 68 | -0.265029781 | -2.827227171 | 0.001626016 | 0.017364006 | APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1 |
| R-HSA-5689603 | 80 | -0.236884306 | -2.818702783 | 0.00212766 | 0.017364006 | UCH proteinases |
| R-HSA-351202 | 51 | -0.305631151 | -2.812785012 | 0.001057082 | 0.017364006 | Metabolism of polyamines |
| R-HSA-179419 | 67 | -0.263592734 | -2.802420851 | 0.0016 | 0.017364006 | APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint |
| R-HSA-69017 | 66 | -0.263893464 | -2.786977365 | 0.001540832 | 0.017364006 | CDK-mediated phosphorylation and removal of Cdc6 |
| R-HSA-174184 | 66 | -0.262982235 | -2.777353885 | 0.001540832 | 0.017364006 | Cdc20:Phospho-APC/C mediated degradation of Cyclin A |
| R-HSA-174143 | 81 | -0.227488391 | -2.709699717 | 0.002237136 | 0.017364006 | APC/C-mediated degradation of cell cycle proteins |
| R-HSA-453276 | 81 | -0.227488391 | -2.709699717 | 0.002237136 | 0.017364006 | Regulation of mitotic cell cycle |
| R-HSA-141424 | 85 | -0.221844261 | -2.709662947 | 0.002457002 | 0.017364006 | Amplification of signal from the kinetochores |
| R-HSA-141444 | 85 | -0.221844261 | -2.709662947 | 0.002457002 | 0.017364006 | Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal |
| R-HSA-174154 | 62 | -0.260260271 | -2.669131185 | 0.001386963 | 0.017364006 | APC/C:Cdc20 mediated degradation of Securin |
| R-HSA-212165 | 81 | -0.222631865 | -2.651851817 | 0.002237136 | 0.017364006 | Epigenetic regulation of gene expression |
| R-HSA-191859 | 48 | -0.292921575 | -2.61927654 | 0.000969932 | 0.017364006 | snRNP Assembly |
| R-HSA-194441 | 48 | -0.292921575 | -2.61927654 | 0.000969932 | 0.017364006 | Metabolism of non-coding RNA |
| R-HSA-8852276 | 61 | -0.258065814 | -2.617551474 | 0.001342282 | 0.017364006 | The role of GTSE1 in G2/M progression after G2 checkpoint |
| R-HSA-427413 | 41 | -0.315245546 | -2.603307754 | 0.001686341 | 0.017364006 | NoRC negatively regulates rRNA expression |
| R-HSA-174084 | 60 | -0.258627112 | -2.601631454 | 0.001293661 | 0.017364006 | Autodegradation of Cdh1 by Cdh1:APC/C |
| R-HSA-159234 | 38 | -0.323790581 | -2.589464834 | 0.001517451 | 0.017364006 | Transport of Mature mRNAs Derived from Intronless Transcripts |
| R-HSA-350562 | 45 | -0.29678011 | -2.589224881 | 0.00178731 | 0.017364006 | Regulation of ornithine decarboxylase (ODC) |
| R-HSA-69190 | 32 | -0.351959803 | -2.557884695 | 0.001346801 | 0.017364006 | DNA strand elongation |
| R-HSA-6790901 | 51 | -0.276414708 | -2.543900205 | 0.001057082 | 0.017364006 | rRNA modification in the nucleus and cytosol |
| R-HSA-5250941 | 44 | -0.294967769 | -2.543499632 | 0.001745201 | 0.017364006 | Negative epigenetic regulation of rRNA expression |
| R-HSA-159231 | 37 | -0.322184864 | -2.54274785 | 0.001485884 | 0.017364006 | Transport of Mature mRNA Derived from an Intronless Transcript |
| R-HSA-72306 | 89 | -0.201841176 | -2.48797108 | 0.002702703 | 0.017364006 | tRNA processing |
| R-HSA-176408 | 74 | -0.218151022 | -2.482057167 | 0.001897533 | 0.017364006 | Regulation of APC/C activators between G1/S and early anaphase |
| R-HSA-1236975 | 87 | -0.199999334 | -2.45971198 | 0.00255102 | 0.017364006 | Antigen processing-Cross presentation |
| R-HSA-450408 | 49 | -0.270113834 | -2.456483969 | 0.001937984 | 0.017364006 | AUF1 (hnRNP D0) binds and destabilizes mRNA |
| R-HSA-180585 | 47 | -0.275009469 | -2.452188681 | 0.001877934 | 0.017364006 | Vif-mediated degradation of APOBEC3G |
| R-HSA-5578749 | 41 | -0.293850377 | -2.42662577 | 0.001686341 | 0.017364006 | Transcriptional regulation by small RNAs |
| R-HSA-73863 | 25 | -0.377646061 | -2.419183094 | 0.001110494 | 0.017364006 | RNA Polymerase I Transcription Termination |
| R-HSA-69601 | 46 | -0.27242889 | -2.410160119 | 0.001833181 | 0.017364006 | Ubiquitin Mediated Degradation of Phosphorylated Cdc25A |
| R-HSA-69610 | 46 | -0.27242889 | -2.410160119 | 0.001833181 | 0.017364006 | p53-Independent DNA Damage Response |
| R-HSA-69613 | 46 | -0.27242889 | -2.410160119 | 0.001833181 | 0.017364006 | p53-Independent G1/S DNA damage checkpoint |
| R-HSA-69615 | 60 | -0.23730928 | -2.387187033 | 0.001293661 | 0.017364006 | G1/S DNA Damage Checkpoints |
| R-HSA-9735869 | 33 | -0.320293653 | -2.376345098 | 0.001346801 | 0.017364006 | SARS-CoV-1 modulates host translation machinery |
| R-HSA-3371453 | 61 | -0.234111979 | -2.374588662 | 0.001342282 | 0.017364006 | Regulation of HSF1-mediated heat shock response |
| R-HSA-69563 | 59 | -0.236773277 | -2.361868713 | 0.00127551 | 0.017364006 | p53-Dependent G1 DNA Damage Response |
| R-HSA-69580 | 59 | -0.236773277 | -2.361868713 | 0.00127551 | 0.017364006 | p53-Dependent G1/S DNA damage checkpoint |
| R-HSA-211733 | 45 | -0.27041091 | -2.35916974 | 0.00178731 | 0.017364006 | Regulation of activated PAK-2p34 by proteasome mediated degradation |
| R-HSA-168325 | 40 | -0.288152454 | -2.356228505 | 0.001640689 | 0.017364006 | Viral Messenger RNA Synthesis |
| R-HSA-177243 | 33 | -0.315143076 | -2.338131576 | 0.001346801 | 0.017364006 | Interactions of Rev with host cellular proteins |
| R-HSA-349425 | 46 | -0.262766291 | -2.324675755 | 0.001833181 | 0.017364006 | Autodegradation of the E3 ubiquitin ligase COP1 |
| R-HSA-8854050 | 49 | -0.254455287 | -2.314081161 | 0.001937984 | 0.017364006 | FBXL7 down-regulates AURKA during mitotic entry and in early mitosis |
| R-HSA-9759194 | 75 | -0.202101968 | -2.302169645 | 0.001945525 | 0.017364006 | Nuclear events mediated by NFE2L2 |
| R-HSA-5696399 | 81 | -0.193136026 | -2.300515789 | 0.002237136 | 0.017364006 | Global Genome Nucleotide Excision Repair (GG-NER) |
| R-HSA-4641258 | 51 | -0.248646801 | -2.28834656 | 0.002114165 | 0.017364006 | Degradation of DVL |
| R-HSA-174417 | 32 | -0.313501146 | -2.278384567 | 0.001346801 | 0.017364006 | Telomere C-strand (Lagging Strand) Synthesis |
| R-HSA-159230 | 31 | -0.317979468 | -2.276089563 | 0.001962067 | 0.017364006 | Transport of the SLBP Dependant Mature mRNA |
| R-HSA-5696394 | 38 | -0.283821823 | -2.269820901 | 0.002276176 | 0.017364006 | DNA Damage Recognition in GG-NER |
| R-HSA-165054 | 31 | -0.316885319 | -2.268257674 | 0.001962067 | 0.017364006 | Rev-mediated nuclear export of HIV RNA |
| R-HSA-70171 | 59 | -0.225389454 | -2.248312417 | 0.00127551 | 0.017364006 | Glycolysis |
| R-HSA-72165 | 49 | -0.246777636 | -2.244258645 | 0.001937984 | 0.017364006 | mRNA Splicing - Minor Pathway |
| R-HSA-75815 | 47 | -0.250245188 | -2.231371956 | 0.001877934 | 0.017364006 | Ubiquitin-dependent degradation of Cyclin D |
| R-HSA-1234176 | 58 | -0.226538614 | -2.230515392 | 0.002493766 | 0.017364006 | Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha |
| R-HSA-159227 | 30 | -0.315547199 | -2.220145193 | 0.001925546 | 0.017364006 | Transport of the SLBP independent Mature mRNA |
| R-HSA-3928662 | 37 | -0.280894678 | -2.216877378 | 0.002228826 | 0.017364006 | EPHB-mediated forward signaling |
| R-HSA-5678895 | 55 | -0.231049754 | -2.21140387 | 0.002314815 | 0.017364006 | Defective CFTR causes cystic fibrosis |
| R-HSA-8939236 | 61 | -0.217843806 | -2.209581211 | 0.001342282 | 0.017364006 | RUNX1 regulates transcription of genes involved in differentiation of HSCs |
| R-HSA-1236978 | 42 | -0.261700768 | -2.203068331 | 0.00170068 | 0.017364006 | Cross-presentation of soluble exogenous antigens (endosomes) |
| R-HSA-4085377 | 31 | -0.30703482 | -2.197748033 | 0.001962067 | 0.017364006 | SUMOylation of SUMOylation proteins |
| R-HSA-180746 | 30 | -0.31129917 | -2.190256663 | 0.001925546 | 0.017364006 | Nuclear import of Rev protein |
| R-HSA-211000 | 61 | -0.215772012 | -2.188567085 | 0.001342282 | 0.017364006 | Gene Silencing by RNA |
| R-HSA-73772 | 26 | -0.334544688 | -2.18840502 | 0.002272727 | 0.017364006 | RNA Polymerase I Promoter Escape |
| R-HSA-167152 | 35 | -0.285777407 | -2.187177763 | 0.002077562 | 0.017364006 | Formation of HIV elongation complex in the absence of HIV Tat |
| R-HSA-1236974 | 76 | -0.190968546 | -2.179553614 | 0.001980198 | 0.017364006 | ER-Phagosome pathway |
