## Reactome
| ID | Description | setSize | enrichmentScore | NES | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 6273658 | Molecules associated with elastic fibres | 40 | 0.810323 | 2.641412 | 0.001795 | 0.011412 | 0.006805 |
| 6273650 | Elastic fibre formation | 43 | 0.795104 | 2.614613 | 0.001832 | 0.011412 | 0.006805 |
| 6273438 | AUF1 (hnRNP D0) destabilizes mRNA | 61 | 0.691767 | 2.442765 | 0.001855 | 0.011412 | 0.006805 |
| 6273434 | Regulation of mRNA stability by proteins that bind AU-rich elements | 94 | 0.627689 | 2.405040 | 0.001754 | 0.011412 | 0.006805 |
| 6272621 | C-type lectin receptors (CLRs) | 113 | 0.600019 | 2.352793 | 0.001757 | 0.011412 | 0.006805 |
| 6273536 | Activation of NF-kappaB in B cells | 68 | 0.648427 | 2.336185 | 0.001832 | 0.011412 | 0.006805 |
| 6273547 | ER-Phagosome pathway | 63 | 0.653436 | 2.326780 | 0.001838 | 0.011412 | 0.006805 |
| 6273768 | Dectin-1 mediated noncanonical NF-kB signaling | 58 | 0.654391 | 2.288078 | 0.001821 | 0.011412 | 0.006805 |
| 6272445 | Stabilization of p53 | 52 | 0.665665 | 2.278880 | 0.001799 | 0.011412 | 0.006805 |
| 6273197 | Regulation of Apoptosis | 52 | 0.671789 | 2.274915 | 0.001901 | 0.011412 | 0.006805 |
| 6272662 | Ubiquitin-dependent degradation of Cyclin D | 51 | 0.665903 | 2.268480 | 0.001869 | 0.011412 | 0.006805 |
| 6272661 | Ubiquitin-dependent degradation of Cyclin D1 | 51 | 0.665903 | 2.268480 | 0.001869 | 0.011412 | 0.006805 |
| 6272425 | CDT1 association with the CDC6:ORC:origin complex | 58 | 0.646093 | 2.267820 | 0.001808 | 0.011412 | 0.006805 |
| 6273196 | Regulation of activated PAK-2p34 by proteasome mediated degradation | 51 | 0.672055 | 2.266911 | 0.001912 | 0.011412 | 0.006805 |
| 6273218 | Regulation of ornithine decarboxylase (ODC) | 49 | 0.674390 | 2.266667 | 0.001938 | 0.011412 | 0.006805 |
| 6273528 | Antigen processing: Ubiquitination & Proteasome degradation | 55 | 0.654968 | 2.264148 | 0.001845 | 0.011412 | 0.006805 |
| 6272435 | CDK-mediated phosphorylation and removal of Cdc6 | 51 | 0.670578 | 2.256236 | 0.001894 | 0.011412 | 0.006805 |
| 6273041 | SCF(Skp2)-mediated degradation of p27/p21 | 55 | 0.651762 | 2.252521 | 0.001835 | 0.011412 | 0.006805 |
| 6273207 | Autodegradation of the E3 ubiquitin ligase COP1 | 51 | 0.662835 | 2.251216 | 0.001828 | 0.011412 | 0.006805 |
| 6272966 | RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways | 44 | 0.681980 | 2.245785 | 0.001795 | 0.011412 | 0.006805 |
| 6273527 | Class I MHC mediated antigen processing & presentation | 93 | 0.588210 | 2.239518 | 0.001773 | 0.011412 | 0.006805 |
| 6273007 | APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1 | 69 | 0.614653 | 2.235638 | 0.001873 | 0.011412 | 0.006805 |
| 6273011 | Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins | 71 | 0.612345 | 2.231578 | 0.001912 | 0.011412 | 0.006805 |
| 6273014 | APC/C:Cdc20 mediated degradation of Securin | 64 | 0.625663 | 2.230410 | 0.001894 | 0.011412 | 0.006805 |
| 6272442 | Cyclin E associated events during G1/S transition | 63 | 0.630113 | 2.223970 | 0.001825 | 0.011412 | 0.006805 |
| 6272446 | p53-Dependent G1 DNA Damage Response | 55 | 0.650577 | 2.223967 | 0.001838 | 0.011412 | 0.006805 |
| 6272447 | p53-Dependent G1/S DNA damage checkpoint | 55 | 0.650577 | 2.223967 | 0.001838 | 0.011412 | 0.006805 |
| 6273010 | APC/C:Cdc20 mediated degradation of mitotic proteins | 70 | 0.609588 | 2.223575 | 0.001894 | 0.011412 | 0.006805 |
| 6273005 | Autodegradation of Cdh1 by Cdh1:APC/C | 61 | 0.629181 | 2.223382 | 0.001852 | 0.011412 | 0.006805 |
| 6272453 | p53-Independent DNA Damage Response | 52 | 0.655916 | 2.222288 | 0.001905 | 0.011412 | 0.006805 |
| 6272454 | p53-Independent G1/S DNA damage checkpoint | 52 | 0.655916 | 2.222288 | 0.001905 | 0.011412 | 0.006805 |
| 6272455 | Ubiquitin Mediated Degradation of Phosphorylated Cdc25A | 52 | 0.655916 | 2.222288 | 0.001905 | 0.011412 | 0.006805 |
| 6273008 | Cdc20:Phospho-APC/C mediated degradation of Cyclin A | 67 | 0.611814 | 2.221609 | 0.001852 | 0.011412 | 0.006805 |
| 6273548 | Antigen processing-Cross presentation | 75 | 0.602363 | 2.219068 | 0.001815 | 0.011412 | 0.006805 |
| 6273009 | APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint | 68 | 0.609889 | 2.207801 | 0.001883 | 0.011412 | 0.006805 |
| 6273598 | degradation of DVL | 59 | 0.625767 | 2.206572 | 0.001859 | 0.011412 | 0.006805 |
| 6272874 | APC/C-mediated degradation of cell cycle proteins | 77 | 0.592623 | 2.197277 | 0.001876 | 0.011412 | 0.006805 |
| 6272875 | Regulation of mitotic cell cycle | 77 | 0.592623 | 2.197277 | 0.001876 | 0.011412 | 0.006805 |
