|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| ID | setSize | enrichmentScore | NES | pvalue | qvalue | Description |
| R-HSA-5683826 | 21 | 0.648484083 | 2.987200203 | 0.000124875 | 0.017364006 | Surfactant metabolism |
| R-HSA-913709 | 38 | 0.453805356 | 2.575628246 | 0.000115154 | 0.017364006 | O-linked glycosylation of mucins |
| R-HSA-909733 | 54 | 0.365437287 | 2.33940834 | 0.000109806 | 0.017364006 | Interferon alpha/beta signaling |
| R-HSA-425366 | 42 | 0.391556392 | 2.29938726 | 0.000339905 | 0.017364006 | Transport of bile salts and organic acids, metal ions and amine compounds |
| R-HSA-5173105 | 66 | 0.326650108 | 2.218963926 | 0.000213835 | 0.017364006 | O-linked glycosylation |
| R-HSA-5576892 | 18 | 0.50896913 | 2.213558539 | 0.000768541 | 0.017364006 | Phase 0 - rapid depolarisation |
| R-HSA-5668914 | 187 | 0.254969876 | 2.201704328 | 0.000100543 | 0.017364006 | Diseases of metabolism |
| R-HSA-8978868 | 130 | 0.265989912 | 2.137181842 | 0.000101906 | 0.017364006 | Fatty acid metabolism |
| R-HSA-8863795 | 24 | 0.429219321 | 2.077221145 | 0.002203722 | 0.017364006 | Downregulation of ERBB2 signaling |
| R-HSA-397014 | 111 | 0.26383023 | 2.051262009 | 0.000615258 | 0.017364006 | Muscle contraction |
| R-HSA-1630316 | 96 | 0.270604707 | 2.028877708 | 0.00041365 | 0.017364006 | Glycosaminoglycan metabolism |
| R-HSA-425407 | 147 | 0.242395991 | 1.999163487 | 0.000506945 | 0.017364006 | SLC-mediated transmembrane transport |
| R-HSA-390918 | 27 | 0.404624925 | 2.042890484 | 0.00301823 | 0.017923597 | Peroxisomal lipid metabolism |
| R-HSA-420029 | 17 | 0.481267402 | 2.048089126 | 0.003491078 | 0.019445494 | Tight junction interactions |
| R-HSA-196849 | 97 | 0.249209636 | 1.873596395 | 0.003510221 | 0.019445494 | Metabolism of water-soluble vitamins and cofactors |
| R-HSA-1250196 | 19 | 0.451453215 | 2.003123374 | 0.00405012 | 0.01985793 | SHC1 events in ERBB2 signaling |
| R-HSA-5576891 | 68 | 0.272089776 | 1.866670685 | 0.004900394 | 0.02160996 | Cardiac conduction |
| R-HSA-450282 | 31 | 0.370376827 | 1.964458905 | 0.005192966 | 0.022370671 | MAPK targets/ Nuclear events mediated by MAP kinases |
| R-HSA-3781865 | 107 | 0.234444196 | 1.806547029 | 0.006575568 | 0.025915887 | Diseases of glycosylation |
| R-HSA-112315 | 137 | 0.215431127 | 1.750666215 | 0.007111653 | 0.026767944 | Transmission across Chemical Synapses |
| R-HSA-877300 | 73 | 0.259632087 | 1.813962618 | 0.007202627 | 0.026974133 | Interferon gamma signaling |
| R-HSA-913531 | 160 | 0.204951102 | 1.721034722 | 0.007367784 | 0.027318098 | Interferon Signaling |
| R-HSA-373760 | 82 | 0.250024112 | 1.801685764 | 0.007634386 | 0.028166469 | L1CAM interactions |
| R-HSA-1227990 | 22 | 0.406121593 | 1.905042746 | 0.007703777 | 0.02828247 | Signaling by ERBB2 in Cancer |
| R-HSA-3560782 | 34 | 0.340813849 | 1.864829215 | 0.008993226 | 0.031622719 | Diseases associated with glycosaminoglycan metabolism |
| R-HSA-3296482 | 18 | 0.433476902 | 1.88523516 | 0.009606763 | 0.03330031 | Defects in vitamin and cofactor metabolism |
| R-HSA-196854 | 143 | 0.209282712 | 1.715338668 | 0.009947219 | 0.034162653 | Metabolism of vitamins and cofactors |
| R-HSA-112316 | 195 | 0.188641268 | 1.640173019 | 0.010245078 | 0.03486429 | Neuronal System |
| R-HSA-419037 | 25 | 0.379958505 | 1.866588776 | 0.010486526 | 0.035394337 | NCAM1 interactions |
| R-HSA-1227986 | 44 | 0.305235801 | 1.822045159 | 0.010614273 | 0.035394337 | Signaling by ERBB2 |
| R-HSA-198753 | 22 | 0.390049783 | 1.829652802 | 0.014040755 | 0.04266832 | ERK/MAPK targets |
| R-HSA-2024096 | 19 | 0.406324711 | 1.802885658 | 0.014934818 | 0.04452148 | HS-GAG degradation |
| R-HSA-9664565 | 21 | 0.391695706 | 1.804321065 | 0.015484515 | 0.045612802 | Signaling by ERBB2 KD Mutants |
| R-HSA-1638091 | 40 | 0.303708029 | 1.758692604 | 0.015484459 | 0.045612802 | Heparan sulfate/heparin (HS-GAG) metabolism |
| R-HSA-9659379 | 41 | 0.295483843 | 1.722982493 | 0.01826225 | 0.052346856 | Sensory processing of sound |
| R-HSA-9753281 | 15 | 0.439675206 | 1.777364018 | 0.019017433 | 0.054302651 | Paracetamol ADME |
| R-HSA-936837 | 37 | 0.308614669 | 1.737044522 | 0.01952403 | 0.055536412 | Ion transport by P-type ATPases |
| R-HSA-421270 | 36 | 0.312192501 | 1.739414907 | 0.019623781 | 0.055607912 | Cell-cell junction organization |
| R-HSA-75105 | 22 | 0.375335096 | 1.760628874 | 0.020626243 | 0.057892547 | Fatty acyl-CoA biosynthesis |
| R-HSA-8848021 | 49 | 0.275578372 | 1.706778591 | 0.0212932 | 0.058557333 | Signaling by PTK6 |
| R-HSA-9006927 | 49 | 0.275578372 | 1.706778591 | 0.0212932 | 0.058557333 | Signaling by Non-Receptor Tyrosine Kinases |
| R-HSA-1638074 | 28 | 0.34011169 | 1.740771328 | 0.021431992 | 0.058647504 | Keratan sulfate/keratin metabolism |
| R-HSA-211859 | 116 | 0.209297896 | 1.64159025 | 0.021483376 | 0.058647504 | Biological oxidations |
| R-HSA-1912408 | 28 | 0.337549504 | 1.727657457 | 0.022030651 | 0.059704119 | Pre-NOTCH Transcription and Translation |
| R-HSA-70895 | 21 | 0.37742382 | 1.738578542 | 0.022477522 | 0.059951809 | Branched-chain amino acid catabolism |
| R-HSA-983712 | 112 | 0.209822021 | 1.635647384 | 0.022622582 | 0.059951809 | Ion channel transport |
| R-HSA-1793185 | 40 | 0.291922584 | 1.690446219 | 0.023682113 | 0.062145797 | Chondroitin sulfate/dermatan sulfate metabolism |
| R-HSA-445095 | 17 | 0.405289441 | 1.724756121 | 0.024308249 | 0.0631221 | Interaction between L1 and Ankyrins |
| R-HSA-2028269 | 18 | 0.39560971 | 1.720546887 | 0.024593314 | 0.063640592 | Signaling by Hippo |
| R-HSA-375165 | 44 | 0.282065136 | 1.683732425 | 0.024841915 | 0.064061467 | NCAM signaling for neurite out-growth |
| R-HSA-2142753 | 37 | 0.298767633 | 1.681620258 | 0.026571165 | 0.067816815 | Arachidonic acid metabolism |
| R-HSA-166658 | 26 | 0.339507069 | 1.692196121 | 0.02669255 | 0.06789411 | Complement cascade |
| R-HSA-8853659 | 29 | 0.326116115 | 1.690358169 | 0.027599334 | 0.069961791 | RET signaling |
| R-HSA-6811558 | 81 | 0.225498217 | 1.620408167 | 0.029827316 | 0.07360662 | PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling |
| R-HSA-9662360 | 39 | 0.287561193 | 1.649412827 | 0.0306566 | 0.0750193 | Sensory processing of sound by inner hair cells of the cochlea |
| R-HSA-196807 | 22 | 0.357938616 | 1.679025141 | 0.0319334 | 0.077773811 | Nicotinate metabolism |
| R-HSA-2219530 | 55 | 0.254890721 | 1.6409417 | 0.032501641 | 0.078899922 | Constitutive Signaling by Aberrant PI3K in Cancer |
| R-HSA-198725 | 54 | 0.255222217 | 1.633848008 | 0.034369167 | 0.083162577 | Nuclear Events (kinase and transcription factor activation) |
| R-HSA-114508 | 22 | 0.352976981 | 1.65575101 | 0.035536779 | 0.085158368 | Effects of PIP2 hydrolysis |
| R-HSA-9665686 | 18 | 0.376909434 | 1.639217484 | 0.037530421 | 0.089647565 | Signaling by ERBB2 TMD/JMD mutants |
| R-HSA-5654736 | 35 | 0.296110712 | 1.633546605 | 0.038209862 | 0.090978922 | Signaling by FGFR1 |
| R-HSA-450294 | 63 | 0.237917118 | 1.596758288 | 0.040012907 | 0.093713703 | MAP kinase activation |
| R-HSA-199418 | 88 | 0.213680874 | 1.570843081 | 0.040095565 | 0.093713703 | Negative regulation of the PI3K/AKT network |
| R-HSA-9694614 | 15 | 0.400393635 | 1.618570319 | 0.041336503 | 0.095082014 | Attachment and Entry |
| R-HSA-425393 | 66 | 0.232715165 | 1.580855307 | 0.042446274 | 0.09733429 | Transport of inorganic cations/anions and amino acids/oligopeptides |
