

Table S3. Gene set enrichment analysis of the core molecular Reactome pathways related to the expression of LMNA in GBM patients from TCGA RNASeq data.

| NAME | GS follow link to MSigDB | SIZE | ES | NES | NOM p-val | FDR q-val | FWER p-val | RANK AT MAX | LEADING EDGE |
|---|---|------|------------|------------|-----------|-------------|------------|-------------|----------------------------------|
| REACTOME_RUNX3 REGULATES RUNX1-MEDIATED | REACTOME_RUNX3 REGULATES RUNX1-MEDIATED TRANSCRIPTION | 3 | 0.9241453 | 0.9241453 | 0 | 0.051445175 | 0.038 | 3716 | tags=100%, list=8%, signal=108% |
| REACTOME_LOCALIZATION OF THE PINCH-ILK-PARVIN COMPLEX TO FOCAL ADHESIONS | REACTOME_LOCALIZATION OF THE PINCH-ILK-PARVIN COMPLEX TO FOCAL ADHESIONS | 4 | 0.9207737 | 0.9207737 | 0 | 0.02892474 | 0.043 | 3882 | tags=100%, list=8%, signal=109% |
| REACTOME_LACTOSE | REACTOME_LACTOSE SYNTHESIS | 3 | 0.8843185 | 0.8843185 | 9.88E-04 | 0.0647311 | 0.1425 | 5666 | tags=100%, list=12%, signal=113% |
| REACTOME_NEUROPHILIN INTERACTIONS WITH VEGF AND VEGFR | REACTOME_NEUROPHILIN INTERACTIONS WITH VEGF AND VEGFR | 4 | 0.86562777 | 0.86562777 | 9.77E-04 | 0.07358983 | 0.2075 | 6582 | tags=100%, list=13%, signal=116% |
| REACTOME_INTERCONVERSION OF POLYAMINES | REACTOME_INTERCONVERSION OF POLYAMINES | 3 | 0.84733063 | 0.84733063 | 0.0071795 | 0.08763774 | 0.2865 | 7477 | tags=100%, list=15%, signal=118% |
| REACTOME_LYSOSOMAL OLIGOSACCHARIDE CATABOLISM | REACTOME_LYSOSOMAL OLIGOSACCHARIDE CATABOLISM | 4 | 0.8390147 | 0.8390147 | 0.0029851 | 0.08392301 | 0.3245 | 7885 | tags=100%, list=16%, signal=119% |
| REACTOME_MET ACTIVATES | REACTOME_MET ACTIVATES STAT3 | 3 | 0.8215555 | 0.8215555 | 0.0077369 | 0.1000432 | 0.4235 | 8739 | tags=100%, list=18%, signal=122% |
| REACTOME_PTK6 ACTIVATES | REACTOME_PTK6 ACTIVATES STAT3 | 4 | 0.80690753 | 0.80690753 | 9.93E-04 | 0.11036967 | 0.507 | 9457 | tags=100%, list=19%, signal=124% |
| REACTOME_PTK6 DOWN-REGULATION | REACTOME_PTK6 DOWN-REGULATION | 3 | 0.8068911 | 0.8068911 | 0.0101317 | 0.09810638 | 0.5075 | 9457 | tags=100%, list=19%, signal=124% |
| REACTOME_CASP8 ACTIVITY IS INHIBITED | REACTOME_CASP8 ACTIVITY IS INHIBITED | 11 | 0.7955558 | 0.7955558 | 0 | 0.106128596 | 0.5765 | 5567 | tags=91%, list=11%, signal=103% |
| REACTOME_DIMERIZATION OF PROCASPASE-8 | REACTOME_DIMERIZATION OF PROCASPASE-8 | 11 | 0.7955558 | 0.7955558 | 0 | 0.09648054 | 0.5765 | 5567 | tags=91%, list=11%, signal=103% |
| REACTOME_REGULATION BY C-FLIP | REACTOME_REGULATION BY C-FLIP | 11 | 0.7955558 | 0.7955558 | 0 | 0.0884405 | 0.5765 | 5567 | tags=91%, list=11%, signal=103% |
| REACTOME_CROSSLINKING OF COLLAGEN FIBRILS | REACTOME_CROSSLINKING OF COLLAGEN FIBRILS | 10 | 0.77763253 | 0.77763253 | 0 | 0.10739531 | 0.679 | 1102 | tags=80%, list=2%, signal=82% |
| REACTOME_RUNX3 REGULATES CDKN1A TRANSCRIPTION | REACTOME_RUNX3 REGULATES CDKN1A TRANSCRIPTION | 7 | 0.7736836 | 0.7736836 | 0 | 0.10527642 | 0.697 | 4091 | tags=86%, list=8%, signal=94% |
| REACTOME_LAMININ | REACTOME_LAMININ INTERACTIONS | 23 | 0.7646043 | 0.7646043 | 0 | 0.11314367 | 0.7425 | 5156 | tags=87%, list=11%, signal=97% |
| REACTOME_ANTAGONISM OF ACTIVIN BY FOLLISTATIN | REACTOME_ANTAGONISM OF ACTIVIN BY FOLLISTATIN | 4 | 0.74794227 | 0.74794227 | 0.0059821 | 0.13218437 | 0.818 | 12344 | tags=100%, list=25%, signal=134% |
| REACTOME_INVADOPODIA FORMATION | REACTOME_INVADOPODIA FORMATION | 4 | 0.7467372 | 0.7467372 | 0.0069307 | 0.12705012 | 0.8245 | 12403 | tags=100%, list=25%, signal=134% |
| REACTOME_PLCG1 EVENTS IN ERBB2 SIGNALING | REACTOME_PLCG1 EVENTS IN ERBB2 SIGNALING | 4 | 0.7436531 | 0.7436531 | 0.0060484 | 0.124367744 | 0.836 | 12554 | tags=100%, list=26%, signal=134% |
| REACTOME_REGULATION OF CYTOSKELETAL REMODELING AND CELL SPREADING BY IPP COMPLEX COMPONENTS | REACTOME_REGULATION OF CYTOSKELETAL REMODELING AND CELL SPREADING BY IPP COMPLEX COMPONENTS | 8 | 0.73836225 | 0.73836225 | 0.001006 | 0.12615298 | 0.85 | 12816 | tags=100%, list=26%, signal=135% |
| REACTOME_CELL-EXTRACELLULAR MATRIX INTERACTIONS | REACTOME_CELL-EXTRACELLULAR MATRIX INTERACTIONS | 16 | 0.73343813 | 0.73343813 | 0 | 0.12777638 | 0.8645 | 3882 | tags=81%, list=8%, signal=88% |
| REACTOME_DEFECTIVE LFNG CAUSES SCDO3 | REACTOME_DEFECTIVE LFNG CAUSES SCDO3 | 4 | 0.73131675 | 0.73131675 | 0.0130916 | 0.12502472 | 0.873 | 13158 | tags=100%, list=27%, signal=137% |
| REACTOME_FORMATION OF THE ACTIVE COFACTOR, UDP-GLUCURONATE | REACTOME_FORMATION OF THE ACTIVE COFACTOR, UDP-GLUCURONATE | 3 | 0.7302398 | 0.7302398 | 0.0346275 | 0.120628394 | 0.8755 | 13210 | tags=100%, list=27%, signal=137% |
| REACTOME_IKBKG DEFICIENCY CAUSES ANHIDROTIC ECTODERMAL DYSPLASIA WITH IMMUNODEFICIENCY (EDA-ID) (VIA TLR) | REACTOME_IKBKG DEFICIENCY CAUSES ANHIDROTIC ECTODERMAL DYSPLASIA WITH IMMUNODEFICIENCY (EDA-ID) (VIA TLR) | 8 | 0.7179438 | 0.7179438 | 0 | 0.13657485 | 0.915 | 7695 | tags=88%, list=16%, signal=104% |

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|--|--|----|------------|------------|-----------|------------|--------|--|
| REACTOME_ANTIGEN PRESENTATION: FOLDING, ASSEMBLY AND PEPTIDE LOADING OF CLASS I MHC | REACTOME_ANTIGEN PRESENTATION: FOLDING, ASSEMBLY AND PEPTIDE LOADING OF CLASS I MHC | 25 | 0.7178913 | 0.7178913 | 0 | 0.13088423 | 0.915 | 5996 tags=84%, list=12%, signal=96% |
| REACTOME_STAT6-MEDIATED INDUCTION OF CHEMOKINES | REACTOME_STAT6-MEDIATED INDUCTION OF CHEMOKINES | 3 | 0.715943 | 0.715943 | 0.0528893 | 0.12870412 | 0.9195 | 13910 tags=100%, list=28%, signal=140% |
| REACTOME_THE ACTIVATION OF ARYLSULFATASES | REACTOME_THE ACTIVATION OF ARYLSULFATASES | 13 | 0.7044138 | 0.7044138 | 0 | 0.1420604 | 0.949 | 10715 tags=92%, list=22%, signal=118% |
| REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 T(7;9)(NOTCH1:M1580_K2555) | REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 T(7;9)(NOTCH1:M1580_K2555) | 7 | 0.70260227 | 0.70260227 | 0.0019841 | 0.13984948 | 0.953 | 7571 tags=86%, list=15%, signal=101% |
| TRANSLOCATION MUTANT REACTOME_SIGNALING BY NOTCH1 T(7;9)(NOTCH1:M1580_K2555) | TRANSLOCATION MUTANT REACTOME_SIGNALING BY NOTCH1 T(7;9)(NOTCH1:M1580_K2555) | 7 | 0.70260227 | 0.70260227 | 0 | 0.13485484 | 0.953 | 7571 tags=86%, list=15%, signal=101% |
| REACTOME_IRS ACTIVATION | REACTOME_IRS ACTIVATION | 5 | 0.70194036 | 0.70194036 | 0.0048077 | 0.13139956 | 0.9545 | 4804 tags=80%, list=10%, signal=89% |
| REACTOME_IKBA VARIANT LEADS TO EDA-ID | REACTOME_IKBA VARIANT LEADS TO EDA-ID | 7 | 0.7000695 | 0.7000695 | 0 | 0.12995693 | 0.957 | 7695 tags=86%, list=16%, signal=102% |
| REACTOME_OXYGEN-DEPENDENT ASPARAGINE HYDROXYLATION OF HYPOXIA-INDUCIBLE FACTOR ALPHA | REACTOME_OXYGEN-DEPENDENT ASPARAGINE HYDROXYLATION OF HYPOXIA-INDUCIBLE FACTOR ALPHA | 3 | 0.6993587 | 0.6993587 | 0.0549451 | 0.12683098 | 0.9585 | 14722 tags=100%, list=30%, signal=143% |
| REACTOME_AMINE OXIDASE REACTIONS | REACTOME_AMINE OXIDASE REACTIONS | 4 | 0.69797903 | 0.69797903 | 0.0107422 | 0.12487799 | 0.9635 | 2549 tags=75%, list=5%, signal=79% |
| REACTOME_HYALURONAN BIOSYNTHESIS AND EXPORT | REACTOME_HYALURONAN BIOSYNTHESIS AND EXPORT | 5 | 0.69321895 | 0.69321895 | 0.0029383 | 0.12848996 | 0.9695 | 5231 tags=80%, list=11%, signal=90% |
| REACTOME_MET ACTIVATES PTK2 SIGNALING | REACTOME_MET ACTIVATES PTK2 SIGNALING | 18 | 0.6924201 | 0.6924201 | 0 | 0.12614985 | 0.97 | 4191 tags=78%, list=9%, signal=85% |
| REACTOME_NOSTRIN MEDIATED ENOS TRAFFICKING | REACTOME_NOSTRIN MEDIATED ENOS TRAFFICKING | 5 | 0.68703026 | 0.68703026 | 0.0047893 | 0.1307439 | 0.977 | 5534 tags=80%, list=11%, signal=90% |
| REACTOME_FASL/ CD95L | REACTOME_FASL/ CD95L SIGNALING | 5 | 0.68635625 | 0.68635625 | 0.0121827 | 0.12802182 | 0.977 | 5567 tags=80%, list=11%, signal=90% |
| REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN DIFFERENTIATION OF MYELOID CELLS | REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN DIFFERENTIATION OF MYELOID CELLS | 7 | 0.6803587 | 0.6803587 | 0 | 0.1328533 | 0.983 | 8660 tags=86%, list=18%, signal=104% |
| REACTOME_ADENOSINE P1 RECEPTORS | REACTOME_ADENOSINE P1 RECEPTORS | 3 | 0.6795066 | 0.6795066 | 0.049904 | 0.1306613 | 0.983 | 15694 tags=100%, list=32%, signal=147% |
| REACTOME_TRAIL SIGNALING | REACTOME_TRAIL SIGNALING | 7 | 0.67476207 | 0.67476207 | 0.0019802 | 0.13421275 | 0.986 | 1939 tags=71%, list=4%, signal=74% |
| REACTOME_REGULATION OF NECROPTOTIC CELL DEATH | REACTOME_REGULATION OF NECROPTOTIC CELL DEATH | 14 | 0.67219263 | 0.67219263 | 0 | 0.13481751 | 0.987 | 5567 tags=79%, list=11%, signal=89% |
| REACTOME_CLEC7A/INFLAMMASOME PATHWAY | REACTOME_CLEC7A/INFLAMMASOME PATHWAY | 6 | 0.6712964 | 0.6712964 | 0.0059055 | 0.13298735 | 0.9875 | 16098 tags=100%, list=33%, signal=149% |
| REACTOME_ACTIVATION OF REACTOME_BINDING AND ENTRY OF HIV VIRION | REACTOME_ACTIVATION OF AKT2 REACTOME_BINDING AND ENTRY OF HIV VIRION | 4 | 0.65484774 | 0.65484774 | 0.0451354 | 0.15667795 | 0.9935 | 16902 tags=100%, list=35%, signal=153% |
| REACTOME_METAL SEQUESTRATION BY | REACTOME_BINDING AND ENTRY OF HIV VIRION | 4 | 0.6531525 | 0.6531525 | 0.0403226 | 0.15615384 | 0.994 | 16985 tags=100%, list=35%, signal=153% |
| REACTOME_LIGAND-DEPENDENT CASPASE ACTIVATION | REACTOME_METAL SEQUESTRATION BY ANTIMICROBIAL PROTEINS | 6 | 0.6523418 | 0.6523418 | 0.0020492 | 0.15409464 | 0.994 | 17026 tags=100%, list=35%, signal=153% |
| REACTOME_CHL1 | REACTOME_LIGAND-DEPENDENT CASPASE ACTIVATION | 17 | 0.6512181 | 0.6512181 | 0 | 0.15266374 | 0.996 | 5567 tags=76%, list=11%, signal=86% |
| REACTOME_HDL ASSEMBLY | REACTOME_CHL1 INTERACTIONS | 9 | 0.6474771 | 0.6474771 | 0 | 0.15614267 | 0.9965 | 6385 tags=78%, list=13%, signal=89% |
| REACTOME_RUNX1 AND FOXP3 CONTROL THE DEVELOPMENT OF REGULATORY T LYMPHOCYTES (TREGS) | REACTOME_HDL ASSEMBLY | 8 | 0.64580655 | 0.64580655 | 9.90E-04 | 0.15592112 | 0.9965 | 5106 tags=75%, list=10%, signal=84% |
| | REACTOME_RUNX1 AND FOXP3 CONTROL THE DEVELOPMENT OF REGULATORY T LYMPHOCYTES (TREGS) | 10 | 0.64033294 | 0.64033294 | 0 | 0.16375242 | 0.997 | 12720 tags=90%, list=26%, signal=122% |