| 6272735 | Cytokine Signaling in Immune system | 144 | 0.535141 | 2.192624 | 0.001745 | 0.011412 | 0.006805 |
| 6272620 | CLEC7A (Dectin-1) signaling | 96 | 0.573236 | 2.192577 | 0.001792 | 0.011412 | 0.006805 |
| 6272448 | G1/S DNA Damage Checkpoints | 58 | 0.636322 | 2.190650 | 0.001866 | 0.011412 | 0.006805 |
| 6273004 | Cyclin A:Cdk2-associated events at S phase entry | 61 | 0.624023 | 2.190150 | 0.001855 | 0.011412 | 0.006805 |
| 6273730 | degradation of AXIN | 55 | 0.636450 | 2.187546 | 0.001908 | 0.011412 | 0.006805 |
| 6273229 | Platelet Aggregation (Plug Formation) | 35 | 0.680467 | 2.169765 | 0.001890 | 0.011412 | 0.006805 |
| 6273549 | Cross-presentation of soluble exogenous antigens (endosomes) | 45 | 0.651649 | 2.153517 | 0.001880 | 0.011412 | 0.006805 |
| 6273114 | Degradation of beta-catenin by the destruction complex | 67 | 0.600754 | 2.149299 | 0.001812 | 0.011412 | 0.006805 |
| 6273490 | Endosomal Sorting Complex Required For Transport (ESCRT) | 29 | 0.714722 | 2.147999 | 0.001876 | 0.011412 | 0.006805 |
| 6273521 | Regulation of Complement cascade | 17 | 0.805094 | 2.145025 | 0.001912 | 0.011412 | 0.006805 |
| 6273748 | RHO GTPases Activate NADPH Oxidases | 11 | 0.894374 | 2.144103 | 0.001988 | 0.011412 | 0.006805 |
| 6273228 | Integrin alphaIIb beta3 signaling | 29 | 0.704650 | 2.132813 | 0.003824 | 0.016699 | 0.009957 |
| 6272566 | Apoptosis | 136 | 0.529018 | 2.132697 | 0.001733 | 0.011412 | 0.006805 |
| 6272567 | Programmed Cell Death | 136 | 0.529018 | 2.132697 | 0.001733 | 0.011412 | 0.006805 |
| 6272957 | Complement cascade | 22 | 0.742747 | 2.117434 | 0.001880 | 0.011412 | 0.006805 |
| 6272595 | Immune System | 642 | 0.444871 | 2.116492 | 0.001517 | 0.011412 | 0.006805 |
| 6273076 | Cholesterol biosynthesis | 22 | 0.738282 | 2.115018 | 0.001866 | 0.011412 | 0.006805 |
| 6273296 | RHO GTPase Effectors | 207 | 0.494739 | 2.114143 | 0.001748 | 0.011412 | 0.006805 |
| 6273755 | Hedgehog ligand biogenesis | 64 | 0.590350 | 2.109904 | 0.001862 | 0.011412 | 0.006805 |
| 6273740 | Asymmetric localization of PCP proteins | 61 | 0.598985 | 2.106733 | 0.001869 | 0.011412 | 0.006805 |
| 6272416 | Assembly of the pre-replicative complex | 63 | 0.591378 | 2.098458 | 0.001832 | 0.011412 | 0.006805 |
| 6272840 | Platelet activation, signaling and aggregation | 192 | 0.496365 | 2.082761 | 0.001799 | 0.011412 | 0.006805 |
| 6273724 | Attenuation phase | 22 | 0.729554 | 2.072754 | 0.001890 | 0.011412 | 0.006805 |
| 6272423 | Regulation of DNA replication | 69 | 0.576518 | 2.066122 | 0.001838 | 0.011412 | 0.006805 |
| 6272432 | Removal of licensing factors from origins | 69 | 0.576518 | 2.066122 | 0.001838 | 0.011412 | 0.006805 |
| 6272433 | Orc1 removal from chromatin | 67 | 0.583637 | 2.063533 | 0.001887 | 0.011412 | 0.006805 |
| 6272434 | Switching of origins to a post-replicative state | 67 | 0.583637 | 2.063533 | 0.001887 | 0.011412 | 0.006805 |
| 6273230 | GRB2:SOS provides linkage to MAPK signaling for Integrins | 18 | 0.746745 | 2.056825 | 0.002008 | 0.011412 | 0.006805 |
| 6272594 | Innate Immune System | 464 | 0.444108 | 2.051662 | 0.001560 | 0.011412 | 0.006805 |
| 6272879 | M Phase | 221 | 0.468434 | 2.039154 | 0.001689 | 0.011412 | 0.006805 |
| 6273016 | Mitotic Anaphase | 156 | 0.490210 | 2.029407 | 0.001783 | 0.011412 | 0.006805 |
| 6273234 | p130Cas linkage to MAPK signaling for integrins | 17 | 0.748021 | 2.029403 | 0.002096 | 0.011412 | 0.006805 |
| 6273015 | Separation of Sister Chromatids | 154 | 0.490816 | 2.029171 | 0.001786 | 0.011412 | 0.006805 |
| 6272510 | Death Receptor Signalling | 16 | 0.768267 | 2.013962 | 0.001976 | 0.011412 | 0.006805 |
| 6272923 | Mitotic Metaphase and Anaphase | 157 | 0.486084 | 2.009163 | 0.001805 | 0.011412 | 0.006805 |
| 6272659 | TNF signaling | 13 | 0.811544 | 2.003167 | 0.001980 | 0.011412 | 0.006805 |
| 6273732 | PCP/CE pathway | 82 | 0.535631 | 1.998444 | 0.001795 | 0.011412 | 0.006805 |
| 6273652 | TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition) | 25 | 0.680419 | 1.992691 | 0.001859 | 0.011412 | 0.006805 |
| 6273721 | Regulation of HSF1-mediated heat shock response | 54 | 0.570667 | 1.991219 | 0.001901 | 0.011412 | 0.006805 |
| 6272969 | Cytosolic sensors of pathogen-associated DNA | 46 | 0.586329 | 1.990165 | 0.003565 | 0.016699 | 0.009957 |
| 6272734 | Signaling by Interleukins | 92 | 0.519134 | 1.989412 | 0.001754 | 0.011412 | 0.006805 |
| 6272991 | TGF-beta receptor signaling activates SMADs | 33 | 0.637541 | 1.985800 | 0.001905 | 0.011412 | 0.006805 |
| 6273410 | RHO GTPases Activate WASPs and WAVEs | 37 | 0.626718 | 1.976443 | 0.001883 | 0.011412 | 0.006805 |