| R-HSA-442742 | 22 | 0.342232223 | 1.605349298 | 0.044358847 | 0.100550868 | CREB1 phosphorylation through NMDA receptor-mediated activation of RAS signaling |
| R-HSA-381426 | 75 | 0.222809765 | 1.571108283 | 0.044793423 | 0.100550868 | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) |
| R-HSA-8957275 | 69 | 0.227961986 | 1.568352585 | 0.044742729 | 0.100550868 | Post-translational protein phosphorylation |
| R-HSA-445355 | 36 | 0.28579723 | 1.59235075 | 0.045750116 | 0.101778734 | Smooth Muscle Contraction |
| R-HSA-2219528 | 81 | 0.215128967 | 1.545895749 | 0.046467818 | 0.102457848 | PI3K/AKT Signaling in Cancer |
| R-HSA-448424 | 67 | 0.228917421 | 1.563444773 | 0.047136611 | 0.103028641 | Interleukin-17 signaling |
| R-HSA-2022854 | 22 | 0.338689195 | 1.588729596 | 0.047837972 | 0.104245258 | Keratan sulfate biosynthesis |
| R-HSA-977606 | 22 | 0.337595157 | 1.583597662 | 0.048707753 | 0.105831178 | Regulation of Complement cascade |
| R-HSA-211945 | 56 | 0.241142781 | 1.561312657 | 0.052096986 | 0.10989603 | Phase I - Functionalization of compounds |
| R-HSA-442755 | 59 | 0.235374091 | 1.548051324 | 0.054567151 | 0.11391285 | Activation of NMDA receptors and postsynaptic events |
| R-HSA-5579029 | 21 | 0.338509695 | 1.559323127 | 0.055194805 | 0.11490127 | Metabolic disorders of biological oxidation enzymes |
| R-HSA-112310 | 23 | 0.322899026 | 1.540461163 | 0.060061538 | 0.123993495 | Neurotransmitter release cycle |
| R-HSA-2022928 | 22 | 0.32796039 | 1.538402716 | 0.061630219 | 0.125351222 | HS-GAG biosynthesis |
| R-HSA-186712 | 20 | 0.340209024 | 1.539956577 | 0.062680206 | 0.126938174 | Regulation of beta-cell development |
| R-HSA-3560783 | 15 | 0.376938453 | 1.523753974 | 0.064844163 | 0.130964676 | Defective B4GALT7 causes EDS, progeroid type |
| R-HSA-9709957 | 116 | 0.185841199 | 1.457611886 | 0.066393862 | 0.13373216 | Sensory Perception |
| R-HSA-425397 | 29 | 0.292910595 | 1.518243946 | 0.067332857 | 0.134532702 | Transport of vitamins, nucleosides, and related molecules |
| R-HSA-5654687 | 18 | 0.347741066 | 1.512361285 | 0.070321506 | 0.138279757 | Downstream signaling of activated FGFR1 |
| R-HSA-438064 | 54 | 0.235117907 | 1.50514688 | 0.070056001 | 0.138279757 | Post NMDA receptor activation events |
| R-HSA-6794361 | 31 | 0.282740652 | 1.499641318 | 0.075534049 | 0.145736978 | Neurexins and neuroligins |
| R-HSA-9619665 | 20 | 0.330431732 | 1.495699653 | 0.07621913 | 0.146146183 | EGR2 and SOX10-mediated initiation of Schwann cell myelination |
| R-HSA-193648 | 54 | 0.232077818 | 1.485685241 | 0.076534534 | 0.146252227 | NRAGE signals death through JNK |
| R-HSA-201451 | 21 | 0.323211047 | 1.488850891 | 0.077297702 | 0.147332813 | Signaling by BMP |
| R-HSA-428157 | 63 | 0.218666707 | 1.467560976 | 0.080025815 | 0.15098808 | Sphingolipid metabolism |
| R-HSA-9634638 | 21 | 0.319117014 | 1.469991992 | 0.083041958 | 0.15510805 | Estrogen-dependent nuclear events downstream of ESR-membrane signaling |
| R-HSA-9616222 | 27 | 0.29024317 | 1.465394177 | 0.087649402 | 0.160891306 | Transcriptional regulation of granulopoiesis |
| R-HSA-182971 | 26 | 0.293101442 | 1.460897781 | 0.090148022 | 0.163067961 | EGFR downregulation |
| R-HSA-3906995 | 40 | 0.249799245 | 1.446521142 | 0.089946488 | 0.163067961 | Diseases associated with O-glycosylation of proteins |
| R-HSA-9033241 | 55 | 0.22466584 | 1.446359227 | 0.091486102 | 0.165087703 | Peroxisomal protein import |
| R-HSA-3781860 | 19 | 0.325130687 | 1.442623195 | 0.096443488 | 0.172852139 | Diseases associated with N-glycosylation of proteins |
| R-HSA-6806667 | 29 | 0.278088315 | 1.441415596 | 0.096716631 | 0.172852139 | Metabolism of fat-soluble vitamins |
| R-HSA-163685 | 75 | 0.201264328 | 1.419183997 | 0.096648398 | 0.172852139 | Integration of energy metabolism |
| R-HSA-196071 | 15 | 0.353752706 | 1.430026807 | 0.098520866 | 0.174179771 | Metabolism of steroid hormones |
| R-HSA-446728 | 61 | 0.21469123 | 1.425972967 | 0.098628065 | 0.174179771 | Cell junction organization |
| R-HSA-1266695 | 19 | 0.323120701 | 1.433704774 | 0.10112644 | 0.178169763 | Interleukin-7 signaling |
| R-HSA-2129379 | 29 | 0.274331168 | 1.42194117 | 0.104449203 | 0.18358996 | Molecules associated with elastic fibres |
| R-HSA-187687 | 31 | 0.269718222 | 1.430571042 | 0.105039537 | 0.18419317 | Signalling to ERKs |
| R-HSA-4420332 | 15 | 0.348451231 | 1.408595871 | 0.107765452 | 0.186775862 | Defective B3GALT6 causes EDSP2 and SEMDJL1 |
| R-HSA-3560801 | 15 | 0.346700214 | 1.401517476 | 0.110802958 | 0.191151302 | Defective B3GAT3 causes JDSSDHD |
| R-HSA-202131 | 16 | 0.336174389 | 1.394406339 | 0.116810232 | 0.200124972 | Metabolism of nitric oxide: NOS3 activation and regulation |
| R-HSA-114608 | 101 | 0.179804463 | 1.366188154 | 0.118586441 | 0.202238228 | Platelet degranulation |
| R-HSA-1660661 | 30 | 0.265743859 | 1.395342543 | 0.118900995 | 0.202311714 | Sphingolipid de novo biosynthesis |
| R-HSA-9639288 | 44 | 0.231877673 | 1.384148222 | 0.120257453 | 0.204153642 | Amino acids regulate mTORC1 |
| R-HSA-77289 | 32 | 0.256324983 | 1.375158871 | 0.128918633 | 0.216392585 | Mitochondrial Fatty Acid Beta-Oxidation |
| R-HSA-191273 | 24 | 0.281988628 | 1.364693323 | 0.12989716 | 0.217545095 | Cholesterol biosynthesis |
| R-HSA-168179 | 109 | 0.173339275 | 1.341720593 | 0.131344202 | 0.218984328 | Toll Like Receptor TLR1:TLR2 Cascade |
| R-HSA-181438 | 109 | 0.173339275 | 1.341720593 | 0.131344202 | 0.218984328 | Toll Like Receptor 2 (TLR2) Cascade |
| R-HSA-211897 | 27 | 0.27150349 | 1.370780346 | 0.132802125 | 0.220428799 | Cytochrome P450 - arranged by substrate type |
| R-HSA-4791275 | 28 | 0.265073193 | 1.356706715 | 0.13829023 | 0.227511288 | Signaling by WNT in cancer |
| R-HSA-881907 | 15 | 0.330922483 | 1.337736824 | 0.144215531 | 0.235182761 | Gastrin-CREB signalling pathway via PKC and MAPK |
| R-HSA-1500931 | 90 | 0.179516253 | 1.327978297 | 0.144990666 | 0.235930571 | Cell-Cell communication |
| R-HSA-416476 | 102 | 0.172979082 | 1.316995243 | 0.14814433 | 0.240537061 | G alpha (q) signalling events |
| R-HSA-1660499 | 50 | 0.212719983 | 1.327785996 | 0.155015535 | 0.249519151 | Synthesis of PIPs at the plasma membrane |
| R-HSA-163125 | 50 | 0.212188257 | 1.32446699 | 0.157345761 | 0.252667925 | Post-translational modification: synthesis of GPI-anchored proteins |
| R-HSA-5654696 | 17 | 0.309998611 | 1.319234965 | 0.159038014 | 0.254345864 | Downstream signaling of activated FGFR2 |
| R-HSA-76005 | 105 | 0.168705948 | 1.295173098 | 0.163428924 | 0.259143736 | Response to elevated platelet cytosolic Ca2+ |
| R-HSA-8948216 | 32 | 0.244157265 | 1.309880232 | 0.165081602 | 0.261208568 | Collagen chain trimerization |
| R-HSA-112314 | 105 | 0.168270101 | 1.291827056 | 0.165690205 | 0.261616112 | Neurotransmitter receptors and postsynaptic signal transmission |
| R-HSA-112409 | 22 | 0.27838843 | 1.305869642 | 0.167246521 | 0.263515159 | RAF-independent MAPK1/3 activation |
| R-HSA-3928663 | 26 | 0.261081662 | 1.301302436 | 0.169376365 | 0.266307942 | EPHA-mediated growth cone collapse |
| R-HSA-1855204 | 24 | 0.26878939 | 1.300815171 | 0.170298727 | 0.267194457 | Synthesis of IP3 and IP4 in the cytosol |
| R-HSA-975634 | 26 | 0.259492986 | 1.293384042 | 0.174714875 | 0.273547394 | Retinoid metabolism and transport |
| R-HSA-422356 | 53 | 0.203028321 | 1.293402336 | 0.17557168 | 0.274312588 | Regulation of insulin secretion |