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|---|---|----|------------|------------|-----------|------------|--------|--|
| REACTOME_TRAF3 DEFICIENCY - HSE | REACTOME_TRAF3 DEFICIENCY - HSE | 3 | 0.63974786 | 0.63974786 | 0.0913605 | 0.16140738 | 0.997 | 1319 tags=67%, list=3%, signal=69% |
| REACTOME_SODIUM-COUPLED PHOSPHATE COTRANSPORTERS | REACTOME_SODIUM-COUPLED PHOSPHATE COTRANSPORTERS | 5 | 0.63713235 | 0.63713235 | 0.0238342 | 0.1635468 | 0.9975 | 7977 tags=80%, list=16%, signal=96% |
| REACTOME_PYRIMIDINE BIOSYNTHESIS | REACTOME_PYRIMIDINE BIOSYNTHESIS | 3 | 0.6349414 | 0.6349414 | 0.0907217 | 0.16457468 | 0.9985 | 17876 tags=100%, list=37%, signal=157% |
| REACTOME_RIPK1-MEDIATED REGULATED NECROSIS | REACTOME_RIPK1-MEDIATED REGULATED NECROSIS | 16 | 0.63081473 | 0.63081473 | 0 | 0.16914149 | 0.999 | 5845 tags=75%, list=12%, signal=85% |
| REACTOME_REGULATED NECROSIS | REACTOME_REGULATED NECROSIS | 16 | 0.63081473 | 0.63081473 | 0 | 0.16595013 | 0.999 | 5845 tags=75%, list=12%, signal=85% |
| REACTOME_LOSS OF FUNCTION OF TGFB2 IN CANCER | REACTOME_LOSS OF FUNCTION OF TGFB2 IN CANCER | 4 | 0.6308031 | 0.6308031 | 0.0448654 | 0.16290064 | 0.999 | 5838 tags=75%, list=12%, signal=85% |
| REACTOME_TGFB1 LBD MUTANTS IN CANCER | REACTOME_TGFB1 LBD MUTANTS IN CANCER | 4 | 0.6308031 | 0.6308031 | 0.0469208 | 0.1599388 | 0.999 | 5838 tags=75%, list=12%, signal=85% |
| REACTOME_TGFB2 KINASE DOMAIN MUTANTS IN CANCER | REACTOME_TGFB2 KINASE DOMAIN MUTANTS IN CANCER | 4 | 0.6308031 | 0.6308031 | 0.0398366 | 0.15708275 | 0.999 | 5838 tags=75%, list=12%, signal=85% |
| REACTOME_ALTERNATIVE COMPLEMENT ACTIVATION | REACTOME_ALTERNATIVE COMPLEMENT ACTIVATION | 4 | 0.6290926 | 0.6290926 | 0.0443996 | 0.15764348 | 0.999 | 18163 tags=100%, list=37%, signal=159% |
| REACTOME_ANCHORING FIBRIL FORMATION | REACTOME_ANCHORING FIBRIL FORMATION | 7 | 0.62876344 | 0.62876344 | 0.004065 | 0.15565756 | 0.999 | 4191 tags=71%, list=9%, signal=78% |
| REACTOME_TYPE II NA+/PI COTRANSPORTERS | REACTOME_TYPE II NA+/PI COTRANSPORTERS | 3 | 0.6280381 | 0.6280381 | 0.123108 | 0.15419634 | 1 | 18214 tags=100%, list=37%, signal=159% |
| REACTOME_ENDOSOMAL/VACUOLAR PATHWAY | REACTOME_ENDOSOMAL/VACUOLAR PATHWAY | 12 | 0.62767863 | 0.62767863 | 0 | 0.15198812 | 1 | 5996 tags=75%, list=12%, signal=85% |
| REACTOME_SYNTHESIS OF PI | REACTOME_SYNTHESIS OF PI | 5 | 0.6264502 | 0.6264502 | 0.0172589 | 0.15180609 | 1 | 8500 tags=80%, list=17%, signal=97% |
| REACTOME_TNFR1-INDUCED PROAPOPTOTIC SIGNALING | REACTOME_TNFR1-INDUCED PROAPOPTOTIC SIGNALING | 13 | 0.624538 | 0.624538 | 0 | 0.15284513 | 1 | 7092 tags=77%, list=14%, signal=90% |
| REACTOME_MET INTERACTS WITH TNS PROTEINS | REACTOME_MET INTERACTS WITH TNS PROTEINS | 5 | 0.6215686 | 0.6215686 | 0.0184426 | 0.15609622 | 1 | 8739 tags=80%, list=18%, signal=97% |
| REACTOME_ARL13B-MEDIATED CILIARY TRAFFICKING OF INPP5E | REACTOME_ARL13B-MEDIATED CILIARY TRAFFICKING OF INPP5E | 3 | 0.6188541 | 0.6188541 | 0.1215686 | 0.15885086 | 1 | 2342 tags=67%, list=5%, signal=70% |
| REACTOME_NR1D1 (REV-ERBA) REPRESSES GENE EXPRESSION | REACTOME_NR1D1 (REV-ERBA) REPRESSES GENE EXPRESSION | 8 | 0.6187675 | 0.6187675 | 0 | 0.15658432 | 1 | 18671 tags=100%, list=38%, signal=162% |
| REACTOME_HHAT G278V ABROGATES PALMITOYLATION OF HH-NP | REACTOME_HHAT G278V ABROGATES PALMITOYLATION OF HH-NP | 3 | 0.61873156 | 0.61873156 | 0.1261445 | 0.15427974 | 1 | 2348 tags=67%, list=5%, signal=70% |
| REACTOME_PTK6 EXPRESSION | REACTOME_PTK6 EXPRESSION | 5 | 0.6069036 | 0.6069036 | 0.031 | 0.1740238 | 1 | 9457 tags=80%, list=19%, signal=99% |
| REACTOME_DEFECTIVE MISMATCH REPAIR ASSOCIATED | REACTOME_DEFECTIVE MISMATCH REPAIR ASSOCIATED WITH MSH2 | 3 | 0.5979331 | 0.5979331 | 0.1539225 | 0.1910249 | 1 | 19688 tags=100%, list=40%, signal=167% |
| REACTOME_SIGNALING BY NOTCH3 | REACTOME_SIGNALING BY NOTCH3 | 11 | 0.59792686 | 0.59792686 | 0 | 0.18826577 | 1 | 6339 tags=73%, list=13%, signal=84% |
| REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN WNT SIGNALING | REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN WNT SIGNALING | 6 | 0.5890507 | 0.5890507 | 0.0204082 | 0.20564455 | 1 | 3803 tags=67%, list=8%, signal=72% |
| REACTOME_CASPASE-MEDIATED CLEAVAGE OF CYTOSKELETAL PROTEINS | REACTOME_CASPASE-MEDIATED CLEAVAGE OF CYTOSKELETAL PROTEINS | 12 | 0.58889824 | 0.58889824 | 0 | 0.2031457 | 1 | 3814 tags=67%, list=8%, signal=72% |
| REACTOME_TNF RECEPTOR SUPERFAMILY (TNFSF) MEMBERS MEDIATING NON-CANONICAL NF-KB PATHWAY | REACTOME_TNF RECEPTOR SUPERFAMILY (TNFSF) MEMBERS MEDIATING NON-CANONICAL NF-KB PATHWAY | 17 | 0.58883977 | 0.58883977 | 0 | 0.200477 | 1 | 5740 tags=71%, list=12%, signal=80% |
| REACTOME_ACTIVATION OF C3 AND C5 | REACTOME_ACTIVATION OF C3 AND C5 | 6 | 0.5861231 | 0.5861231 | 0.0172239 | 0.20382991 | 1 | 20268 tags=100%, list=41%, signal=171% |
| REACTOME_MITOCHONDRIAL ABC TRANSPORTERS | REACTOME_MITOCHONDRIAL ABC TRANSPORTERS | 4 | 0.58360225 | 0.58360225 | 0.0777454 | 0.2070922 | 1 | 8149 tags=75%, list=17%, signal=90% |
| REACTOME_TYPE I HEMIDESMOSOME ASSEMBLY | REACTOME_TYPE I HEMIDESMOSOME ASSEMBLY | 9 | 0.5811613 | 0.5811613 | 0.0019084 | 0.21058372 | 1 | 4191 tags=67%, list=9%, signal=73% |

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|--|--|----|------------|------------|-----------|------------|---|--|
| REACTOME DISSOLUTION OF FIBRIN CLOT | REACTOME DISSOLUTION OF FIBRIN CLOT | 13 | 0.5776538 | 0.5776538 | 0 | 0.21647505 | 1 | 1854 tags=62%, list=4%, signal=64% |
| REACTOME_TRAF3-DEPENDENT IRF ACTIVATION PATHWAY | REACTOME_TRAF3-DEPENDENT IRF ACTIVATION PATHWAY | 14 | 0.5732059 | 0.5732059 | 0 | 0.22429603 | 1 | 13910 tags=86%, list=28%, signal=120% |
| REACTOME_HDL CLEARANCE | REACTOME_HDL CLEARANCE | 5 | 0.57148695 | 0.57148695 | 0.0432161 | 0.2257464 | 1 | 11191 tags=80%, list=23%, signal=104% |
| REACTOME_SYNTHESIS OF GDP-MANNOSE | REACTOME_SYNTHESIS OF GDP-MANNOSE | 5 | 0.5700163 | 0.5700163 | 0.0406674 | 0.22646251 | 1 | 11263 tags=80%, list=23%, signal=104% |
| REACTOME_PRE-NOTCH PROCESSING IN THE ENDOPLASMIC RETICULUM | REACTOME_PRE-NOTCH PROCESSING IN THE ENDOPLASMIC RETICULUM | 6 | 0.5646596 | 0.5646596 | 0.0179641 | 0.23712938 | 1 | 13158 tags=83%, list=27%, signal=114% |
| REACTOME_GLI PROTEINS BIND PROMOTERS OF HH RESPONSIVE GENES TO PROMOTE TRANSCRIPTION | REACTOME_GLI PROTEINS BIND PROMOTERS OF HH RESPONSIVE GENES TO PROMOTE TRANSCRIPTION | 7 | 0.56160384 | 0.56160384 | 0.0114504 | 0.242047 | 1 | 7479 tags=71%, list=15%, signal=84% |
| REACTOME_NEF MEDIATED DOWNREGULATION OF MHC CLASS I COMPLEX CELL SURFACE EXPRESSION | REACTOME_NEF MEDIATED DOWNREGULATION OF MHC CLASS I COMPLEX CELL SURFACE EXPRESSION | 10 | 0.55749154 | 0.55749154 | 0.005 | 0.24987137 | 1 | 21672 tags=100%, list=44%, signal=179% |
| REACTOME_METABOLISM OF VITAMIN K | REACTOME_METABOLISM OF VITAMIN K | 3 | 0.5545389 | 0.5545389 | 0.2009756 | 0.2545208 | 1 | 5491 tags=67%, list=11%, signal=75% |
| REACTOME_GALACTOSE CATABOLISM | REACTOME_GALACTOSE CATABOLISM | 6 | 0.55103934 | 0.55103934 | 0.0288557 | 0.26059273 | 1 | 5664 tags=67%, list=12%, signal=75% |
| REACTOME_LRR FLII-INTERACTING PROTEIN 1 (LRRFIP1) ACTIVATES TYPE I IFN | REACTOME_LRR FLII-INTERACTING PROTEIN 1 (LRRFIP1) ACTIVATES TYPE I IFN PRODUCTION | 5 | 0.55085784 | 0.55085784 | 0.0669331 | 0.25799718 | 1 | 12201 tags=80%, list=25%, signal=107% |
| REACTOME_PLATELET ADHESION TO EXPOSED | REACTOME_PLATELET ADHESION TO EXPOSED COLLAGEN | 12 | 0.55040044 | 0.55040044 | 0 | 0.25621033 | 1 | 9779 tags=75%, list=20%, signal=94% |
| REACTOME_HS-GAG | REACTOME_HS-GAG DEGRADATION | 21 | 0.5494715 | 0.5494715 | 0 | 0.25570154 | 1 | 5749 tags=67%, list=12%, signal=76% |
| REACTOME_CHOLESTEROL BIOSYNTHESIS VIA | REACTOME_CHOLESTEROL BIOSYNTHESIS VIA DESMOSTEROL | 4 | 0.5477574 | 0.5477574 | 0.1232742 | 0.25694463 | 1 | 9904 tags=75%, list=20%, signal=94% |
| REACTOME_CHOLESTEROL BIOSYNTHESIS VIA | REACTOME_CHOLESTEROL BIOSYNTHESIS VIA LATHOSTEROL | 4 | 0.5477574 | 0.5477574 | 0.1436059 | 0.25405762 | 1 | 9904 tags=75%, list=20%, signal=94% |
| REACTOME_INSULIN-LIKE GROWTH FACTOR-2 MRNA BINDING PROTEINS | REACTOME_INSULIN-LIKE GROWTH FACTOR-2 MRNA BINDING PROTEINS (IGF2BPS/IMPS/VICKZS) BIND RNA | 8 | 0.5475366 | 0.5475366 | 0.0091185 | 0.25185776 | 1 | 9917 tags=75%, list=20%, signal=94% |
| REACTOME_VEGF BINDS TO VEGFR LEADING TO RECEPTOR DIMERIZATION | REACTOME_VEGF BINDS TO VEGFR LEADING TO RECEPTOR DIMERIZATION | 8 | 0.5467936 | 0.5467936 | 0.014 | 0.2509417 | 1 | 16074 tags=88%, list=33%, signal=130% |
| REACTOME_VEGF LIGAND-RECEPTOR INTERACTIONS | REACTOME_VEGF LIGAND-RECEPTOR INTERACTIONS | 8 | 0.5467936 | 0.5467936 | 0.007913 | 0.24821408 | 1 | 16074 tags=88%, list=33%, signal=130% |
| REACTOME_SEMA3A-PLEXIN REPULSION SIGNALING BY INHIBITING INTEGRIN ADHESION | REACTOME_SEMA3A-PLEXIN REPULSION SIGNALING BY INHIBITING INTEGRIN ADHESION | 14 | 0.5464138 | 0.5464138 | 0 | 0.2464687 | 1 | 4729 tags=64%, list=10%, signal=71% |
| REACTOME_CROSS-PRESENTATION OF PARTICULATE EXOGENOUS | REACTOME_CROSS-PRESENTATION OF PARTICULATE EXOGENOUS ANTIGENS (PHAGOSOMES) | 8 | 0.54639786 | 0.54639786 | 0.0151057 | 0.24391584 | 1 | 22214 tags=100%, list=45%, signal=183% |
| REACTOME_SYNTHESIS OF UDP-N-ACETYL-GLUCOSAMINE | REACTOME_SYNTHESIS OF UDP-N-ACETYL-GLUCOSAMINE | 8 | 0.54611444 | 0.54611444 | 0.0039254 | 0.2419243 | 1 | 3866 tags=63%, list=8%, signal=68% |
| REACTOME_NEGATIVE REGULATION OF TCF-DEPENDENT SIGNALING BY DVL- | REACTOME_NEGATIVE REGULATION OF TCF-DEPENDENT SIGNALING BY DVL-INTERACTING PROTEINS | 5 | 0.54405636 | 0.54405636 | 0.0705522 | 0.24472003 | 1 | 12534 tags=80%, list=26%, signal=108% |
| REACTOME_FIBRONECTIN MATRIX FORMATION | REACTOME_FIBRONECTIN MATRIX FORMATION | 6 | 0.5421918 | 0.5421918 | 0.0223124 | 0.24713701 | 1 | 14258 tags=83%, list=29%, signal=118% |
| REACTOME_PLC-MEDIATED HYDROLYSIS OF PIP2 | REACTOME_PLC-MEDIATED HYDROLYSIS OF PIP2 | 4 | 0.5387758 | 0.5387758 | 0.1233831 | 0.25350112 | 1 | 22585 tags=100%, list=46%, signal=186% |

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|--|--|----|------------|------------|-----------|------------|---|--|
| REACTOME_FORMATION OF ANNULAR GAP JUNCTIONS | REACTOME_FORMATION OF ANNULAR GAP JUNCTIONS | 9 | 0.53672457 | 0.53672457 | 0.0050505 | 0.25611737 | 1 | 11807 tags=78%, list=24%, signal=102% |
| REACTOME_METALLOTHIONEINS BIND METALS | REACTOME_METALLOTHIONEINS BIND METALS | 11 | 0.5354062 | 0.5354062 | 0.001001 | 0.2569884 | 1 | 13851 tags=82%, list=28%, signal=114% |
| REACTOME_DEFECTIVE AVP CAUSES NEUROHYPOPHYSEAL DIABETES INSIPIDUS (NDI) | REACTOME_DEFECTIVE AVP CAUSES NEUROHYPOPHYSEAL DIABETES INSIPIDUS (NDI) | 4 | 0.53348076 | 0.53348076 | 0.1166501 | 0.25966275 | 1 | 10603 tags=75%, list=22%, signal=96% |
| REACTOME_CONDENSATION OF PROMETAPHASE | REACTOME_CONDENSATION OF PROMETAPHASE CHROMOSOMES | 11 | 0.5330515 | 0.5330515 | 0.002994 | 0.25841528 | 1 | 22869 tags=100%, list=47%, signal=188% |
| REACTOME_INTERLEUKIN-15 SIGNALING | REACTOME_INTERLEUKIN-15 SIGNALING | 6 | 0.5321868 | 0.5321868 | 0.0308642 | 0.25833377 | 1 | 6587 tags=67%, list=13%, signal=77% |
| REACTOME_COLLAGEN | REACTOME_COLLAGEN FORMATION | 90 | 0.53166467 | 0.53166467 | 0 | 0.25711486 | 1 | 4481 tags=62%, list=9%, signal=68% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF DEATH RECEPTORS AND LIGANDS | REACTOME_TP53 REGULATES TRANSCRIPTION OF DEATH RECEPTORS AND LIGANDS | 12 | 0.5314809 | 0.5314809 | 0.0020182 | 0.25517616 | 1 | 18866 tags=92%, list=39%, signal=149% |
| REACTOME_COLLAGEN BIOSYNTHESIS AND MODIFYING ENZYMES | REACTOME_COLLAGEN BIOSYNTHESIS AND MODIFYING ENZYMES | 67 | 0.5308604 | 0.5308604 | 0 | 0.25447845 | 1 | 2543 tags=58%, list=5%, signal=61% |
| REACTOME_SCAVENGING BY CLASS F RECEPTORS | REACTOME_SCAVENGING BY CLASS F RECEPTORS | 6 | 0.5283026 | 0.5283026 | 0.0575968 | 0.25876683 | 1 | 14938 tags=83%, list=31%, signal=120% |
| REACTOME_SYNDECAN INTERACTIONS | REACTOME_SYNDECAN INTERACTIONS | 20 | 0.5274083 | 0.5274083 | 0 | 0.2586908 | 1 | 13357 tags=80%, list=27%, signal=110% |
| REACTOME_FGFR1C AND KLOTHO LIGAND BINDING AND | REACTOME_FGFR1C AND KLOTHO LIGAND BINDING AND ACTIVATION | 3 | 0.52694607 | 0.52694607 | 0.2763819 | 0.25742516 | 1 | 6842 tags=67%, list=14%, signal=77% |
| REACTOME_ELASTIC FIBRE FORMATION | REACTOME_ELASTIC FIBRE FORMATION | 41 | 0.5242985 | 0.5242985 | 0 | 0.26189452 | 1 | 8982 tags=71%, list=18%, signal=87% |
| REACTOME_HYALURONAN METABOLISM | REACTOME_HYALURONAN METABOLISM | 17 | 0.5231783 | 0.5231783 | 0 | 0.26245642 | 1 | 8954 tags=71%, list=18%, signal=86% |
| REACTOME_TERMINAL PATHWAY OF COMPLEMENT | REACTOME_TERMINAL PATHWAY OF COMPLEMENT | 8 | 0.5227113 | 0.5227113 | 0.0132248 | 0.26135218 | 1 | 17253 tags=88%, list=35%, signal=135% |
| REACTOME_NF-KB ACTIVATION THROUGH FADD/RIP-1 PATHWAY MEDIATED BY CASPASE-8 AND -10 | REACTOME_NF-KB ACTIVATION THROUGH FADD/RIP-1 PATHWAY MEDIATED BY CASPASE-8 AND -10 | 12 | 0.52174366 | 0.52174366 | 0 | 0.26158696 | 1 | 3021 tags=58%, list=6%, signal=62% |
| REACTOME_COLLAGEN DEGRADATION | REACTOME_COLLAGEN DEGRADATION | 40 | 0.52101433 | 0.52101433 | 0 | 0.2612079 | 1 | 10008 tags=73%, list=20%, signal=91% |
| REACTOME_SYNTHESIS OF LIPOXINS (LX) | REACTOME_SYNTHESIS OF LIPOXINS (LX) | 6 | 0.5184985 | 0.5184985 | 0.0504032 | 0.26547706 | 1 | 15418 tags=83%, list=31%, signal=122% |
| REACTOME_TRIF-MEDIATED PROGRAMMED CELL DEATH | REACTOME_TRIF-MEDIATED PROGRAMMED CELL DEATH | 10 | 0.517414 | 0.517414 | 0.0042328 | 0.26614916 | 1 | 4048 tags=60%, list=8%, signal=65% |
| REACTOME_ASSEMBLY OF COLLAGEN FIBRILS AND OTHER MULTIMERIC STRUCTURES | REACTOME_ASSEMBLY OF COLLAGEN FIBRILS AND OTHER MULTIMERIC STRUCTURES | 58 | 0.51633745 | 0.51633745 | 0 | 0.26692992 | 1 | 6827 tags=66%, list=14%, signal=76% |
| REACTOME_SYNTHESIS OF DOLICHYL-PHOSPHATE | REACTOME_SYNTHESIS OF DOLICHYL-PHOSPHATE MANNOSE | 3 | 0.5123566 | 0.5123566 | 0.3123753 | 0.27516922 | 1 | 23878 tags=100%, list=49%, signal=195% |
| REACTOME_A THIRD PROTEOLYTIC CLEAVAGE RELEASES NICD | REACTOME_A THIRD PROTEOLYTIC CLEAVAGE RELEASES NICD | 9 | 0.5121197 | 0.5121197 | 0.0102145 | 0.27350482 | 1 | 7571 tags=67%, list=15%, signal=79% |
| REACTOME_NON-INTEGRIN MEMBRANE-ECM INTERACTIONS | REACTOME_NON-INTEGRIN MEMBRANE-ECM INTERACTIONS | 42 | 0.51006347 | 0.51006347 | 0 | 0.27676645 | 1 | 4191 tags=60%, list=9%, signal=65% |
| REACTOME_PHOSPHORYLATION OF EMI1 | REACTOME_PHOSPHORYLATION OF EMI1 | 6 | 0.50979394 | 0.50979394 | 0.0673171 | 0.2752341 | 1 | 24005 tags=100%, list=49%, signal=196% |
| REACTOME_HISTAMINE | REACTOME_HISTAMINE RECEPTORS | 4 | 0.50797063 | 0.50797063 | 0.1841564 | 0.27786925 | 1 | 11852 tags=75%, list=24%, signal=99% |
| REACTOME_SIGNALING BY PLASMA MEMBRANE FGFR1 | REACTOME_SIGNALING BY PLASMA MEMBRANE FGFR1 FUSIONS | 3 | 0.50768626 | 0.50768626 | 0.3306773 | 0.27645156 | 1 | 7785 tags=67%, list=16%, signal=79% |