| 6272844 | Extracellular matrix organization | 216 | 0.455304 | 1.974227 | 0.001733 | 0.011412 | 0.006805 |
| 6273316 | Eicosanoid ligand-binding receptors | 13 | 0.791007 | 1.971783 | 0.001912 | 0.011412 | 0.006805 |
| 6273445 | Growth hormone receptor signaling | 26 | 0.663588 | 1.962641 | 0.001923 | 0.011412 | 0.006805 |
| 6273424 | Hedgehog 'on' state | 78 | 0.522240 | 1.951484 | 0.001812 | 0.011412 | 0.006805 |
| 6272736 | Gastrin-CREB signalling pathway via PKC and MAPK | 147 | 0.476598 | 1.948927 | 0.001730 | 0.011412 | 0.006805 |
| 6273001 | Downregulation of TGF-beta receptor signaling | 27 | 0.653458 | 1.948904 | 0.001934 | 0.011412 | 0.006805 |
| 6273323 | Signal amplification | 21 | 0.699376 | 1.941832 | 0.001927 | 0.011412 | 0.006805 |
| 6272997 | p38MAPK events | 16 | 0.757815 | 1.941105 | 0.001912 | 0.011412 | 0.006805 |
| 6272417 | DNA Replication Pre-Initiation | 76 | 0.535139 | 1.940942 | 0.001776 | 0.011412 | 0.006805 |
| 6272418 | M/G1 Transition | 76 | 0.535139 | 1.940942 | 0.001776 | 0.011412 | 0.006805 |
| 6273504 | Negative regulators of RIG-I/MDA5 signaling | 22 | 0.686382 | 1.937005 | 0.001996 | 0.011412 | 0.006805 |
| 6272847 | G alpha (q) signalling events | 120 | 0.488046 | 1.929000 | 0.001792 | 0.011412 | 0.006805 |
| 6272617 | VEGFA-VEGFR2 Pathway | 106 | 0.496446 | 1.926698 | 0.001835 | 0.011412 | 0.006805 |
| 6273603 | Activation of Matrix Metalloproteinases | 20 | 0.687352 | 1.910809 | 0.005629 | 0.021610 | 0.012886 |
| 6273729 | Regulated Necrosis | 17 | 0.715128 | 1.904947 | 0.003891 | 0.016699 | 0.009957 |
| 6273727 | Regulation of necroptotic cell death | 17 | 0.715128 | 1.904947 | 0.003891 | 0.016699 | 0.009957 |
| 6273728 | RIPK1-mediated regulated necrosis | 17 | 0.715128 | 1.904947 | 0.003891 | 0.016699 | 0.009957 |
| 6273113 | Signaling by Rho GTPases | 320 | 0.422635 | 1.904574 | 0.001664 | 0.011412 | 0.006805 |
| 6273474 | Interferon Signaling | 39 | 0.577080 | 1.903023 | 0.003650 | 0.016699 | 0.009957 |
| 6273777 | CD209 (DC-SIGN) signaling | 18 | 0.704699 | 1.886906 | 0.003846 | 0.016699 | 0.009957 |
| 6273154 | TCR signaling | 36 | 0.583124 | 1.875633 | 0.005587 | 0.021610 | 0.012886 |
| 6272964 | TAK1 activates NFkB by phosphorylation and activation of IKKs complex | 22 | 0.660149 | 1.870673 | 0.001905 | 0.011412 | 0.006805 |
| 6273725 | HSF1-dependent transactivation | 31 | 0.612142 | 1.868366 | 0.001835 | 0.011412 | 0.006805 |
| 6272972 | NOD1/2 Signaling Pathway | 26 | 0.620681 | 1.866583 | 0.003711 | 0.016699 | 0.009957 |
| 6273733 | RHO GTPases Activate Formins | 90 | 0.488469 | 1.865437 | 0.001845 | 0.011412 | 0.006805 |
| 6273425 | Signaling by Hedgehog | 101 | 0.478278 | 1.862909 | 0.001838 | 0.011412 | 0.006805 |
| 6272449 | Cell Cycle Checkpoints | 108 | 0.483261 | 1.860856 | 0.001786 | 0.011412 | 0.006805 |
| 6273722 | Cellular response to heat stress | 77 | 0.503122 | 1.860135 | 0.001742 | 0.011412 | 0.006805 |
| 6272618 | Signaling by VEGF | 111 | 0.478728 | 1.859748 | 0.001842 | 0.011412 | 0.006805 |
| 6272430 | G1/S Transition | 99 | 0.491151 | 1.856978 | 0.001783 | 0.011412 | 0.006805 |
| 6273159 | Cell surface interactions at the vascular wall | 77 | 0.501458 | 1.853261 | 0.001866 | 0.011412 | 0.006805 |
| 6272974 | Interleukin-1 signaling | 34 | 0.594990 | 1.848340 | 0.007859 | 0.027410 | 0.016344 |
| 6273281 | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 14 | 0.721177 | 1.848221 | 0.005837 | 0.021856 | 0.013032 |
| 6273781 | RHO GTPases activate CIT | 19 | 0.676757 | 1.847782 | 0.001923 | 0.011412 | 0.006805 |
| 6272992 | Signaling by TGF-beta Receptor Complex | 76 | 0.501277 | 1.842143 | 0.003643 | 0.016699 | 0.009957 |
| 6273220 | Platelet degranulation | 91 | 0.489448 | 1.841160 | 0.001894 | 0.011412 | 0.006805 |
| 6273250 | Sema4D in semaphorin signaling | 35 | 0.586562 | 1.825715 | 0.001818 | 0.011412 | 0.006805 |
| 6272839 | Thrombin signalling through proteinase activated receptors (PARs) | 22 | 0.642449 | 1.822293 | 0.005769 | 0.021739 | 0.012963 |
| 6273718 | HATs acetylate histones | 79 | 0.488121 | 1.819750 | 0.001848 | 0.011412 | 0.006805 |
| 6273483 | Interferon alpha/beta signaling | 11 | 0.756117 | 1.812019 | 0.011450 | 0.037096 | 0.022120 |
| 6272842 | Response to elevated platelet cytosolic Ca2+ | 98 | 0.473566 | 1.803922 | 0.001890 | 0.011412 | 0.006805 |
| 6273614 | Regulation of cholesterol biosynthesis by SREBP (SREBF) | 36 | 0.567263 | 1.798017 | 0.005338 | 0.021377 | 0.012747 |
| 6272763 | MyD88-independent TLR3/TLR4 cascade | 64 | 0.503473 | 1.793429 | 0.003810 | 0.016699 | 0.009957 |
| 6272764 | Toll Like Receptor 3 (TLR3) Cascade | 64 | 0.503473 | 1.793429 | 0.003810 | 0.016699 | 0.009957 |