| R-HSA-162710 | 18 | 0.298572749 | 1.298523271 | 0.175995901 | 0.274400128 | Synthesis of glycosylphosphatidylinositol (GPI) |
| R-HSA-3000157 | 28 | 0.252002808 | 1.289809422 | 0.179477969 | 0.276932336 | Laminin interactions |
| R-HSA-5686938 | 15 | 0.318354205 | 1.286930216 | 0.179344955 | 0.276932336 | Regulation of TLR by endogenous ligand |
| R-HSA-2672351 | 60 | 0.194688678 | 1.286327587 | 0.18019287 | 0.277460966 | Stimuli-sensing channels |
| R-HSA-202427 | 17 | 0.302693447 | 1.288146994 | 0.181794673 | 0.278811507 | Phosphorylation of CD3 and TCR zeta chains |
| R-HSA-1566948 | 36 | 0.230353202 | 1.283438242 | 0.186600093 | 0.285268194 | Elastic fibre formation |
| R-HSA-975576 | 19 | 0.288439476 | 1.279822221 | 0.188583724 | 0.285268194 | N-glycan antennae elongation in the medial/trans-Golgi |
| R-HSA-177929 | 45 | 0.212260835 | 1.277935544 | 0.18799955 | 0.285268194 | Signaling by EGFR |
| R-HSA-201722 | 28 | 0.249131081 | 1.275111249 | 0.188697318 | 0.285268194 | Formation of the beta-catenin:TCF transactivating complex |
| R-HSA-193368 | 16 | 0.30618199 | 1.270001883 | 0.188723571 | 0.285268194 | Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol |
| R-HSA-3769402 | 38 | 0.224826158 | 1.276028576 | 0.193689544 | 0.289277918 | Deactivation of the beta-catenin transactivating complex |
| R-HSA-400253 | 62 | 0.189307302 | 1.264668899 | 0.195237582 | 0.290185801 | Circadian Clock |
| R-HSA-1474228 | 91 | 0.170221437 | 1.262159623 | 0.195854922 | 0.290185801 | Degradation of the extracellular matrix |
| R-HSA-9614657 | 15 | 0.312156133 | 1.261874834 | 0.197569995 | 0.292146107 | FOXO-mediated transcription of cell death genes |
| R-HSA-1483166 | 24 | 0.260780818 | 1.262057421 | 0.200538688 | 0.295363825 | Synthesis of PA |
| R-HSA-4641262 | 26 | 0.251784228 | 1.254961481 | 0.202378064 | 0.296185411 | Disassembly of the destruction complex and recruitment of AXIN to the membrane |
| R-HSA-187037 | 102 | 0.163097449 | 1.241760343 | 0.202268041 | 0.296185411 | Signaling by NTRK1 (TRKA) |
| R-HSA-166016 | 136 | 0.151772139 | 1.230922105 | 0.202686203 | 0.296185411 | Toll Like Receptor 4 (TLR4) Cascade |
| R-HSA-9662361 | 29 | 0.242655518 | 1.257756725 | 0.204496788 | 0.297083669 | Sensory processing of sound by outer hair cells of the cochlea |
| R-HSA-2243919 | 15 | 0.310385474 | 1.254717038 | 0.204305335 | 0.297083669 | Crosslinking of collagen fibrils |
| R-HSA-383280 | 37 | 0.222970932 | 1.254996848 | 0.206561922 | 0.299317375 | Nuclear Receptor transcription pathway |
| R-HSA-5654726 | 20 | 0.276466854 | 1.251427566 | 0.208349003 | 0.300699592 | Negative regulation of FGFR1 signaling |
| R-HSA-5625900 | 20 | 0.276416618 | 1.251200173 | 0.208599724 | 0.300699592 | RHO GTPases activate CIT |
| R-HSA-381070 | 45 | 0.208161314 | 1.25325401 | 0.210401891 | 0.300887522 | IRE1alpha activates chaperones |
| R-HSA-168142 | 93 | 0.166202723 | 1.237346164 | 0.211152493 | 0.300887522 | Toll Like Receptor 10 (TLR10) Cascade |
| R-HSA-168176 | 93 | 0.166202723 | 1.237346164 | 0.211152493 | 0.300887522 | Toll Like Receptor 5 (TLR5) Cascade |
| R-HSA-975871 | 93 | 0.166202723 | 1.237346164 | 0.211152493 | 0.300887522 | MyD88 cascade initiated on plasma membrane |
| R-HSA-1912422 | 43 | 0.210581447 | 1.249085279 | 0.212850045 | 0.302151042 | Pre-NOTCH Expression and Processing |
| R-HSA-168164 | 101 | 0.162068676 | 1.231428304 | 0.212754997 | 0.302151042 | Toll Like Receptor 3 (TLR3) Cascade |
| R-HSA-5669034 | 15 | 0.306802409 | 1.240232688 | 0.21737982 | 0.306247961 | TNFs bind their physiological receptors |
| R-HSA-9013695 | 17 | 0.287749608 | 1.224551759 | 0.228600983 | 0.319639569 | NOTCH4 Intracellular Domain Regulates Transcription |
| R-HSA-196299 | 16 | 0.294040605 | 1.219641044 | 0.229313495 | 0.320035392 | Beta-catenin phosphorylation cascade |
| R-HSA-1971475 | 19 | 0.275508393 | 1.222446276 | 0.231109986 | 0.321939735 | A tetrasaccharide linker sequence is required for GAG synthesis |
| R-HSA-437239 | 33 | 0.22530521 | 1.220254887 | 0.233063285 | 0.323451545 | Recycling pathway of L1 |
| R-HSA-5620922 | 21 | 0.264491828 | 1.218364585 | 0.23513986 | 0.325726905 | BBSome-mediated cargo-targeting to cilium |
| R-HSA-381038 | 43 | 0.205342922 | 1.218012434 | 0.238934056 | 0.330242272 | XBP1(S) activates chaperone genes |
| R-HSA-373080 | 40 | 0.209090098 | 1.210785273 | 0.245701924 | 0.336604029 | Class B/2 (Secretin family receptors) |
| R-HSA-5654732 | 20 | 0.265693744 | 1.20266307 | 0.249467218 | 0.33926775 | Negative regulation of FGFR3 signaling |
| R-HSA-8956319 | 23 | 0.251652772 | 1.200565163 | 0.249353846 | 0.33926775 | Nucleotide catabolism |
| R-HSA-380972 | 26 | 0.239817293 | 1.195315002 | 0.25272992 | 0.342455088 | Energy dependent regulation of mTOR by LKB1-AMPK |
| R-HSA-425410 | 19 | 0.26942034 | 1.195433243 | 0.253765346 | 0.343234053 | Metal ion SLC transporters |
| R-HSA-389357 | 22 | 0.25578385 | 1.199835659 | 0.255094433 | 0.343334313 | CD28 dependent PI3K/Akt signaling |
| R-HSA-109704 | 27 | 0.235521503 | 1.189112699 | 0.255221538 | 0.343334313 | PI3K Cascade |
| R-HSA-2022870 | 15 | 0.294519872 | 1.190581172 | 0.256075013 | 0.343861753 | Chondroitin sulfate biosynthesis |
| R-HSA-174824 | 50 | 0.191135276 | 1.193055484 | 0.256546826 | 0.343875716 | Plasma lipoprotein assembly, remodeling, and clearance |
| R-HSA-156580 | 57 | 0.181836037 | 1.183879248 | 0.262807935 | 0.350377588 | Phase II - Conjugation of compounds |
| R-HSA-5654708 | 16 | 0.285187086 | 1.182917836 | 0.261942052 | 0.350377588 | Downstream signaling of activated FGFR3 |
| R-HSA-8957322 | 110 | 0.151430201 | 1.174698509 | 0.262402624 | 0.350377588 | Metabolism of steroids |
| R-HSA-5654741 | 31 | 0.22264669 | 1.180906149 | 0.263424997 | 0.350573116 | Signaling by FGFR3 |
| R-HSA-204998 | 70 | 0.171179275 | 1.18227136 | 0.269206214 | 0.356357857 | Cell death signalling via NRAGE, NRIF and NADE |
| R-HSA-8964038 | 15 | 0.290345954 | 1.173708329 | 0.269017433 | 0.356357857 | LDL clearance |
| R-HSA-168898 | 152 | 0.139885183 | 1.161357771 | 0.270059698 | 0.356853801 | Toll-like Receptor Cascades |
| R-HSA-5654727 | 21 | 0.254982549 | 1.174560704 | 0.273101898 | 0.360221347 | Negative regulation of FGFR2 signaling |
| R-HSA-445717 | 31 | 0.220534904 | 1.169705353 | 0.273574885 | 0.360221347 | Aquaporin-mediated transport |
| R-HSA-9683701 | 29 | 0.225993496 | 1.171392443 | 0.275279562 | 0.361810533 | Translation of Structural Proteins |
| R-HSA-9665348 | 15 | 0.28876447 | 1.167315261 | 0.275752773 | 0.361810533 | Signaling by ERBB2 ECD mutants |
| R-HSA-6802957 | 71 | 0.1689755 | 1.171712582 | 0.279744817 | 0.366403349 | Oncogenic MAPK signaling |
| R-HSA-1296071 | 36 | 0.208810403 | 1.163410163 | 0.284254529 | 0.371476988 | Potassium Channels |
| R-HSA-74752 | 56 | 0.178954163 | 1.158663753 | 0.285823504 | 0.372401621 | Signaling by Insulin receptor |
| R-HSA-3899300 | 42 | 0.198311253 | 1.164568826 | 0.288579198 | 0.374681959 | SUMOylation of transcription cofactors |
| R-HSA-400042 | 19 | 0.260244175 | 1.15471808 | 0.291228958 | 0.377464719 | Adrenaline,noradrenaline inhibits insulin secretion |
| R-HSA-6804758 | 28 | 0.224818241 | 1.150672439 | 0.293821839 | 0.380164222 | Regulation of TP53 Activity through Acetylation |
| R-HSA-416482 | 66 | 0.16998407 | 1.154717263 | 0.296161659 | 0.380886432 | G alpha (12/13) signalling events |