| R-HSA-5693538 | 86 | -0.177751335 | -2.157388065 | 0.002604167 | 0.017364006 | Homology Directed Repair |
| R-HSA-168271 | 28 | -0.318338082 | -2.155897124 | 0.001212121 | 0.017364006 | Transport of Ribonucleoproteins into the Host Nucleus |
| R-HSA-4615885 | 42 | -0.255913 | -2.154345322 | 0.00170068 | 0.017364006 | SUMOylation of DNA replication proteins |
| R-HSA-72202 | 74 | -0.189028604 | -2.150710994 | 0.001897533 | 0.017364006 | Transport of Mature Transcript to Cytoplasm |
| R-HSA-168274 | 28 | -0.317290824 | -2.148804722 | 0.001212121 | 0.017364006 | Export of Viral Ribonucleoproteins from Nucleus |
| R-HSA-168333 | 28 | -0.317290824 | -2.148804722 | 0.001212121 | 0.017364006 | NEP/NS2 Interacts with the Cellular Export Machinery |
| R-HSA-157579 | 58 | -0.217661745 | -2.143113113 | 0.002493766 | 0.017364006 | Telomere Maintenance |
| R-HSA-167169 | 33 | -0.288721989 | -2.142106397 | 0.002693603 | 0.017364006 | HIV Transcription Elongation |
| R-HSA-167200 | 33 | -0.288721989 | -2.142106397 | 0.002693603 | 0.017364006 | Formation of HIV-1 elongation complex containing HIV-1 Tat |
| R-HSA-167246 | 33 | -0.288721989 | -2.142106397 | 0.002693603 | 0.017364006 | Tat-mediated elongation of the HIV-1 transcript |
| R-HSA-73762 | 41 | -0.256540314 | -2.118518076 | 0.001686341 | 0.017364006 | RNA Polymerase I Transcription Initiation |
| R-HSA-5693567 | 80 | -0.177974476 | -2.117730623 | 0.00212766 | 0.017364006 | HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA) |
| R-HSA-187577 | 56 | -0.219203228 | -2.113567087 | 0.002364066 | 0.017364006 | SCF(Skp2)-mediated degradation of p27/p21 |
| R-HSA-5658442 | 61 | -0.207050085 | -2.100100924 | 0.001342282 | 0.017364006 | Regulation of RAS by GAPs |
| R-HSA-73864 | 44 | -0.238346532 | -2.055256132 | 0.002617801 | 0.017364006 | RNA Polymerase I Transcription |
| R-HSA-73854 | 44 | -0.238346532 | -2.055256132 | 0.002617801 | 0.017364006 | RNA Polymerase I Promoter Clearance |
| R-HSA-5250913 | 42 | -0.240794128 | -2.027070542 | 0.00255102 | 0.017364006 | Positive epigenetic regulation of rRNA expression |
| R-HSA-70326 | 75 | -0.176557967 | -2.011194637 | 0.001945525 | 0.017364006 | Glucose metabolism |
| R-HSA-3371556 | 79 | -0.17004762 | -2.000891308 | 0.002123142 | 0.017364006 | Cellular response to heat stress |
| R-HSA-9609690 | 58 | -0.202963352 | -1.998391684 | 0.002493766 | 0.017364006 | HCMV Early Events |
| R-HSA-4570464 | 43 | -0.233900222 | -1.984433503 | 0.002617801 | 0.017364006 | SUMOylation of RNA binding proteins |
| R-HSA-8852135 | 61 | -0.19525182 | -1.980431583 | 0.002684564 | 0.017364006 | Protein ubiquitination |
| R-HSA-9664407 | 56 | -0.203490555 | -1.962064812 | 0.002364066 | 0.017364006 | Parasite infection |
| R-HSA-9664417 | 56 | -0.203490555 | -1.962064812 | 0.002364066 | 0.017364006 | Leishmania phagocytosis |
| R-HSA-9664422 | 56 | -0.203490555 | -1.962064812 | 0.002364066 | 0.017364006 | FCGR3A-mediated phagocytosis |
| R-HSA-674695 | 68 | -0.183426604 | -1.95671852 | 0.001626016 | 0.017364006 | RNA Polymerase II Pre-transcription Events |
| R-HSA-8854518 | 64 | -0.186795514 | -1.935696743 | 0.001457726 | 0.017364006 | AURKA Activation by TPX2 |
| R-HSA-975956 | 90 | -0.240961453 | -2.982905922 | 0.002777778 | 0.017693807 | Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) |
| R-HSA-72695 | 47 | -0.230686747 | -2.056974375 | 0.002816901 | 0.017766569 | Formation of the ternary complex, and subsequently, the 43S complex |
| R-HSA-8939902 | 63 | -0.187053001 | -1.930947014 | 0.002836879 | 0.017766569 | Regulation of RUNX2 expression and activity |
| R-HSA-9633012 | 95 | -0.271152373 | -3.471608442 | 0.003030303 | 0.017923597 | Response of EIF2AK4 (GCN2) to amino acid deficiency |
| R-HSA-72689 | 95 | -0.261235668 | -3.344643241 | 0.003030303 | 0.017923597 | Formation of a pool of free 40S subunits |
| R-HSA-69002 | 95 | -0.242391165 | -3.10337397 | 0.003030303 | 0.017923597 | DNA Replication Pre-Initiation |
| R-HSA-9648025 | 96 | -0.193436653 | -2.490955407 | 0.003012048 | 0.017923597 | EML4 and NUDC in mitotic spindle formation |
| R-HSA-5362768 | 50 | -0.233448201 | -2.124298212 | 0.003030303 | 0.017923597 | Hh mutants are degraded by ERAD |
| R-HSA-9604323 | 50 | -0.230540495 | -2.097839085 | 0.003030303 | 0.017923597 | Negative regulation of NOTCH4 signaling |
| R-HSA-69541 | 51 | -0.243384054 | -2.239912447 | 0.003171247 | 0.018398834 | Stabilization of p53 |
| R-HSA-8941858 | 52 | -0.210354906 | -1.952800853 | 0.003184713 | 0.018398834 | Regulation of RUNX3 expression and activity |
| R-HSA-5387390 | 51 | -0.21194162 | -1.950541399 | 0.003171247 | 0.018398834 | Hh mutants abrogate ligand secretion |
| R-HSA-174411 | 24 | -0.343615194 | -2.148523878 | 0.003271538 | 0.01875505 | Polymerase switching on the C-strand of the telomere |
| R-HSA-2408522 | 100 | -0.239977314 | -3.100363562 | 0.003311258 | 0.018837853 | Selenoamino acid metabolism |
| R-HSA-69618 | 101 | -0.20711036 | -2.702353258 | 0.003378378 | 0.019074098 | Mitotic Spindle Checkpoint |
| R-HSA-156827 | 104 | -0.242607664 | -3.200502676 | 0.003571429 | 0.019445494 | L13a-mediated translational silencing of Ceruloplasmin expression |
| R-HSA-2500257 | 104 | -0.224110315 | -2.956483933 | 0.003571429 | 0.019445494 | Resolution of Sister Chromatid Cohesion |
| R-HSA-9754678 | 45 | -0.226376776 | -1.974998862 | 0.00357462 | 0.019445494 | SARS-CoV-2 modulates host translation machinery |
| R-HSA-72706 | 105 | -0.228300223 | -3.012824125 | 0.003663004 | 0.019632165 | GTP hydrolysis and joining of the 60S ribosomal subunit |
| R-HSA-5696398 | 107 | -0.178879019 | -2.401058726 | 0.003717472 | 0.019632165 | Nucleotide Excision Repair |
| R-HSA-606279 | 23 | -0.329356505 | -2.008068106 | 0.003729355 | 0.019632165 | Deposition of new CENPA-containing nucleosomes at the centromere |
| R-HSA-774815 | 23 | -0.329356505 | -2.008068106 | 0.003729355 | 0.019632165 | Nucleosome assembly |
| R-HSA-167172 | 58 | -0.198476928 | -1.954218026 | 0.003740648 | 0.019632165 | Transcription of the HIV genome |
| R-HSA-1799339 | 106 | -0.216539135 | -2.86110148 | 0.003846154 | 0.019803974 | SRP-dependent cotranslational protein targeting to membrane |
| R-HSA-927802 | 108 | -0.202040377 | -2.716689404 | 0.00390625 | 0.019803974 | Nonsense-Mediated Decay (NMD) |
| R-HSA-975957 | 108 | -0.202040377 | -2.716689404 | 0.00390625 | 0.019803974 | Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) |
| R-HSA-179409 | 25 | -0.32239284 | -2.065233536 | 0.00388673 | 0.019803974 | APC-Cdc20 mediated degradation of Nek2A |
| R-HSA-180910 | 30 | -0.290043552 | -2.040705161 | 0.003851091 | 0.019803974 | Vpr-mediated nuclear import of PICs |
| R-HSA-68962 | 32 | -0.282851328 | -2.05563555 | 0.004040404 | 0.01985793 | Activation of the pre-replicative complex |
| R-HSA-6796648 | 50 | -0.210139681 | -1.912198709 | 0.004040404 | 0.01985793 | TP53 Regulates Transcription of DNA Repair Genes |
| R-HSA-4641257 | 50 | -0.207794808 | -1.890861175 | 0.004040404 | 0.01985793 | Degradation of AXIN |
| R-HSA-174113 | 50 | -0.201837634 | -1.83665294 | 0.004040404 | 0.01985793 | SCF-beta-TrCP mediated degradation of Emi1 |
| R-HSA-69239 | 114 | -0.238591933 | -3.357856321 | 0.004201681 | 0.020466391 | Synthesis of DNA |
| R-HSA-72613 | 112 | -0.222034731 | -3.045326463 | 0.004291845 | 0.020635834 | Eukaryotic Translation Initiation |
| R-HSA-72737 | 112 | -0.222034731 | -3.045326463 | 0.004291845 | 0.020635834 | Cap-dependent Translation Initiation |
| R-HSA-162599 | 116 | -0.196452202 | -2.785876605 | 0.004405286 | 0.020711247 | Late Phase of HIV Life Cycle |
| R-HSA-72662 | 54 | -0.218686915 | -2.078875582 | 0.004469274 | 0.020711247 | Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S |
| R-HSA-72649 | 53 | -0.215019799 | -2.005651151 | 0.004415011 | 0.020711247 | Translation initiation complex formation |