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|--|---|----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_SIGNALING BY REACTOME_SIGNALLING TO REACTOME_NEF MEDIATED CD8 DOWN-REGULATION | REACTOME_SIGNALING BY NOTCH4 REACTOME_SIGNALLING TO STAT3 REACTOME_NEF MEDIATED CD8 DOWN- REGULATION | 11 | 0.5069973 | 0.5069973 | 0.0040984 | 0.2760106 | 1 | 6339 tags=64%, list=13%, signal=73% |
| REACTOME_OPTINEURIN AND MYOSIN PHOSPHATASE NEGATIVELY REGULATE PLK1 | REACTOME_OPTINEURIN AND MYOSIN PHOSPHATASE NEGATIVELY REGULATE PLK1 | 3 | 0.50548047 | 0.50548047 | 0.3212928 | 0.27801064 | 1 | 7893 tags=67%, list=16%, signal=79% |
| REACTOME_ACTIVATION OF PUMA AND TRANSLOCATION TO MITOCHONDRIA | REACTOME_ACTIVATION OF PUMA AND TRANSLOCATION TO MITOCHONDRIA | 7 | 0.5049022 | 0.5049022 | 0.0385376 | 0.2773282 | 1 | 10255 tags=71%, list=21%, signal=90% |
| REACTOME_SLC TRANSPORTER DISORDERS | REACTOME_SLC TRANSPORTER DISORDERS | 3 | 0.5048269 | 0.5048269 | 0.32999 | 0.27537686 | 1 | 7925 tags=67%, list=16%, signal=80% |
| REACTOME_NGF PROCESSING | REACTOME_NGF PROCESSING | 9 | 0.50366545 | 0.50366545 | 0.0129225 | 0.27637482 | 1 | 18866 tags=89%, list=39%, signal=145% |
| REACTOME_MOLECULES ASSOCIATED WITH ELASTIC FIBRES | REACTOME_MOLECULES ASSOCIATED WITH ELASTIC FIBRES | 7 | 0.49779406 | 0.49779406 | 0.0372984 | 0.29004017 | 1 | 10603 tags=71%, list=22%, signal=91% |
| REACTOME_GDP-FUCOSE BIOSYNTHESIS | REACTOME_GDP-FUCOSE BIOSYNTHESIS | 4 | 0.49562916 | 0.49562916 | 0.1957619 | 0.2937462 | 1 | 215 tags=50%, list=0%, signal=50% |
| REACTOME_RECEPTOR-LIGAND BINDING INITIATES THE SECOND PROTEOLYTIC CLEAVAGE OF NOTCH RECEPTOR | REACTOME_RECEPTOR-LIGAND BINDING INITIATES THE SECOND PROTEOLYTIC CLEAVAGE OF NOTCH RECEPTOR | 30 | 0.4947107 | 0.4947107 | 0 | 0.29394174 | 1 | 11698 tags=73%, list=24%, signal=96% |
| REACTOME_KERATAN SULFATE DEGRADATION | REACTOME_KERATAN SULFATE DEGRADATION | 6 | 0.48970228 | 0.48970228 | 0.0629302 | 0.3061298 | 1 | 8667 tags=67%, list=18%, signal=81% |
| REACTOME_PROGRESSIVE TRIMMING OF ALPHA-1,2-LINKED MANNOSE RESIDUES FROM MAN9/8/7GLCNAC2 TO PRODUCE MAN5GLCNAC2 | REACTOME_PROGRESSIVE TRIMMING OF ALPHA-1,2-LINKED MANNOSE RESIDUES FROM MAN9/8/7GLCNAC2 TO PRODUCE MAN5GLCNAC2 | 14 | 0.48835573 | 0.48835573 | 0.0029098 | 0.3076914 | 1 | 7571 tags=64%, list=15%, signal=76% |
| REACTOME_HYALURONAN UPTAKE AND DEGRADATION | REACTOME_HYALURONAN UPTAKE AND DEGRADATION | 12 | 0.48701647 | 0.48701647 | 0.0096339 | 0.30922753 | 1 | 4721 tags=58%, list=10%, signal=65% |
| REACTOME_TRANSPORT AND SYNTHESIS OF PAPS | REACTOME_TRANSPORT AND SYNTHESIS OF PAPS | 3 | 0.48683333 | 0.48683333 | 0.361658 | 0.3074705 | 1 | 8806 tags=67%, list=18%, signal=81% |
| REACTOME_WNT5A-DEPENDENT INTERNALIZATION OF FZD2, FZD5 AND ROR2 | REACTOME_WNT5A-DEPENDENT INTERNALIZATION OF FZD2, FZD5 AND ROR2 | 12 | 0.48389953 | 0.48389953 | 0.0039254 | 0.31397265 | 1 | 8954 tags=67%, list=18%, signal=82% |
| REACTOME_RUNX3 REGULATES YAP1-MEDIATED TRANSCRIPTION | REACTOME_RUNX3 REGULATES YAP1- MEDIATED TRANSCRIPTION | 6 | 0.48328537 | 0.48328537 | 0.0782953 | 0.31351948 | 1 | 17142 tags=83%, list=35%, signal=128% |
| REACTOME_REGULATED PROTEOLYSIS OF P75NTR | REACTOME_REGULATED PROTEOLYSIS OF P75NTR | 13 | 0.48140723 | 0.48140723 | 0.005 | 0.3170939 | 1 | 10332 tags=69%, list=21%, signal=88% |
| REACTOME_CASPASE ACTIVATION VIA EXTRINSIC APOPTOTIC SIGNALLING | REACTOME_CASPASE ACTIVATION VIA EXTRINSIC APOPTOTIC SIGNALLING PATHWAY | 22 | 0.48125094 | 0.48125094 | 0 | 0.31534016 | 1 | 5379 tags=59%, list=11%, signal=66% |
| REACTOME_REGULATION OF GENE EXPRESSION BY HYPOXIA- INDUCIBLE FACTOR | REACTOME_REGULATION OF GENE EXPRESSION BY HYPOXIA-INDUCIBLE FACTOR | 10 | 0.48055357 | 0.48055357 | 0.0119522 | 0.315104 | 1 | 10749 tags=70%, list=22%, signal=90% |
| REACTOME_MET PROMOTES CELL MOTILITY | REACTOME_MET PROMOTES CELL MOTILITY | 27 | 0.47914293 | 0.47914293 | 0 | 0.31696254 | 1 | 5567 tags=59%, list=11%, signal=67% |
| REACTOME_REGULATION OF TNFR1 SIGNALING | REACTOME_REGULATION OF TNFR1 SIGNALING | 11 | 0.47818175 | 0.47818175 | 0.0089374 | 0.31760788 | 1 | 12201 tags=73%, list=25%, signal=97% |
| REACTOME_TRANSPORT OF NUCLEOTIDE SUGARS | REACTOME_TRANSPORT OF NUCLEOTIDE SUGARS | 29 | 0.47696003 | 0.47696003 | 0 | 0.31914815 | 1 | 8739 tags=66%, list=18%, signal=80% |
| | | 33 | 0.4743138 | 0.4743138 | 0 | 0.32475746 | 1 | 10917 tags=70%, list=22%, signal=90% |
| | | 9 | 0.47382912 | 0.47382912 | 0.0232558 | 0.32396805 | 1 | 4005 tags=56%, list=8%, signal=60% |

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| REACTOME_PTK6 REGULATES RTKS AND THEIR EFFECTORS AKT1 AND DOK1 | REACTOME_PTK6 REGULATES RTKS AND THEIR EFFECTORS AKT1 AND DOK1 | 9 | 0.47359535 | 0.47359535 | 0.0328358 | 0.32250014 | 1 | 9457 tags=67%, list=19%, signal=83% |
| REACTOME_INTERLEUKIN-1 PROCESSING | REACTOME_INTERLEUKIN-1 PROCESSING | 7 | 0.47199643 | 0.47199643 | 0.0482283 | 0.32530847 | 1 | 4871 tags=57%, list=10%, signal=63% |
| REACTOME_CHONDROITIN SULFATE/DERMATAN SULFATE METABOLISM | REACTOME_CHONDROITIN SULFATE/DERMATAN SULFATE METABOLISM | 50 | 0.47132778 | 0.47132778 | 0 | 0.32508138 | 1 | 6323 tags=60%, list=13%, signal=69% |
| REACTOME_CHONDROITIN SULFATE BIOSYNTHESIS | REACTOME_CHONDROITIN SULFATE BIOSYNTHESIS | 20 | 0.47103894 | 0.47103894 | 0 | 0.32370687 | 1 | 6323 tags=60%, list=13%, signal=69% |
| REACTOME_SYNTHESIS OF DOLICHYL-PHOSPHATE | REACTOME_SYNTHESIS OF DOLICHYL-PHOSPHATE | 6 | 0.46895024 | 0.46895024 | 0.0929773 | 0.3279084 | 1 | 9683 tags=67%, list=20%, signal=83% |
| REACTOME_RHO GTPASES ACTIVATE IQGAPS | REACTOME_RHO GTPASES ACTIVATE IQGAPS | 11 | 0.46652332 | 0.46652332 | 0.008008 | 0.33355713 | 1 | 3869 tags=55%, list=8%, signal=59% |
| REACTOME_DEFECTIVE EXT1 CAUSES EXOSTOSES 1, TRPS2 AND CHDS | REACTOME_DEFECTIVE EXT1 CAUSES EXOSTOSES 1, TRPS2 AND CHDS | 12 | 0.46601674 | 0.46601674 | 0.0098328 | 0.33288562 | 1 | 5749 tags=58%, list=12%, signal=66% |
| REACTOME_DEFECTIVE EXT2 CAUSES EXOSTOSES 2 | REACTOME_DEFECTIVE EXT2 CAUSES EXOSTOSES 2 | 12 | 0.46601674 | 0.46601674 | 0.0051546 | 0.3307099 | 1 | 5749 tags=58%, list=12%, signal=66% |
| REACTOME_UNWINDING OF DNA | REACTOME_UNWINDING OF DNA | 12 | 0.46535626 | 0.46535626 | 0.0110442 | 0.33066857 | 1 | 22103 tags=92%, list=45%, signal=167% |
| REACTOME_G2/M DNA REPLICATION CHECKPOINT | REACTOME_G2/M DNA REPLICATION CHECKPOINT | 5 | 0.46343955 | 0.46343955 | 0.1661507 | 0.3346996 | 1 | 26274 tags=100%, list=54%, signal=216% |
| REACTOME_NEF-MEDIATES DOWN MODULATION OF CELL SURFACE RECEPTORS BY RECRUITING THEM TO CLATHRIN | REACTOME_NEF-MEDIATES DOWN MODULATION OF CELL SURFACE RECEPTORS BY RECRUITING THEM TO CLATHRIN ADAPTERS | 21 | 0.46233794 | 0.46233794 | 0 | 0.33592865 | 1 | 21672 tags=90%, list=44%, signal=162% |
| REACTOME_ATTACHMENT OF GPI ANCHOR TO UPAR | REACTOME_ATTACHMENT OF GPI ANCHOR TO UPAR | 7 | 0.460027 | 0.460027 | 0.0694864 | 0.34090436 | 1 | 12452 tags=71%, list=25%, signal=96% |
| REACTOME_MITOTIC TELOPHASE/CYTOKINESIS | REACTOME_MITOTIC TELOPHASE/CYTOKINESIS | 14 | 0.45912245 | 0.45912245 | 0.0020429 | 0.34138077 | 1 | 22992 tags=93%, list=47%, signal=175% |
| REACTOME_GAP JUNCTION DEGRADATION | REACTOME_GAP JUNCTION DEGRADATION | 10 | 0.45894188 | 0.45894188 | 0.0149402 | 0.33977878 | 1 | 11807 tags=70%, list=24%, signal=92% |
| REACTOME_NUCLEOBASE BIOSYNTHESIS | REACTOME_NUCLEOBASE BIOSYNTHESIS | 15 | 0.45829082 | 0.45829082 | 0.004065 | 0.33982414 | 1 | 20002 tags=87%, list=41%, signal=146% |
| REACTOME_PTK6 PROMOTES HIF1A STABILIZATION | REACTOME_PTK6 PROMOTES HIF1A STABILIZATION | 7 | 0.4579436 | 0.4579436 | 0.0733198 | 0.3388057 | 1 | 12554 tags=71%, list=26%, signal=96% |
| REACTOME_UPTAKE AND FUNCTION OF DIPHTHERIA TOXIN | REACTOME_UPTAKE AND FUNCTION OF DIPHTHERIA TOXIN | 6 | 0.45740655 | 0.45740655 | 0.1115538 | 0.33833677 | 1 | 18409 tags=83%, list=38%, signal=134% |
| REACTOME_TRANSCRIPTIONAL ACTIVATION OF CELL CYCLE INHIBITOR P21 | REACTOME_TRANSCRIPTIONAL ACTIVATION OF CELL CYCLE INHIBITOR P21 | 4 | 0.4549233 | 0.4549233 | 0.2941177 | 0.34431326 | 1 | 2208 tags=50%, list=5%, signal=52% |
| REACTOME_TRANSCRIPTIONAL ACTIVATION OF P53 RESPONSIVE GENES | REACTOME_TRANSCRIPTIONAL ACTIVATION OF P53 RESPONSIVE GENES | 4 | 0.4549233 | 0.4549233 | 0.2621167 | 0.34221378 | 1 | 2208 tags=50%, list=5%, signal=52% |
| REACTOME_CS/DS | REACTOME_CS/DS DEGRADATION | 14 | 0.4535556 | 0.4535556 | 0.0019474 | 0.34450197 | 1 | 5777 tags=57%, list=12%, signal=65% |
| REACTOME_LOSS OF FUNCTION OF TGFB1 IN CANCER | REACTOME_LOSS OF FUNCTION OF TGFB1 IN CANCER | 7 | 0.45224482 | 0.45224482 | 0.0721443 | 0.34651455 | 1 | 5838 tags=57%, list=12%, signal=65% |
| REACTOME_TGFB1 KD MUTANTS IN CANCER | REACTOME_TGFB1 KD MUTANTS IN CANCER | 7 | 0.45224482 | 0.45224482 | 0.0869565 | 0.3444396 | 1 | 5838 tags=57%, list=12%, signal=65% |
| REACTOME_PROTON-COUPLED MONOCARBOXYLATE TRANSPORT | REACTOME_PROTON-COUPLED MONOCARBOXYLATE TRANSPORT | 6 | 0.45046538 | 0.45046538 | 0.1300403 | 0.34823865 | 1 | 10588 tags=67%, list=22%, signal=85% |