| R-HSA-373755 | 61 | 0.173198482 | 1.150379326 | 0.296424328 | 0.380886432 | Semaphorin interactions |
| R-HSA-3000178 | 55 | 0.178011633 | 1.146007635 | 0.298643029 | 0.383076845 | ECM proteoglycans |
| R-HSA-6794362 | 45 | 0.190042657 | 1.144168999 | 0.308341776 | 0.392608785 | Protein-protein interactions at synapses |
| R-HSA-5663084 | 29 | 0.21922358 | 1.136301925 | 0.308708066 | 0.392608785 | Diseases of carbohydrate metabolism |
| R-HSA-9006936 | 110 | 0.145642886 | 1.129804227 | 0.314473145 | 0.398580355 | Signaling by TGFB family members |
| R-HSA-3000171 | 51 | 0.179995205 | 1.131733587 | 0.315481449 | 0.399029237 | Non-integrin membrane-ECM interactions |
| R-HSA-5654733 | 21 | 0.245404815 | 1.130441487 | 0.316433566 | 0.399029237 | Negative regulation of FGFR4 signaling |
| R-HSA-9031628 | 32 | 0.210052979 | 1.12691402 | 0.316308559 | 0.399029237 | NGF-stimulated transcription |
| R-HSA-166520 | 114 | 0.144102754 | 1.126576513 | 0.317697665 | 0.399946562 | Signaling by NTRKs |
| R-HSA-6785807 | 82 | 0.156208889 | 1.125648759 | 0.322003765 | 0.403243023 | Interleukin-4 and Interleukin-13 signaling |
| R-HSA-180024 | 24 | 0.232009403 | 1.122817205 | 0.321988247 | 0.403243023 | DARPP-32 events |
| R-HSA-5627123 | 24 | 0.230574211 | 1.115871546 | 0.327987267 | 0.407394711 | RHO GTPases activate PAKs |
| R-HSA-2559580 | 60 | 0.168851391 | 1.115618047 | 0.32972153 | 0.408867402 | Oxidative Stress Induced Senescence |
| R-HSA-204174 | 15 | 0.274374749 | 1.109145567 | 0.333333333 | 0.412659556 | Regulation of pyruvate dehydrogenase (PDH) complex |
| R-HSA-4085001 | 25 | 0.225661635 | 1.108588093 | 0.337397878 | 0.414251886 | Sialic acid metabolism |
| R-HSA-74751 | 36 | 0.198766739 | 1.107450782 | 0.339061774 | 0.414251886 | Insulin receptor signalling cascade |
| R-HSA-211976 | 16 | 0.266604894 | 1.10584139 | 0.337770817 | 0.414251886 | Endogenous sterols |
| R-HSA-975155 | 98 | 0.146278265 | 1.101622808 | 0.345490237 | 0.420034494 | MyD88 dependent cascade initiated on endosome |
| R-HSA-166058 | 106 | 0.143075156 | 1.10108571 | 0.34541162 | 0.420034494 | MyD88:MAL(TIRAP) cascade initiated on plasma membrane |
| R-HSA-168188 | 106 | 0.143075156 | 1.10108571 | 0.34541162 | 0.420034494 | Toll Like Receptor TLR6:TLR2 Cascade |
| R-HSA-5083635 | 22 | 0.234101127 | 1.098125934 | 0.35139165 | 0.423752833 | Defective B3GALTL causes PpS |
| R-HSA-350054 | 27 | 0.216802946 | 1.094605518 | 0.350839068 | 0.423752833 | Notch-HLH transcription pathway |
| R-HSA-400685 | 24 | 0.226048116 | 1.093967357 | 0.351371205 | 0.423752833 | Sema4D in semaphorin signaling |
| R-HSA-392517 | 15 | 0.268720206 | 1.086287374 | 0.357501321 | 0.426975262 | Rap1 signalling |
| R-HSA-216083 | 70 | 0.156894381 | 1.083610933 | 0.369014684 | 0.431909173 | Integrin cell surface interactions |
| R-HSA-9614085 | 51 | 0.171522527 | 1.078460982 | 0.372681095 | 0.433300296 | FOXO-mediated transcription |
| R-HSA-168181 | 99 | 0.142456272 | 1.075895165 | 0.374600227 | 0.43485319 | Toll Like Receptor 7/8 (TLR7/8) Cascade |
| R-HSA-9009391 | 64 | 0.159759189 | 1.076682069 | 0.375375698 | 0.435075704 | Extra-nuclear estrogen signaling |
| R-HSA-9609736 | 17 | 0.250677099 | 1.066785403 | 0.379751746 | 0.438782923 | Assembly and cell surface presentation of NMDA receptors |
| R-HSA-111885 | 69 | 0.155006811 | 1.066429262 | 0.390113987 | 0.446963825 | Opioid Signalling |
| R-HSA-2187338 | 52 | 0.16817572 | 1.064375672 | 0.388962472 | 0.446963825 | Visual phototransduction |
| R-HSA-163841 | 29 | 0.20434725 | 1.059193418 | 0.391030217 | 0.446963825 | Gamma carboxylation, hypusine formation and arylsulfatase activation |
| R-HSA-5654716 | 17 | 0.248609269 | 1.057985514 | 0.389319886 | 0.446963825 | Downstream signaling of activated FGFR4 |
| R-HSA-975138 | 97 | 0.141490128 | 1.063744559 | 0.392009085 | 0.447396522 | TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation |
| R-HSA-199992 | 66 | 0.156189749 | 1.061011188 | 0.392922057 | 0.447752803 | trans-Golgi Network Vesicle Budding |
| R-HSA-9013026 | 61 | 0.158548862 | 1.053076973 | 0.397645025 | 0.451753334 | RHOB GTPase cycle |
| R-HSA-449836 | 17 | 0.244423918 | 1.04017427 | 0.407551073 | 0.460899544 | Other interleukin signaling |
| R-HSA-9013149 | 169 | 0.123463755 | 1.047654744 | 0.414457103 | 0.463093432 | RAC1 GTPase cycle |
| R-HSA-2980736 | 42 | 0.177548799 | 1.042642784 | 0.410378427 | 0.463093432 | Peptide hormone metabolism |
| R-HSA-1251985 | 26 | 0.209003862 | 1.041732433 | 0.411186605 | 0.463093432 | Nuclear signaling by ERBB4 |
| R-HSA-1839124 | 21 | 0.225636543 | 1.039380217 | 0.413586414 | 0.463093432 | FGFR1 mutant receptor activation |
| R-HSA-4090294 | 26 | 0.208472641 | 1.039084681 | 0.41421985 | 0.463093432 | SUMOylation of intracellular receptors |
| R-HSA-2426168 | 40 | 0.179327826 | 1.038439853 | 0.414436981 | 0.463093432 | Activation of gene expression by SREBF (SREBP) |
| R-HSA-2173789 | 46 | 0.171900328 | 1.043271712 | 0.415217147 | 0.463242579 | TGF-beta receptor signaling activates SMADs |
| R-HSA-373753 | 16 | 0.24944739 | 1.034674361 | 0.417645523 | 0.464939219 | Nephrin family interactions |
| R-HSA-163615 | 15 | 0.254515981 | 1.028867535 | 0.420892763 | 0.466318051 | PKA activation |
| R-HSA-432720 | 31 | 0.19392532 | 1.028569541 | 0.421102325 | 0.466318051 | Lysosome Vesicle Biogenesis |
| R-HSA-2514856 | 18 | 0.23605844 | 1.026642178 | 0.422185218 | 0.466823574 | The phototransduction cascade |
| R-HSA-5675221 | 42 | 0.17509061 | 1.028207241 | 0.425220938 | 0.469483702 | Negative regulation of MAPK pathway |
| R-HSA-1482839 | 16 | 0.247375422 | 1.026080118 | 0.426128948 | 0.469790245 | Acyl chain remodelling of PE |
| R-HSA-5173214 | 23 | 0.214635754 | 1.023967299 | 0.427815385 | 0.470952798 | O-glycosylation of TSR domain-containing proteins |
| R-HSA-5633008 | 40 | 0.176767073 | 1.023611214 | 0.430490721 | 0.472502024 | TP53 Regulates Transcription of Cell Death Genes |
| R-HSA-389948 | 17 | 0.238939019 | 1.016832646 | 0.432764417 | 0.474299082 | PD-1 signaling |
| R-HSA-168138 | 101 | 0.135529914 | 1.029781793 | 0.434576551 | 0.475585745 | Toll Like Receptor 9 (TLR9) Cascade |
| R-HSA-1483206 | 90 | 0.138791806 | 1.026717656 | 0.436009127 | 0.476453869 | Glycerophospholipid biosynthesis |
| R-HSA-9013508 | 21 | 0.22037468 | 1.015141784 | 0.440934066 | 0.481130182 | NOTCH3 Intracellular Domain Regulates Transcription |
| R-HSA-1236394 | 45 | 0.168613648 | 1.015153708 | 0.44433187 | 0.48342215 | Signaling by ERBB4 |
| R-HSA-983170 | 23 | 0.2112217 | 1.0076798 | 0.445292308 | 0.483760862 | Antigen Presentation: Folding, assembly and peptide loading of class I MHC |
| R-HSA-6783589 | 18 | 0.229520695 | 0.99820886 | 0.45254259 | 0.488080057 | Interleukin-6 family signaling |
| R-HSA-166166 | 105 | 0.13274661 | 1.019109524 | 0.455648062 | 0.489305063 | MyD88-independent TLR4 cascade |
| R-HSA-937061 | 105 | 0.13274661 | 1.019109524 | 0.455648062 | 0.489305063 | TRIF(TICAM1)-mediated TLR4 signaling |
| R-HSA-4086398 | 44 | 0.167931633 | 1.002434895 | 0.45697832 | 0.489323428 | Ca2+ pathway |
| R-HSA-194138 | 105 | 0.131931048 | 1.012848363 | 0.463254189 | 0.495331821 | Signaling by VEGF |
| R-HSA-432040 | 28 | 0.194035808 | 0.993120733 | 0.464918582 | 0.496399271 | Vasopressin regulates renal water homeostasis via Aquaporins |
| R-HSA-6811440 | 45 | 0.165371577 | 0.995634531 | 0.468085106 | 0.497641347 | Retrograde transport at the Trans-Golgi-Network |