| R-HSA-450531 | 81 | -0.16333874 | -1.945589124 | 0.004474273 | 0.020711247 | Regulation of mRNA stability by proteins that bind AU-rich elements |
| R-HSA-180786 | 45 | -0.22040117 | -1.922865357 | 0.004468275 | 0.020711247 | Extension of Telomeres |
| R-HSA-73884 | 45 | -0.219090038 | -1.911426534 | 0.004468275 | 0.020711247 | Base Excision Repair |
| R-HSA-5663220 | 118 | -0.182152472 | -2.600654448 | 0.004587156 | 0.020973241 | RHO GTPases Activate Formins |
| R-HSA-162909 | 118 | -0.179993355 | -2.56982798 | 0.004587156 | 0.020973241 | Host Interactions of HIV factors |
| R-HSA-69306 | 120 | -0.25168052 | -3.642920818 | 0.00462963 | 0.021038368 | DNA Replication |
| R-HSA-112382 | 47 | -0.217892364 | -1.942890153 | 0.004694836 | 0.021077639 | Formation of RNA Pol II elongation complex |
| R-HSA-75955 | 47 | -0.217892364 | -1.942890153 | 0.004694836 | 0.021077639 | RNA Polymerase II Transcription Elongation |
| R-HSA-69481 | 117 | -0.223403541 | -3.136106877 | 0.004739336 | 0.021150017 | G2/M Checkpoints |
| R-HSA-169911 | 48 | -0.217457268 | -1.944481968 | 0.004849661 | 0.021513532 | Regulation of Apoptosis |
| R-HSA-69206 | 124 | -0.152800146 | -2.212167882 | 0.005050505 | 0.022140914 | G1/S Transition |
| R-HSA-168273 | 127 | -0.248092926 | -3.737957574 | 0.005154639 | 0.022370671 | Influenza Viral RNA Transcription and Replication |
| R-HSA-2995410 | 60 | -0.189221293 | -1.903451126 | 0.005174644 | 0.022370671 | Nuclear Envelope (NE) Reassembly |
| R-HSA-162587 | 129 | -0.182516413 | -2.791397841 | 0.005405405 | 0.023152009 | HIV Life Cycle |
| R-HSA-72702 | 53 | -0.213729229 | -1.99361304 | 0.005518764 | 0.0232369 | Ribosomal scanning and start codon recognition |
| R-HSA-5693607 | 53 | -0.212089464 | -1.978317716 | 0.005518764 | 0.0232369 | Processing of DNA double-strand break ends |
| R-HSA-389958 | 21 | -0.331352678 | -1.929145225 | 0.00551655 | 0.0232369 | Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding |
| R-HSA-5368287 | 90 | -0.153274595 | -1.897414258 | 0.005555556 | 0.023260398 | Mitochondrial translation |
| R-HSA-8866652 | 29 | -0.289775647 | -1.998215407 | 0.005639098 | 0.023478278 | Synthesis of active ubiquitin: roles of E1 and E2 enzymes |
| R-HSA-113418 | 27 | -0.29179486 | -1.941762367 | 0.005817336 | 0.023899917 | Formation of the Early Elongation Complex |
| R-HSA-167158 | 27 | -0.29179486 | -1.941762367 | 0.005817336 | 0.023899917 | Formation of the HIV-1 Early Elongation Complex |
| R-HSA-6781827 | 75 | -0.169990989 | -1.936389342 | 0.005836576 | 0.023899917 | Transcription-Coupled Nucleotide Excision Repair (TC-NER) |
| R-HSA-170822 | 26 | -0.305787704 | -2.000292849 | 0.00625 | 0.025064824 | Regulation of Glucokinase by Glucokinase Regulatory Protein |
| R-HSA-5619107 | 26 | -0.305787704 | -2.000292849 | 0.00625 | 0.025064824 | Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC) |
| R-HSA-2424491 | 26 | -0.30205787 | -1.975894355 | 0.00625 | 0.025064824 | DAP12 signaling |
| R-HSA-429914 | 45 | -0.21473619 | -1.873441872 | 0.006255585 | 0.025064824 | Deadenylation-dependent mRNA decay |
| R-HSA-9711097 | 139 | -0.150880496 | -2.382653842 | 0.006369427 | 0.025384487 | Cellular response to starvation |
| R-HSA-453279 | 142 | -0.131590658 | -2.105107217 | 0.006711409 | 0.025915887 | Mitotic G1 phase and G1/S transition |
| R-HSA-5610785 | 54 | -0.20054868 | -1.90645038 | 0.006703911 | 0.025915887 | GLI3 is processed to GLI3R by the proteasome |
| R-HSA-5358346 | 54 | -0.199470947 | -1.896205267 | 0.006703911 | 0.025915887 | Hedgehog ligand biogenesis |
| R-HSA-380259 | 61 | -0.179810889 | -1.823814827 | 0.006711409 | 0.025915887 | Loss of Nlp from mitotic centrosomes |
| R-HSA-380284 | 61 | -0.179810889 | -1.823814827 | 0.006711409 | 0.025915887 | Loss of proteins required for interphase microtubule organization from the centrosome |
| R-HSA-168255 | 144 | -0.227675316 | -3.681190531 | 0.006993007 | 0.026767944 | Influenza Infection |
| R-HSA-5368286 | 84 | -0.14664207 | -1.791993454 | 0.007109005 | 0.026767944 | Mitochondrial translation initiation |
| R-HSA-5389840 | 84 | -0.146520443 | -1.79050715 | 0.007109005 | 0.026767944 | Mitochondrial translation elongation |
| R-HSA-5419276 | 84 | -0.146430238 | -1.78940483 | 0.007109005 | 0.026767944 | Mitochondrial translation termination |
| R-HSA-5689880 | 149 | -0.106315525 | -1.755682477 | 0.007352941 | 0.027318098 | Ub-specific processing proteases |
| R-HSA-9762114 | 49 | -0.200262746 | -1.821240392 | 0.007751938 | 0.028319773 | GSK3B and BTRC:CUL1-mediated-degradation of NFE2L2 |
| R-HSA-168276 | 36 | -0.250968737 | -1.952213602 | 0.007913669 | 0.02876959 | NS1 Mediated Effects on Host Pathways |
| R-HSA-176187 | 33 | -0.261098434 | -1.937159788 | 0.008080808 | 0.029152268 | Activation of ATR in response to replication stress |
| R-HSA-380320 | 77 | -0.161459246 | -1.845214602 | 0.008097166 | 0.029152268 | Recruitment of NuMA to mitotic centrosomes |
| R-HSA-9010553 | 151 | -0.166403042 | -2.744193102 | 0.008333333 | 0.029822455 | Regulation of expression of SLITs and ROBOs |
| R-HSA-5693532 | 114 | -0.141443014 | -1.990617675 | 0.008403361 | 0.029822455 | DNA Double-Strand Break Repair |
| R-HSA-9609646 | 78 | -0.159895275 | -1.855548493 | 0.008385744 | 0.029822455 | HCMV Infection |
| R-HSA-1234174 | 65 | -0.175380724 | -1.842776 | 0.008995502 | 0.031622719 | Cellular response to hypoxia |
| R-HSA-73933 | 38 | -0.235337583 | -1.882075735 | 0.009104704 | 0.031856341 | Resolution of Abasic Sites (AP sites) |
| R-HSA-69242 | 154 | -0.168341595 | -2.79759075 | 0.009259259 | 0.032245723 | S Phase |
| R-HSA-69186 | 20 | -0.3287689 | -1.859215387 | 0.009876543 | 0.034076962 | Lagging Strand Synthesis |
| R-HSA-6803529 | 26 | -0.281209542 | -1.839516201 | 0.010227273 | 0.03486429 | FGFR2 alternative splicing |
| R-HSA-2467813 | 163 | -0.206395053 | -3.478409918 | 0.010638298 | 0.035394337 | Separation of Sister Chromatids |
| R-HSA-9615933 | 25 | -0.29207285 | -1.871005087 | 0.010549695 | 0.035394337 | Postmitotic nuclear pore complex (NPC) reformation |
| R-HSA-6781823 | 51 | -0.193248427 | -1.778504181 | 0.010570825 | 0.035394337 | Formation of TC-NER Pre-Incision Complex |
| R-HSA-69275 | 166 | -0.133537651 | -2.273549209 | 0.010752688 | 0.035458329 | G2/M Transition |
| R-HSA-9705683 | 166 | -0.103621549 | -1.764211734 | 0.010752688 | 0.035458329 | SARS-CoV-2-host interactions |
| R-HSA-9610379 | 46 | -0.202420889 | -1.790804034 | 0.010999083 | 0.036111064 | HCMV Late Events |
| R-HSA-174048 | 23 | -0.297793828 | -1.81563224 | 0.011188066 | 0.03657041 | APC/C:Cdc20 mediated degradation of Cyclin B |
| R-HSA-5687128 | 74 | -0.161921853 | -1.842298474 | 0.011385199 | 0.036990596 | MAPK6/MAPK4 signaling |
| R-HSA-3214858 | 28 | -0.270675694 | -1.833110716 | 0.011515152 | 0.036990596 | RMTs methylate histone arginines |
| R-HSA-3247509 | 167 | -0.099890695 | -1.70413626 | 0.011494253 | 0.036990596 | Chromatin modifying enzymes |
| R-HSA-4839726 | 167 | -0.099890695 | -1.70413626 | 0.011494253 | 0.036990596 | Chromatin organization |
| R-HSA-9013407 | 34 | -0.248687373 | -1.873787913 | 0.011805556 | 0.037760711 | RHOH GTPase cycle |
| R-HSA-210991 | 19 | -0.335182413 | -1.859228708 | 0.011899096 | 0.037897255 | Basigin interactions |
| R-HSA-159236 | 65 | -0.170192467 | -1.788261486 | 0.011994003 | 0.038036973 | Transport of Mature mRNA derived from an Intron-Containing Transcript |
| R-HSA-110373 | 25 | -0.288474318 | -1.847953059 | 0.012215436 | 0.038575061 | Resolution of AP sites via the multiple-nucleotide patch replacement pathway |
| R-HSA-389957 | 20 | -0.323736749 | -1.830758159 | 0.012345679 | 0.038821855 | Prefoldin mediated transfer of substrate to CCT/TriC |
| R-HSA-6791226 | 168 | -0.259630237 | -4.381929167 | 0.012658228 | 0.039471594 | Major pathway of rRNA processing in the nucleolus and cytosol |
| R-HSA-453274 | 168 | -0.135981652 | -2.295040731 | 0.012658228 | 0.039471594 | Mitotic G2-G2/M phases |
| R-HSA-69205 | 27 | -0.267946535 | -1.783062591 | 0.013379872 | 0.041548024 | G1/S-Specific Transcription |