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| REACTOME_VASOPRESSIN-LIKE RECEPTORS | REACTOME_VASOPRESSIN-LIKE RECEPTORS | 6 | 0.45015898 | 0.45015898 | 0.1193416 | 0.34712338 | 1 | 10603 tags=67%, list=22%, signal=85% |
| REACTOME_TRAF6 MEDIATED IRF7 ACTIVATION | REACTOME_TRAF6 MEDIATED IRF7 ACTIVATION | 30 | 0.4495079 | 0.4495079 | 0 | 0.34702203 | 1 | 13910 tags=73%, list=28%, signal=102% |
| REACTOME_ACTIVATION OF SMO | REACTOME_ACTIVATION OF SMO | 18 | 0.44942603 | 0.44942603 | 0 | 0.34521106 | 1 | 7924 tags=61%, list=16%, signal=73% |
| REACTOME_PRE-NOTCH PROCESSING IN GOLGI | REACTOME_PRE-NOTCH PROCESSING IN GOLGI | 18 | 0.4488744 | 0.4488744 | 0 | 0.34497017 | 1 | 7951 tags=61%, list=16%, signal=73% |
| REACTOME_ACTIVATION OF NOXA AND TRANSLOCATION TO MITOCHONDRIA | REACTOME_ACTIVATION OF NOXA AND TRANSLOCATION TO MITOCHONDRIA | 5 | 0.44775328 | 0.44775328 | 0.2102102 | 0.3467182 | 1 | 17249 tags=80%, list=35%, signal=123% |
| REACTOME_NEUROFASCIN INTERACTIONS | REACTOME_NEUROFASCIN INTERACTIONS | 7 | 0.44728136 | 0.44728136 | 0.0891473 | 0.34624007 | 1 | 6081 tags=57%, list=12%, signal=65% |
| REACTOME_RUNX3 REGULATES BCL2L11 (BIM) TRANSCRIPTION | REACTOME_RUNX3 REGULATES BCL2L11 (BIM) TRANSCRIPTION | 5 | 0.4468546 | 0.4468546 | 0.1981707 | 0.34574997 | 1 | 17293 tags=80%, list=35%, signal=124% |
| REACTOME_RUNX1 REGULATES ESTROGEN RECEPTOR MEDIATED TRANSCRIPTION | REACTOME_RUNX1 REGULATES ESTROGEN RECEPTOR MEDIATED TRANSCRIPTION | 6 | 0.44685352 | 0.44685352 | 0.1363184 | 0.3437855 | 1 | 2604 tags=50%, list=5%, signal=53% |
| REACTOME_PYRIMIDINE | REACTOME_PYRIMIDINE SALVAGE | 11 | 0.4444692 | 0.4444692 | 0.0221519 | 0.34964767 | 1 | 9400 tags=64%, list=19%, signal=79% |
| REACTOME_G2 PHASE | REACTOME_G2 PHASE | 5 | 0.443893 | 0.443893 | 0.1941177 | 0.34945968 | 1 | 27231 tags=100%, list=56%, signal=225% |
| REACTOME_PHOSPHORYLATION OF PROTEINS INVOLVED IN THE G2/M TRANSITION BY CYCLIN A:CDC2 COMPLEXES | REACTOME_PHOSPHORYLATION OF PROTEINS INVOLVED IN THE G2/M TRANSITION BY CYCLIN A:CDC2 COMPLEXES | 3 | 0.44387487 | 0.44387487 | 0.4708786 | 0.3475607 | 1 | 27231 tags=100%, list=56%, signal=225% |
| REACTOME_LINOLEIC ACID (LA) METABOLISM | REACTOME_LINOLEIC ACID (LA) METABOLISM | 8 | 0.44359592 | 0.44359592 | 0.0629515 | 0.34655014 | 1 | 8885 tags=63%, list=18%, signal=76% |
| REACTOME_NEF MEDIATED CD4 DOWN-REGULATION | REACTOME_NEF MEDIATED CD4 DOWN-REGULATION | 9 | 0.44322112 | 0.44322112 | 0.0303644 | 0.34584716 | 1 | 10944 tags=67%, list=22%, signal=86% |
| REACTOME_ALKBH3 MEDIATED REVERSAL OF ALKYLATION | REACTOME_ALKBH3 MEDIATED REVERSAL OF ALKYLATION | 4 | 0.44191295 | 0.44191295 | 0.2981557 | 0.34800676 | 1 | 2845 tags=50%, list=6%, signal=53% |
| REACTOME_DISEASES OF MISMATCH REPAIR (MMR) | REACTOME_DISEASES OF MISMATCH REPAIR (MMR) | 5 | 0.44180965 | 0.44180965 | 0.2126607 | 0.3464265 | 1 | 7747 tags=60%, list=16%, signal=71% |
| REACTOME_COLLAGEN CHAIN TRIMERIZATION | REACTOME_COLLAGEN CHAIN TRIMERIZATION | 44 | 0.43988362 | 0.43988362 | 0 | 0.35062072 | 1 | 9639 tags=64%, list=20%, signal=79% |
| REACTOME_DEFECTIVE AMN CAUSES HEREDITARY MEGALOBlastic ANEMIA 1 | REACTOME_DEFECTIVE AMN CAUSES HEREDITARY MEGALOBlastic ANEMIA 1 | 3 | 0.4381221 | 0.4381221 | 0.4757185 | 0.3544044 | 1 | 11191 tags=67%, list=23%, signal=86% |
| REACTOME_DEFECTIVE CUBN CAUSES HEREDITARY MEGALOBlastic ANEMIA 1 | REACTOME_DEFECTIVE CUBN CAUSES HEREDITARY MEGALOBlastic ANEMIA 1 | 3 | 0.4381221 | 0.4381221 | 0.4856294 | 0.352499 | 1 | 11191 tags=67%, list=23%, signal=86% |
| REACTOME_UPTAKE AND FUNCTION OF ANTHRAX TOXINS | REACTOME_UPTAKE AND FUNCTION OF ANTHRAX TOXINS | 11 | 0.43723795 | 0.43723795 | 0.024558 | 0.35340998 | 1 | 9754 tags=64%, list=20%, signal=79% |
| REACTOME_FGFR1B LIGAND BINDING AND ACTIVATION | REACTOME_FGFR1B LIGAND BINDING AND ACTIVATION | 6 | 0.4371447 | 0.4371447 | 0.1444333 | 0.35182458 | 1 | 19401 tags=83%, list=40%, signal=138% |
| REACTOME_VLDLR INTERNALISATION AND DEGRADATION | REACTOME_VLDLR INTERNALISATION AND DEGRADATION | 12 | 0.43687487 | 0.43687487 | 0.0158259 | 0.35081342 | 1 | 11256 tags=67%, list=23%, signal=87% |
| REACTOME_PD-1 SIGNALING | REACTOME_PD-1 SIGNALING | 24 | 0.4342244 | 0.4342244 | 0 | 0.357482 | 1 | 21592 tags=88%, list=44%, signal=156% |
| REACTOME_BETA-OXIDATION OF PRISTANOYL-COA | REACTOME_BETA-OXIDATION OF PRISTANOYL-COA | 9 | 0.4329761 | 0.4329761 | 0.0482546 | 0.35953304 | 1 | 6005 tags=56%, list=12%, signal=63% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF GENES INVOLVED IN G1 CELL CYCLE ARREST | REACTOME_TP53 REGULATES TRANSCRIPTION OF GENES INVOLVED IN G1 CELL CYCLE ARREST | 14 | 0.4323916 | 0.4323916 | 0.00611 | 0.35932982 | 1 | 6813 tags=57%, list=14%, signal=66% |

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|--|--|-----|------------|------------|-----------|------------|---|--|
| REACTOME_RESPONSE TO METAL IONS | REACTOME_RESPONSE TO METAL IONS | 14 | 0.4315132 | 0.4315132 | 0.0128079 | 0.36021245 | 1 | 13851 tags=71%, list=28%, signal=100% |
| REACTOME_TNFR1-INDUCED NFKAPPAB SIGNALING PATHWAY | REACTOME_TNFR1-INDUCED NFKAPPAB SIGNALING PATHWAY | 26 | 0.4310995 | 0.4310995 | 0 | 0.35964105 | 1 | 10917 tags=65%, list=22%, signal=84% |
| REACTOME_COHESIN LOADING ONTO CHROMATIN | REACTOME_COHESIN LOADING ONTO CHROMATIN | 10 | 0.4305076 | 0.4305076 | 0.048583 | 0.3596388 | 1 | 22992 tags=90%, list=47%, signal=170% |
| REACTOME_ENOS ACTIVATION | REACTOME_ENOS ACTIVATION | 10 | 0.4302727 | 0.4302727 | 0.0389474 | 0.3584809 | 1 | 8314 tags=60%, list=17%, signal=72% |
| REACTOME_INHIBITION OF TSC COMPLEX FORMATION BY PKB | REACTOME_INHIBITION OF TSC COMPLEX FORMATION BY PKB | 3 | 0.43006825 | 0.43006825 | 0.5300493 | 0.35732195 | 1 | 27907 tags=100%, list=57%, signal=233% |
| REACTOME_SMOOTH MUSCLE CONTRACTION | REACTOME_SMOOTH MUSCLE CONTRACTION | 35 | 0.4289393 | 0.4289393 | 0 | 0.35920075 | 1 | 6991 tags=57%, list=14%, signal=67% |
| REACTOME_PURINE RIBONUCLEOSIDE MONOPHOSPHATE | REACTOME_PURINE RIBONUCLEOSIDE MONOPHOSPHATE BIOSYNTHESIS | 12 | 0.4249212 | 0.4249212 | 0.0106486 | 0.37033302 | 1 | 20002 tags=83%, list=41%, signal=141% |
| REACTOME_SPERM MOTILITY AND TAXES | REACTOME_SPERM MOTILITY AND TAXES | 9 | 0.42456266 | 0.42456266 | 0.0485537 | 0.36954698 | 1 | 17298 tags=78%, list=35%, signal=120% |
| REACTOME_RUNX3 REGULATES IMMUNE RESPONSE AND CELL MIGRATION | REACTOME_RUNX3 REGULATES IMMUNE RESPONSE AND CELL MIGRATION | 6 | 0.42414063 | 0.42414063 | 0.170297 | 0.36913863 | 1 | 3716 tags=50%, list=8%, signal=54% |
| REACTOME_SCAVENGING BY CLASS A RECEPTORS | REACTOME_SCAVENGING BY CLASS A RECEPTORS | 19 | 0.42367208 | 0.42367208 | 9.70E-04 | 0.36885548 | 1 | 5033 tags=53%, list=10%, signal=59% |
| REACTOME_EXTRACELLULAR MATRIX ORGANIZATION | REACTOME_EXTRACELLULAR MATRIX ORGANIZATION | 295 | 0.42242044 | 0.42242044 | 0 | 0.37111149 | 1 | 6827 tags=56%, list=14%, signal=65% |
| REACTOME_PLASMA LIPOPROTEIN ASSEMBLY | REACTOME_PLASMA LIPOPROTEIN ASSEMBLY | 19 | 0.42218062 | 0.42218062 | 0 | 0.3701236 | 1 | 5106 tags=53%, list=10%, signal=59% |
| REACTOME_A TETRASACCHARIDE LINKER SEQUENCE IS REQUIRED FOR | REACTOME_A TETRASACCHARIDE LINKER SEQUENCE IS REQUIRED FOR GAG SYNTHESIS | 26 | 0.42068228 | 0.42068228 | 0 | 0.37321317 | 1 | 5777 tags=54%, list=12%, signal=61% |
| REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN DIFFERENTIATION OF KERATINOCYTES | REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN DIFFERENTIATION OF KERATINOCYTES | 8 | 0.4206574 | 0.4206574 | 0.0843965 | 0.37149796 | 1 | 10008 tags=63%, list=20%, signal=79% |
| REACTOME_N-GLYCAN TRIMMING AND ELONGATION IN | REACTOME_N-GLYCAN TRIMMING AND ELONGATION IN THE CIS-GOLGI | 5 | 0.42017975 | 0.42017975 | 0.2487258 | 0.37118647 | 1 | 8806 tags=60%, list=18%, signal=73% |
| REACTOME_PROCESSIVE SYNTHESIS ON THE C-STRAND OF THE TELOMERE | REACTOME_PROCESSIVE SYNTHESIS ON THE C-STRAND OF THE TELOMERE | 11 | 0.41945317 | 0.41945317 | 0.0156709 | 0.37179115 | 1 | 15076 tags=73%, list=31%, signal=105% |
| REACTOME_CREB3 FACTORS ACTIVATE GENES | REACTOME_CREB3 FACTORS ACTIVATE GENES | 9 | 0.41704342 | 0.41704342 | 0.0732422 | 0.3778764 | 1 | 6785 tags=56%, list=14%, signal=64% |
| REACTOME_LYSOSOMAL GLYCOGEN CATABOLISM | REACTOME_LYSOSOMAL GLYCOGEN CATABOLISM | 3 | 0.41602334 | 0.41602334 | 0.5429418 | 0.37955466 | 1 | 12273 tags=67%, list=25%, signal=89% |
| REACTOME_MISSPLICED LRP5 MUTANTS HAVE ENHANCED BETA-CATENIN-DEPENDENT SIGNALING | REACTOME_MISSPLICED LRP5 MUTANTS HAVE ENHANCED BETA-CATENIN-DEPENDENT SIGNALING | 5 | 0.4157884 | 0.4157884 | 0.2731855 | 0.37856635 | 1 | 9021 tags=60%, list=18%, signal=74% |
| REACTOME_PTK6 REGULATES RHO GTPASES, RAS GTPASE AND MAP KINASES | REACTOME_PTK6 REGULATES RHO GTPASES, RAS GTPASE AND MAP KINASES | 18 | 0.41498062 | 0.41498062 | 0.0019704 | 0.37955284 | 1 | 9610 tags=61%, list=20%, signal=76% |
| REACTOME_GLYCINE | REACTOME_GLYCINE DEGRADATION | 4 | 0.41497827 | 0.41497827 | 0.3792757 | 0.37778014 | 1 | 16405 tags=75%, list=34%, signal=113% |
| REACTOME_THE ROLE OF NEF IN HIV-1 REPLICATION AND DISEASE PATHOGENESIS | REACTOME_THE ROLE OF NEF IN HIV-1 REPLICATION AND DISEASE PATHOGENESIS | 28 | 0.4147578 | 0.4147578 | 0 | 0.37670675 | 1 | 21672 tags=86%, list=44%, signal=154% |

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|---|---|-----|------------|------------|-----------|------------|---|--|
| REACTOME_TRANSLOCATION OF ZAP-70 TO IMMUNOLOGICAL SYNAPSE | REACTOME_TRANSLOCATION OF ZAP-70 TO IMMUNOLOGICAL SYNAPSE | 20 | 0.41368884 | 0.41368884 | 9.64E-04 | 0.37880638 | 1 | 28716 tags=100%, list=59%, signal=242% |
| REACTOME_PHOSPHORYLATION OF PROTEINS INVOLVED IN G1/S TRANSITION BY ACTIVE CYCLIN E:CDK2 COMPLEXES | REACTOME_PHOSPHORYLATION OF PROTEINS INVOLVED IN G1/S TRANSITION BY ACTIVE CYCLIN E:CDK2 COMPLEXES | 4 | 0.41162354 | 0.41162354 | 0.4040896 | 0.384208 | 1 | 4328 tags=50%, list=9%, signal=55% |
| REACTOME_CHREBP ACTIVATES METABOLIC GENE EXPRESSION | REACTOME_CHREBP ACTIVATES METABOLIC GENE EXPRESSION | 8 | 0.41138396 | 0.41138396 | 0.1014199 | 0.3833146 | 1 | 10462 tags=63%, list=21%, signal=79% |
| REACTOME_ZINC INFLUX INTO CELLS BY THE SLC39 GENE | REACTOME_ZINC INFLUX INTO CELLS BY THE SLC39 GENE FAMILY | 10 | 0.41064242 | 0.41064242 | 0.0460784 | 0.38403845 | 1 | 9275 tags=60%, list=19%, signal=74% |
| REACTOME_DEFECTIVE B3GALT6 CAUSES EDSP2 AND SEMDHL | REACTOME_DEFECTIVE B3GALT6 CAUSES EDSP2 AND SEMDHL | 19 | 0.40847164 | 0.40847164 | 0 | 0.3895812 | 1 | 5777 tags=53%, list=12%, signal=60% |
| REACTOME_DEFECTIVE B3GAT3 CAUSES JDSSDHD | REACTOME_DEFECTIVE B3GAT3 CAUSES JDSSDHD | 19 | 0.40847164 | 0.40847164 | 0.0031847 | 0.38781038 | 1 | 5777 tags=53%, list=12%, signal=60% |
| REACTOME_DEFECTIVE B4GALT7 CAUSES EDS, PROGEROID TYPE | REACTOME_DEFECTIVE B4GALT7 CAUSES EDS, PROGEROID TYPE | 19 | 0.40847164 | 0.40847164 | 0.0041494 | 0.38605556 | 1 | 5777 tags=53%, list=12%, signal=60% |
| REACTOME_RNF MUTANTS SHOW ENHANCED WNT SIGNALING AND PROLIFERATION | REACTOME_RNF MUTANTS SHOW ENHANCED WNT SIGNALING AND PROLIFERATION | 8 | 0.40787068 | 0.40787068 | 0.1033797 | 0.38637233 | 1 | 10634 tags=63%, list=22%, signal=80% |
| REACTOME_KERATAN SULFATE/KERATIN METABOLISM | REACTOME_KERATAN SULFATE/KERATIN METABOLISM | 33 | 0.40720147 | 0.40720147 | 0 | 0.38688856 | 1 | 6782 tags=55%, list=14%, signal=63% |
| REACTOME_SMAC BINDS TO IAPs | REACTOME_SMAC BINDS TO IAPs | 5 | 0.40700573 | 0.40700573 | 0.2781726 | 0.3858096 | 1 | 9451 tags=60%, list=19%, signal=74% |
| REACTOME_SMAC-MEDIATED APOPTOTIC RESPONSE | REACTOME_SMAC-MEDIATED APOPTOTIC RESPONSE | 5 | 0.40700573 | 0.40700573 | 0.2918707 | 0.3840949 | 1 | 9451 tags=60%, list=19%, signal=74% |
| REACTOME_SMAC-MEDIATED DISSOCIATION OF IAP:CASPASE COMPLEXES | REACTOME_SMAC-MEDIATED DISSOCIATION OF IAP:CASPASE COMPLEXES | 5 | 0.40700573 | 0.40700573 | 0.2821256 | 0.38239536 | 1 | 9451 tags=60%, list=19%, signal=74% |
| REACTOME_ECM | REACTOME_ECM PROTEOGLYCANS | 55 | 0.40599614 | 0.40599614 | 0 | 0.384048 | 1 | 10411 tags=62%, list=21%, signal=78% |
| REACTOME_LDL CLEARANCE | REACTOME_LDL CLEARANCE | 19 | 0.40582213 | 0.40582213 | 0 | 0.38292122 | 1 | 13638 tags=68%, list=28%, signal=95% |
| REACTOME_P75NTR SIGNALS VIA NF-KB | REACTOME_P75NTR SIGNALS VIA NF-KB | 16 | 0.40558797 | 0.40558797 | 0.002994 | 0.38202682 | 1 | 10749 tags=63%, list=22%, signal=80% |
| REACTOME_SCAVENGING BY CLASS H RECEPTORS | REACTOME_SCAVENGING BY CLASS H RECEPTORS | 4 | 0.4031474 | 0.4031474 | 0.4414683 | 0.38845712 | 1 | 4743 tags=50%, list=10%, signal=55% |
| REACTOME_TNFS BIND THEIR PHYSIOLOGICAL RECEPTORS | REACTOME_TNFS BIND THEIR PHYSIOLOGICAL RECEPTORS | 27 | 0.40289223 | 0.40289223 | 0 | 0.387648 | 1 | 3858 tags=48%, list=8%, signal=52% |
| REACTOME_DEGRADATION OF THE EXTRACELLULAR MATRIX | REACTOME_DEGRADATION OF THE EXTRACELLULAR MATRIX | 111 | 0.4023533 | 0.4023533 | 0 | 0.38771582 | 1 | 6810 tags=54%, list=14%, signal=63% |
| REACTOME_SIGNAL | REACTOME_SIGNAL ATTENUATION | 10 | 0.40195078 | 0.40195078 | 0.074331 | 0.38739923 | 1 | 4804 tags=50%, list=10%, signal=55% |
| REACTOME_HUR (ELAVL1) BINDS AND STABILIZES MRNA | REACTOME_HUR (ELAVL1) BINDS AND STABILIZES MRNA | 10 | 0.40131754 | 0.40131754 | 0.0653218 | 0.3879464 | 1 | 14628 tags=70%, list=30%, signal=100% |
| REACTOME_HEPARAN SULFATE/HEPARIN (HS-GAG) METABOLISM | REACTOME_HEPARAN SULFATE/HEPARIN (HS-GAG) METABOLISM | 54 | 0.40095806 | 0.40095806 | 0 | 0.38745353 | 1 | 5777 tags=52%, list=12%, signal=59% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF SEVERAL ADDITIONAL CELL DEATH GENES WHOSE SPECIFIC ROLES IN P53-DEPENDENT APOPTOSIS REMAIN UNCERTAIN | REACTOME_TP53 REGULATES TRANSCRIPTION OF SEVERAL ADDITIONAL CELL DEATH GENES WHOSE SPECIFIC ROLES IN P53-DEPENDENT APOPTOSIS REMAIN UNCERTAIN | 14 | 0.40051278 | 0.40051278 | 0.0166503 | 0.38729984 | 1 | 18866 tags=79%, list=39%, signal=128% |