| R-HSA-70268 | 24 | 0.204558581 | 0.989968039 | 0.467433888 | 0.497641347 | Pyruvate metabolism |
| R-HSA-381676 | 27 | 0.195822884 | 0.988680333 | 0.466859833 | 0.497641347 | Glucagon-like Peptide-1 (GLP1) regulates insulin secretion |
| R-HSA-399954 | 15 | 0.243835462 | 0.985692097 | 0.471870048 | 0.500238068 | Sema3A PAK dependent Axon repulsion |
| R-HSA-112043 | 40 | 0.170906173 | 0.989672297 | 0.47375612 | 0.501194442 | PLC beta mediated events |
| R-HSA-3371571 | 19 | 0.221399766 | 0.982363249 | 0.4741172 | 0.501194442 | HSF1-dependent transactivation |
| R-HSA-418555 | 61 | 0.148384247 | 0.985563892 | 0.478340715 | 0.504942935 | G alpha (s) signalling events |
| R-HSA-389661 | 21 | 0.213203977 | 0.982110402 | 0.479395604 | 0.50534071 | Glyoxylate metabolism and glycine degradation |
| R-HSA-8964043 | 28 | 0.191160707 | 0.978405292 | 0.482279693 | 0.505503963 | Plasma lipoprotein clearance |
| R-HSA-5654743 | 31 | 0.184345921 | 0.977760916 | 0.481175499 | 0.505503963 | Signaling by FGFR4 |
| R-HSA-392451 | 17 | 0.228705354 | 0.973282103 | 0.483061805 | 0.505503963 | G beta:gamma signalling through PI3Kgamma |
| R-HSA-2428924 | 34 | 0.178051556 | 0.974243696 | 0.489138052 | 0.50868156 | IGF1R signaling cascade |
| R-HSA-5684264 | 16 | 0.23486406 | 0.974184664 | 0.489950405 | 0.50868156 | MAP3K8 (TPL2)-dependent MAPK1/3 activation |
| R-HSA-165159 | 38 | 0.171086541 | 0.971022758 | 0.489175495 | 0.50868156 | MTOR signalling |
| R-HSA-167044 | 18 | 0.222169324 | 0.966237 | 0.490073011 | 0.50868156 | Signalling to RAS |
| R-HSA-1592389 | 16 | 0.233865002 | 0.970040705 | 0.494648917 | 0.511636256 | Activation of Matrix Metalloproteinases |
| R-HSA-8864260 | 30 | 0.184011353 | 0.966189288 | 0.495973472 | 0.511636256 | Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors |
| R-HSA-416572 | 21 | 0.209552902 | 0.965291958 | 0.496503497 | 0.511636256 | Sema4D induced cell migration and growth-cone collapse |
| R-HSA-2173791 | 15 | 0.238314601 | 0.963374305 | 0.496434231 | 0.511636256 | TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition) |
| R-HSA-189445 | 19 | 0.217549894 | 0.965281149 | 0.497911657 | 0.511827881 | Metabolism of porphyrins |
| R-HSA-1839117 | 16 | 0.232632923 | 0.964930208 | 0.501044114 | 0.513630975 | Signaling by cytosolic FGFR1 fusion mutants |
| R-HSA-5655302 | 28 | 0.187839502 | 0.961406587 | 0.503472222 | 0.515411124 | Signaling by FGFR1 in disease |
| R-HSA-111465 | 32 | 0.179408132 | 0.962507365 | 0.505694493 | 0.515561525 | Apoptotic cleavage of cellular proteins |
| R-HSA-1660662 | 33 | 0.177276492 | 0.960130953 | 0.504872608 | 0.515561525 | Glycosphingolipid metabolism |
| R-HSA-112399 | 31 | 0.180445956 | 0.95707571 | 0.505606043 | 0.515561525 | IRS-mediated signalling |
| R-HSA-71406 | 48 | 0.154604109 | 0.952571165 | 0.518336863 | 0.526290691 | Pyruvate metabolism and Citric Acid (TCA) cycle |
| R-HSA-2514859 | 17 | 0.221670984 | 0.943346524 | 0.520687872 | 0.527241152 | Inactivation, recovery and regulation of the phototransduction cascade |
| R-HSA-1483257 | 166 | 0.114868294 | 0.971560746 | 0.525885559 | 0.531193793 | Phospholipid metabolism |
| R-HSA-199220 | 15 | 0.23232596 | 0.939165539 | 0.526016904 | 0.531193793 | Vitamin B5 (pantothenate) metabolism |
| R-HSA-381119 | 82 | 0.132702208 | 0.956258489 | 0.532210835 | 0.533114418 | Unfolded Protein Response (UPR) |
| R-HSA-917937 | 50 | 0.151758629 | 0.947268701 | 0.528739458 | 0.533114418 | Iron uptake and transport |
| R-HSA-77387 | 21 | 0.203392127 | 0.936912744 | 0.530594406 | 0.533114418 | Insulin receptor recycling |
| R-HSA-5627117 | 20 | 0.206766356 | 0.935928171 | 0.531277423 | 0.533114418 | RHO GTPases Activate ROCKs |
| R-HSA-416700 | 18 | 0.214874208 | 0.934509797 | 0.531830409 | 0.533114418 | Other semaphorin interactions |
| R-HSA-5218920 | 29 | 0.180220012 | 0.934134669 | 0.529740661 | 0.533114418 | VEGFR2 mediated vascular permeability |
| R-HSA-6811438 | 40 | 0.162150241 | 0.938969019 | 0.534783104 | 0.534972006 | Intra-Golgi traffic |
| R-HSA-9007101 | 107 | 0.123757665 | 0.953634367 | 0.539093805 | 0.537840363 | Rab regulation of trafficking |
| R-HSA-9603798 | 19 | 0.209296892 | 0.928662114 | 0.538919124 | 0.537840363 | Class I peroxisomal membrane protein import |
| R-HSA-5620924 | 39 | 0.162146437 | 0.930050436 | 0.543582704 | 0.538712982 | Intraflagellar transport |
| R-HSA-114452 | 30 | 0.176851859 | 0.928596899 | 0.542278541 | 0.538712982 | Activation of BH3-only proteins |
| R-HSA-5637810 | 15 | 0.229155279 | 0.926348225 | 0.54318542 | 0.538712982 | Constitutive Signaling by EGFRvIII |
| R-HSA-5637812 | 15 | 0.229155279 | 0.926348225 | 0.54318542 | 0.538712982 | Signaling by EGFRvIII in Cancer |
| R-HSA-194068 | 27 | 0.183312947 | 0.925519539 | 0.542798503 | 0.538712982 | Bile acid and bile salt metabolism |
| R-HSA-917977 | 24 | 0.19050653 | 0.921962671 | 0.550195886 | 0.543100296 | Transferrin endocytosis and recycling |
| R-HSA-1643713 | 22 | 0.196170471 | 0.920200108 | 0.549950298 | 0.543100296 | Signaling by EGFR in Cancer |
| R-HSA-4420097 | 97 | 0.125050774 | 0.940150961 | 0.55244683 | 0.544114856 | VEGFA-VEGFR2 Pathway |
| R-HSA-166208 | 22 | 0.195866755 | 0.918775428 | 0.552683897 | 0.544114856 | mTORC1-mediated signalling |
| R-HSA-2404192 | 35 | 0.167178056 | 0.922267025 | 0.553517177 | 0.544216305 | Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R) |
| R-HSA-1483191 | 21 | 0.198320513 | 0.913550682 | 0.556568432 | 0.545059063 | Synthesis of PC |
| R-HSA-1655829 | 53 | 0.143923585 | 0.916872584 | 0.562115215 | 0.549048179 | Regulation of cholesterol biosynthesis by SREBP (SREBF) |
| R-HSA-432722 | 52 | 0.144920236 | 0.917192881 | 0.565121413 | 0.549486156 | Golgi Associated Vesicle Biogenesis |
| R-HSA-1442490 | 45 | 0.151446243 | 0.911795797 | 0.566250141 | 0.549486156 | Collagen degradation |
| R-HSA-9694631 | 15 | 0.225025974 | 0.909655725 | 0.565636556 | 0.549486156 | Maturation of nucleoprotein |
| R-HSA-418597 | 30 | 0.172795794 | 0.907299698 | 0.564187589 | 0.549486156 | G alpha (z) signalling events |
| R-HSA-9659787 | 17 | 0.210179336 | 0.89444249 | 0.579519007 | 0.560174015 | Aberrant regulation of mitotic G1/S transition in cancer due to RB1 defects |
| R-HSA-9661069 | 17 | 0.210179336 | 0.89444249 | 0.579519007 | 0.560174015 | Defective binding of RB1 mutants to E2F1,(E2F2, E2F3) |
| R-HSA-9634815 | 21 | 0.194287884 | 0.894974634 | 0.581918082 | 0.561764388 | Transcriptional Regulation by NPAS4 |
| R-HSA-446193 | 67 | 0.132144956 | 0.902514712 | 0.588887704 | 0.567757193 | Biosynthesis of the N-glycan precursor (dolichol lipid-linked oligosaccharide, LLO) and transfer to a nascent protein |
| R-HSA-9609507 | 136 | 0.113058803 | 0.916944181 | 0.595034595 | 0.568775733 | Protein localization |
| R-HSA-373752 | 38 | 0.156456906 | 0.887990461 | 0.592699217 | 0.568775733 | Netrin-1 signaling |
| R-HSA-1483249 | 42 | 0.151134344 | 0.887525763 | 0.594946748 | 0.568775733 | Inositol phosphate metabolism |
| R-HSA-9696270 | 36 | 0.159129565 | 0.8866079 | 0.596725499 | 0.568775733 | RND2 GTPase cycle |
| R-HSA-1650814 | 46 | 0.14598952 | 0.886017718 | 0.59757603 | 0.568775733 | Collagen biosynthesis and modifying enzymes |
| R-HSA-9696273 | 38 | 0.155721377 | 0.883815874 | 0.597305389 | 0.568775733 | RND1 GTPase cycle |
| R-HSA-6799198 | 46 | 0.14517329 | 0.881063977 | 0.603972618 | 0.572286389 | Complex I biogenesis |