| R-HSA-8868773 | 176 | -0.253502279 | -4.546046368 | 0.013513514 | 0.041788895 | rRNA processing in the nucleus and cytosol |
| R-HSA-76046 | 36 | -0.236621182 | -1.840608095 | 0.013669065 | 0.042095249 | RNA Polymerase III Transcription Initiation |
| R-HSA-72163 | 175 | -0.185575594 | -3.267285872 | 0.013888889 | 0.042421628 | mRNA Splicing - Major Pathway |
| R-HSA-1169091 | 62 | -0.168871221 | -1.731879553 | 0.013869626 | 0.042421628 | Activation of NF-kappaB in B cells |
| R-HSA-180534 | 47 | -0.192218994 | -1.713967318 | 0.014084507 | 0.04266832 | Vpu mediated degradation of CD4 |
| R-HSA-1268020 | 50 | -0.188075621 | -1.71142336 | 0.014141414 | 0.04266832 | Mitochondrial protein import |
| R-HSA-68877 | 174 | -0.164306706 | -2.844381478 | 0.014285714 | 0.042929905 | Mitotic Prometaphase |
| R-HSA-3232142 | 34 | -0.243831517 | -1.83720043 | 0.014583333 | 0.043648277 | SUMOylation of ubiquitinylation proteins |
| R-HSA-72312 | 181 | -0.24026922 | -4.358821737 | 0.015384615 | 0.045612802 | rRNA processing |
| R-HSA-5250924 | 28 | -0.261427852 | -1.770481088 | 0.015757576 | 0.046234412 | B-WICH complex positively regulates rRNA expression |
| R-HSA-72172 | 183 | -0.175575593 | -3.136513435 | 0.015873016 | 0.046390486 | mRNA Splicing |
| R-HSA-198933 | 74 | -0.154381741 | -1.756509332 | 0.017077799 | 0.049716618 | Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell |
| R-HSA-1433559 | 15 | -0.365987556 | -1.801760271 | 0.017695473 | 0.051314336 | Regulation of KIT signaling |
| R-HSA-5693579 | 35 | -0.231426442 | -1.771206387 | 0.01800554 | 0.052011107 | Homologous DNA Pairing and Strand Exchange |
| R-HSA-9755511 | 94 | -0.128097844 | -1.622316849 | 0.018181818 | 0.052317526 | KEAP1-NFE2L2 pathway |
| R-HSA-5610780 | 53 | -0.179822054 | -1.677335356 | 0.01986755 | 0.056085427 | Degradation of GLI1 by the proteasome |
| R-HSA-141405 | 20 | -0.302745587 | -1.712051396 | 0.020740741 | 0.057892547 | Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components |
| R-HSA-141430 | 20 | -0.302745587 | -1.712051396 | 0.020740741 | 0.057892547 | Inactivation of APC/C via direct inhibition of the APC/C complex |
| R-HSA-376176 | 194 | -0.151037967 | -2.795693962 | 0.020833333 | 0.057934014 | Signaling by ROBO receptors |
| R-HSA-5610783 | 54 | -0.177191721 | -1.684415102 | 0.02122905 | 0.058557333 | Degradation of GLI2 by the proteasome |
| R-HSA-983705 | 105 | -0.129624289 | -1.710621127 | 0.021978022 | 0.059704119 | Signaling by the B Cell Receptor (BCR) |
| R-HSA-6782210 | 62 | -0.162133101 | -1.662775938 | 0.022191401 | 0.05992186 | Gap-filling DNA repair synthesis and ligation in TC-NER |
| R-HSA-512988 | 41 | -0.208267307 | -1.719878051 | 0.022765599 | 0.059951809 | Interleukin-3, Interleukin-5 and GM-CSF signaling |
| R-HSA-6807505 | 67 | -0.160405465 | -1.70537182 | 0.0224 | 0.059951809 | RNA polymerase II transcribes snRNA genes |
| R-HSA-1538133 | 25 | -0.263274797 | -1.686526099 | 0.02276513 | 0.059951809 | G0 and Early G1 |
| R-HSA-167287 | 25 | -0.263192785 | -1.686000733 | 0.02276513 | 0.059951809 | HIV elongation arrest and recovery |
| R-HSA-167290 | 25 | -0.263192785 | -1.686000733 | 0.02276513 | 0.059951809 | Pausing and recovery of HIV elongation |
| R-HSA-380270 | 72 | -0.150506365 | -1.685340336 | 0.023890785 | 0.062254972 | Recruitment of mitotic centrosome proteins and complexes |
| R-HSA-380287 | 72 | -0.150506365 | -1.685340336 | 0.023890785 | 0.062254972 | Centrosome maturation |
| R-HSA-9013694 | 76 | -0.15095563 | -1.722880004 | 0.025742574 | 0.066155145 | Signaling by NOTCH4 |
| R-HSA-69473 | 50 | -0.180894897 | -1.646081251 | 0.026262626 | 0.067259683 | G2/M DNA damage checkpoint |
| R-HSA-5685942 | 55 | -0.170814486 | -1.634885165 | 0.027777778 | 0.070175439 | HDR through Homologous Recombination (HRR) |
| R-HSA-9675136 | 33 | -0.223752054 | -1.660076904 | 0.028282828 | 0.070908353 | Diseases of DNA Double-Strand Break Repair |
| R-HSA-9701190 | 33 | -0.223752054 | -1.660076904 | 0.028282828 | 0.070908353 | Defective homologous recombination repair (HRR) due to BRCA2 loss of function |
| R-HSA-190828 | 24 | -0.26478984 | -1.655652325 | 0.028353326 | 0.070908353 | Gap junction trafficking |
| R-HSA-72086 | 27 | -0.246818735 | -1.64246667 | 0.028504945 | 0.071049114 | mRNA Capping |
| R-HSA-176033 | 32 | -0.228568545 | -1.661132828 | 0.028956229 | 0.071933369 | Interactions of Vpr with host cellular proteins |
| R-HSA-389960 | 15 | -0.341704491 | -1.682214508 | 0.02962963 | 0.073361699 | Formation of tubulin folding intermediates by CCT/TriC |
| R-HSA-8953750 | 33 | -0.218642988 | -1.62217137 | 0.03030303 | 0.074533769 | Transcriptional Regulation by E2F6 |
| R-HSA-75067 | 29 | -0.241995939 | -1.668739314 | 0.030701754 | 0.0750193 | Processing of Capped Intronless Pre-mRNA |
| R-HSA-3301854 | 32 | -0.219846725 | -1.597746586 | 0.035016835 | 0.084183087 | Nuclear Pore Complex (NPC) Disassembly |
| R-HSA-5693616 | 32 | -0.219046909 | -1.591933882 | 0.035016835 | 0.084183087 | Presynaptic phase of homologous DNA pairing and strand exchange |
| R-HSA-76071 | 28 | -0.238189351 | -1.613101811 | 0.039393939 | 0.093465458 | RNA Polymerase III Transcription Initiation From Type 3 Promoter |
| R-HSA-176412 | 19 | -0.284474979 | -1.577958825 | 0.039504998 | 0.093465458 | Phosphorylation of the APC/C |
| R-HSA-9646399 | 29 | -0.233065833 | -1.60715969 | 0.040100251 | 0.093713703 | Aggrephagy |
| R-HSA-157858 | 26 | -0.242816758 | -1.588371993 | 0.040340909 | 0.093713703 | Gap junction trafficking and regulation |
| R-HSA-167238 | 23 | -0.259415351 | -1.581640821 | 0.040490144 | 0.093713703 | Pausing and recovery of Tat-mediated HIV elongation |
| R-HSA-167243 | 23 | -0.259415351 | -1.581640821 | 0.040490144 | 0.093713703 | Tat-mediated HIV elongation arrest and recovery |
| R-HSA-9687136 | 19 | -0.284161921 | -1.576222318 | 0.040456925 | 0.093713703 | Aberrant regulation of mitotic exit in cancer due to RB1 defects |
| R-HSA-5619084 | 64 | -0.150745764 | -1.56212576 | 0.040816327 | 0.094176175 | ABC transporter disorders |
| R-HSA-5218859 | 49 | -0.168462205 | -1.53203818 | 0.042635659 | 0.097468668 | Regulated Necrosis |
| R-HSA-2172127 | 32 | -0.211784087 | -1.539150976 | 0.043771044 | 0.099758246 | DAP12 interactions |
| R-HSA-4551638 | 52 | -0.165950572 | -1.54057933 | 0.044585987 | 0.100550868 | SUMOylation of chromatin organization proteins |
| R-HSA-69656 | 80 | -0.128780229 | -1.532364869 | 0.044680851 | 0.100550868 | Cyclin A:Cdk2-associated events at S phase entry |
| R-HSA-9705671 | 96 | -0.117696779 | -1.515625011 | 0.045180723 | 0.1011157 | SARS-CoV-2 activates/modulates innate and adaptive immune responses |
| R-HSA-73856 | 63 | -0.149144308 | -1.539615802 | 0.045390071 | 0.101280083 | RNA Polymerase II Transcription Termination |
| R-HSA-975163 | 15 | -0.320732125 | -1.578967344 | 0.046090535 | 0.102033416 | IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation |
| R-HSA-5651801 | 21 | -0.269017381 | -1.566227255 | 0.046138415 | 0.102033416 | PCNA-Dependent Long Patch Base Excision Repair |
| R-HSA-5693554 | 21 | -0.268859512 | -1.565308137 | 0.04663992 | 0.102533964 | Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA) |
| R-HSA-69273 | 21 | -0.268522077 | -1.563343584 | 0.047141424 | 0.103028641 | Cyclin A/B1/B2 associated events during G2/M transition |
| R-HSA-3214841 | 31 | -0.218687173 | -1.565357651 | 0.049051668 | 0.106268607 | PKMTs methylate histone lysines |
| R-HSA-167242 | 19 | -0.277191109 | -1.537555811 | 0.050452166 | 0.108985914 | Abortive elongation of HIV-1 transcript in the absence of Tat |
| R-HSA-167161 | 43 | -0.180991538 | -1.5355508 | 0.051483421 | 0.109001979 | HIV Transcription Initiation |
| R-HSA-167162 | 43 | -0.180991538 | -1.5355508 | 0.051483421 | 0.109001979 | RNA Polymerase II HIV Promoter Escape |
| R-HSA-73776 | 43 | -0.180991538 | -1.5355508 | 0.051483421 | 0.109001979 | RNA Polymerase II Promoter Escape |