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|---|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_ATF6 (ATF6-ALPHA) ACTIVATES CHAPERONES | REACTOME_ATF6 (ATF6-ALPHA) ACTIVATES CHAPERONES | 11 | 0.39995062 | 0.39995062 | 0.039666 | 0.38758382 | 1 | 7128 tags=55%, list=15%, signal=64% |
| REACTOME_MISMATCH REPAIR | REACTOME_MISMATCH REPAIR | 15 | 0.39878792 | 0.39878792 | 0.0107527 | 0.3899788 | 1 | 16386 tags=73%, list=33%, signal=110% |
| REACTOME_INTEGRIN CELL SURFACE INTERACTIONS | REACTOME_INTEGRIN CELL SURFACE INTERACTIONS | 66 | 0.39807874 | 0.39807874 | 0 | 0.39079052 | 1 | 10951 tags=62%, list=22%, signal=80% |
| REACTOME_TELOMERE EXTENSION BY TELOMERASE | REACTOME_TELOMERE EXTENSION BY TELOMERASE | 6 | 0.39756057 | 0.39756057 | 0.2270434 | 0.39086103 | 1 | 21339 tags=83%, list=44%, signal=148% |
| REACTOME_TFAP2 (AP-2) FAMILY REGULATES TRANSCRIPTION OF CELL CYCLE FACTORS | REACTOME_TFAP2 (AP-2) FAMILY REGULATES TRANSCRIPTION OF CELL CYCLE FACTORS | 5 | 0.39748776 | 0.39748776 | 0.3415113 | 0.3894936 | 1 | 9917 tags=60%, list=20%, signal=75% |
| REACTOME_CHYLOMICRON ASSEMBLY | REACTOME_CHYLOMICRON ASSEMBLY | 10 | 0.397273 | 0.397273 | 0.0525803 | 0.38858214 | 1 | 5033 tags=50%, list=10%, signal=56% |
| REACTOME_DEATH RECEPTOR SIGNALLING | REACTOME_DEATH RECEPTOR SIGNALLING | 50 | 0.3970009 | 0.3970009 | 0 | 0.3878593 | 1 | 10938 tags=62%, list=22%, signal=80% |
| REACTOME_ACYL CHAIN REMODELING OF DAG AND TAG | REACTOME_ACYL CHAIN REMODELING OF DAG AND TAG | 8 | 0.3965342 | 0.3965342 | 0.1080808 | 0.3879151 | 1 | 11189 tags=63%, list=23%, signal=81% |
| REACTOME_TFAP2 (AP-2) FAMILY REGULATES TRANSCRIPTION OF OTHER TRANSCRIPTION | REACTOME_TFAP2 (AP-2) FAMILY REGULATES TRANSCRIPTION OF OTHER TRANSCRIPTION FACTORS | 4 | 0.3961061 | 0.3961061 | 0.4540059 | 0.38775325 | 1 | 17329 tags=75%, list=35%, signal=116% |
| REACTOME_NF-KB IS ACTIVATED AND SIGNALS SURVIVAL | REACTOME_NF-KB IS ACTIVATED AND SIGNALS SURVIVAL | 13 | 0.3959452 | 0.3959452 | 0.016129 | 0.38674057 | 1 | 10749 tags=62%, list=22%, signal=79% |
| REACTOME_VEGFR2 MEDIATED VASCULAR PERMEABILITY | REACTOME_VEGFR2 MEDIATED VASCULAR PERMEABILITY | 27 | 0.3957532 | 0.3957532 | 9.79E-04 | 0.38583618 | 1 | 16902 tags=74%, list=35%, signal=113% |
| REACTOME_SEMA3A PAK DEPENDENT AXON REPULSION | REACTOME_SEMA3A PAK DEPENDENT AXON REPULSION | 16 | 0.39501828 | 0.39501828 | 0.0099206 | 0.38672847 | 1 | 17387 tags=75%, list=36%, signal=116% |
| REACTOME_NOTCH2 ACTIVATION AND TRANSMISSION OF SIGNAL TO THE NUCLEUS | REACTOME_NOTCH2 ACTIVATION AND TRANSMISSION OF SIGNAL TO THE NUCLEUS | 21 | 0.3944985 | 0.3944985 | 0.002006 | 0.38689154 | 1 | 6339 tags=52%, list=13%, signal=60% |
| REACTOME_RUNX3 REGULATES NOTCH SIGNALING | REACTOME_RUNX3 REGULATES NOTCH SIGNALING | 14 | 0.39377135 | 0.39377135 | 0.0153218 | 0.38792565 | 1 | 12201 tags=64%, list=25%, signal=86% |
| REACTOME_POST-TRANSLATIONAL PROTEIN | REACTOME_POST-TRANSLATIONAL PROTEIN PHOSPHORYLATION | 107 | 0.3937361 | 0.3937361 | 0 | 0.38652247 | 1 | 6846 tags=53%, list=14%, signal=62% |
| REACTOME_GP1B-IX-V ACTIVATION SIGNALLING | REACTOME_GP1B-IX-V ACTIVATION SIGNALLING | 9 | 0.39278808 | 0.39278808 | 0.1060456 | 0.38822928 | 1 | 13413 tags=67%, list=27%, signal=92% |
| REACTOME_Glutathione SYNTHESIS AND RECYCLING | REACTOME_Glutathione SYNTHESIS AND RECYCLING | 13 | 0.39238912 | 0.39238912 | 0.027027 | 0.38798055 | 1 | 3390 tags=46%, list=7%, signal=50% |
| REACTOME_REMOVAL OF THE FLAP INTERMEDIATE FROM THE | REACTOME_REMOVAL OF THE FLAP INTERMEDIATE FROM THE C-STRAND | 10 | 0.3921663 | 0.3921663 | 0.0770732 | 0.3872302 | 1 | 15076 tags=70%, list=31%, signal=101% |
| REACTOME_PROSTANOID LIGAND RECEPTORS | REACTOME_PROSTANOID LIGAND RECEPTORS | 9 | 0.39155114 | 0.39155114 | 0.0922053 | 0.3878809 | 1 | 8033 tags=56%, list=16%, signal=66% |
| REACTOME_ACTIVATION OF NIMA KINASES NEK9, NEK6, NEK7 | REACTOME_ACTIVATION OF NIMA KINASES NEK9, NEK6, NEK7 | 7 | 0.39013037 | 0.39013037 | 0.2099609 | 0.39119905 | 1 | 22869 tags=86%, list=47%, signal=161% |
| REACTOME_REGULATION OF IFNA SIGNALING | REACTOME_REGULATION OF IFNA SIGNALING | 23 | 0.38897777 | 0.38897777 | 0.0020471 | 0.3936926 | 1 | 21411 tags=83%, list=44%, signal=147% |
| REACTOME_CALNEXIN/CALRETICULIN CYCLE | REACTOME_CALNEXIN/CALRETICULIN CYCLE | 26 | 0.38888758 | 0.38888758 | 0 | 0.39250958 | 1 | 7333 tags=54%, list=15%, signal=63% |
| REACTOME_PLASMA LIPOPROTEIN CLEARANCE | REACTOME_PLASMA LIPOPROTEIN CLEARANCE | 33 | 0.38838252 | 0.38838252 | 0 | 0.39264196 | 1 | 13638 tags=67%, list=28%, signal=92% |
| REACTOME_MISMATCH REPAIR (MMR) DIRECTED BY MSH2:MSH3 (MUTSBETA) | REACTOME_MISMATCH REPAIR (MMR) DIRECTED BY MSH2:MSH3 (MUTSBETA) | 14 | 0.388225 | 0.388225 | 0.0210843 | 0.39165986 | 1 | 22965 tags=86%, list=47%, signal=161% |

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|---|---|-----|------------|------------|-----------|------------|---|--|
| REACTOME_MISMATCH REPAIR (MMR) DIRECTED BY MSH2:MSH6 (MUTSALPHA) | REACTOME_MISMATCH REPAIR (MMR) DIRECTED BY MSH2:MSH6 (MUTSALPHA) | 14 | 0.388225 | 0.388225 | 0.0221774 | 0.39015925 | 1 | 22965 tags=86%, list=47%, signal=161% |
| REACTOME_GLYCOSAMINOGLYCAN METABOLISM | REACTOME_GLYCOSAMINOGLYCAN METABOLISM | 122 | 0.3882072 | 0.3882072 | 0 | 0.38870472 | 1 | 6323 tags=52%, list=13%, signal=59% |
| REACTOME_FATTY ACIDS BOUND TO GPR40 (FFAR1) REGULATE INSULIN SECRETION | REACTOME_FATTY ACIDS BOUND TO GPR40 (FFAR1) REGULATE INSULIN SECRETION | 8 | 0.38777906 | 0.38777906 | 0.1324245 | 0.3886077 | 1 | 5497 tags=50%, list=11%, signal=56% |
| REACTOME_FREE FATTY ACIDS REGULATE INSULIN SECRETION | REACTOME_FREE FATTY ACIDS REGULATE INSULIN SECRETION | 8 | 0.38777906 | 0.38777906 | 0.1135647 | 0.3871357 | 1 | 5497 tags=50%, list=11%, signal=56% |
| REACTOME_AKT-MEDIATED INACTIVATION OF FOXO1A | REACTOME_AKT-MEDIATED INACTIVATION OF FOXO1A | 4 | 0.38719594 | 0.38719594 | 0.4888889 | 0.3875344 | 1 | 5524 tags=50%, list=11%, signal=56% |
| REACTOME_ROLE OF ABL IN ROBO-SLIT SIGNALING | REACTOME_ROLE OF ABL IN ROBO-SLIT SIGNALING | 9 | 0.3861177 | 0.3861177 | 0.097371 | 0.3895573 | 1 | 8299 tags=56%, list=17%, signal=67% |
| REACTOME_NEGATIVE FEEDBACK REGULATION OF REACTOME_TNF SIGNALING | REACTOME_NEGATIVE FEEDBACK REGULATION OF MAPK PATHWAY | 6 | 0.38469267 | 0.38469267 | 0.2530864 | 0.3928872 | 1 | 21969 tags=83%, list=45%, signal=151% |
| REACTOME_TNF SIGNALING | REACTOME_TNF SIGNALING | 43 | 0.38158178 | 0.38158178 | 0 | 0.40220746 | 1 | 10938 tags=60%, list=22%, signal=78% |
| REACTOME_SIGNALING BY TGF-BETA RECEPTOR COMPLEX IN CANCER | REACTOME_SIGNALING BY TGF-BETA RECEPTOR COMPLEX IN CANCER | 8 | 0.38081378 | 0.38081378 | 0.1438776 | 0.40345994 | 1 | 5838 tags=50%, list=12%, signal=57% |
| REACTOME_SMAD2/3 PHOSPHORYLATION MOTIF MUTANTS IN CANCER | REACTOME_SMAD2/3 PHOSPHORYLATION MOTIF MUTANTS IN CANCER | 6 | 0.38079822 | 0.38079822 | 0.2864173 | 0.40201548 | 1 | 5838 tags=50%, list=12%, signal=57% |
| REACTOME_FORMATION OF SENESENCE-ASSOCIATED HETEROCHROMATIN FOCI (SAHF) | REACTOME_FORMATION OF SENESENCE-ASSOCIATED HETEROCHROMATIN FOCI (SAHF) | 17 | 0.38059238 | 0.38059238 | 0.0121581 | 0.40121248 | 1 | 13053 tags=65%, list=27%, signal=88% |
| REACTOME_HEME DEGRADATION | REACTOME_HEME DEGRADATION | 5 | 0.3805147 | 0.3805147 | 0.3501027 | 0.39999497 | 1 | 20541 tags=80%, list=42%, signal=138% |
| REACTOME_TRAF6 MEDIATED NF-KB ACTIVATION | REACTOME_TRAF6 MEDIATED NF-KB ACTIVATION | 26 | 0.38017187 | 0.38017187 | 0 | 0.3997319 | 1 | 3993 tags=46%, list=8%, signal=50% |
| REACTOME_FORMYL PEPTIDE RECEPTORS BIND FORMYL PEPTIDES AND MANY OTHER LIGANDS | REACTOME_FORMYL PEPTIDE RECEPTORS BIND FORMYL PEPTIDES AND MANY OTHER LIGANDS | 9 | 0.37908417 | 0.37908417 | 0.1151151 | 0.40210247 | 1 | 24965 tags=89%, list=51%, signal=181% |
| REACTOME_STING MEDIATED INDUCTION OF HOST IMMUNE RESPONSES | REACTOME_STING MEDIATED INDUCTION OF HOST IMMUNE RESPONSES | 15 | 0.37897176 | 0.37897176 | 0.0219436 | 0.40102565 | 1 | 7563 tags=53%, list=15%, signal=63% |
| REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 HD DOMAIN MUTANTS | REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 HD DOMAIN MUTANTS | 15 | 0.37880832 | 0.37880832 | 0.0194473 | 0.40010488 | 1 | 7571 tags=53%, list=15%, signal=63% |
| REACTOME_SIGNALING BY NOTCH1 HD DOMAIN MUTANTS IN CANCER | REACTOME_SIGNALING BY NOTCH1 HD DOMAIN MUTANTS IN CANCER | 15 | 0.37880832 | 0.37880832 | 0.018664 | 0.39866045 | 1 | 7571 tags=53%, list=15%, signal=63% |
| REACTOME_MAPK3 (ERK1) ACTIVATION | REACTOME_MAPK3 (ERK1) ACTIVATION | 10 | 0.37853128 | 0.37853128 | 0.083089 | 0.39820364 | 1 | 30433 tags=100%, list=62%, signal=264% |
| REACTOME_MAPK1 (ERK2) ACTIVATION | REACTOME_MAPK1 (ERK2) ACTIVATION | 9 | 0.3785236 | 0.3785236 | 0.1295716 | 0.39680886 | 1 | 30433 tags=100%, list=62%, signal=264% |
| REACTOME_ELECTRIC TRANSMISSION ACROSS GAP JUNCTIONS | REACTOME_ELECTRIC TRANSMISSION ACROSS GAP JUNCTIONS | 5 | 0.3782067 | 0.3782067 | 0.3721841 | 0.39651802 | 1 | 20654 tags=80%, list=42%, signal=138% |
| REACTOME_TRANSMISSION ACROSS ELECTRICAL SYNAPSES | REACTOME_TRANSMISSION ACROSS ELECTRICAL SYNAPSES | 5 | 0.3782067 | 0.3782067 | 0.3892216 | 0.39510694 | 1 | 20654 tags=80%, list=42%, signal=138% |
| REACTOME_INTERLEUKIN-6 FAMILY SIGNALING | REACTOME_INTERLEUKIN-6 FAMILY SIGNALING | 24 | 0.3782003 | 0.3782003 | 0.0020121 | 0.3937195 | 1 | 5972 tags=50%, list=12%, signal=57% |