| 6272612 | Signaling by the B Cell Receptor (BCR) | 158 | 0.435809 | 1.793137 | 0.001692 | 0.011412 | 0.006805 |
| 6273153 | Downstream TCR signaling | 22 | 0.631739 | 1.790307 | 0.001908 | 0.011412 | 0.006805 |
| 6273221 | Clathrin derived vesicle budding | 49 | 0.528607 | 1.787769 | 0.001908 | 0.011412 | 0.006805 |
| 6273222 | trans-Golgi Network Vesicle Budding | 49 | 0.528607 | 1.787769 | 0.001908 | 0.011412 | 0.006805 |
| 6273100 | p75NTR signals via NF-kB | 18 | 0.665491 | 1.784788 | 0.009921 | 0.032753 | 0.019530 |
| 6273526 | Antigen Presentation: Folding, assembly and peptide loading of class I MHC | 23 | 0.602439 | 1.781814 | 0.009191 | 0.031192 | 0.018600 |
| 6273334 | EGFR Transactivation by Gastrin | 11 | 0.752425 | 1.780830 | 0.003745 | 0.016699 | 0.009957 |
| 6273156 | FCERI mediated NF-kB activation | 21 | 0.634236 | 1.780163 | 0.003817 | 0.016699 | 0.009957 |
| 6272427 | Synthesis of DNA | 91 | 0.477495 | 1.778585 | 0.001783 | 0.011412 | 0.006805 |
| 6273788 | Recognition of DNA damage by PCNA-containing replication complex | 22 | 0.624362 | 1.776734 | 0.007299 | 0.025998 | 0.015502 |
| 6273133 | Downstream signaling events of B Cell Receptor (BCR) | 132 | 0.441756 | 1.776702 | 0.001704 | 0.011412 | 0.006805 |
| 6272956 | Initial triggering of complement | 12 | 0.726783 | 1.773728 | 0.003953 | 0.016699 | 0.009957 |
| 6272665 | RNA Polymerase II Promoter Escape | 40 | 0.538521 | 1.768804 | 0.003922 | 0.016699 | 0.009957 |
| 6272668 | RNA Polymerase II Transcription Initiation | 40 | 0.538521 | 1.768804 | 0.003922 | 0.016699 | 0.009957 |
| 6272666 | RNA Polymerase II Transcription Initiation And Promoter Clearance | 40 | 0.538521 | 1.768804 | 0.003922 | 0.016699 | 0.009957 |
| 6272646 | RNA Polymerase II Transcription Pre-Initiation And Promoter Opening | 40 | 0.538521 | 1.768804 | 0.003922 | 0.016699 | 0.009957 |
| 6272841 | Hemostasis | 408 | 0.386886 | 1.768624 | 0.001656 | 0.011412 | 0.006805 |
| 6272431 | Mitotic G1-G1/S phases | 121 | 0.448859 | 1.765834 | 0.001745 | 0.011412 | 0.006805 |
| 6273354 | ADP signalling through P2Y purinoceptor 1 | 14 | 0.710355 | 1.763918 | 0.013944 | 0.043544 | 0.025965 |
| 6273238 | Class A/1 (Rhodopsin-like receptors) | 177 | 0.423765 | 1.761961 | 0.001751 | 0.011412 | 0.006805 |
| 6273542 | Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha | 22 | 0.624237 | 1.759928 | 0.005566 | 0.021610 | 0.012886 |
| 6272762 | TRIF-mediated TLR3/TLR4 signaling | 62 | 0.495541 | 1.759837 | 0.003766 | 0.016699 | 0.009957 |
| 6272421 | DNA Replication | 95 | 0.463588 | 1.750857 | 0.001742 | 0.011412 | 0.006805 |
| 6273492 | TRAF3-dependent IRF activation pathway | 12 | 0.714979 | 1.746809 | 0.009747 | 0.032426 | 0.019335 |
| 6273497 | TRAF6 mediated IRF7 activation | 13 | 0.708788 | 1.738116 | 0.003976 | 0.016699 | 0.009957 |
| 6273643 | Signaling by Hippo | 25 | 0.587832 | 1.730015 | 0.009560 | 0.031929 | 0.019039 |
| 6272613 | Adaptive Immune System | 274 | 0.394571 | 1.729906 | 0.001647 | 0.011412 | 0.006805 |
| 6273149 | TCF dependent signaling in response to WNT | 143 | 0.420183 | 1.723676 | 0.001721 | 0.011412 | 0.006805 |
| 6272637 | Signalling to RAS | 35 | 0.545713 | 1.720828 | 0.005445 | 0.021610 | 0.012886 |
| 6272565 | Caspase activation via extrinsic apoptotic signalig pathway | 19 | 0.623360 | 1.717410 | 0.008130 | 0.028018 | 0.016707 |
| 6272693 | mRNA Capping | 28 | 0.559683 | 1.717299 | 0.005894 | 0.021975 | 0.013104 |
| 6272757 | Toll-Like Receptors Cascades | 88 | 0.455643 | 1.716304 | 0.001862 | 0.011412 | 0.006805 |
| 6273369 | Golgi Associated Vesicle Biogenesis | 31 | 0.556674 | 1.714572 | 0.009434 | 0.031752 | 0.018934 |
| 6272820 | Formation of the Early Elongation Complex | 31 | 0.549999 | 1.712193 | 0.005941 | 0.022054 | 0.013151 |
| 6273237 | Peptide ligand-binding receptors | 98 | 0.449571 | 1.710197 | 0.001815 | 0.011412 | 0.006805 |
| 6273067 | Membrane Trafficking | 161 | 0.415325 | 1.703255 | 0.001701 | 0.011412 | 0.006805 |
| 6272694 | RNA Pol II CTD phosphorylation and interaction with CE | 27 | 0.558362 | 1.701980 | 0.003960 | 0.016699 | 0.009957 |
| 6273544 | Cellular response to hypoxia | 28 | 0.570174 | 1.699532 | 0.003656 | 0.016699 | 0.009957 |
| 6273543 | Regulation of Hypoxia-inducible Factor (HIF) by oxygen | 28 | 0.570174 | 1.699532 | 0.003656 | 0.016699 | 0.009957 |
| 6272638 | Signalling to ERKs | 47 | 0.507448 | 1.691077 | 0.003704 | 0.016699 | 0.009957 |
| 6272511 | Signal Transduction | 1456 | 0.337151 | 1.684171 | 0.001418 | 0.011412 | 0.006805 |
| 6273249 | Sema4D induced cell migration and growth-cone collapse | 31 | 0.561340 | 1.683143 | 0.011070 | 0.036135 | 0.021547 |