| R-HSA-73779 | 43 | -0.180991538 | -1.5355508 | 0.051483421 | 0.109001979 | RNA Polymerase II Transcription Pre-Initiation And Promoter Opening |
| R-HSA-75953 | 43 | -0.180991538 | -1.5355508 | 0.051483421 | 0.109001979 | RNA Polymerase II Transcription Initiation |
| R-HSA-76042 | 43 | -0.180991538 | -1.5355508 | 0.051483421 | 0.109001979 | RNA Polymerase II Transcription Initiation And Promoter Clearance |
| R-HSA-202403 | 108 | -0.112426054 | -1.511711046 | 0.05078125 | 0.109001979 | TCR signaling |
| R-HSA-5620971 | 22 | -0.260233773 | -1.552528692 | 0.052200614 | 0.10989603 | Pyroptosis |
| R-HSA-2980766 | 48 | -0.165157895 | -1.476826006 | 0.053346266 | 0.111991568 | Nuclear Envelope Breakdown |
| R-HSA-1168372 | 78 | -0.130623417 | -1.515855209 | 0.054507338 | 0.11391285 | Downstream signaling events of B Cell Receptor (BCR) |
| R-HSA-6783310 | 31 | -0.21422857 | -1.533443073 | 0.056245912 | 0.116763249 | Fanconi Anemia Pathway |
| R-HSA-5626467 | 22 | -0.25529602 | -1.52307055 | 0.058341863 | 0.120777892 | RHO GTPases activate IQGAPs |
| R-HSA-5693537 | 25 | -0.233768243 | -1.497508488 | 0.060521932 | 0.124255555 | Resolution of D-Loop Structures |
| R-HSA-5693568 | 25 | -0.233768243 | -1.497508488 | 0.060521932 | 0.124255555 | Resolution of D-loop Structures through Holliday Junction Intermediates |
| R-HSA-69202 | 78 | -0.127300822 | -1.477297241 | 0.060796646 | 0.124476649 | Cyclin E associated events during G1/S transition |
| R-HSA-2029482 | 58 | -0.150329894 | -1.480158884 | 0.061097257 | 0.12474941 | Regulation of actin dynamics for phagocytic cup formation |
| R-HSA-69183 | 15 | -0.308573661 | -1.519111109 | 0.061728395 | 0.125351222 | Processive synthesis on the lagging strand |
| R-HSA-167160 | 25 | -0.228931995 | -1.466527708 | 0.067184897 | 0.134532702 | RNA Pol II CTD phosphorylation and interaction with CE during HIV infection |
| R-HSA-77075 | 25 | -0.228931995 | -1.466527708 | 0.067184897 | 0.134532702 | RNA Pol II CTD phosphorylation and interaction with CE |
| R-HSA-5617472 | 48 | -0.160335317 | -1.433702975 | 0.067895247 | 0.13493287 | Activation of anterior HOX genes in hindbrain development during early embryogenesis |
| R-HSA-5619507 | 48 | -0.160335317 | -1.433702975 | 0.067895247 | 0.13493287 | Activation of HOX genes during differentiation |
| R-HSA-176407 | 19 | -0.265091471 | -1.470440133 | 0.068538791 | 0.135849563 | Conversion from APC/C:Cdc20 to APC/C:Cdh1 in late anaphase |
| R-HSA-9664323 | 34 | -0.193831933 | -1.460467927 | 0.070138889 | 0.138279757 | FCGR3A-mediated IL10 synthesis |
| R-HSA-9692914 | 86 | -0.121140239 | -1.470292789 | 0.072916667 | 0.14243285 | SARS-CoV-1-host interactions |
| R-HSA-9701192 | 20 | -0.259697959 | -1.468613492 | 0.073580247 | 0.14243285 | Defective HDR through Homologous Recombination (HRR) due to BRCA1 loss-of-function |
| R-HSA-9701193 | 20 | -0.259697959 | -1.468613492 | 0.073580247 | 0.14243285 | Defective HDR through Homologous Recombination (HRR) due to PALB2 loss of function |
| R-HSA-9704331 | 20 | -0.259697959 | -1.468613492 | 0.073580247 | 0.14243285 | Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA1 binding function |
| R-HSA-9704646 | 20 | -0.259697959 | -1.468613492 | 0.073580247 | 0.14243285 | Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA2/RAD51/RAD51C binding function |
| R-HSA-9709603 | 20 | -0.259697959 | -1.468613492 | 0.073580247 | 0.14243285 | Impaired BRCA2 binding to PALB2 |
| R-HSA-2995383 | 19 | -0.262528156 | -1.456221644 | 0.075678248 | 0.145736978 | Initiation of Nuclear Envelope (NE) Reformation |
| R-HSA-6782135 | 62 | -0.140455004 | -1.440453546 | 0.07628294 | 0.146146183 | Dual incision in TC-NER |
| R-HSA-2871837 | 75 | -0.123884669 | -1.411186279 | 0.077821012 | 0.14795187 | FCERI mediated NF-kB activation |
| R-HSA-9675135 | 43 | -0.169740032 | -1.440091861 | 0.078534031 | 0.148927532 | Diseases of DNA repair |
| R-HSA-75893 | 45 | -0.163954381 | -1.43040166 | 0.079535299 | 0.150443473 | TNF signaling |
| R-HSA-380108 | 31 | -0.203606427 | -1.457410023 | 0.081098757 | 0.152241602 | Chemokine receptors bind chemokines |
| R-HSA-983189 | 39 | -0.175140018 | -1.417485845 | 0.080952381 | 0.152241602 | Kinesins |
| R-HSA-174414 | 19 | -0.259767914 | -1.440910812 | 0.081865778 | 0.153295348 | Processive synthesis on the C-strand of the telomere |
| R-HSA-186763 | 29 | -0.207826683 | -1.433117256 | 0.083333333 | 0.155263158 | Downstream signal transduction |
| R-HSA-445989 | 41 | -0.171242136 | -1.414123008 | 0.086003373 | 0.159640395 | TAK1-dependent IKK and NF-kappa-B activation |
| R-HSA-5663213 | 34 | -0.187179292 | -1.410342194 | 0.086111111 | 0.159640395 | RHO GTPases Activate WASPs and WAVEs |
| R-HSA-76061 | 28 | -0.210139865 | -1.423140859 | 0.086666667 | 0.160271647 | RNA Polymerase III Transcription Initiation From Type 1 Promoter |
| R-HSA-9662851 | 61 | -0.138614272 | -1.405959149 | 0.087248322 | 0.160550519 | Anti-inflammatory response favouring Leishmania parasite infection |
| R-HSA-9664433 | 61 | -0.138614272 | -1.405959149 | 0.087248322 | 0.160550519 | Leishmania parasite growth and survival |
| R-HSA-5607761 | 55 | -0.146089038 | -1.398235048 | 0.087962963 | 0.161070161 | Dectin-1 mediated noncanonical NF-kB signaling |
| R-HSA-9709570 | 29 | -0.205492054 | -1.417018278 | 0.088972431 | 0.162121944 | Impaired BRCA2 binding to RAD51 |
| R-HSA-8948751 | 62 | -0.137078386 | -1.405824228 | 0.088765603 | 0.162121944 | Regulation of PTEN stability and activity |
| R-HSA-168638 | 36 | -0.180190741 | -1.40165193 | 0.089928058 | 0.163067961 | NOD1/2 Signaling Pathway |
| R-HSA-2565942 | 77 | -0.118132032 | -1.350055544 | 0.093117409 | 0.167625542 | Regulation of PLK1 Activity at G2/M Transition |
| R-HSA-5632684 | 75 | -0.12013259 | -1.368445862 | 0.097276265 | 0.173436402 | Hedgehog 'on' state |
| R-HSA-5620916 | 17 | -0.267385506 | -1.402356053 | 0.098324515 | 0.174179771 | VxPx cargo-targeting to cilium |
| R-HSA-9758274 | 18 | -0.257507058 | -1.385745103 | 0.097949886 | 0.174179771 | Regulation of NF-kappa B signaling |
| R-HSA-168643 | 55 | -0.140344811 | -1.343256394 | 0.105324074 | 0.184258573 | Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways |
| R-HSA-5676590 | 54 | -0.142234313 | -1.35210394 | 0.106145251 | 0.185260293 | NIK-->noncanonical NF-kB signaling |
| R-HSA-9670095 | 19 | -0.249192702 | -1.382251 | 0.107091861 | 0.186475744 | Inhibition of DNA recombination at telomere |
| R-HSA-4086400 | 83 | -0.113436162 | -1.384017089 | 0.107551487 | 0.186775862 | PCP/CE pathway |
| R-HSA-68875 | 76 | -0.115970775 | -1.32359243 | 0.108910891 | 0.188323143 | Mitotic Prophase |
| R-HSA-5696395 | 40 | -0.163970361 | -1.34078899 | 0.113207547 | 0.194848531 | Formation of Incision Complex in GG-NER |
| R-HSA-76066 | 27 | -0.204628253 | -1.361708157 | 0.115183246 | 0.197792234 | RNA Polymerase III Transcription Initiation From Type 2 Promoter |
| R-HSA-110314 | 30 | -0.192891069 | -1.357154112 | 0.118100128 | 0.201870813 | Recognition of DNA damage by PCNA-containing replication complex |
| R-HSA-5685938 | 32 | -0.185740629 | -1.349878903 | 0.121212121 | 0.205306655 | HDR through Single Strand Annealing (SSA) |
| R-HSA-5619115 | 126 | -0.087327886 | -1.29200292 | 0.123076923 | 0.207992509 | Disorders of transmembrane transporters |
| R-HSA-450513 | 17 | -0.256650037 | -1.346051764 | 0.123897707 | 0.208905875 | Tristetraprolin (TTP, ZFP36) binds and destabilizes mRNA |
| R-HSA-8866654 | 42 | -0.156531564 | -1.317725332 | 0.125 | 0.210288701 | E3 ubiquitin ligases ubiquitinate target proteins |
| R-HSA-4608870 | 58 | -0.133191395 | -1.311411997 | 0.132169576 | 0.219868562 | Asymmetric localization of PCP proteins |
| R-HSA-9022692 | 26 | -0.202218845 | -1.322803057 | 0.133522727 | 0.220642061 | Regulation of MECP2 expression and activity |
| R-HSA-2151201 | 50 | -0.141340981 | -1.28615424 | 0.133333333 | 0.220642061 | Transcriptional activation of mitochondrial biogenesis |