| R-HSA-5620920 | 43 | 0.148445046 | 0.880516893 | 0.604336043 | 0.572286389 | Cargo trafficking to the periciliary membrane |
| R-HSA-5668599 | 21 | 0.189787765 | 0.874245128 | 0.606643357 | 0.572438648 | RHO GTPases Activate NADPH Oxidases |
| R-HSA-140877 | 17 | 0.204969064 | 0.872269572 | 0.606025343 | 0.572438648 | Formation of Fibrin Clot (Clotting Cascade) |
| R-HSA-418990 | 17 | 0.20473885 | 0.871289872 | 0.606801138 | 0.572438648 | Adherens junctions interactions |
| R-HSA-1483255 | 77 | 0.12525754 | 0.889007505 | 0.609276399 | 0.573322289 | PI Metabolism |
| R-HSA-156590 | 28 | 0.17036198 | 0.871952534 | 0.608596743 | 0.573322289 | Glutathione conjugation |
| R-HSA-9012852 | 44 | 0.146381024 | 0.87379277 | 0.611449864 | 0.574641938 | Signaling by NOTCH3 |
| R-HSA-9707616 | 40 | 0.150340493 | 0.870581897 | 0.617101218 | 0.577301125 | Heme signaling |
| R-HSA-2428928 | 33 | 0.160213625 | 0.867718322 | 0.619701773 | 0.577301125 | IRS-related events triggered by IGF1R |
| R-HSA-1614635 | 21 | 0.187702864 | 0.864641165 | 0.61963037 | 0.577301125 | Sulfur amino acid metabolism |
| R-HSA-399719 | 19 | 0.194673475 | 0.863777187 | 0.619035565 | 0.577301125 | Trafficking of AMPA receptors |
| R-HSA-399721 | 19 | 0.194673475 | 0.863777187 | 0.619035565 | 0.577301125 | Glutamate binding, activation of AMPA receptors and synaptic plasticity |
| R-HSA-1222556 | 27 | 0.17130244 | 0.864880296 | 0.621634673 | 0.578051421 | ROS and RNS production in phagocytes |
| R-HSA-9008059 | 17 | 0.201773931 | 0.858672314 | 0.622058443 | 0.578051421 | Interleukin-37 signaling |
| R-HSA-8980692 | 135 | 0.109942944 | 0.890557457 | 0.631418404 | 0.58473233 | RHOA GTPase cycle |
| R-HSA-2132295 | 95 | 0.117240963 | 0.876492365 | 0.633995037 | 0.585493362 | MHC class II antigen presentation |
| R-HSA-9772573 | 66 | 0.127361208 | 0.865176285 | 0.635945686 | 0.586567933 | Late SARS-CoV-2 Infection Events |
| R-HSA-9748784 | 51 | 0.136482602 | 0.858144775 | 0.637809187 | 0.587559566 | Drug ADME |
| R-HSA-8936459 | 24 | 0.174455507 | 0.844283213 | 0.641160627 | 0.58873341 | RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function |
| R-HSA-445144 | 17 | 0.198219792 | 0.843547263 | 0.641453323 | 0.58873341 | Signal transduction by L1 |
| R-HSA-418592 | 18 | 0.193235157 | 0.840399361 | 0.650185731 | 0.594917255 | ADP signalling through P2Y purinoceptor 1 |
| R-HSA-5674400 | 25 | 0.170581922 | 0.838002824 | 0.651383978 | 0.594917255 | Constitutive Signaling by AKT1 E17K in Cancer |
| R-HSA-532668 | 33 | 0.155776949 | 0.843689252 | 0.652459786 | 0.595170429 | N-glycan trimming in the ER and Calnexin/Calreticulin cycle |
| R-HSA-163200 | 88 | 0.116836643 | 0.858907158 | 0.655448219 | 0.595451463 | Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. |
| R-HSA-3214847 | 62 | 0.126925765 | 0.847928559 | 0.655963797 | 0.595451463 | HATs acetylate histones |
| R-HSA-9656223 | 36 | 0.150464767 | 0.838331022 | 0.654435671 | 0.595451463 | Signaling by RAF1 mutants |
| R-HSA-192105 | 25 | 0.16958441 | 0.833102438 | 0.65796854 | 0.596544662 | Synthesis of bile acids and bile salts |
| R-HSA-9013106 | 66 | 0.122919241 | 0.835001595 | 0.670693895 | 0.604405623 | RHOC GTPase cycle |
| R-HSA-3238698 | 16 | 0.198248953 | 0.822310103 | 0.670582093 | 0.604405623 | WNT ligand biogenesis and trafficking |
| R-HSA-1606322 | 20 | 0.181553145 | 0.821800539 | 0.670552839 | 0.604405623 | ZBP1(DAI) mediated induction of type I IFNs |
| R-HSA-9660826 | 23 | 0.172092705 | 0.821006281 | 0.6752 | 0.606998413 | Purinergic signaling in leishmaniasis infection |
| R-HSA-9664424 | 23 | 0.172092705 | 0.821006281 | 0.6752 | 0.606998413 | Cell recruitment (pro-inflammatory response) |
| R-HSA-1428517 | 132 | 0.105901334 | 0.853891533 | 0.676066375 | 0.607045014 | The citric acid (TCA) cycle and respiratory electron transport |
| R-HSA-8874081 | 27 | 0.162273832 | 0.819296211 | 0.683568755 | 0.609876148 | MET activates PTK2 signaling |
| R-HSA-112040 | 44 | 0.137187121 | 0.818911573 | 0.682475158 | 0.609876148 | G-protein mediated events |
| R-HSA-982772 | 19 | 0.183721874 | 0.815184318 | 0.682192128 | 0.609876148 | Growth hormone receptor signaling |
| R-HSA-5609975 | 15 | 0.20107766 | 0.81284592 | 0.683967248 | 0.609876148 | Diseases associated with glycosylation precursor biosynthesis |
| R-HSA-392518 | 23 | 0.169969864 | 0.8108788 | 0.685907692 | 0.610535886 | Signal amplification |
| R-HSA-1482788 | 18 | 0.185032125 | 0.80472354 | 0.69309594 | 0.61279762 | Acyl chain remodelling of PC |
| R-HSA-9013507 | 24 | 0.166273699 | 0.804687083 | 0.691234084 | 0.61279762 | NOTCH3 Activation and Transmission of Signal to the Nucleus |
| R-HSA-3214842 | 20 | 0.177689405 | 0.804311319 | 0.691864109 | 0.61279762 | HDMs demethylate histones |
| R-HSA-111996 | 28 | 0.156538041 | 0.801198372 | 0.701628352 | 0.618813919 | Ca-dependent events |
| R-HSA-190236 | 68 | 0.118358736 | 0.811999579 | 0.703313093 | 0.619566591 | Signaling by FGFR |
| R-HSA-193704 | 88 | 0.111410823 | 0.819020055 | 0.705411862 | 0.620681785 | p75 NTR receptor-mediated signalling |
| R-HSA-9617828 | 15 | 0.196551273 | 0.794548236 | 0.708267301 | 0.622459346 | FOXO-mediated transcription of cell cycle genes |
| R-HSA-9006115 | 20 | 0.17429058 | 0.788926531 | 0.710918892 | 0.62353436 | Signaling by NTRK2 (TRKB) |
| R-HSA-163359 | 21 | 0.170932699 | 0.787390481 | 0.711163836 | 0.62353436 | Glucagon signaling in metabolic regulation |
| R-HSA-8873719 | 53 | 0.125050541 | 0.796640888 | 0.715259455 | 0.625038384 | RAB geranylgeranylation |
| R-HSA-8979227 | 22 | 0.167057142 | 0.78363476 | 0.716202783 | 0.625038384 | Triglyceride metabolism |
| R-HSA-1474290 | 65 | 0.116684988 | 0.789275738 | 0.727262989 | 0.627076645 | Collagen formation |
| R-HSA-6802946 | 39 | 0.136661338 | 0.783871294 | 0.726378403 | 0.627076645 | Signaling by moderate kinase activity BRAF mutants |
| R-HSA-6802949 | 39 | 0.136661338 | 0.783871294 | 0.726378403 | 0.627076645 | Signaling by RAS mutants |
| R-HSA-6802955 | 39 | 0.136661338 | 0.783871294 | 0.726378403 | 0.627076645 | Paradoxical activation of RAF signaling by kinase inactive BRAF |
| R-HSA-9649948 | 39 | 0.136661338 | 0.783871294 | 0.726378403 | 0.627076645 | Signaling downstream of RAS mutants |
| R-HSA-2122947 | 46 | 0.128933415 | 0.782503361 | 0.727527775 | 0.627076645 | NOTCH1 Intracellular Domain Regulates Transcription |
| R-HSA-6803157 | 17 | 0.182924601 | 0.778456808 | 0.727825187 | 0.627076645 | Antimicrobial peptides |
| R-HSA-456926 | 22 | 0.164869935 | 0.773374969 | 0.728752485 | 0.627150552 | Thrombin signalling through proteinase activated receptors (PARs) |
| R-HSA-611105 | 85 | 0.109171957 | 0.794613197 | 0.735487233 | 0.629312902 | Respiratory electron transport |
| R-HSA-6802952 | 57 | 0.120166907 | 0.782370257 | 0.735120994 | 0.629312902 | Signaling by BRAF and RAF1 fusions |
| R-HSA-5673000 | 33 | 0.143222752 | 0.775695613 | 0.735000587 | 0.629312902 | RAF activation |
| R-HSA-9772572 | 32 | 0.142120182 | 0.762461101 | 0.749442292 | 0.639899916 | Early SARS-CoV-2 Infection Events |
| R-HSA-8939243 | 35 | 0.137542703 | 0.758778409 | 0.756134611 | 0.642553327 | RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known |
| R-HSA-8963899 | 16 | 0.18150962 | 0.752877591 | 0.760506395 | 0.64479795 | Plasma lipoprotein remodeling |
| R-HSA-9717189 | 20 | 0.16545262 | 0.748921494 | 0.759809452 | 0.64479795 | Sensory perception of taste |