| 6272939 | GPCR ligand binding | 230 | 0.389893 | 1.679639 | 0.003571 | 0.016699 | 0.009957 |
| 6272761 | TRAF6 Mediated Induction of proinflammatory cytokines | 60 | 0.476017 | 1.670610 | 0.005769 | 0.021739 | 0.012963 |
| 6272755 | Activated TLR4 signalling | 73 | 0.456028 | 1.664477 | 0.003623 | 0.016699 | 0.009957 |
| 6272756 | Toll Like Receptor 4 (TLR4) Cascade | 73 | 0.456028 | 1.664477 | 0.003623 | 0.016699 | 0.009957 |
| 6273332 | Regulation of actin dynamics for phagocytic cup formation | 62 | 0.472696 | 1.652403 | 0.012727 | 0.040033 | 0.023871 |
| 6273613 | Activation of gene expression by SREBF (SREBP) | 23 | 0.577989 | 1.648352 | 0.016514 | 0.049599 | 0.029575 |
| 6272428 | S Phase | 117 | 0.421523 | 1.645206 | 0.003565 | 0.016699 | 0.009957 |
| 6273696 | Syndecan interactions | 13 | 0.648819 | 1.644472 | 0.015873 | 0.048176 | 0.028727 |
| 6272452 | Cellular responses to stress | 207 | 0.382696 | 1.639838 | 0.001712 | 0.011412 | 0.006805 |
| 6272790 | DNA Damage Bypass | 36 | 0.517068 | 1.633022 | 0.009381 | 0.031697 | 0.018901 |
| 6272769 | MyD88 cascade initiated on plasma membrane | 67 | 0.451964 | 1.622314 | 0.005566 | 0.021610 | 0.012886 |
| 6272770 | Toll Like Receptor 10 (TLR10) Cascade | 67 | 0.451964 | 1.622314 | 0.005566 | 0.021610 | 0.012886 |
| 6272771 | Toll Like Receptor 5 (TLR5) Cascade | 67 | 0.451964 | 1.622314 | 0.005566 | 0.021610 | 0.012886 |
| 6272766 | MyD88 dependent cascade initiated on endosome | 71 | 0.448067 | 1.621646 | 0.005660 | 0.021610 | 0.012886 |
| 6272768 | Toll Like Receptor 7/8 (TLR7/8) Cascade | 71 | 0.448067 | 1.621646 | 0.005660 | 0.021610 | 0.012886 |
| 6273735 | EPH-Ephrin signaling | 100 | 0.426137 | 1.620658 | 0.006885 | 0.024711 | 0.014735 |
| 6273145 | Apoptotic cleavage of cellular proteins | 36 | 0.515660 | 1.620445 | 0.016158 | 0.048699 | 0.029039 |
| 6272961 | Fcgamma receptor (FCGR) dependent phagocytosis | 83 | 0.440440 | 1.619355 | 0.003630 | 0.016699 | 0.009957 |
| 6272733 | Interleukin-2 signaling | 40 | 0.489760 | 1.611145 | 0.010870 | 0.035614 | 0.021236 |
| 6272581 | Signaling by GPCR | 414 | 0.349152 | 1.607613 | 0.001631 | 0.011412 | 0.006805 |
| 6272838 | GPCR downstream signaling | 338 | 0.357281 | 1.607494 | 0.001684 | 0.011412 | 0.006805 |
| 6272767 | Toll Like Receptor 9 (TLR9) Cascade | 73 | 0.441928 | 1.606760 | 0.005660 | 0.021610 | 0.012886 |
| 6273444 | Interleukin-3, 5 and GM-CSF signaling | 37 | 0.496317 | 1.585485 | 0.012433 | 0.039251 | 0.023405 |
| 6273068 | Vesicle-mediated transport | 195 | 0.376132 | 1.581627 | 0.003367 | 0.016699 | 0.009957 |
| 6272642 | mRNA Splicing - Minor Pathway | 45 | 0.463613 | 1.572391 | 0.011278 | 0.036675 | 0.021869 |
| 6272765 | TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation | 70 | 0.435380 | 1.569704 | 0.005671 | 0.021610 | 0.012886 |
| 6272419 | Cell Cycle, Mitotic | 373 | 0.342221 | 1.563615 | 0.001603 | 0.011412 | 0.006805 |
| 6273578 | Degradation of the extracellular matrix | 83 | 0.412828 | 1.557996 | 0.014085 | 0.043824 | 0.026132 |
| 6272754 | MyD88:Mal cascade initiated on plasma membrane | 69 | 0.429996 | 1.546418 | 0.007394 | 0.025998 | 0.015502 |
| 6272759 | Toll Like Receptor 2 (TLR2) Cascade | 69 | 0.429996 | 1.546418 | 0.007394 | 0.025998 | 0.015502 |
| 6272758 | Toll Like Receptor TLR1:TLR2 Cascade | 69 | 0.429996 | 1.546418 | 0.007394 | 0.025998 | 0.015502 |
| 6272760 | Toll Like Receptor TLR6:TLR2 Cascade | 69 | 0.429996 | 1.546418 | 0.007394 | 0.025998 | 0.015502 |
| 6273251 | Semaphorin interactions | 66 | 0.435000 | 1.542198 | 0.016071 | 0.048608 | 0.028984 |
| 6272420 | Cell Cycle | 410 | 0.330613 | 1.521319 | 0.001595 | 0.011412 | 0.006805 |
| 6273612 | Mitotic Prometaphase | 104 | 0.373380 | 1.459448 | 0.014760 | 0.045598 | 0.027190 |
| 6272505 | Metabolism of lipids and lipoproteins | 486 | -0.263086 | -1.279664 | 0.008043 | 0.027828 | 0.016594 |
| 6272464 | Metabolism | 1418 | -0.264443 | -1.368030 | 0.003546 | 0.016699 | 0.009957 |
| 6272486 | The citric acid (TCA) cycle and respiratory electron transport | 135 | -0.343100 | -1.426497 | 0.009547 | 0.031929 | 0.019039 |
| 6273348 | Ion channel transport | 134 | -0.350194 | -1.464251 | 0.004640 | 0.018669 | 0.011132 |
| 6273577 | Collagen degradation | 52 | -0.415259 | -1.519688 | 0.006726 | 0.024243 | 0.014456 |
| 6272928 | Respiratory electron transport | 70 | -0.405137 | -1.525154 | 0.013363 | 0.041881 | 0.024973 |
| 6272929 | Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. | 93 | -0.392906 | -1.537833 | 0.009195 | 0.031192 | 0.018600 |
| 6273412 | CREB phosphorylation through the activation of Ras | 38 | -0.467941 | -1.539407 | 0.015453 | 0.047231 | 0.028163 |