| R-HSA-427389 | 15 | -0.271077979 | -1.334519506 | 0.135390947 | 0.223234257 | ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression |
| R-HSA-5601884 | 19 | -0.237214238 | -1.315807464 | 0.142313184 | 0.233614038 | PIWI-interacting RNA (piRNA) biogenesis |
| R-HSA-9645723 | 40 | -0.158571909 | -1.296645738 | 0.142739951 | 0.233799619 | Diseases of programmed cell death |
| R-HSA-8854214 | 42 | -0.151993142 | -1.279519657 | 0.143707483 | 0.234868186 | TBC/RABGAPs |
| R-HSA-174437 | 17 | -0.2465456 | -1.293057052 | 0.149029982 | 0.240925283 | Removal of the Flap Intermediate from the C-strand |
| R-HSA-202733 | 99 | -0.096528257 | -1.244985787 | 0.148867314 | 0.240925283 | Cell surface interactions at the vascular wall |
| R-HSA-3214815 | 32 | -0.178598401 | -1.297972419 | 0.151515152 | 0.244412685 | HDACs deacetylate histones |
| R-HSA-70263 | 27 | -0.192794767 | -1.282961678 | 0.157649796 | 0.252667925 | Gluconeogenesis |
| R-HSA-8856688 | 109 | -0.095770513 | -1.291770387 | 0.16064257 | 0.256361861 | Golgi-to-ER retrograde transport |
| R-HSA-381042 | 30 | -0.180330792 | -1.268781789 | 0.161103979 | 0.256548847 | PERK regulates gene expression |
| R-HSA-5696400 | 38 | -0.15859347 | -1.26832662 | 0.162367223 | 0.258009188 | Dual Incision in GG-NER |
| R-HSA-391251 | 71 | -0.110400281 | -1.223780113 | 0.177554439 | 0.276252154 | Protein folding |
| R-HSA-9711123 | 170 | -0.073923247 | -1.248860018 | 0.178082192 | 0.276496035 | Cellular response to chemical stress |
| R-HSA-9705462 | 22 | -0.211060178 | -1.259163939 | 0.178607984 | 0.276735863 | Inactivation of CSF3 (G-CSF) signaling |
| R-HSA-114604 | 31 | -0.172836364 | -1.237158633 | 0.181818182 | 0.278811507 | GPVI-mediated activation cascade |
| R-HSA-1362277 | 18 | -0.229540595 | -1.235246745 | 0.188610478 | 0.285268194 | Transcription of E2F targets under negative control by DREAM complex |
| R-HSA-2173782 | 28 | -0.181903082 | -1.231911457 | 0.189090909 | 0.285268194 | Binding and Uptake of Ligands by Scavenger Receptors |
| R-HSA-9696264 | 37 | -0.154996536 | -1.223263888 | 0.188707281 | 0.285268194 | RND3 GTPase cycle |
| R-HSA-9674555 | 27 | -0.185595122 | -1.235051309 | 0.190226876 | 0.286402187 | Signaling by CSF3 (G-CSF) |
| R-HSA-5357956 | 27 | -0.185355152 | -1.233454416 | 0.191390343 | 0.287572927 | TNFR1-induced NFkappaB signaling pathway |
| R-HSA-9679191 | 88 | -0.098741062 | -1.213253746 | 0.192 | 0.287908504 | Potential therapeutics for SARS |
| R-HSA-6811436 | 39 | -0.150925609 | -1.221507891 | 0.192857143 | 0.288613099 | COPI-independent Golgi-to-ER retrograde traffic |
| R-HSA-912631 | 22 | -0.207702182 | -1.239130471 | 0.194472876 | 0.28986694 | Regulation of signaling by CBL |
| R-HSA-6783783 | 34 | -0.162230602 | -1.22236098 | 0.195833333 | 0.290185801 | Interleukin-10 signaling |
| R-HSA-164938 | 20 | -0.218450909 | -1.235358004 | 0.198518519 | 0.292967402 | Nef-mediates down modulation of cell surface receptors by recruiting them to clathrin adapters |
| R-HSA-5696397 | 25 | -0.189433296 | -1.213500878 | 0.202665186 | 0.296185411 | Gap-filling DNA repair synthesis and ligation in GG-NER |
| R-HSA-72187 | 54 | -0.125498159 | -1.193007169 | 0.203351955 | 0.296576752 | mRNA 3'-end processing |
| R-HSA-937072 | 16 | -0.240066443 | -1.218998003 | 0.206837607 | 0.299317375 | TRAF6-mediated induction of TAK1 complex within TLR4 complex |
| R-HSA-8853884 | 33 | -0.163215532 | -1.210940102 | 0.210774411 | 0.300887522 | Transcriptional Regulation by VENTX |
| R-HSA-2029480 | 80 | -0.100798202 | -1.199404789 | 0.210638298 | 0.300887522 | Fcgamma receptor (FCGR) dependent phagocytosis |
| R-HSA-6811442 | 171 | -0.071236436 | -1.196364382 | 0.214285714 | 0.303034626 | Intra-Golgi and retrograde Golgi-to-ER traffic |
| R-HSA-9607240 | 37 | -0.15026666 | -1.185934754 | 0.213967311 | 0.303034626 | FLT3 Signaling |
| R-HSA-5607764 | 95 | -0.091612244 | -1.172926636 | 0.215151515 | 0.303682761 | CLEC7A (Dectin-1) signaling |
| R-HSA-983695 | 30 | -0.169030426 | -1.189274027 | 0.221437741 | 0.311376207 | Antigen activates B Cell Receptor (BCR) leading to generation of second messengers |
| R-HSA-5603041 | 15 | -0.243800325 | -1.200231351 | 0.223868313 | 0.314201141 | IRAK4 deficiency (TLR2/4) |
| R-HSA-1632852 | 110 | -0.088136037 | -1.201564127 | 0.227642276 | 0.318897372 | Macroautophagy |
| R-HSA-77595 | 20 | -0.211666561 | -1.19699195 | 0.231604938 | 0.32202729 | Processing of Intronless Pre-mRNAs |
| R-HSA-9020702 | 104 | -0.089579779 | -1.181744706 | 0.239285714 | 0.330242272 | Interleukin-1 signaling |
| R-HSA-5357905 | 36 | -0.15029377 | -1.169091996 | 0.241007194 | 0.332003295 | Regulation of TNFR1 signaling |
| R-HSA-912526 | 20 | -0.208340146 | -1.178180802 | 0.242469136 | 0.333400948 | Interleukin receptor SHC signaling |
| R-HSA-113510 | 21 | -0.201555019 | -1.173459366 | 0.244232698 | 0.335207425 | E2F mediated regulation of DNA replication |
| R-HSA-2022090 | 50 | -0.125277205 | -1.139979413 | 0.246464646 | 0.337029396 | Assembly of collagen fibrils and other multimeric structures |
| R-HSA-9615017 | 18 | -0.215798748 | -1.16129655 | 0.246924829 | 0.337040253 | FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes |
| R-HSA-5610787 | 94 | -0.091034653 | -1.152923782 | 0.251515152 | 0.341429829 | Hedgehog 'off' state |
| R-HSA-9748787 | 20 | -0.205843906 | -1.164064357 | 0.254320988 | 0.343334313 | Azathioprine ADME |
| R-HSA-8982491 | 24 | -0.18370885 | -1.148676948 | 0.264449291 | 0.351308937 | Glycogen metabolism |
| R-HSA-1296065 | 16 | -0.222296769 | -1.128767995 | 0.284615385 | 0.371476988 | Inwardly rectifying K+ channels |
| R-HSA-5358508 | 15 | -0.230696657 | -1.135721868 | 0.286419753 | 0.372527207 | Mismatch Repair |
| R-HSA-9682385 | 27 | -0.168343775 | -1.120251422 | 0.296102385 | 0.380886432 | FLT3 signaling in disease |
| R-HSA-937041 | 23 | -0.18269444 | -1.113877738 | 0.296217368 | 0.380886432 | IKK complex recruitment mediated by RIP1 |
| R-HSA-5223345 | 19 | -0.200462012 | -1.111945953 | 0.304616849 | 0.390068239 | Miscellaneous transport and binding events |
| R-HSA-164952 | 27 | -0.166986053 | -1.111216399 | 0.305991856 | 0.391156873 | The role of Nef in HIV-1 replication and disease pathogenesis |
| R-HSA-9706574 | 34 | -0.146288841 | -1.102244389 | 0.306944444 | 0.391702716 | RHOBTB GTPase Cycle |
| R-HSA-9612973 | 121 | -0.074924064 | -1.0781453 | 0.310679612 | 0.394443047 | Autophagy |
| R-HSA-933542 | 21 | -0.187278066 | -1.090338517 | 0.31995988 | 0.402115194 | TRAF6 mediated NF-kB activation |
| R-HSA-9020591 | 36 | -0.140497246 | -1.092887654 | 0.323021583 | 0.403243023 | Interleukin-12 signaling |
| R-HSA-6807878 | 83 | -0.089131503 | -1.087479704 | 0.322654462 | 0.403243023 | COPI-mediated anterograde transport |
| R-HSA-9013404 | 81 | -0.090364244 | -1.076362468 | 0.324384787 | 0.404267611 | RAC2 GTPase cycle |
| R-HSA-8866427 | 15 | -0.222887444 | -1.09727704 | 0.327983539 | 0.407394711 | VLDLR internalisation and degradation |
| R-HSA-1500620 | 43 | -0.126842891 | -1.076148112 | 0.335078534 | 0.413446501 | Meiosis |
| R-HSA-9668328 | 18 | -0.199247155 | -1.072226028 | 0.334851936 | 0.413446501 | Sealing of the nuclear envelope (NE) by ESCRT-III |
| R-HSA-9663891 | 63 | -0.103497214 | -1.068401123 | 0.336170213 | 0.414107891 | Selective autophagy |
| R-HSA-6804756 | 82 | -0.090174154 | -1.077920959 | 0.338636364 | 0.414251886 | Regulation of TP53 Activity through Phosphorylation |
| R-HSA-5620912 | 85 | -0.086691006 | -1.058866279 | 0.339066339 | 0.414251886 | Anchoring of the basal body to the plasma membrane |
| R-HSA-1362300 | 16 | -0.212445948 | -1.078747962 | 0.346153846 | 0.420155877 | Transcription of E2F targets under negative control by p107 (RBL1) and p130 (RBL2) in complex with HDAC1 |
| R-HSA-1660516 | 16 | -0.212273475 | -1.077872189 | 0.347008547 | 0.420508432 | Synthesis of PIPs at the early endosome membrane |
| R-HSA-111471 | 18 | -0.196167337 | -1.055652332 | 0.35261959 | 0.424546671 | Apoptotic factor-mediated response |