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|---|--|-----|------------|------------|-----------|------------|---|--|
| REACTOME_REGULATION OF INSULIN-LIKE GROWTH FACTOR (IGF) TRANSPORT AND UPTAKE BY INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS | REACTOME_REGULATION OF INSULIN-LIKE GROWTH FACTOR (IGF) TRANSPORT AND UPTAKE BY INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS (IGFBPS) | 124 | 0.3772498 | 0.3772498 | 0 | 0.39553076 | 1 | 6846 tags=52%, list=14%, signal=60% |
| REACTOME_DISEASES ASSOCIATED WITH THE TLR | REACTOME_DISEASES ASSOCIATED WITH THE TLR SIGNALING CASCADE | 24 | 0.37582582 | 0.37582582 | 0 | 0.39899176 | 1 | 4048 tags=46%, list=8%, signal=50% |
| REACTOME_DISEASES OF IMMUNE SYSTEM | REACTOME_DISEASES OF IMMUNE SYSTEM | 24 | 0.37582582 | 0.37582582 | 0 | 0.39759177 | 1 | 4048 tags=46%, list=8%, signal=50% |
| REACTOME_YAP1- AND WWTR1 (TAZ)-STIMULATED GENE EXPRESSION | REACTOME_YAP1- AND WWTR1 (TAZ)-STIMULATED GENE EXPRESSION | 29 | 0.37506482 | 0.37506482 | 9.96E-04 | 0.39873588 | 1 | 8660 tags=55%, list=18%, signal=67% |
| REACTOME_METABOLISM OF INGESTED H2SEO4 AND H2SEO3 INTO H2SE | REACTOME_METABOLISM OF INGESTED H2SEO4 AND H2SEO3 INTO H2SE | 4 | 0.37404773 | 0.37404773 | 0.523301 | 0.40102962 | 1 | 18409 tags=75%, list=38%, signal=120% |
| REACTOME_LYSINE CATABOLISM | REACTOME_LYSINE CATABOLISM | 12 | 0.37363052 | 0.37363052 | 0.0659341 | 0.40108514 | 1 | 14352 tags=67%, list=29%, signal=94% |
| REACTOME_NICOTINAMIDE SALVAGING | REACTOME_NICOTINAMIDE SALVAGING | 19 | 0.37230936 | 0.37230936 | 0.0071356 | 0.4044372 | 1 | 7547 tags=53%, list=15%, signal=62% |
| REACTOME_MULTIFUNCTIONAL ANION EXCHANGERS | REACTOME_MULTIFUNCTIONAL ANION EXCHANGERS | 9 | 0.37217775 | 0.37217775 | 0.131579 | 0.40350336 | 1 | 14422 tags=67%, list=29%, signal=94% |
| REACTOME_RSK ACTIVATION | REACTOME_RSK ACTIVATION | 6 | 0.37180433 | 0.37180433 | 0.320398 | 0.40332735 | 1 | 22600 tags=83%, list=46%, signal=155% |
| REACTOME_SODIUM/PROTON EXCHANGERS | REACTOME_SODIUM/PROTON EXCHANGERS | 9 | 0.3715536 | 0.3715536 | 0.1146045 | 0.40282798 | 1 | 9012 tags=56%, list=18%, signal=68% |
| REACTOME_IRE1ALPHA ACTIVATES CHAPERONES | REACTOME_IRE1ALPHA ACTIVATES CHAPERONES | 55 | 0.37070313 | 0.37070313 | 0 | 0.4044703 | 1 | 5015 tags=47%, list=10%, signal=53% |
| REACTOME_ACETYLCHOLINE REGULATES INSULIN SECRETION | REACTOME_ACETYLCHOLINE REGULATES INSULIN SECRETION | 10 | 0.3706976 | 0.3706976 | 0.0861723 | 0.40311414 | 1 | 6334 tags=50%, list=13%, signal=57% |
| REACTOME_REVERSAL OF ALKYLATION DAMAGE BY DNA DIOXYGENASES | REACTOME_REVERSAL OF ALKYLATION DAMAGE BY DNA DIOXYGENASES | 7 | 0.37050128 | 0.37050128 | 0.2440538 | 0.4024193 | 1 | 2845 tags=43%, list=6%, signal=45% |
| REACTOME_PHOSPHORYLATION OF CD3 AND TCR ZETA CHAINS | REACTOME_PHOSPHORYLATION OF CD3 AND TCR ZETA CHAINS | 23 | 0.37021554 | 0.37021554 | 0.00409 | 0.4020297 | 1 | 28716 tags=96%, list=59%, signal=231% |
| REACTOME_SEMA4D IN SEMAPHORIN SIGNALING | REACTOME_SEMA4D IN SEMAPHORIN SIGNALING | 27 | 0.3694024 | 0.3694024 | 0.0019305 | 0.4034806 | 1 | 12751 tags=63%, list=26%, signal=85% |
| REACTOME_THE AIM2 INFLAMMASOME | REACTOME_THE AIM2 INFLAMMASOME | 3 | 0.36932728 | 0.36932728 | 0.6880642 | 0.4023813 | 1 | 30881 tags=100%, list=63%, signal=271% |
| REACTOME_METABOLISM OF ANGIOTENSINOGEN TO ANGIOTENSINS | REACTOME_METABOLISM OF ANGIOTENSINOGEN TO ANGIOTENSINS | 16 | 0.3688699 | 0.3688699 | 0.0194872 | 0.40270793 | 1 | 9486 tags=56%, list=19%, signal=70% |
| REACTOME_MITOCHONDRIAL TRNA AMINOACYLATION | REACTOME_MITOCHONDRIAL TRNA AMINOACYLATION | 21 | 0.368244 | 0.368244 | 0.0077519 | 0.4036165 | 1 | 14619 tags=67%, list=30%, signal=95% |
| REACTOME_GLYCOSPHINGOLIPID METABOLISM | REACTOME_GLYCOSPHINGOLIPID METABOLISM | 46 | 0.36726105 | 0.36726105 | 0 | 0.40577823 | 1 | 5451 tags=48%, list=11%, signal=54% |
| REACTOME_MET ACTIVATES RAS SIGNALING | REACTOME_MET ACTIVATES RAS SIGNALING | 11 | 0.36704218 | 0.36704218 | 0.0506586 | 0.40523508 | 1 | 8739 tags=55%, list=18%, signal=66% |
| REACTOME_NRCAM | REACTOME_NRCAM INTERACTIONS | 7 | 0.36639574 | 0.36639574 | 0.2237903 | 0.4062267 | 1 | 17036 tags=71%, list=35%, signal=110% |
| REACTOME_PHOSPHATE BOND HYDROLYSIS BY NTPDASE PROTEINS | REACTOME_PHOSPHATE BOND HYDROLYSIS BY NTPDASE PROTEINS | 8 | 0.36621422 | 0.36621422 | 0.1819106 | 0.4055142 | 1 | 18794 tags=75%, list=38%, signal=122% |
| REACTOME_N-GLYCAN TRIMMING IN THE ER AND CALNEXIN/CALRETICULIN CYCLE | REACTOME_N-GLYCAN TRIMMING IN THE ER AND CALNEXIN/CALRETICULIN CYCLE | 35 | 0.36212957 | 0.36212957 | 9.93E-04 | 0.41893065 | 1 | 10260 tags=57%, list=21%, signal=72% |
| REACTOME_CREB PHOSPHORYLATION | REACTOME_CREB PHOSPHORYLATION | 7 | 0.36100334 | 0.36100334 | 0.2535787 | 0.42165908 | 1 | 3310 tags=43%, list=7%, signal=46% |

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|---|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_DEX/H-BOX HELICASES ACTIVATE TYPE I IFN AND INFLAMMATORY CYTOKINES PRODUCTION | REACTOME_DEX/H-BOX HELICASES ACTIVATE TYPE I IFN AND INFLAMMATORY CYTOKINES PRODUCTION | 13 | 0.3603986 | 0.3603986 | 0.0510204 | 0.42254743 | 1 | 4956 tags=46%, list=10%, signal=51% |
| REACTOME_RETROGRADE NEUROTROPHIN SIGNALLING | REACTOME_RETROGRADE NEUROTROPHIN SIGNALLING | 14 | 0.3597884 | 0.3597884 | 0.0362538 | 0.42346293 | 1 | 10367 tags=57%, list=21%, signal=72% |
| REACTOME_DISEASES ASSOCIATED WITH VISUAL TRANSDUCTION | REACTOME_DISEASES ASSOCIATED WITH VISUAL TRANSDUCTION | 7 | 0.35943055 | 0.35943055 | 0.2632114 | 0.42341834 | 1 | 3387 tags=43%, list=7%, signal=46% |
| REACTOME_RETINOID CYCLE DISEASE EVENTS | REACTOME_RETINOID CYCLE DISEASE EVENTS | 7 | 0.35943055 | 0.35943055 | 0.2306911 | 0.42205247 | 1 | 3387 tags=43%, list=7%, signal=46% |
| REACTOME_PROCESSIVE SYNTHESIS ON THE LAGGING STRAND | REACTOME_PROCESSIVE SYNTHESIS ON THE LAGGING STRAND | 15 | 0.35886282 | 0.35886282 | 0.0319767 | 0.42271984 | 1 | 15076 tags=67%, list=31%, signal=96% |
| REACTOME_SIGNAL TRANSDUCTION BY L1 | REACTOME_SIGNAL TRANSDUCTION BY L1 | 21 | 0.35877058 | 0.35877058 | 0.0050302 | 0.42170224 | 1 | 12751 tags=62%, list=26%, signal=84% |
| REACTOME_EICOSANOID LIGAND- BINDING RECEPTORS | REACTOME_EICOSANOID LIGAND- BINDING RECEPTORS | 15 | 0.35672456 | 0.35672456 | 0.0363815 | 0.42784035 | 1 | 8652 tags=53%, list=18%, signal=65% |
| REACTOME_NICD TRAFFICS TO NUCLEUS | REACTOME_NICD TRAFFICS TO NUCLEUS | 13 | 0.35632396 | 0.35632396 | 0.0546341 | 0.42792612 | 1 | 8922 tags=54%, list=18%, signal=66% |
| REACTOME_NOTCH-HLH TRANSCRIPTION PATHWAY | REACTOME_NOTCH-HLH TRANSCRIPTION PATHWAY | 13 | 0.35632396 | 0.35632396 | 0.0608108 | 0.4265676 | 1 | 8922 tags=54%, list=18%, signal=66% |
| REACTOME_INTERACTION WITH THE ZONA PELLUCIDA | REACTOME_INTERACTION WITH THE ZONA PELLUCIDA | 10 | 0.3550097 | 0.3550097 | 0.14 | 0.42982212 | 1 | 26688 tags=90%, list=55%, signal=198% |
| REACTOME_RIP-MEDIATED NFKB ACTIVATION VIA ZBP1 | REACTOME_RIP-MEDIATED NFKB ACTIVATION VIA ZBP1 | 23 | 0.35338014 | 0.35338014 | 0.0050607 | 0.43449453 | 1 | 3993 tags=43%, list=8%, signal=47% |
| REACTOME_TERMINATION OF O- GLYCAN BIOSYNTHESIS | REACTOME_TERMINATION OF O- GLYCAN BIOSYNTHESIS | 25 | 0.35332653 | 0.35332653 | 0.0020387 | 0.4333078 | 1 | 8169 tags=52%, list=17%, signal=62% |
| REACTOME_NOD1/2 SIGNALING PATHWAY | REACTOME_NOD1/2 SIGNALING PATHWAY | 31 | 0.35192892 | 0.35192892 | 0 | 0.43715876 | 1 | 11209 tags=58%, list=23%, signal=75% |
| REACTOME_RUNX3 REGULATES P14-ARF | REACTOME_RUNX3 REGULATES P14- ARF | 10 | 0.35087326 | 0.35087326 | 0.1150713 | 0.4396838 | 1 | 12201 tags=60%, list=25%, signal=80% |
| REACTOME_XBP1(S) ACTIVATES CHAPERONE GENES | REACTOME_XBP1(S) ACTIVATES CHAPERONE GENES | 53 | 0.35076934 | 0.35076934 | 0 | 0.43874648 | 1 | 5015 tags=45%, list=10%, signal=50% |
| REACTOME_PLATELET DEGRANULATION | REACTOME_PLATELET DEGRANULATION | 128 | 0.35021618 | 0.35021618 | 0 | 0.43938982 | 1 | 12351 tags=60%, list=25%, signal=80% |
| REACTOME_NEF AND SIGNAL TRANSDUCTION | REACTOME_NEF AND SIGNAL TRANSDUCTION | 8 | 0.34938312 | 0.34938312 | 0.2492401 | 0.44109482 | 1 | 19618 tags=75%, list=40%, signal=125% |
| REACTOME_APOBEC3G MEDIATED RESISTANCE TO HIV-1 | REACTOME_APOBEC3G MEDIATED RESISTANCE TO HIV-1 INFECTION | 5 | 0.34932598 | 0.34932598 | 0.4582485 | 0.43997332 | 1 | 12275 tags=60%, list=25%, signal=80% |
| REACTOME_RUNX1 REGULATES EXPRESSION OF COMPONENTS OF TIGHT JUNCTIONS | REACTOME_RUNX1 REGULATES EXPRESSION OF COMPONENTS OF TIGHT JUNCTIONS | 5 | 0.34683415 | 0.34683415 | 0.4556098 | 0.4479447 | 1 | 2604 tags=40%, list=5%, signal=42% |
| REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN INTERLEUKIN SIGNALING | REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN INTERLEUKIN SIGNALING | 5 | 0.34683415 | 0.34683415 | 0.5 | 0.44657063 | 1 | 2604 tags=40%, list=5%, signal=42% |
| REACTOME_PHYSIOLOGICAL FACTORS | REACTOME_PHYSIOLOGICAL FACTORS | 12 | 0.34611773 | 0.34611773 | 0.0765358 | 0.44795004 | 1 | 7538 tags=50%, list=15%, signal=59% |
| REACTOME_ACTIVATION OF MATRIX METALLOPROTEINASES | REACTOME_ACTIVATION OF MATRIX METALLOPROTEINASES | 33 | 0.3459823 | 0.3459823 | 0.0010225 | 0.44709906 | 1 | 6810 tags=48%, list=14%, signal=56% |
| REACTOME_OVARIAN TUMOR DOMAIN PROTEASES | REACTOME_OVARIAN TUMOR DOMAIN PROTEASES | 38 | 0.34594074 | 0.34594074 | 0 | 0.4458941 | 1 | 3690 tags=42%, list=8%, signal=46% |

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| REACTOME_ACTIVATION OF IRF3/IRF7 MEDIATED BY TBK1/IKK EPSILON | REACTOME_ACTIVATION OF IRF3/IRF7 MEDIATED BY TBK1/IKK EPSILON | 18 | 0.3457311 | 0.3457311 | 0.0243902 | 0.44534117 | 1 | 7559 tags=50%, list=15%, signal=59% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF CASPASE ACTIVATORS AND CASPASES | REACTOME_TP53 REGULATES TRANSCRIPTION OF CASPASE ACTIVATORS AND CASPASES | 12 | 0.3454232 | 0.3454232 | 0.0833333 | 0.44519347 | 1 | 7572 tags=50%, list=15%, signal=59% |
| REACTOME_PENTOSE PHOSPHATE PATHWAY (HEXOSE MONOPHOSPHATE SHUNT) | REACTOME_PENTOSE PHOSPHATE PATHWAY (HEXOSE MONOPHOSPHATE SHUNT) | 15 | 0.3442152 | 0.3442152 | 0.0486815 | 0.44852263 | 1 | 6000 tags=47%, list=12%, signal=53% |
| REACTOME_DISEASES ASSOCIATED WITH GLYCOSAMINOGLYCAN | REACTOME_DISEASES ASSOCIATED WITH GLYCOSAMINOGLYCAN METABOLISM | 26 | 0.34371832 | 0.34371832 | 0.0010163 | 0.44906783 | 1 | 5777 tags=46%, list=12%, signal=52% |
| REACTOME_DEFECTIVE C1GALT1C1 CAUSES TN POLYAGGLUTINATION | REACTOME_DEFECTIVE C1GALT1C1 CAUSES TN POLYAGGLUTINATION SYNDROME (TNPS) | 17 | 0.34331393 | 0.34331393 | 0.0240964 | 0.44924432 | 1 | 17758 tags=71%, list=36%, signal=111% |
| REACTOME_DEFECTIVE GALNT12 CAUSES COLORECTAL CANCER 1 (CRCS1) | REACTOME_DEFECTIVE GALNT12 CAUSES COLORECTAL CANCER 1 (CRCS1) | 17 | 0.34331393 | 0.34331393 | 0.0300971 | 0.44790328 | 1 | 17758 tags=71%, list=36%, signal=111% |
| REACTOME_DEFECTIVE GALNT3 CAUSES FAMILIAL HYPERPHOSPHATEMIC TUMORAL CALCINOSIS (HFTC) | REACTOME_DEFECTIVE GALNT3 CAUSES FAMILIAL HYPERPHOSPHATEMIC TUMORAL CALCINOSIS (HFTC) | 17 | 0.34331393 | 0.34331393 | 0.0214724 | 0.44657028 | 1 | 17758 tags=71%, list=36%, signal=111% |
| REACTOME_INTERLEUKIN-10 SIGNALING | REACTOME_INTERLEUKIN-10 SIGNALING | 46 | 0.34318265 | 0.34318265 | 0 | 0.4457489 | 1 | 16209 tags=67%, list=33%, signal=101% |
| REACTOME_DEREGULATED CDK5 TRIGGERS MULTIPLE NEURODEGENERATIVE PATHWAYS IN ALZHEIMER'S | REACTOME_DEREGULATED CDK5 TRIGGERS MULTIPLE NEURODEGENERATIVE PATHWAYS IN ALZHEIMER'S DISEASE MODELS | 22 | 0.3409848 | 0.3409848 | 0.0112936 | 0.45264742 | 1 | 5567 tags=45%, list=11%, signal=51% |
| REACTOME_NEURODEGENERATIVE DISEASES | REACTOME_NEURODEGENERATIVE DISEASES | 22 | 0.3409848 | 0.3409848 | 0.0050201 | 0.45131215 | 1 | 5567 tags=45%, list=11%, signal=51% |
| REACTOME_ZINC | REACTOME_ZINC TRANSPORTERS | 17 | 0.3400884 | 0.3400884 | 0.0317164 | 0.45329422 | 1 | 9275 tags=53%, list=19%, signal=65% |
| REACTOME_INTERLEUKIN-9 SIGNALING | REACTOME_INTERLEUKIN-9 SIGNALING | 3 | 0.33973968 | 0.33973968 | 0.7805826 | 0.45340908 | 1 | 16008 tags=67%, list=33%, signal=99% |
| REACTOME_SIGNALING BY PTK6 | REACTOME_SIGNALING BY PTK6 | 59 | 0.3393712 | 0.3393712 | 0 | 0.45344183 | 1 | 9959 tags=54%, list=20%, signal=68% |
| REACTOME_PROTON/OLIGOPEPTIDE COTRANSPORTERS | REACTOME_PROTON/OLIGOPEPTIDE COTRANSPORTERS | 4 | 0.33852455 | 0.33852455 | 0.626601 | 0.45519406 | 1 | 7907 tags=50%, list=16%, signal=60% |
| REACTOME_LIGAND-RECEPTOR INTERACTIONS | REACTOME_LIGAND-RECEPTOR INTERACTIONS | 8 | 0.33820495 | 0.33820495 | 0.2634731 | 0.45502344 | 1 | 7924 tags=50%, list=16%, signal=60% |
| REACTOME_HS-GAG | REACTOME_HS-GAG BIOSYNTHESIS | 31 | 0.3377551 | 0.3377551 | 0.002006 | 0.45540106 | 1 | 4005 tags=42%, list=8%, signal=46% |
| REACTOME_RESPONSE TO ELEVATED PLATELET CYTOSOLIC CA2+ | REACTOME_RESPONSE TO ELEVATED PLATELET CYTOSOLIC CA2+ | 133 | 0.33683047 | 0.33683047 | 0 | 0.45763665 | 1 | 7113 tags=48%, list=15%, signal=56% |
| REACTOME_CELL JUNCTION ORGANIZATION | REACTOME_CELL JUNCTION ORGANIZATION | 87 | 0.33623007 | 0.33623007 | 0 | 0.4585941 | 1 | 13394 tags=61%, list=27%, signal=84% |
| REACTOME_SYNTHESIS OF EPOXY (EET) AND DIHYDROXYEICOSATRIENOIC ACIDS (DHET) | REACTOME_SYNTHESIS OF EPOXY (EET) AND DIHYDROXYEICOSATRIENOIC ACIDS (DHET) | 8 | 0.335907 | 0.335907 | 0.2512219 | 0.45855284 | 1 | 32519 tags=100%, list=66%, signal=298% |
| REACTOME_LEADING STRAND SYNTHESIS | REACTOME_LEADING STRAND SYNTHESIS | 14 | 0.33503914 | 0.33503914 | 0.0704663 | 0.46068445 | 1 | 15076 tags=64%, list=31%, signal=93% |
| REACTOME_POLYMERASE SWITCHING | REACTOME_POLYMERASE SWITCHING | 14 | 0.33503914 | 0.33503914 | 0.0549793 | 0.4593682 | 1 | 15076 tags=64%, list=31%, signal=93% |