| R-HSA-9013406 | 58 | 0.115469338 | 0.755946867 | 0.762173913 | 0.645477429 | RHOQ GTPase cycle |
| R-HSA-1489509 | 32 | 0.139526574 | 0.748546643 | 0.765997417 | 0.646511499 | DAG and IP3 signaling |
| R-HSA-3232118 | 18 | 0.171262896 | 0.744839763 | 0.767516331 | 0.646768201 | SUMOylation of transcription factors |
| R-HSA-111931 | 17 | 0.174944727 | 0.744497531 | 0.768037238 | 0.646768201 | PKA-mediated phosphorylation of CREB |
| R-HSA-73980 | 23 | 0.154291196 | 0.736080247 | 0.773292308 | 0.649725217 | RNA Polymerase III Transcription Termination |
| R-HSA-5358351 | 123 | 0.09726871 | 0.772423505 | 0.779865224 | 0.653951755 | Signaling by Hedgehog |
| R-HSA-201681 | 142 | 0.093167763 | 0.762740001 | 0.788186339 | 0.657391789 | TCF dependent signaling in response to WNT |
| R-HSA-375276 | 56 | 0.113618439 | 0.73563847 | 0.78877239 | 0.657391789 | Peptide ligand-binding receptors |
| R-HSA-451326 | 21 | 0.158150093 | 0.728508226 | 0.787837163 | 0.657391789 | Activation of kainate receptors upon glutamate binding |
| R-HSA-170834 | 91 | 0.099942123 | 0.741051857 | 0.794507772 | 0.658640012 | Signaling by TGF-beta Receptor Complex |
| R-HSA-2173788 | 26 | 0.145558762 | 0.725504694 | 0.792526086 | 0.658640012 | Downregulation of TGF-beta receptor signaling |
| R-HSA-9024446 | 33 | 0.133780664 | 0.724557188 | 0.794058941 | 0.658640012 | NR1H2 and NR1H3-mediated signaling |
| R-HSA-499943 | 24 | 0.14937181 | 0.722889833 | 0.793584721 | 0.658640012 | Interconversion of nucleotide di- and triphosphates |
| R-HSA-389356 | 33 | 0.133229387 | 0.721571468 | 0.798168369 | 0.660939421 | CD28 co-stimulation |
| R-HSA-432142 | 16 | 0.172895809 | 0.717148659 | 0.802531976 | 0.662609605 | Platelet sensitization by LDL |
| R-HSA-901042 | 24 | 0.148045131 | 0.716469322 | 0.801297747 | 0.662609605 | Calnexin/calreticulin cycle |
| R-HSA-8941326 | 27 | 0.14177346 | 0.715792907 | 0.805263793 | 0.662609605 | RUNX2 regulates bone development |
| R-HSA-5339562 | 25 | 0.144718444 | 0.710945589 | 0.804901841 | 0.662609605 | Uptake and actions of bacterial toxins |
| R-HSA-6802948 | 31 | 0.133356893 | 0.707317839 | 0.811282899 | 0.666614394 | Signaling by high-kinase activity BRAF mutants |
| R-HSA-901032 | 19 | 0.157719182 | 0.699808906 | 0.818757119 | 0.672014886 | ER Quality Control Compartment (ERQC) |
| R-HSA-2730905 | 16 | 0.169645697 | 0.70366763 | 0.819759854 | 0.672097709 | Role of LAT2/NTAL/LAB on calcium mobilization |
| R-HSA-9013148 | 145 | 0.088960239 | 0.731607354 | 0.822055392 | 0.672500107 | CDC42 GTPase cycle |
| R-HSA-8876198 | 76 | 0.100048735 | 0.707820196 | 0.821943772 | 0.672500107 | RAB GEFs exchange GTP for GDP on RABs |
| R-HSA-1810476 | 17 | 0.164202819 | 0.698784101 | 0.823894492 | 0.673265582 | RIP-mediated NFkB activation via ZBP1 |
| R-HSA-500792 | 145 | 0.088569917 | 0.728397357 | 0.82580907 | 0.673353474 | GPCR ligand binding |
| R-HSA-9694635 | 56 | 0.107785588 | 0.697872865 | 0.825360419 | 0.673353474 | Translation of Structural Proteins |
| R-HSA-5668541 | 80 | 0.097242957 | 0.696369896 | 0.834137642 | 0.676203872 | TNFR2 non-canonical NF-kB pathway |
| R-HSA-111933 | 26 | 0.137609911 | 0.685885446 | 0.834748847 | 0.676203872 | Calmodulin induced events |
| R-HSA-111997 | 26 | 0.137609911 | 0.685885446 | 0.834748847 | 0.676203872 | CaM pathway |
| R-HSA-73887 | 132 | 0.088982487 | 0.717473417 | 0.839356612 | 0.677851427 | Death Receptor Signalling |
| R-HSA-5218921 | 21 | 0.147862539 | 0.681119271 | 0.840034965 | 0.677851427 | VEGFR2 mediated cell proliferation |
| R-HSA-1834949 | 60 | 0.102806572 | 0.679253316 | 0.846137176 | 0.678602593 | Cytosolic sensors of pathogen-associated DNA |
| R-HSA-6806834 | 73 | 0.097145688 | 0.678724452 | 0.850333651 | 0.678602593 | Signaling by MET |
| R-HSA-1295596 | 16 | 0.163346757 | 0.677540469 | 0.84742887 | 0.678602593 | Spry regulation of FGF signaling |
| R-HSA-5578775 | 33 | 0.124985435 | 0.676922156 | 0.848185981 | 0.678602593 | Ion homeostasis |
| R-HSA-202433 | 28 | 0.132183366 | 0.67654544 | 0.845665709 | 0.678602593 | Generation of second messenger molecules |
| R-HSA-168928 | 62 | 0.100602013 | 0.672072525 | 0.852278849 | 0.678602593 | DDX58/IFIH1-mediated induction of interferon-alpha/beta |
| R-HSA-5674135 | 34 | 0.122693229 | 0.671339849 | 0.851553375 | 0.678602593 | MAP2K and MAPK activation |
| R-HSA-446219 | 52 | 0.105990181 | 0.670806522 | 0.850551876 | 0.678602593 | Synthesis of substrates in N-glycan biosythesis |
| R-HSA-5362517 | 28 | 0.131009148 | 0.67053552 | 0.850814176 | 0.678602593 | Signaling by Retinoic Acid |
| R-HSA-5625740 | 31 | 0.126368644 | 0.670252538 | 0.849994099 | 0.678602593 | RHO GTPases activate PKNs |
| R-HSA-8875878 | 38 | 0.118489631 | 0.672502509 | 0.856287425 | 0.679893741 | MET promotes cell motility |
| R-HSA-1368082 | 17 | 0.156269734 | 0.665023937 | 0.85971037 | 0.679893741 | RORA activates gene expression |
| R-HSA-8986944 | 41 | 0.114046014 | 0.665008564 | 0.859119782 | 0.679893741 | Transcriptional Regulation by MECP2 |
| R-HSA-1221632 | 26 | 0.132880037 | 0.66231046 | 0.861198738 | 0.679893741 | Meiotic synapsis |
| R-HSA-1368108 | 21 | 0.143453799 | 0.660810697 | 0.86038961 | 0.679893741 | BMAL1:CLOCK,NPAS2 activates circadian gene expression |
| R-HSA-2029485 | 22 | 0.140690725 | 0.659954676 | 0.864686879 | 0.681925157 | Role of phospholipids in phagocytosis |
| R-HSA-111447 | 15 | 0.163629903 | 0.661465321 | 0.865689382 | 0.681994083 | Activation of BAD and translocation to mitochondria |
| R-HSA-210993 | 17 | 0.154329775 | 0.656768219 | 0.867985518 | 0.682797527 | Tie2 Signaling |
| R-HSA-1980143 | 68 | 0.095542932 | 0.655471853 | 0.8685416 | 0.682797527 | Signaling by NOTCH1 |
| R-HSA-2559583 | 117 | 0.085452135 | 0.67184358 | 0.871208252 | 0.683126789 | Cellular Senescence |
| R-HSA-388841 | 63 | 0.096975316 | 0.650840683 | 0.871679036 | 0.683126789 | Costimulation by the CD28 family |
| R-HSA-9700206 | 52 | 0.102039638 | 0.645803733 | 0.872626932 | 0.683126789 | Signaling by ALK in cancer |
| R-HSA-9725370 | 52 | 0.102039638 | 0.645803733 | 0.872626932 | 0.683126789 | Signaling by ALK fusions and activated point mutants |
| R-HSA-3928664 | 17 | 0.153020019 | 0.651194399 | 0.874062581 | 0.683532675 | Ephrin signaling |
| R-HSA-109606 | 53 | 0.100777151 | 0.642006008 | 0.875549692 | 0.683977912 | Intrinsic Pathway for Apoptosis |
| R-HSA-8878171 | 143 | 0.08201722 | 0.672235695 | 0.88134389 | 0.686045935 | Transcriptional regulation by RUNX1 |
| R-HSA-373076 | 95 | 0.086408878 | 0.645991977 | 0.8808933 | 0.686045935 | Class A/1 (Rhodopsin-like receptors) |
| R-HSA-428930 | 16 | 0.154947319 | 0.642700725 | 0.880318455 | 0.686045935 | Thromboxane signalling through TP receptor |
| R-HSA-1236382 | 19 | 0.143797995 | 0.638039812 | 0.882799646 | 0.686045935 | Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants |
| R-HSA-5637815 | 19 | 0.143797995 | 0.638039812 | 0.882799646 | 0.686045935 | Signaling by Ligand-Responsive EGFR Variants in Cancer |
| R-HSA-390471 | 35 | 0.114380663 | 0.63100096 | 0.890278102 | 0.689342651 | Association of TriC/CCT with target proteins during biosynthesis |
| R-HSA-2559582 | 46 | 0.103794753 | 0.629935561 | 0.890023566 | 0.689342651 | Senescence-Associated Secretory Phenotype (SASP) |
| R-HSA-195253 | 76 | 0.088897961 | 0.628931215 | 0.891018216 | 0.689342651 | Degradation of beta-catenin by the destruction complex |