| 6273466 | Keratan sulfate biosynthesis | 32 | -0.489278 | -1.557205 | 0.015748 | 0.047965 | 0.028601 |
| 6273217 | ABC-family proteins mediated transport | 35 | -0.491993 | -1.598613 | 0.011561 | 0.037313 | 0.022250 |
| 6273347 | Ion transport by P-type ATPases | 36 | -0.492911 | -1.617081 | 0.012320 | 0.039037 | 0.023277 |
| 6272522 | Phase 1 - Functionalization of compounds | 67 | -0.443980 | -1.640734 | 0.008639 | 0.029538 | 0.017613 |
| 6272684 | Cytochrome P450 - arranged by substrate type | 53 | -0.466458 | -1.643801 | 0.010799 | 0.035518 | 0.021179 |
| 6273533 | Inwardly rectifying K+ channels | 38 | -0.499177 | -1.645334 | 0.012121 | 0.038547 | 0.022985 |
| 6272805 | Post NMDA receptor activation events | 41 | -0.499125 | -1.670616 | 0.004425 | 0.017885 | 0.010665 |
| 6273053 | FGFR1 ligand binding and activation | 15 | -0.618359 | -1.673435 | 0.008032 | 0.027828 | 0.016594 |
| 6273054 | FGFR1c ligand binding and activation | 12 | -0.664160 | -1.676680 | 0.012097 | 0.038547 | 0.022985 |
| 6273513 | Ligand-gated ion channel transport | 18 | -0.610343 | -1.682658 | 0.011881 | 0.038205 | 0.022781 |
| 6272730 | NCAM signaling for neurite out-growth | 62 | -0.450022 | -1.684931 | 0.006623 | 0.023969 | 0.014292 |
| 6272462 | Glucose metabolism | 83 | -0.438387 | -1.688797 | 0.002137 | 0.011412 | 0.006805 |
| 6272883 | Peptide chain elongation | 87 | -0.431494 | -1.712444 | 0.002062 | 0.011412 | 0.006805 |
| 6272469 | Biological oxidations | 151 | -0.408724 | -1.713002 | 0.002252 | 0.011675 | 0.006962 |
| 6273346 | Reduction of cytosolic Ca++ levels | 15 | -0.655365 | -1.718019 | 0.014286 | 0.044291 | 0.026410 |
| 6273657 | Abacavir transport and metabolism | 15 | -0.646430 | -1.731461 | 0.011976 | 0.038368 | 0.022878 |
| 6273059 | FGFR3 ligand binding and activation | 11 | -0.695610 | -1.733679 | 0.015385 | 0.047190 | 0.028139 |
| 6273058 | FGFR3c ligand binding and activation | 11 | -0.695610 | -1.733679 | 0.015385 | 0.047190 | 0.028139 |
| 6272899 | Metabolism of porphyrins | 29 | -0.563207 | -1.737166 | 0.008421 | 0.028906 | 0.017236 |
| 6272884 | Eukaryotic Translation Elongation | 90 | -0.436217 | -1.741014 | 0.002058 | 0.011412 | 0.006805 |
| 6272670 | Peroxisomal lipid metabolism | 22 | -0.602016 | -1.759364 | 0.009921 | 0.032753 | 0.019530 |
| 6273309 | Amine ligand-binding receptors | 32 | -0.556657 | -1.768216 | 0.007797 | 0.027306 | 0.016282 |
| 6273085 | Synthesis of bile acids and bile salts via 24-hydroxycholesterol | 16 | -0.658011 | -1.778598 | 0.006135 | 0.022389 | 0.013350 |
| 6273610 | Keratan sulfate degradation | 12 | -0.728209 | -1.778636 | 0.003854 | 0.016699 | 0.009957 |
| 6272461 | Gluconeogenesis | 38 | -0.534029 | -1.778748 | 0.004000 | 0.016699 | 0.009957 |
| 6272988 | GABA receptor activation | 53 | -0.502208 | -1.789178 | 0.002101 | 0.011412 | 0.006805 |
| 6273239 | Class C/3 (Metabotropic glutamate/pheromone receptors) | 15 | -0.688726 | -1.804455 | 0.005780 | 0.021739 | 0.012963 |
| 6273061 | FGFR4 ligand binding and activation | 16 | -0.675884 | -1.813033 | 0.006012 | 0.022169 | 0.013219 |
| 6272806 | Activation of NMDA receptor upon glutamate binding and postsynaptic events | 49 | -0.527465 | -1.823826 | 0.002268 | 0.011675 | 0.006962 |
| 6273208 | Acetylcholine Neurotransmitter Release Cycle | 16 | -0.675609 | -1.827806 | 0.004237 | 0.017208 | 0.010261 |
| 6273516 | Retinoid metabolism and transport | 13 | -0.723991 | -1.836144 | 0.004008 | 0.016699 | 0.009957 |
| 6273371 | Sodium/Calcium exchangers | 11 | -0.754282 | -1.838623 | 0.002070 | 0.011412 | 0.006805 |
| 6273531 | Activation of G protein gated Potassium channels | 27 | -0.597521 | -1.847444 | 0.004057 | 0.016699 | 0.009957 |
| 6273532 | G protein gated Potassium channels | 27 | -0.597521 | -1.847444 | 0.004057 | 0.016699 | 0.009957 |
| 6273530 | Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits | 27 | -0.597521 | -1.847444 | 0.004057 | 0.016699 | 0.009957 |
| 6272807 | Neurotransmitter Receptor Binding And Downstream Transmission In The Postsynaptic Cell | 143 | -0.435933 | -1.852775 | 0.002257 | 0.011675 | 0.006962 |
| 6273081 | Synthesis of bile acids and bile salts | 24 | -0.620965 | -1.859419 | 0.006024 | 0.022169 | 0.013219 |
| 6272999 | Lipoprotein metabolism | 21 | -0.645278 | -1.860046 | 0.006160 | 0.022389 | 0.013350 |
| 6273055 | FGFR2c ligand binding and activation | 14 | -0.719518 | -1.885654 | 0.006048 | 0.022169 | 0.013219 |
| 6272898 | Heme degradation | 18 | -0.679937 | -1.896894 | 0.002033 | 0.011412 | 0.006805 |