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| REACTOME_POLYMERASE SWITCHING ON THE C-STRAND OF THE TELOMERE | REACTOME_POLYMERASE SWITCHING ON THE C-STRAND OF THE TELOMERE | 14 | 0.33503914 | 0.33503914 | 0.0720632 | 0.45805946 | 1 | 15076 tags=64%, list=31%, signal=93% |
| REACTOME_REMOVAL OF THE FLAP INTERMEDIATE | REACTOME_REMOVAL OF THE FLAP INTERMEDIATE | 14 | 0.33503914 | 0.33503914 | 0.0414079 | 0.45675814 | 1 | 15076 tags=64%, list=31%, signal=93% |
| REACTOME_ACYL CHAIN REMODELLING OF PI | REACTOME_ACYL CHAIN REMODELLING OF PI | 17 | 0.33278054 | 0.33278054 | 0.026 | 0.4642657 | 1 | 12513 tags=59%, list=26%, signal=79% |
| REACTOME_GAP JUNCTION TRAFFICKING | REACTOME_GAP JUNCTION TRAFFICKING | 28 | 0.33046573 | 0.33046573 | 9.75E-04 | 0.4724442 | 1 | 11807 tags=57%, list=24%, signal=75% |
| REACTOME_VLDL ASSEMBLY | REACTOME_VLDL ASSEMBLY | 5 | 0.33018792 | 0.33018792 | 0.547379 | 0.4721829 | 1 | 13212 tags=60%, list=27%, signal=82% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF CELL DEATH GENES | REACTOME_TP53 REGULATES TRANSCRIPTION OF CELL DEATH GENES | 44 | 0.3267583 | 0.3267583 | 0 | 0.48499945 | 1 | 9609 tags=52%, list=20%, signal=65% |
| REACTOME_5-PHOSPHORIBOSE 1-DIPHOSPHATE BIOSYNTHESIS | REACTOME_5-PHOSPHORIBOSE 1-DIPHOSPHATE BIOSYNTHESIS | 3 | 0.32643002 | 0.32643002 | 0.8092428 | 0.48495108 | 1 | 338 tags=33%, list=1%, signal=34% |
| REACTOME_METAL ION SLC TRANSPORTERS | REACTOME_METAL ION SLC TRANSPORTERS | 26 | 0.32621774 | 0.32621774 | 0.0112016 | 0.48454 | 1 | 10400 tags=54%, list=21%, signal=68% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF GENES INVOLVED IN G2 CELL CYCLE ARREST | REACTOME_TP53 REGULATES TRANSCRIPTION OF GENES INVOLVED IN G2 CELL CYCLE ARREST | 18 | 0.3261941 | 0.3261941 | 0.0241206 | 0.48327252 | 1 | 5795 tags=44%, list=12%, signal=50% |
| REACTOME_ZBP1(DAI) MEDIATED INDUCTION OF TYPE I IFNS | REACTOME_ZBP1(DAI) MEDIATED INDUCTION OF TYPE I IFNS | 27 | 0.32601872 | 0.32601872 | 0.008 | 0.4826433 | 1 | 3993 tags=41%, list=8%, signal=44% |
| REACTOME_KERATAN SULFATE BIOSYNTHESIS | REACTOME_KERATAN SULFATE BIOSYNTHESIS | 28 | 0.3259446 | 0.3259446 | 0.007992 | 0.4816153 | 1 | 6782 tags=46%, list=14%, signal=54% |
| REACTOME_ACTIVATION, MYRISTOLYLATION OF BID AND TRANSLOCATION TO MITOCHONDRIA | REACTOME_ACTIVATION, MYRISTOLYLATION OF BID AND TRANSLOCATION TO MITOCHONDRIA | 4 | 0.3257593 | 0.3257593 | 0.6922301 | 0.48105133 | 1 | 8532 tags=50%, list=17%, signal=61% |
| REACTOME_SIGNALING BY MET | REACTOME_SIGNALING BY MET | 67 | 0.3257112 | 0.3257112 | 0 | 0.47992882 | 1 | 5997 tags=45%, list=12%, signal=51% |
| REACTOME_DISEASES ASSOCIATED WITH O-GLYCOSYLATION OF PROTEINS | REACTOME_DISEASES ASSOCIATED WITH O-GLYCOSYLATION OF PROTEINS | 59 | 0.3248688 | 0.3248688 | 0 | 0.48215875 | 1 | 13158 tags=59%, list=27%, signal=81% |
| REACTOME_P130CAS LINKAGE TO MAPK SIGNALING FOR CELL MIGRATION AND GROWTH-CONE COLLAPSE | REACTOME_P130CAS LINKAGE TO MAPK SIGNALING FOR INTEGRINS | 15 | 0.32432416 | 0.32432416 | 0.0572597 | 0.48316708 | 1 | 20031 tags=73%, list=41%, signal=124% |
| REACTOME_SEMA4D INDUCED CELL MIGRATION AND GROWTH-CONE COLLAPSE | REACTOME_SEMA4D INDUCED CELL MIGRATION AND GROWTH-CONE COLLAPSE | 24 | 0.32306078 | 0.32306078 | 0.0154589 | 0.48703265 | 1 | 12751 tags=58%, list=26%, signal=79% |
| REACTOME_ATF6 (ATF6-ALPHA) ACTIVATES CHAPERONE GENES | REACTOME_ATF6 (ATF6-ALPHA) ACTIVATES CHAPERONE GENES | 9 | 0.32244602 | 0.32244602 | 0.229572 | 0.48819318 | 1 | 535 tags=33%, list=1%, signal=34% |
| REACTOME_CONSTITUTIVE SIGNALING BY EGFRVIII | REACTOME_CONSTITUTIVE SIGNALING BY EGFRVIII | 15 | 0.32221317 | 0.32221317 | 0.0761079 | 0.4878116 | 1 | 7077 tags=47%, list=14%, signal=55% |
| REACTOME_SIGNALING BY EGFRVIII IN CANCER | REACTOME_SIGNALING BY EGFRVIII IN CANCER | 15 | 0.32221317 | 0.32221317 | 0.0884692 | 0.4864896 | 1 | 7077 tags=47%, list=14%, signal=55% |
| REACTOME_ACTIVATION OF CASPASES THROUGH APOPTOSOME-MEDIATED CLEAVAGE | REACTOME_ACTIVATION OF CASPASES THROUGH APOPTOSOME-MEDIATED CLEAVAGE | 5 | 0.3221201 | 0.3221201 | 0.5777549 | 0.48554355 | 1 | 3814 tags=40%, list=8%, signal=43% |
| REACTOME_CYTOCHROME C-MEDIATED APOPTOTIC RESPONSE | REACTOME_CYTOCHROME C-MEDIATED APOPTOTIC RESPONSE | 5 | 0.3221201 | 0.3221201 | 0.5888224 | 0.4842348 | 1 | 3814 tags=40%, list=8%, signal=43% |
| REACTOME_SIGNALING BY HIPPO | REACTOME_SIGNALING BY HIPPO | 20 | 0.32204005 | 0.32204005 | 0.0256158 | 0.48329425 | 1 | 16064 tags=65%, list=33%, signal=97% |
| REACTOME_MET RECEPTOR ACTIVATION | REACTOME_MET RECEPTOR ACTIVATION | 6 | 0.3215446 | 0.3215446 | 0.4699507 | 0.48419136 | 1 | 8739 tags=50%, list=18%, signal=61% |
| REACTOME_CHEMOKINE RECEPTORS BIND CHEMOKINES | REACTOME_CHEMOKINE RECEPTORS BIND CHEMOKINES | 48 | 0.32017118 | 0.32017118 | 0 | 0.488584 | 1 | 11880 tags=56%, list=24%, signal=74% |

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| REACTOME_P75NTR RECRUITS SIGNALLING COMPLEXES | REACTOME_P75NTR RECRUITS SIGNALLING COMPLEXES | 13 | 0.31900167 | 0.31900167 | 0.1118744 | 0.4921977 | 1 | 10749 tags=54%, list=22%, signal=69% |
| REACTOME_RORA ACTIVATES GENE EXPRESSION | REACTOME_RORA ACTIVATES GENE EXPRESSION | 27 | 0.31864506 | 0.31864506 | 0.0049702 | 0.49239174 | 1 | 18862 tags=70%, list=39%, signal=114% |
| REACTOME_FMO OXIDISES NUCLEOPHILES | REACTOME_FMO OXIDISES NUCLEOPHILES | 3 | 0.3183898 | 0.3183898 | 0.8087649 | 0.492166 | 1 | 33375 tags=100%, list=68%, signal=314% |
| REACTOME_TGF-BETA RECEPTOR SIGNALING IN EMT (EPITHELIAL TO MESENCHYMAL TRANSITION) | REACTOME_TGF-BETA RECEPTOR SIGNALING IN EMT (EPITHELIAL TO MESENCHYMAL TRANSITION) | 16 | 0.3183556 | 0.3183556 | 0.0634441 | 0.49099642 | 1 | 5838 tags=44%, list=12%, signal=50% |
| REACTOME_PRE-NOTCH EXPRESSION AND PROCESSING | REACTOME_PRE-NOTCH EXPRESSION AND PROCESSING | 48 | 0.31807962 | 0.31807962 | 0 | 0.4908356 | 1 | 8922 tags=50%, list=18%, signal=61% |
| REACTOME_IL-6-TYPE CYTOKINE RECEPTOR LIGAND | REACTOME_IL-6-TYPE CYTOKINE RECEPTOR LIGAND INTERACTIONS | 17 | 0.3177586 | 0.3177586 | 0.0471888 | 0.49087837 | 1 | 10368 tags=53%, list=21%, signal=67% |
| REACTOME_DNA STRAND ELONGATION | REACTOME_DNA STRAND ELONGATION | 32 | 0.31729355 | 0.31729355 | 0.004012 | 0.49152935 | 1 | 15076 tags=63%, list=31%, signal=90% |
| REACTOME_INTERLEUKIN-4 AND 13 SIGNALING | REACTOME_INTERLEUKIN-4 AND 13 SIGNALING | 111 | 0.31725067 | 0.31725067 | 0 | 0.49039626 | 1 | 19349 tags=71%, list=40%, signal=117% |
| REACTOME_DEFECTS IN COBALAMIN (B12) METABOLISM | REACTOME_DEFECTS IN COBALAMIN (B12) METABOLISM | 11 | 0.31695434 | 0.31695434 | 0.1525424 | 0.49033982 | 1 | 11191 tags=55%, list=23%, signal=71% |
| REACTOME_DNA DAMAGE REVERSAL | REACTOME_DNA DAMAGE REVERSAL | 8 | 0.31692863 | 0.31692863 | 0.3190377 | 0.48916465 | 1 | 2845 tags=38%, list=6%, signal=40% |
| REACTOME_P75NTR NEGATIVELY REGULATES CELL CYCLE VIA SC1 | REACTOME_P75NTR NEGATIVELY REGULATES CELL CYCLE VIA SC1 | 6 | 0.3162306 | 0.3162306 | 0.4829015 | 0.4908527 | 1 | 17160 tags=67%, list=35%, signal=103% |
| REACTOME_GLYCOGEN | REACTOME_GLYCOGEN SYNTHESIS | 16 | 0.3148966 | 0.3148966 | 0.0800801 | 0.49507472 | 1 | 2947 tags=38%, list=6%, signal=40% |
| REACTOME_POST-TRANSCRIPTIONAL SILENCING BY SMALL RNAS | REACTOME_POST-TRANSCRIPTIONAL SILENCING BY SMALL RNAS | 3 | 0.3145773 | 0.3145773 | 0.8481519 | 0.49507976 | 1 | 17240 tags=67%, list=35%, signal=103% |
| REACTOME_PLASMA LIPOPROTEIN ASSEMBLY, REMODELING, AND CLEARANCE | REACTOME_PLASMA LIPOPROTEIN ASSEMBLY, REMODELING, AND CLEARANCE | 71 | 0.3134579 | 0.3134579 | 0 | 0.49850306 | 1 | 13638 tags=59%, list=28%, signal=82% |
| REACTOME_RESOLUTION OF D-LOOP STRUCTURES | REACTOME_RESOLUTION OF D-LOOP STRUCTURES | 32 | 0.31262007 | 0.31262007 | 0.003012 | 0.50095123 | 1 | 18365 tags=69%, list=38%, signal=110% |
| REACTOME_JOSEPHIN DOMAIN DUBS | REACTOME_JOSEPHIN DOMAIN DUBS | 12 | 0.31214637 | 0.31214637 | 0.1538462 | 0.50158936 | 1 | 9201 tags=50%, list=19%, signal=62% |
| REACTOME_INTERFERON ALPHA/BETA SIGNALING | REACTOME_INTERFERON ALPHA/BETA SIGNALING | 67 | 0.31174183 | 0.31174183 | 0 | 0.50209254 | 1 | 11065 tags=54%, list=23%, signal=69% |
| REACTOME_PURINE | REACTOME_PURINE CATABOLISM | 18 | 0.3101972 | 0.3101972 | 0.0506823 | 0.5071841 | 1 | 6578 tags=44%, list=13%, signal=51% |
| REACTOME_GAMMA-CARBOXYLATION, TRANSPORT, AND AMINO-TERMINAL CLEAVAGE OF PROTEINS | REACTOME_GAMMA-CARBOXYLATION, TRANSPORT, AND AMINO-TERMINAL CLEAVAGE OF PROTEINS | 11 | 0.30968776 | 0.30968776 | 0.1880597 | 0.5080683 | 1 | 2644 tags=36%, list=5%, signal=38% |
| REACTOME_LOSS OF FUNCTION OF SMAD2/3 IN CANCER | REACTOME_LOSS OF FUNCTION OF SMAD2/3 IN CANCER | 7 | 0.30936724 | 0.30936724 | 0.4157303 | 0.5081307 | 1 | 5838 tags=43%, list=12%, signal=49% |
| REACTOME_SMAD2/3 MH2 DOMAIN MUTANTS IN CANCER | REACTOME_SMAD2/3 MH2 DOMAIN MUTANTS IN CANCER | 7 | 0.30936724 | 0.30936724 | 0.4249513 | 0.50684434 | 1 | 5838 tags=43%, list=12%, signal=49% |
| REACTOME_GROWTH HORMONE RECEPTOR SIGNALING | REACTOME_GROWTH HORMONE RECEPTOR SIGNALING | 22 | 0.30915186 | 0.30915186 | 0.0258373 | 0.5064254 | 1 | 7125 tags=45%, list=15%, signal=53% |
| REACTOME_PTK6 REGULATES CELL CYCLE | REACTOME_PTK6 REGULATES CELL CYCLE | 6 | 0.30687925 | 0.30687925 | 0.5341797 | 0.51457417 | 1 | 9457 tags=50%, list=19%, signal=62% |
| REACTOME_O-LINKED GLYCOSYLATION OF MUCINS | REACTOME_O-LINKED GLYCOSYLATION OF MUCINS | 65 | 0.30573383 | 0.30573383 | 0 | 0.51821655 | 1 | 12921 tags=57%, list=26%, signal=77% |