| R-HSA-5694530 | 26 | 0.125498154 | 0.625517135 | 0.894928415 | 0.69043186 | Cargo concentration in the ER |
| R-HSA-5655253 | 30 | 0.118977014 | 0.624713171 | 0.894362861 | 0.69043186 | Signaling by FGFR2 in disease |
| R-HSA-8856828 | 125 | 0.080865437 | 0.645201628 | 0.896544695 | 0.690694421 | Clathrin-mediated endocytosis |
| R-HSA-5357769 | 23 | 0.130305209 | 0.621649797 | 0.899815385 | 0.692052895 | Caspase activation via extrinsic apoptotic signalling pathway |
| R-HSA-3858494 | 120 | 0.080138388 | 0.633113728 | 0.901900674 | 0.692941593 | Beta-catenin independent WNT signaling |
| R-HSA-5617833 | 162 | 0.075533786 | 0.635593206 | 0.909751666 | 0.693409155 | Cilium Assembly |
| R-HSA-196757 | 15 | 0.153926893 | 0.622241412 | 0.903592182 | 0.693409155 | Metabolism of folate and pterines |
| R-HSA-6807004 | 19 | 0.138175633 | 0.613093075 | 0.905961271 | 0.693409155 | Negative regulation of MET activity |
| R-HSA-5689901 | 17 | 0.143965447 | 0.61266162 | 0.908714766 | 0.693409155 | Metalloprotease DUBs |
| R-HSA-9609523 | 18 | 0.140548895 | 0.611261448 | 0.909952607 | 0.693409155 | Insertion of tail-anchored proteins into the endoplasmic reticulum membrane |
| R-HSA-264876 | 17 | 0.143552186 | 0.61090294 | 0.909878459 | 0.693409155 | Insulin processing |
| R-HSA-6805567 | 28 | 0.118395402 | 0.60597541 | 0.909123563 | 0.693409155 | Keratinization |
| R-HSA-6809371 | 28 | 0.118395402 | 0.60597541 | 0.909123563 | 0.693409155 | Formation of the cornified envelope |
| R-HSA-9013409 | 53 | 0.093766216 | 0.597342489 | 0.911059807 | 0.693543727 | RHOJ GTPase cycle |
| R-HSA-9006931 | 195 | 0.073155257 | 0.636060605 | 0.920550422 | 0.694777978 | Signaling by Nuclear Receptors |
| R-HSA-8939211 | 143 | 0.075747231 | 0.620845138 | 0.917884693 | 0.694777978 | ESR-mediated signaling |
| R-HSA-948021 | 153 | 0.074511511 | 0.619737878 | 0.916388636 | 0.694777978 | Transport to the Golgi and subsequent modification |
| R-HSA-199977 | 129 | 0.07688521 | 0.617008134 | 0.914943465 | 0.694777978 | ER to Golgi Anterograde Transport |
| R-HSA-71403 | 22 | 0.127196752 | 0.5966569 | 0.921346918 | 0.694777978 | Citric acid cycle (TCA cycle) |
| R-HSA-446353 | 18 | 0.136684979 | 0.594456885 | 0.923786346 | 0.694777978 | Cell-extracellular matrix interactions |
| R-HSA-75153 | 40 | 0.102193703 | 0.591776614 | 0.921666856 | 0.694777978 | Apoptotic execution phase |
| R-HSA-2871796 | 32 | 0.110006375 | 0.590173616 | 0.918163673 | 0.694777978 | FCERI mediated MAPK activation |
| R-HSA-15869 | 75 | 0.083612439 | 0.589580063 | 0.917685497 | 0.694777978 | Metabolism of nucleotides |
| R-HSA-397795 | 24 | 0.121463831 | 0.587828242 | 0.926665034 | 0.694777978 | G-protein beta:gamma signalling |
| R-HSA-2871809 | 33 | 0.107815609 | 0.583930232 | 0.92485617 | 0.694777978 | FCERI mediated Ca+2 mobilization |
| R-HSA-8943724 | 55 | 0.090303972 | 0.581361114 | 0.926242066 | 0.694777978 | Regulation of PTEN gene transcription |
| R-HSA-381340 | 75 | 0.08218729 | 0.579530851 | 0.92358769 | 0.694777978 | Transcriptional regulation of white adipocyte differentiation |
| R-HSA-9694548 | 36 | 0.1042643 | 0.58092003 | 0.927775197 | 0.69491123 | Maturation of spike protein |
| R-HSA-6807070 | 123 | 0.074883767 | 0.59466176 | 0.92883398 | 0.695005768 | PTEN Regulation |
| R-HSA-5205685 | 19 | 0.130518287 | 0.579117 | 0.931147956 | 0.695340948 | PINK1-PRKN Mediated Mitophagy |
| R-HSA-6804115 | 16 | 0.140193311 | 0.581503077 | 0.933829287 | 0.696645209 | TP53 regulates transcription of additional cell cycle genes whose exact role in the p53 pathway remain uncertain |
| R-HSA-1980145 | 30 | 0.108408033 | 0.569218575 | 0.938654666 | 0.697001025 | Signaling by NOTCH2 |
| R-HSA-8856825 | 87 | 0.077569728 | 0.568205853 | 0.937252862 | 0.697001025 | Cargo recognition for clathrin-mediated endocytosis |
| R-HSA-933541 | 15 | 0.141127433 | 0.570500263 | 0.944268357 | 0.698693964 | TRAF6 mediated IRF7 activation |
| R-HSA-1169410 | 74 | 0.077630935 | 0.545154875 | 0.945013193 | 0.698693964 | Antiviral mechanism by IFN-stimulated genes |
| R-HSA-9013418 | 22 | 0.119298246 | 0.559606437 | 0.946073559 | 0.698784706 | RHOBTB2 GTPase cycle |
| R-HSA-8862803 | 18 | 0.125620052 | 0.546334388 | 0.954912258 | 0.70211766 | Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models |
| R-HSA-8863678 | 18 | 0.125620052 | 0.546334388 | 0.954912258 | 0.70211766 | Neurodegenerative Diseases |
| R-HSA-6803204 | 18 | 0.125523547 | 0.545914679 | 0.955296529 | 0.70211766 | TP53 Regulates Transcription of Genes Involved in Cytochrome C Release |
| R-HSA-3371497 | 39 | 0.094823531 | 0.543895187 | 0.952528026 | 0.70211766 | HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand |
| R-HSA-73929 | 17 | 0.125521477 | 0.53417117 | 0.962244634 | 0.702375587 | Base-Excision Repair, AP Site Formation |
| R-HSA-8940973 | 20 | 0.117761964 | 0.533049681 | 0.957001379 | 0.702375587 | RUNX2 regulates osteoblast differentiation |
| R-HSA-9707564 | 53 | 0.081935257 | 0.521972758 | 0.959212841 | 0.702375587 | Cytoprotection by HMOX1 |
| R-HSA-9018519 | 83 | 0.071785588 | 0.518693877 | 0.961108207 | 0.702375587 | Estrogen-dependent gene expression |
| R-HSA-2122948 | 27 | 0.10302306 | 0.520147957 | 0.964747072 | 0.70351316 | Activated NOTCH1 Transmits Signal to the Nucleus |
| R-HSA-400206 | 102 | 0.067183281 | 0.51150729 | 0.966185567 | 0.703873418 | Regulation of lipid metabolism by PPARalpha |
| R-HSA-1989781 | 100 | 0.06615955 | 0.50112206 | 0.96742268 | 0.704086408 | PPARA activates gene expression |
| R-HSA-389513 | 21 | 0.112402507 | 0.517774915 | 0.969280719 | 0.704750449 | CTLA4 inhibitory signaling |
| R-HSA-9615710 | 29 | 0.098730762 | 0.511751313 | 0.970735189 | 0.705120051 | Late endosomal microautophagy |
| R-HSA-446652 | 128 | 0.06077403 | 0.48674362 | 0.977066558 | 0.705918625 | Interleukin-1 family signaling |
| R-HSA-418594 | 150 | 0.058549353 | 0.484730544 | 0.978943106 | 0.705918625 | G alpha (i) signalling events |
| R-HSA-9013424 | 35 | 0.087369085 | 0.48198686 | 0.979784996 | 0.705918625 | RHOV GTPase cycle |
| R-HSA-9613829 | 20 | 0.106013016 | 0.47986805 | 0.980819857 | 0.705918625 | Chaperone Mediated Autophagy |
| R-HSA-186797 | 53 | 0.075318098 | 0.479817808 | 0.979221636 | 0.705918625 | Signaling by PDGF |
| R-HSA-5205647 | 25 | 0.097340284 | 0.478195062 | 0.984148275 | 0.705918625 | Mitophagy |
| R-HSA-2454202 | 127 | 0.058296419 | 0.466288404 | 0.982463295 | 0.705918625 | Fc epsilon receptor (FCERI) signaling |
| R-HSA-9013408 | 68 | 0.067741896 | 0.464742973 | 0.983807393 | 0.705918625 | RHOG GTPase cycle |
| R-HSA-1226099 | 48 | 0.073185015 | 0.450919034 | 0.986846505 | 0.706008735 | Signaling by FGFR in disease |
| R-HSA-204005 | 62 | 0.06667793 | 0.445442427 | 0.987716841 | 0.706008735 | COPII-mediated vesicle transport |
| R-HSA-157118 | 158 | 0.051459284 | 0.43102144 | 0.991114701 | 0.706008735 | Signaling by NOTCH |
| R-HSA-3295583 | 15 | 0.105606461 | 0.426908592 | 0.995641838 | 0.706008735 | TRP channels |
| R-HSA-5619102 | 62 | 0.063724903 | 0.425714708 | 0.99170348 | 0.706008735 | SLC transporter disorders |
| R-HSA-382556 | 84 | 0.057505808 | 0.417082398 | 0.992066806 | 0.706008735 | ABC-family proteins mediated transport |
| R-HSA-1474165 | 52 | 0.063989764 | 0.404988 | 0.994701987 | 0.706008735 | Reproduction |
| R-HSA-936440 | 34 | 0.065167934 | 0.356579019 | 0.999182434 | 0.707845871 | Negative regulators of DDX58/IFIH1 signaling |