| R-HSA-110328 | 15 | -0.217049345 | -1.068536021 | 0.356790123 | 0.426809846 | Recognition and association of DNA glycosylase with site containing an affected pyrimidine |
| R-HSA-110329 | 15 | -0.217049345 | -1.068536021 | 0.356790123 | 0.426809846 | Cleavage of the damaged pyrimidine |
| R-HSA-73928 | 15 | -0.217049345 | -1.068536021 | 0.356790123 | 0.426809846 | Depyrimidination |
| R-HSA-5693606 | 37 | -0.134727016 | -1.063292748 | 0.356612184 | 0.426809846 | DNA Double Strand Break Response |
| R-HSA-8956321 | 19 | -0.192092191 | -1.065519259 | 0.358400762 | 0.427364613 | Nucleotide salvage |
| R-HSA-202424 | 87 | -0.086695181 | -1.066229432 | 0.359693878 | 0.427688447 | Downstream TCR signaling |
| R-HSA-390466 | 65 | -0.101106839 | -1.062358802 | 0.35982009 | 0.427688447 | Chaperonin-mediated protein folding |
| R-HSA-8878166 | 104 | -0.08039297 | -1.060551471 | 0.364285714 | 0.43025154 | Transcriptional regulation by RUNX2 |
| R-HSA-352230 | 22 | -0.177612023 | -1.059615584 | 0.363868987 | 0.43025154 | Amino acid transport across the plasma membrane |
| R-HSA-74158 | 41 | -0.127813457 | -1.055487596 | 0.363406408 | 0.43025154 | RNA Polymerase III Transcription |
| R-HSA-749476 | 41 | -0.127813457 | -1.055487596 | 0.363406408 | 0.43025154 | RNA Polymerase III Abortive And Retractive Initiation |
| R-HSA-917729 | 27 | -0.159242927 | -1.05968941 | 0.365910413 | 0.430804976 | Endosomal Sorting Complex Required For Transport (ESCRT) |
| R-HSA-3108214 | 70 | -0.096937684 | -1.057924905 | 0.36589404 | 0.430804976 | SUMOylation of DNA damage response and repair proteins |
| R-HSA-8876384 | 18 | -0.193962529 | -1.043787406 | 0.367198178 | 0.431639233 | Listeria monocytogenes entry into host cells |
| R-HSA-8878159 | 91 | -0.084791046 | -1.061464791 | 0.369318182 | 0.431909173 | Transcriptional regulation by RUNX3 |
| R-HSA-8950505 | 31 | -0.147320454 | -1.054516352 | 0.370830608 | 0.431909173 | Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation |
| R-HSA-6814122 | 25 | -0.164546984 | -1.054080322 | 0.370905053 | 0.431909173 | Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding |
| R-HSA-9669938 | 20 | -0.186045037 | -1.052100111 | 0.370864198 | 0.431909173 | Signaling by KIT in disease |
| R-HSA-9670439 | 20 | -0.186045037 | -1.052100111 | 0.370864198 | 0.431909173 | Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants |
| R-HSA-9717207 | 16 | -0.207298785 | -1.052611942 | 0.379487179 | 0.438782923 | Sensory perception of sweet, bitter, and umami (glutamate) taste |
| R-HSA-5357801 | 181 | -0.057753129 | -1.047723025 | 0.384615385 | 0.443714669 | Programmed Cell Death |
| R-HSA-450385 | 17 | -0.198247312 | -1.039747148 | 0.386684303 | 0.445412002 | Butyrate Response Factor 1 (BRF1) binds and destabilizes mRNA |
| R-HSA-9035034 | 40 | -0.126535567 | -1.034683918 | 0.390484003 | 0.446963825 | RHOF GTPase cycle |
| R-HSA-9725371 | 18 | -0.189361252 | -1.019026156 | 0.396810934 | 0.451494 | Nuclear events stimulated by ALK signaling in cancer |
| R-HSA-912446 | 18 | -0.188181176 | -1.012675711 | 0.405922551 | 0.460455285 | Meiotic recombination |
| R-HSA-9635486 | 23 | -0.16755101 | -1.021549092 | 0.407032499 | 0.460899544 | Infection with Mycobacterium tuberculosis |
| R-HSA-9675126 | 36 | -0.131215065 | -1.020684239 | 0.414388489 | 0.463093432 | Diseases of mitotic cell cycle |
| R-HSA-110320 | 17 | -0.193285077 | -1.013721728 | 0.414462081 | 0.463093432 | Translesion Synthesis by POLH |
| R-HSA-5693565 | 36 | -0.130914069 | -1.01834288 | 0.417985612 | 0.464939219 | Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks |
| R-HSA-9703465 | 19 | -0.18394935 | -1.0203516 | 0.420752023 | 0.466318051 | Signaling by FLT3 fusion proteins |
| R-HSA-6804760 | 16 | -0.19910838 | -1.011023096 | 0.429059829 | 0.471626081 | Regulation of TP53 Activity through Methylation |
| R-HSA-379724 | 23 | -0.16348095 | -0.996734168 | 0.443793287 | 0.48342215 | tRNA Aminoacylation |
| R-HSA-1660514 | 15 | -0.202152387 | -0.995198153 | 0.447736626 | 0.485197368 | Synthesis of PIPs at the Golgi membrane |
| R-HSA-451927 | 34 | -0.131558687 | -0.991256908 | 0.447916667 | 0.485197368 | Interleukin-2 family signaling |
| R-HSA-429947 | 19 | -0.178258506 | -0.988784969 | 0.451213708 | 0.488059438 | Deadenylation of mRNA |
| R-HSA-9687139 | 35 | -0.129248394 | -0.989193707 | 0.452216066 | 0.488080057 | Aberrant regulation of mitotic cell cycle due to RB1 defects |
| R-HSA-6811434 | 77 | -0.088569007 | -1.012198615 | 0.453441296 | 0.488342618 | COPI-dependent Golgi-to-ER retrograde traffic |
| R-HSA-8978934 | 19 | -0.17750832 | -0.984623746 | 0.45644931 | 0.489323428 | Metabolism of cofactors |
| R-HSA-201556 | 24 | -0.156302895 | -0.977315638 | 0.471646674 | 0.500238068 | Signaling by ALK |
| R-HSA-162588 | 24 | -0.155117512 | -0.969903788 | 0.483097056 | 0.505503963 | Budding and maturation of HIV virion |
| R-HSA-9637690 | 20 | -0.170786386 | -0.965811173 | 0.480493827 | 0.505503963 | Response of Mtb to phagocytosis |
| R-HSA-2559586 | 25 | -0.150702738 | -0.965394729 | 0.483620211 | 0.505503963 | DNA Damage/Telomere Stress Induced Senescence |
| R-HSA-3299685 | 32 | -0.13228032 | -0.96135355 | 0.485521886 | 0.506780915 | Detoxification of Reactive Oxygen Species |
| R-HSA-8955332 | 22 | -0.159621997 | -0.95228889 | 0.492323439 | 0.510306705 | Carboxyterminal post-translational modifications of tubulin |
| R-HSA-73780 | 18 | -0.177725789 | -0.956411231 | 0.497038724 | 0.511636256 | RNA Polymerase III Chain Elongation |
| R-HSA-9013422 | 23 | -0.156413574 | -0.953644776 | 0.500799148 | 0.513630975 | RHOBTB1 GTPase cycle |
| R-HSA-9634597 | 30 | -0.133569355 | -0.939774978 | 0.51283697 | 0.522129098 | GPER1 signaling |
| R-HSA-9648002 | 22 | -0.157011706 | -0.936716152 | 0.517400205 | 0.526056358 | RAS processing |
| R-HSA-380994 | 25 | -0.146760684 | -0.940142112 | 0.519156024 | 0.526405249 | ATF4 activates genes in response to endoplasmic reticulum stress |
| R-HSA-163560 | 15 | -0.187497192 | -0.923050485 | 0.548559671 | 0.54292339 | Triglyceride catabolism |
| R-HSA-9619483 | 17 | -0.174837913 | -0.916971936 | 0.55643739 | 0.545059063 | Activation of AMPK downstream of NMDARs |
| R-HSA-5656121 | 17 | -0.174773471 | -0.916633957 | 0.55643739 | 0.545059063 | Translesion synthesis by POLI |
| R-HSA-5654738 | 58 | -0.093880129 | -0.924350461 | 0.561097257 | 0.548773115 | Signaling by FGFR2 |
| R-HSA-450604 | 17 | -0.173662643 | -0.910808002 | 0.565696649 | 0.549486156 | KSRP (KHSRP) binds and destabilizes mRNA |
| R-HSA-203927 | 20 | -0.160184582 | -0.905857093 | 0.567407407 | 0.549893155 | MicroRNA (miRNA) biogenesis |
| R-HSA-379726 | 17 | -0.17007594 | -0.891996831 | 0.592151675 | 0.568775733 | Mitochondrial tRNA aminoacylation |
| R-HSA-5693571 | 29 | -0.129300113 | -0.891619018 | 0.59085213 | 0.568775733 | Nonhomologous End-Joining (NHEJ) |
| R-HSA-76009 | 27 | -0.13391328 | -0.891132102 | 0.597440372 | 0.568775733 | Platelet Aggregation (Plug Formation) |
| R-HSA-6782315 | 33 | -0.119720887 | -0.888241591 | 0.596632997 | 0.568775733 | tRNA modification in the nucleus and cytosol |
| R-HSA-5621481 | 121 | -0.061989658 | -0.89202126 | 0.601941748 | 0.571471347 | C-type lectin receptors (CLRs) |
| R-HSA-168927 | 19 | -0.159677566 | -0.885718052 | 0.601618277 | 0.571471347 | TICAM1, RIP1-mediated IKK complex recruitment |
| R-HSA-9703648 | 15 | -0.177810315 | -0.875361895 | 0.612757202 | 0.575145299 | Signaling by FLT3 ITD and TKD mutants |
| R-HSA-983231 | 105 | -0.067243827 | -0.887400907 | 0.619047619 | 0.577301125 | Factors involved in megakaryocyte development and platelet production |
| R-HSA-1433557 | 41 | -0.107046183 | -0.88399079 | 0.623102867 | 0.578300884 | Signaling by SCF-KIT |
| R-HSA-5633007 | 141 | -0.056759198 | -0.907271625 | 0.632258065 | 0.58473233 | Regulation of TP53 Activity |
| R-HSA-3000170 | 26 | -0.132137068 | -0.864367107 | 0.632386364 | 0.58473233 | Syndecan interactions |