| 6273418 | GABA synthesis, release, reuptake and degradation | 24 | -0.635078 | -1.897409 | 0.001946 | 0.011412 | 0.006805 |
| 6272467 | Glucuronidation | 16 | -0.707067 | -1.898543 | 0.004132 | 0.016860 | 0.010054 |
| 6273262 | Nuclear Receptor transcription pathway | 53 | -0.528293 | -1.904581 | 0.002020 | 0.011412 | 0.006805 |
| 6272481 | Transmembrane transport of small molecules | 470 | -0.394860 | -1.907438 | 0.002558 | 0.012862 | 0.007670 |
| 6273232 | Norepinephrine Neurotransmitter Release Cycle | 16 | -0.705725 | -1.915777 | 0.002049 | 0.011412 | 0.006805 |
| 6272687 | Fatty acids | 14 | -0.731517 | -1.921185 | 0.004073 | 0.016699 | 0.009957 |
| 6273403 | Bile salt and organic anion SLC transporters | 16 | -0.715978 | -1.930466 | 0.001901 | 0.011412 | 0.006805 |
| 6273095 | Recycling of bile acids and salts | 12 | -0.774800 | -1.940065 | 0.001908 | 0.011412 | 0.006805 |
| 6273226 | Na+/Cl- dependent neurotransmitter transporters | 16 | -0.736276 | -1.945714 | 0.004024 | 0.016699 | 0.009957 |
| 6272494 | Glutamate Neurotransmitter Release Cycle | 26 | -0.638781 | -1.963767 | 0.002004 | 0.011412 | 0.006805 |
| 6273413 | CREB phosphorylation through the activation of CaMKII | 23 | -0.655946 | -1.970722 | 0.002008 | 0.011412 | 0.006805 |
| 6273307 | Striated Muscle Contraction | 56 | -0.560887 | -1.981426 | 0.002119 | 0.011412 | 0.006805 |
| 6273414 | Ras activation uopn Ca2+ infux through NMDA receptor | 26 | -0.650495 | -1.984309 | 0.002119 | 0.011412 | 0.006805 |
| 6273663 | Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET) | 17 | -0.731499 | -1.999185 | 0.002092 | 0.011412 | 0.006805 |
| 6272480 | SLC-mediated transmembrane transport | 249 | -0.445204 | -2.010229 | 0.002375 | 0.012086 | 0.007207 |
| 6272574 | The canonical retinoid cycle in rods (twilight vision) | 20 | -0.717981 | -2.024506 | 0.001961 | 0.011412 | 0.006805 |
| 6273047 | Transport of glucose and other sugars, bile salts and organic acids, metal ions and amine compounds | 89 | -0.525787 | -2.032732 | 0.002208 | 0.011573 | 0.006901 |
| 6273227 | Amine compound SLC transporters | 28 | -0.660380 | -2.038962 | 0.002041 | 0.011412 | 0.006805 |
| 6273225 | Transport of inorganic cations/anions and amino acids/oligopeptides | 104 | -0.513929 | -2.041776 | 0.002151 | 0.011412 | 0.006805 |
| 6273402 | Type I hemidesmosome assembly | 23 | -0.697031 | -2.049269 | 0.002024 | 0.011412 | 0.006805 |
| 6273581 | Collagen formation | 63 | -0.556347 | -2.050684 | 0.002141 | 0.011412 | 0.006805 |
| 6272513 | Tryptophan catabolism | 13 | -0.804178 | -2.054235 | 0.002123 | 0.011412 | 0.006805 |
| 6273082 | Bile acid and bile salt metabolism | 34 | -0.649614 | -2.066516 | 0.002079 | 0.011412 | 0.006805 |
| 6272570 | Inactivation, recovery and regulation of the phototransduction cascade | 42 | -0.611880 | -2.077346 | 0.002062 | 0.011412 | 0.006805 |
| 6272571 | The phototransduction cascade | 43 | -0.610034 | -2.084405 | 0.002075 | 0.011412 | 0.006805 |
| 6273224 | Amino acid and oligopeptide SLC transporters | 57 | -0.592088 | -2.094821 | 0.002110 | 0.011412 | 0.006805 |
| 6273399 | Unblocking of NMDA receptor, glutamate binding and activation | 23 | -0.721170 | -2.125945 | 0.002088 | 0.011412 | 0.006805 |
| 6272492 | Transmission across Chemical Synapses | 213 | -0.479780 | -2.136675 | 0.002421 | 0.012248 | 0.007303 |
| 6273254 | NCAM1 interactions | 31 | -0.665512 | -2.151027 | 0.002079 | 0.011412 | 0.006805 |
| 6273580 | Assembly of collagen fibrils and other multimeric structures | 36 | -0.649163 | -2.162806 | 0.002096 | 0.011412 | 0.006805 |
| 6273083 | Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol | 17 | -0.810649 | -2.172703 | 0.002049 | 0.011412 | 0.006805 |
| 6273534 | Potassium Channels | 104 | -0.547901 | -2.191483 | 0.002169 | 0.011441 | 0.006822 |
| 6273606 | Collagen biosynthesis and modifying enzymes | 55 | -0.605353 | -2.192691 | 0.002101 | 0.011412 | 0.006805 |
| 6272495 | Neurotransmitter Release Cycle | 51 | -0.625598 | -2.236210 | 0.002128 | 0.011412 | 0.006805 |
| 6273564 | Voltage gated Potassium channels | 45 | -0.656586 | -2.250122 | 0.002151 | 0.011412 | 0.006805 |
| 6272493 | Neuronal System | 295 | -0.489955 | -2.253567 | 0.002364 | 0.012086 | 0.007207 |
| 6272572 | Visual phototransduction | 73 | -0.630320 | -2.387105 | 0.002132 | 0.011412 | 0.006805 |
| 6272935 | Lipid digestion, mobilization, and transport | 39 | -0.739192 | -2.464425 | 0.002114 | 0.011412 | 0.006805 |

## KEGG
| ID | Description | setSize | enrichmentScore | NES | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- | --- |
| dre04060 | Cytokine-cytokine receptor interaction | 109 | 0.647372 | 2.535759 | 0.001887 | 0.014101 | 0.008452 |