| R-HSA-2173796 | 36 | -0.110765092 | -0.861609786 | 0.639568345 | 0.588452747 | SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription |
| R-HSA-2173793 | 50 | -0.097300166 | -0.885397989 | 0.643434343 | 0.589825228 | Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer |
| R-HSA-447115 | 42 | -0.102430793 | -0.862290307 | 0.651360544 | 0.594917255 | Interleukin-12 family signaling |
| R-HSA-525793 | 19 | -0.153405202 | -0.850925777 | 0.654926226 | 0.595451463 | Myogenesis |
| R-HSA-1592230 | 69 | -0.080155295 | -0.871602073 | 0.66504065 | 0.602223931 | Mitochondrial biogenesis |
| R-HSA-9658195 | 138 | -0.054791253 | -0.863064702 | 0.666666667 | 0.60296372 | Leishmania infection |
| R-HSA-9660821 | 29 | -0.121956501 | -0.840979434 | 0.677944862 | 0.607999192 | ADORA2B mediated anti-inflammatory cytokines production |
| R-HSA-1169408 | 66 | -0.080509044 | -0.850255555 | 0.68412943 | 0.609876148 | ISG15 antiviral mechanism |
| R-HSA-6804114 | 17 | -0.158808266 | -0.832901292 | 0.686507937 | 0.610535886 | TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest |
| R-HSA-1839126 | 20 | -0.147253034 | -0.832728117 | 0.687901235 | 0.611045824 | FGFR2 mutant receptor activation |
| R-HSA-110312 | 16 | -0.161631472 | -0.820724626 | 0.693162393 | 0.61279762 | Translesion synthesis by REV1 |
| R-HSA-9013420 | 39 | -0.103135722 | -0.834723142 | 0.698412698 | 0.616707646 | RHOU GTPase cycle |
| R-HSA-2644602 | 55 | -0.085519926 | -0.818521089 | 0.71875 | 0.625038384 | Signaling by NOTCH1 PEST Domain Mutants in Cancer |
| R-HSA-2644603 | 55 | -0.085519926 | -0.818521089 | 0.71875 | 0.625038384 | Signaling by NOTCH1 in Cancer |
| R-HSA-2644606 | 55 | -0.085519926 | -0.818521089 | 0.71875 | 0.625038384 | Constitutive Signaling by NOTCH1 PEST Domain Mutants |
| R-HSA-2894858 | 55 | -0.085519926 | -0.818521089 | 0.71875 | 0.625038384 | Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer |
| R-HSA-2894862 | 55 | -0.085519926 | -0.818521089 | 0.71875 | 0.625038384 | Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants |
| R-HSA-2990846 | 157 | -0.049732139 | -0.83019764 | 0.727272727 | 0.627076645 | SUMOylation |
| R-HSA-73893 | 45 | -0.093787306 | -0.818236859 | 0.73458445 | 0.629312902 | DNA Damage Bypass |
| R-HSA-354192 | 24 | -0.128080616 | -0.800850097 | 0.733369684 | 0.629312902 | Integrin signaling |
| R-HSA-5213460 | 27 | -0.117936076 | -0.78481106 | 0.7504363 | 0.639899916 | RIPK1-mediated regulated necrosis |
| R-HSA-5675482 | 27 | -0.117936076 | -0.78481106 | 0.7504363 | 0.639899916 | Regulation of necroptotic cell death |
| R-HSA-6791312 | 42 | -0.093961383 | -0.790992508 | 0.755102041 | 0.642408369 | TP53 Regulates Transcription of Cell Cycle Genes |
| R-HSA-844456 | 15 | -0.157974109 | -0.777708065 | 0.75473251 | 0.642408369 | The NLRP3 inflammasome |
| R-HSA-418346 | 59 | -0.080343963 | -0.801449784 | 0.764030612 | 0.646315399 | Platelet homeostasis |
| R-HSA-6806003 | 34 | -0.103112734 | -0.776924826 | 0.765277778 | 0.646511499 | Regulation of TP53 Expression and Degradation |
| R-HSA-110313 | 36 | -0.100249336 | -0.779810743 | 0.771942446 | 0.649323098 | Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template |
| R-HSA-1445148 | 60 | -0.078558432 | -0.790250046 | 0.78007762 | 0.653951755 | Translocation of SLC2A4 (GLUT4) to the plasma membrane |
| R-HSA-8851708 | 19 | -0.136174733 | -0.755349811 | 0.78486435 | 0.657225263 | Signaling by FGFR2 IIIa TM |
| R-HSA-2682334 | 83 | -0.062910185 | -0.767557446 | 0.789473684 | 0.657391789 | EPH-Ephrin signaling |
| R-HSA-9735871 | 15 | -0.151896828 | -0.74778955 | 0.788477366 | 0.657391789 | SARS-CoV-1 targets host intracellular signalling and regulatory pathways |
| R-HSA-450302 | 23 | -0.122923589 | -0.749458215 | 0.804475226 | 0.662609605 | activated TAK1 mediates p38 MAPK activation |
| R-HSA-2559585 | 30 | -0.10636635 | -0.748378507 | 0.805519897 | 0.662609605 | Oncogene Induced Senescence |
| R-HSA-69231 | 46 | -0.085803589 | -0.759098594 | 0.829514207 | 0.674897792 | Cyclin D associated events in G1 |
| R-HSA-69236 | 46 | -0.085803589 | -0.759098594 | 0.829514207 | 0.674897792 | G1 Phase |
| R-HSA-5628897 | 73 | -0.067302733 | -0.754960735 | 0.830659537 | 0.675092638 | TP53 Regulates Metabolic Genes |
| R-HSA-9678108 | 129 | -0.049753744 | -0.760931534 | 0.837837838 | 0.677851427 | SARS-CoV-1 Infection |
| R-HSA-9006335 | 24 | -0.115295729 | -0.720909992 | 0.841330425 | 0.677851427 | Signaling by Erythropoietin |
| R-HSA-622312 | 20 | -0.1273039 | -0.719914107 | 0.840493827 | 0.677851427 | Inflammasomes |
| R-HSA-109581 | 157 | -0.043030236 | -0.718320214 | 0.848484848 | 0.678602593 | Apoptosis |
| R-HSA-9029569 | 28 | -0.10614946 | -0.718881367 | 0.853939394 | 0.679199114 | NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux |
| R-HSA-977444 | 22 | -0.118840621 | -0.708991273 | 0.860286592 | 0.679893741 | GABA B receptor activation |
| R-HSA-991365 | 22 | -0.118840621 | -0.708991273 | 0.860286592 | 0.679893741 | Activation of GABAB receptors |
| R-HSA-9013405 | 50 | -0.07763082 | -0.706413719 | 0.88989899 | 0.689342651 | RHOD GTPase cycle |
| R-HSA-3108232 | 151 | -0.0413207 | -0.681429733 | 0.891666667 | 0.689342651 | SUMO E3 ligases SUMOylate target proteins |
| R-HSA-977225 | 36 | -0.0879226 | -0.683924612 | 0.897122302 | 0.690694421 | Amyloid fiber formation |
| R-HSA-9692916 | 36 | -0.083667207 | -0.650823133 | 0.926618705 | 0.694777978 | SARS-CoV-1 activates/modulates innate immune responses |
| R-HSA-6804757 | 33 | -0.087600114 | -0.649928898 | 0.922558923 | 0.694777978 | Regulation of TP53 Degradation |
| R-HSA-5689896 | 37 | -0.081486349 | -0.643106677 | 0.930163447 | 0.695302455 | Ovarian tumor domain proteases |
| R-HSA-9671555 | 20 | -0.111856017 | -0.632555048 | 0.939259259 | 0.697001025 | Signaling by PDGFR in disease |
| R-HSA-1912420 | 16 | -0.122487383 | -0.621960629 | 0.938888889 | 0.697001025 | Pre-NOTCH Processing in Golgi |
| R-HSA-4655427 | 16 | -0.122175468 | -0.620376802 | 0.939316239 | 0.697001025 | SUMOylation of DNA methylation proteins |
| R-HSA-140534 | 15 | -0.123844717 | -0.609688737 | 0.939917695 | 0.697001025 | Caspase activation via Death Receptors in the presence of ligand |
| R-HSA-3928665 | 45 | -0.07300768 | -0.636947335 | 0.943699732 | 0.698693964 | EPH-ephrin mediated repulsion of cells |
| R-HSA-977443 | 24 | -0.098010254 | -0.612829042 | 0.948200654 | 0.69966239 | GABA receptor activation |
| R-HSA-5260271 | 28 | -0.089058246 | -0.603133671 | 0.961818182 | 0.702375587 | Diseases of Immune System |
| R-HSA-5602358 | 28 | -0.089058246 | -0.603133671 | 0.961818182 | 0.702375587 | Diseases associated with the TLR signaling cascade |
| R-HSA-9734009 | 21 | -0.100932247 | -0.587630565 | 0.959879639 | 0.702375587 | Defective Intrinsic Pathway for Apoptosis |
| R-HSA-5656169 | 31 | -0.081776122 | -0.58535156 | 0.971877044 | 0.705262079 | Termination of translesion DNA synthesis |
| R-HSA-9013423 | 84 | -0.048528602 | -0.593028569 | 0.973933649 | 0.705918625 | RAC3 GTPase cycle |
| R-HSA-936964 | 17 | -0.106586826 | -0.559015645 | 0.975308642 | 0.705918625 | Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon |
| R-HSA-2173795 | 29 | -0.080866415 | -0.557633185 | 0.978070175 | 0.705918625 | Downregulation of SMAD2/3:SMAD4 transcriptional activity |
| R-HSA-450321 | 22 | -0.092815794 | -0.553729754 | 0.983111566 | 0.705918625 | JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1 |
| R-HSA-5655862 | 17 | -0.101710864 | -0.533442698 | 0.986772487 | 0.706008735 | Translesion synthesis by POLK |
| R-HSA-5621575 | 20 | -0.0939177 | -0.531112381 | 0.988148148 | 0.706008735 | CD209 (DC-SIGN) signaling |
| R-HSA-2979096 | 21 | -0.089126564 | -0.518897528 | 0.98996991 | 0.706008735 | NOTCH2 Activation and Transmission of Signal to the Nucleus |
| R-HSA-418360 | 19 | -0.09176925 | -0.509036325 | 0.992860543 | 0.706008735 | Platelet calcium homeostasis |
| R-HSA-171319 | 19 | -0.091000281 | -0.504770922 | 0.994288434 | 0.706008735 | Telomere Extension By Telomerase |