| dre04620 | Toll-like receptor signaling pathway | 78 | 0.659403 | 2.440707 | 0.001805 | 0.014101 | 0.008452 |
| dre04621 | NOD-like receptor signaling pathway | 47 | 0.717351 | 2.412803 | 0.001825 | 0.014101 | 0.008452 |
| dre05132 | Salmonella infection | 81 | 0.650703 | 2.408212 | 0.001931 | 0.014101 | 0.008452 |
| dre04622 | RIG-I-like receptor signaling pathway | 51 | 0.675001 | 2.307518 | 0.001880 | 0.014101 | 0.008452 |
| dre03050 | Proteasome | 45 | 0.671254 | 2.241621 | 0.001890 | 0.014101 | 0.008452 |
| dre04630 | Jak-STAT signaling pathway | 105 | 0.544197 | 2.119904 | 0.001912 | 0.014101 | 0.008452 |
| dre04141 | Protein processing in endoplasmic reticulum | 172 | 0.484090 | 2.014558 | 0.001681 | 0.014101 | 0.008452 |
| dre04623 | Cytosolic DNA-sensing pathway | 34 | 0.630937 | 1.995778 | 0.001984 | 0.014101 | 0.008452 |
| dre04115 | p53 signaling pathway | 68 | 0.544458 | 1.981893 | 0.001848 | 0.014101 | 0.008452 |
| dre04210 | Apoptosis | 88 | 0.517619 | 1.945269 | 0.001855 | 0.014101 | 0.008452 |
| dre04370 | VEGF signaling pathway | 74 | 0.530966 | 1.936510 | 0.001815 | 0.014101 | 0.008452 |
| dre05168 | Herpes simplex infection | 144 | 0.473221 | 1.927887 | 0.001706 | 0.014101 | 0.008452 |
| dre04130 | SNARE interactions in vesicular transport | 42 | 0.551358 | 1.842043 | 0.001942 | 0.014101 | 0.008452 |
| dre04142 | Lysosome | 120 | 0.454151 | 1.786929 | 0.001748 | 0.014101 | 0.008452 |
| dre00900 | Terpenoid backbone biosynthesis | 21 | 0.630932 | 1.785050 | 0.007890 | 0.033415 | 0.020029 |
| dre04810 | Regulation of actin cytoskeleton | 225 | 0.412026 | 1.779215 | 0.001675 | 0.014101 | 0.008452 |
| dre00970 | Aminoacyl-tRNA biosynthesis | 37 | 0.544410 | 1.735311 | 0.007435 | 0.032443 | 0.019447 |
| dre04530 | Tight junction | 153 | 0.421417 | 1.718139 | 0.001767 | 0.014101 | 0.008452 |
| dre03008 | Ribosome biogenesis in eukaryotes | 64 | 0.476825 | 1.708675 | 0.001842 | 0.014101 | 0.008452 |
| dre04144 | Endocytosis | 297 | 0.388314 | 1.703584 | 0.001664 | 0.014101 | 0.008452 |
| dre04350 | TGF-beta signaling pathway | 86 | 0.441370 | 1.641281 | 0.003839 | 0.020473 | 0.012272 |
| dre00590 | Arachidonic acid metabolism | 44 | 0.467018 | 1.567938 | 0.015444 | 0.048346 | 0.028980 |
| dre04120 | Ubiquitin mediated proteolysis | 131 | 0.380416 | 1.526017 | 0.005396 | 0.025899 | 0.015524 |
| dre03040 | Spliceosome | 129 | 0.381993 | 1.522535 | 0.003717 | 0.020473 | 0.012272 |
| dre04010 | MAPK signaling pathway | 283 | 0.345270 | 1.520130 | 0.003165 | 0.018228 | 0.010926 |
| dre04520 | Adherens junction | 87 | 0.399421 | 1.494778 | 0.014388 | 0.046043 | 0.027599 |
| dre04145 | Phagosome | 126 | 0.377009 | 1.492889 | 0.014235 | 0.046043 | 0.027599 |
| dre04510 | Focal adhesion | 219 | 0.332146 | 1.412419 | 0.011824 | 0.041529 | 0.024893 |
| dre01100 | Metabolic pathways | 1153 | -0.253414 | -1.303366 | 0.003125 | 0.018228 | 0.010926 |
| dre01230 | Biosynthesis of amino acids | 77 | -0.387657 | -1.485419 | 0.011416 | 0.041096 | 0.024634 |
| dre01200 | Carbon metabolism | 116 | -0.363726 | -1.517708 | 0.004405 | 0.021875 | 0.013112 |
| dre04260 | Cardiac muscle contraction | 86 | -0.399529 | -1.522819 | 0.007160 | 0.032220 | 0.019313 |
| dre00010 | Glycolysis / Gluconeogenesis | 70 | -0.402429 | -1.523229 | 0.008602 | 0.033479 | 0.020068 |
| dre00020 | Citrate cycle (TCA cycle) | 31 | -0.509402 | -1.624335 | 0.016000 | 0.049021 | 0.029384 |
| dre00040 | Pentose and glucuronate interconversions | 27 | -0.536075 | -1.631841 | 0.014056 | 0.046043 | 0.027599 |
| dre02010 | ABC transporters | 33 | -0.512754 | -1.634613 | 0.014344 | 0.046043 | 0.027599 |
| dre00500 | Starch and sucrose metabolism | 37 | -0.515282 | -1.681186 | 0.008475 | 0.033479 | 0.020068 |
| dre00360 | Phenylalanine metabolism | 16 | -0.626265 | -1.681899 | 0.008547 | 0.033479 | 0.020068 |
| dre00410 | beta-Alanine metabolism | 31 | -0.537849 | -1.708086 | 0.010288 | 0.038986 | 0.023369 |
| dre01210 | 2-Oxocarboxylic acid metabolism | 16 | -0.623669 | -1.714402 | 0.010571 | 0.039031 | 0.023396 |
| dre00983 | Drug metabolism - other enzymes | 32 | -0.540721 | -1.726048 | 0.004057 | 0.020864 | 0.012506 |
| dre00340 | Histidine metabolism | 23 | -0.621031 | -1.832182 | 0.005780 | 0.026851 | 0.016095 |
| dre00830 | Retinol metabolism | 37 | -0.569270 | -1.882598 | 0.002119 | 0.014101 | 0.008452 |
| dre00350 | Tyrosine metabolism | 30 | -0.615109 | -1.925633 | 0.002212 | 0.014101 | 0.008452 |
| dre00380 | Tryptophan metabolism | 47 | -0.576394 | -2.018140 | 0.002252 | 0.014101 | 0.008452 |
| dre04744 | Phototransduction | 31 | -0.679337 | -2.127648 | 0.002110 | 0.014101 | 0.008452 |