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| REACTOME_CYTOSOLIC TRNA AMINOACYLATION | REACTOME_CYTOSOLIC TRNA AMINOACYLATION | 24 | 0.30567676 | 0.30567676 | 0.019861 | 0.51715195 | 1 | 15642 tags=63%, list=32%, signal=92% |
| REACTOME_GAP JUNCTION TRAFFICKING AND REGULATION | REACTOME_GAP JUNCTION TRAFFICKING AND REGULATION | 30 | 0.305429 | 0.305429 | 0.0070922 | 0.5168886 | 1 | 16064 tags=63%, list=33%, signal=94% |
| REACTOME_HIGHLY CALCIUM PERMEABLE POSTSYNAPTIC NICOTINIC ACETYLCHOLINE RECEPTORS | REACTOME_HIGHLY CALCIUM PERMEABLE POSTSYNAPTIC NICOTINIC ACETYLCHOLINE RECEPTORS | 11 | 0.30426154 | 0.30426154 | 0.1935484 | 0.5204392 | 1 | 7361 tags=45%, list=15%, signal=53% |
| REACTOME_DOWNREGULATION OF ERBB2 SIGNALING | REACTOME_DOWNREGULATION OF ERBB2 SIGNALING | 29 | 0.3039036 | 0.3039036 | 0.0069583 | 0.52065074 | 1 | 7077 tags=45%, list=14%, signal=52% |
| REACTOME_P38MAPK EVENTS | REACTOME_P38MAPK EVENTS | 13 | 0.30358154 | 0.30358154 | 0.1329423 | 0.5206759 | 1 | 26570 tags=85%, list=54%, signal=185% |
| REACTOME_MRNA EDITING | REACTOME_MRNA EDITING | 9 | 0.3032973 | 0.3032973 | 0.2979146 | 0.5206047 | 1 | 6913 tags=44%, list=14%, signal=52% |
| REACTOME_RESOLUTION OF D-LOOP STRUCTURES THROUGH HOLLIDAY JUNCTION | REACTOME_RESOLUTION OF D-LOOP STRUCTURES THROUGH HOLLIDAY JUNCTION INTERMEDIATES | 31 | 0.30252662 | 0.30252662 | 0.0076923 | 0.52266186 | 1 | 18365 tags=68%, list=38%, signal=108% |
| REACTOME_RHO GTPASES ACTIVATE ROCKS | REACTOME_RHO GTPASES ACTIVATE ROCKS | 18 | 0.3017595 | 0.3017595 | 0.0574018 | 0.52467215 | 1 | 6991 tags=44%, list=14%, signal=52% |
| REACTOME_OTHER INTERLEUKIN SIGNALING | REACTOME_OTHER INTERLEUKIN SIGNALING | 34 | 0.3012928 | 0.3012928 | 0.0020222 | 0.5254317 | 1 | 29901 tags=91%, list=61%, signal=234% |
| REACTOME_CARGO CONCENTRATION IN THE ER | REACTOME_CARGO CONCENTRATION IN THE ER | 33 | 0.3010963 | 0.3010963 | 0.0038835 | 0.52499 | 1 | 4555 tags=39%, list=9%, signal=43% |
| REACTOME_WAX BIOSYNTHESIS | REACTOME_WAX BIOSYNTHESIS | 4 | 0.3010917 | 0.3010917 | 0.7664974 | 0.5237187 | 1 | 21981 tags=75%, list=45%, signal=136% |
| REACTOME_REGULATION OF TP53 ACTIVITY THROUGH ASSOCIATION WITH CO-FACTORS | REACTOME_REGULATION OF TP53 ACTIVITY THROUGH ASSOCIATION WITH CO-FACTORS | 14 | 0.30081105 | 0.30081105 | 0.13381 | 0.5236963 | 1 | 20249 tags=71%, list=41%, signal=122% |
| REACTOME_ESTABLISHMENT OF SISTER CHROMATID COHESION | REACTOME_ESTABLISHMENT OF SISTER CHROMATID COHESION | 11 | 0.3005326 | 0.3005326 | 0.208498 | 0.5236051 | 1 | 25349 tags=82%, list=52%, signal=170% |
| REACTOME_NUCLEOTIDE-LIKE (PURINERGIC) RECEPTORS | REACTOME_NUCLEOTIDE-LIKE (PURINERGIC) RECEPTORS | 15 | 0.30039498 | 0.30039498 | 0.1009901 | 0.5229677 | 1 | 8145 tags=47%, list=17%, signal=56% |
| REACTOME_GAP JUNCTION ASSEMBLY | REACTOME_GAP JUNCTION ASSEMBLY | 19 | 0.30032992 | 0.30032992 | 0.0571705 | 0.52198696 | 1 | 8493 tags=47%, list=17%, signal=57% |
| REACTOME_REGULATION OF RUNX1 EXPRESSION AND ACTIVITY | REACTOME_REGULATION OF RUNX1 EXPRESSION AND ACTIVITY | 17 | 0.2999582 | 0.2999582 | 0.075 | 0.52229303 | 1 | 8359 tags=47%, list=17%, signal=57% |
| REACTOME_DDX58/IFIH1-MEDIATED INDUCTION OF INTERFERON-ALPHA/BETA | REACTOME_DDX58/IFIH1-MEDIATED INDUCTION OF INTERFERON-ALPHA/BETA | 80 | 0.29988238 | 0.29988238 | 0 | 0.52132076 | 1 | 12270 tags=55%, list=25%, signal=73% |
| REACTOME_TRNA AMINOACYLATION | REACTOME_TRNA AMINOACYLATION | 42 | 0.29983172 | 0.29983172 | 0 | 0.5203068 | 1 | 15642 tags=62%, list=32%, signal=91% |
| REACTOME_EPH-EPHRIN SIGNALING | REACTOME_EPH-EPHRIN SIGNALING | 95 | 0.29930213 | 0.29930213 | 0 | 0.52134675 | 1 | 12174 tags=55%, list=25%, signal=73% |
| REACTOME_GAMMA CARBOXYLATION, HYPUSINE FORMATION AND ARYLSULFATASE ACTIVATION | REACTOME_GAMMA CARBOXYLATION, HYPUSINE FORMATION AND ARYLSULFATASE ACTIVATION | 39 | 0.29914984 | 0.29914984 | 0 | 0.5206644 | 1 | 5451 tags=41%, list=11%, signal=46% |
| REACTOME_METABOLISM OF CARBOHYDRATES | REACTOME_METABOLISM OF CARBOHYDRATES | 271 | 0.29678404 | 0.29678404 | 0 | 0.5294922 | 1 | 7410 tags=45%, list=15%, signal=52% |
| REACTOME_DISEASES OF GLYCOSYLATION | REACTOME_DISEASES OF GLYCOSYLATION | 85 | 0.2964776 | 0.2964776 | 0 | 0.5295876 | 1 | 13158 tags=56%, list=27%, signal=77% |
| REACTOME_UNFOLDED PROTEIN RESPONSE (UPR) | REACTOME_UNFOLDED PROTEIN RESPONSE (UPR) | 93 | 0.2958283 | 0.2958283 | 0 | 0.5311535 | 1 | 7128 tags=44%, list=15%, signal=51% |
| REACTOME_ARACHIDONATE PRODUCTION FROM DAG | REACTOME_ARACHIDONATE PRODUCTION FROM DAG | 5 | 0.2956495 | 0.2956495 | 0.6901408 | 0.5307092 | 1 | 24696 tags=80%, list=50%, signal=161% |
| REACTOME_CYTOSOLIC IRON-SULFUR CLUSTER ASSEMBLY | REACTOME_CYTOSOLIC IRON-SULFUR CLUSTER ASSEMBLY | 13 | 0.2951714 | 0.2951714 | 0.1914894 | 0.5316405 | 1 | 8149 tags=46%, list=17%, signal=55% |
| REACTOME_NECTIN/NECL TRANS HETERODIMERIZATION | REACTOME_NECTIN/NECL TRANS HETERODIMERIZATION | 7 | 0.29433396 | 0.29433396 | 0.4744233 | 0.5341229 | 1 | 20564 tags=71%, list=42%, signal=123% |
| REACTOME_GLYCOLYSIS | REACTOME_GLYCOLYSIS | 70 | 0.29320994 | 0.29320994 | 0 | 0.53766733 | 1 | 7347 tags=44%, list=15%, signal=52% |

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| REACTOME_CLASSICAL ANTIBODY-MEDIATED COMPLEMENT ACTIVATION | REACTOME_CLASSICAL ANTIBODY-MEDIATED COMPLEMENT ACTIVATION | 83 | 0.29315418 | 0.29315418 | 0 | 0.5366456 | 1 | 25195 tags=81%, list=51%, signal=166% |
| REACTOME_RHO GTPASES ACTIVATE PAKS | REACTOME_RHO GTPASES ACTIVATE PAKS | 21 | 0.29294705 | 0.29294705 | 0.0360531 | 0.5362289 | 1 | 20636 tags=71%, list=42%, signal=123% |
| REACTOME_LAGGING STRAND SYNTHESIS | REACTOME_LAGGING STRAND SYNTHESIS | 20 | 0.29220554 | 0.29220554 | 0.0540541 | 0.53817743 | 1 | 15076 tags=60%, list=31%, signal=87% |
| REACTOME_WNT MEDIATED ACTIVATION OF DVL | REACTOME_WNT MEDIATED ACTIVATION OF DVL | 8 | 0.29210836 | 0.29210836 | 0.4041096 | 0.53731424 | 1 | 22422 tags=75%, list=46%, signal=138% |
| REACTOME_REGULATION OF CHOLESTEROL BIOSYNTHESIS BY SREBP (SREBF) | REACTOME_REGULATION OF CHOLESTEROL BIOSYNTHESIS BY SREBP (SREBF) | 55 | 0.29066187 | 0.29066187 | 0 | 0.5421619 | 1 | 6259 tags=42%, list=13%, signal=48% |
| REACTOME_INTERLEUKIN-35 SIGNALLING | REACTOME_INTERLEUKIN-35 SIGNALLING | 7 | 0.29002416 | 0.29002416 | 0.5093966 | 0.54367155 | 1 | 34765 tags=100%, list=71%, signal=345% |
| REACTOME_ACYL CHAIN REMODELLING OF PS | REACTOME_ACYL CHAIN REMODELLING OF PS | 22 | 0.29001456 | 0.29001456 | 0.0392562 | 0.54246366 | 1 | 12513 tags=55%, list=26%, signal=73% |
| REACTOME_MET ACTIVATES | REACTOME_MET ACTIVATES PTPN11 | 5 | 0.28968546 | 0.28968546 | 0.6900585 | 0.54264116 | 1 | 34781 tags=100%, list=71%, signal=345% |
| REACTOME_ORGANIC CATION TRANSPORT | REACTOME_ORGANIC CATION TRANSPORT | 9 | 0.28930515 | 0.28930515 | 0.3564357 | 0.54304224 | 1 | 7598 tags=44%, list=16%, signal=53% |
| REACTOME_SIGNALING BY | REACTOME_SIGNALING BY ACTIVIN | 13 | 0.28858253 | 0.28858253 | 0.1863231 | 0.5449764 | 1 | 4705 tags=38%, list=10%, signal=43% |
| REACTOME_RECYCLING PATHWAY OF L1 | REACTOME_RECYCLING PATHWAY OF L1 | 28 | 0.28842187 | 0.28842187 | 0.0110664 | 0.54445636 | 1 | 10367 tags=50%, list=21%, signal=63% |
| REACTOME_O-LINKED GLYCOSYLATION | REACTOME_O-LINKED GLYCOSYLATION | 114 | 0.28835642 | 0.28835642 | 0 | 0.5435201 | 1 | 10395 tags=50%, list=21%, signal=63% |
| REACTOME_REGULATION OF KIT SIGNALING | REACTOME_REGULATION OF KIT SIGNALING | 16 | 0.28815323 | 0.28815323 | 0.118593 | 0.5431579 | 1 | 13437 tags=56%, list=27%, signal=77% |
| REACTOME_REACTIONS SPECIFIC TO THE COMPLEX N-GLYCAN SYNTHESIS PATHWAY | REACTOME_REACTIONS SPECIFIC TO THE COMPLEX N-GLYCAN SYNTHESIS PATHWAY | 10 | 0.2870289 | 0.2870289 | 0.3346939 | 0.5467845 | 1 | 20223 tags=70%, list=41%, signal=119% |
| REACTOME_PRE-NOTCH TRANSCRIPTION AND | REACTOME_PRE-NOTCH TRANSCRIPTION AND TRANSLATION | 32 | 0.28670517 | 0.28670517 | 0.009901 | 0.54692364 | 1 | 8922 tags=47%, list=18%, signal=57% |
| REACTOME_SIGNALING BY | REACTOME_SIGNALING BY NOTCH2 | 32 | 0.28670517 | 0.28670517 | 0.0133333 | 0.54568344 | 1 | 8922 tags=47%, list=18%, signal=57% |
| REACTOME_VITAMINS B6 ACTIVATION TO PYRIDOXAL PHOSPHATE | REACTOME_VITAMINS B6 ACTIVATION TO PYRIDOXAL PHOSPHATE | 3 | 0.28639898 | 0.28639898 | 0.9170041 | 0.5457979 | 1 | 2298 tags=33%, list=5%, signal=35% |
| REACTOME_TAK1 ACTIVATES NFKB BY PHOSPHORYLATION AND ACTIVATION OF IKKS | REACTOME_TAK1 ACTIVATES NFKB BY PHOSPHORYLATION AND ACTIVATION OF IKKS COMPLEX | 30 | 0.28527302 | 0.28527302 | 0.0092402 | 0.54937786 | 1 | 3993 tags=37%, list=8%, signal=40% |
| REACTOME_MET ACTIVATES RAP1 AND RAC1 | REACTOME_MET ACTIVATES RAP1 AND RAC1 | 11 | 0.28508767 | 0.28508767 | 0.2602339 | 0.5489587 | 1 | 12751 tags=55%, list=26%, signal=74% |
| REACTOME_INTEGRIN ALPHAII B BETA3 SIGNALING | REACTOME_INTEGRIN ALPHAII B BETA3 SIGNALING | 27 | 0.28506893 | 0.28506893 | 0.0219342 | 0.5477947 | 1 | 5997 tags=41%, list=12%, signal=46% |
| REACTOME_GRB7 EVENTS IN ERBB2 SIGNALING | REACTOME_GRB7 EVENTS IN ERBB2 SIGNALING | 5 | 0.2850286 | 0.2850286 | 0.7175421 | 0.5467253 | 1 | 5630 tags=40%, list=11%, signal=45% |
| REACTOME_ER QUALITY CONTROL COMPARTMENT | REACTOME_ER QUALITY CONTROL COMPARTMENT (ERQC) | 21 | 0.28476763 | 0.28476763 | 0.0561685 | 0.5466526 | 1 | 9378 tags=48%, list=19%, signal=59% |
| REACTOME_HSF1-DEPENDENT TRANSACTIVATION | REACTOME_HSF1-DEPENDENT TRANSACTIVATION | 34 | 0.28333655 | 0.28333655 | 0.0112821 | 0.5517544 | 1 | 14938 tags=59%, list=31%, signal=85% |
| REACTOME_INTERFERON GAMMA SIGNALING | REACTOME_INTERFERON GAMMA SIGNALING | 91 | 0.2830245 | 0.2830245 | 0 | 0.5519354 | 1 | 10918 tags=51%, list=22%, signal=65% |
| REACTOME_REGULATION OF INNATE IMMUNE RESPONSES TO CYTOSOLIC DNA | REACTOME_REGULATION OF INNATE IMMUNE RESPONSES TO CYTOSOLIC DNA | 14 | 0.28219038 | 0.28219038 | 0.1831276 | 0.55434406 | 1 | 3673 tags=36%, list=8%, signal=39% |
| REACTOME_MTF1 ACTIVATES GENE EXPRESSION | REACTOME_MTF1 ACTIVATES GENE EXPRESSION | 3 | 0.2820691 | 0.2820691 | 0.9322866 | 0.5536595 | 1 | 2510 tags=33%, list=5%, signal=35% |

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|--|--|----|------------|------------|-----------|------------|---|--|
| REACTOME_INITIAL TRIGGERING OF COMPLEMENT | REACTOME_INITIAL TRIGGERING OF COMPLEMENT | 98 | 0.28191096 | 0.28191096 | 0 | 0.5530564 | 1 | 25195 tags=80%, list=51%, signal=164% |
| REACTOME_EGFR TRANSACTIVATION BY GASTRIN | REACTOME_EGFR TRANSACTIVATION BY GASTRIN | 9 | 0.28156805 | 0.28156805 | 0.3985944 | 0.55336887 | 1 | 29739 tags=89%, list=61%, signal=226% |
| REACTOME_EPH-EPHRIN MEDIATED REPULSION OF CELLS | REACTOME_EPH-EPHRIN MEDIATED REPULSION OF CELLS | 48 | 0.28151172 | 0.28151172 | 0.0019666 | 0.55239636 | 1 | 12751 tags=54%, list=26%, signal=73% |
| REACTOME_ADVANCED GLYCOSYLATION ENDPRODUCT RECEPTOR SIGNALING | REACTOME_ADVANCED GLYCOSYLATION ENDPRODUCT RECEPTOR SIGNALING | 13 | 0.28119698 | 0.28119698 | 0.2077922 | 0.5525913 | 1 | 1300 tags=31%, list=3%, signal=32% |
| REACTOME_CHOLINE | REACTOME_CHOLINE CATABOLISM | 6 | 0.28053066 | 0.28053066 | 0.6632653 | 0.5541742 | 1 | 10747 tags=50%, list=22%, signal=64% |
| REACTOME_MAP3K8 (TPL2)-DEPENDENT MAPK1/3 | REACTOME_MAP3K8 (TPL2)-DEPENDENT MAPK1/3 ACTIVATION | 16 | 0.28041813 | 0.28041813 | 0.1189516 | 0.55345047 | 1 | 7695 tags=44%, list=16%, signal=52% |
| REACTOME_METABOLISM OF NITRIC OXIDE | REACTOME_METABOLISM OF NITRIC OXIDE | 20 | 0.2802993 | 0.2802993 | 0.0651068 | 0.5527724 | 1 | 8314 tags=45%, list=17%, signal=54% |
| REACTOME_ENOS ACTIVATION AND REGULATION | REACTOME_ENOS ACTIVATION AND REGULATION | 20 | 0.2802993 | 0.2802993 | 0.0618661 | 0.5515681 | 1 | 8314 tags=45%, list=17%, signal=54% |
| REACTOME_PECAM1 | REACTOME_PECAM1 INTERACTIONS | 12 | 0.2802263 | 0.2802263 | 0.2589852 | 0.55068994 | 1 | 14844 tags=58%, list=30%, signal=84% |
| REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN BCR SIGNALING | REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN BCR SIGNALING | 6 | 0.28016642 | 0.28016642 | 0.6669951 | 0.54973775 | 1 | 2604 tags=33%, list=5%, signal=35% |
| REACTOME_PKMTS METHYLATE HISTONE LYSINES | REACTOME_PKMTS METHYLATE HISTONE LYSINES | 45 | 0.2800945 | 0.2800945 | 9.90E-04 | 0.54886705 | 1 | 8059 tags=44%, list=16%, signal=53% |
| REACTOME_RESOLUTION OF D-LOOP STRUCTURES THROUGH SYNTHESIS-DEPENDENT STRAND ANNEALING (SDSA) | REACTOME_RESOLUTION OF D-LOOP STRUCTURES THROUGH SYNTHESIS-DEPENDENT STRAND ANNEALING (SDSA) | 26 | 0.27891004 | 0.27891004 | 0.025641 | 0.55281675 | 1 | 18365 tags=65%, list=38%, signal=105% |
| REACTOME_ACTIVATED NOTCH1 TRANSMITS SIGNAL TO THE NUCLEUS | REACTOME_ACTIVATED NOTCH1 TRANSMITS SIGNAL TO THE NUCLEUS | 30 | 0.27886313 | 0.27886313 | 0.0091556 | 0.5518093 | 1 | 7571 tags=43%, list=15%, signal=51% |
| REACTOME_TIGHT JUNCTION INTERACTIONS | REACTOME_TIGHT JUNCTION INTERACTIONS | 29 | 0.27865317 | 0.27865317 | 0.0173077 | 0.55161065 | 1 | 13378 tags=55%, list=27%, signal=76% |
| REACTOME_CRMPS IN SEMA3A SIGNALING | REACTOME_CRMPS IN SEMA3A SIGNALING | 16 | 0.27849138 | 0.27849138 | 0.1325301 | 0.5511438 | 1 | 4729 tags=38%, list=10%, signal=41% |
| REACTOME_REGULATION OF THYROID HORMONE ACTIVITY | REACTOME_REGULATION OF THYROID HORMONE ACTIVITY | 3 | 0.27817494 | 0.27817494 | 0.9381339 | 0.5514128 | 1 | 35344 tags=100%, list=72%, signal=359% |
| REACTOME_ASSEMBLY OF ACTIVE LPL AND LIPC LIPASE | REACTOME_ASSEMBLY OF ACTIVE LPL AND LIPC LIPASE COMPLEXES | 19 | 0.277797 | 0.277797 | 0.0861723 | 0.55191493 | 1 | 12173 tags=53%, list=25%, signal=70% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF CELL CYCLE GENES | REACTOME_TP53 REGULATES TRANSCRIPTION OF CELL CYCLE GENES | 48 | 0.27777836 | 0.27777836 | 9.71E-04 | 0.55081356 | 1 | 6813 tags=42%, list=14%, signal=48% |
| REACTOME_AUTOINTEGRATION RESULTS IN VIRAL DNA CIRCLES | REACTOME_AUTOINTEGRATION RESULTS IN VIRAL DNA CIRCLES | 3 | 0.27757582 | 0.27757582 | 0.9324727 | 0.5505357 | 1 | 2730 tags=33%, list=6%, signal=35% |
| REACTOME_INTEGRATION OF VIRAL DNA INTO HOST GENOMIC | REACTOME_INTEGRATION OF VIRAL DNA INTO HOST GENOMIC DNA | 3 | 0.27757582 | 0.27757582 | 0.9424032 | 0.5493668 | 1 | 2730 tags=33%, list=6%, signal=35% |
| REACTOME_METABOLISM OF FOLATE AND PTERINES | REACTOME_METABOLISM OF FOLATE AND PTERINES | 17 | 0.27753222 | 0.27753222 | 0.1166181 | 0.54839236 | 1 | 12337 tags=53%, list=25%, signal=71% |
| REACTOME_SMAD2/SMAD3:SMAD4 HETEROTRIMER REGULATES TRANSCRIPTION | REACTOME_SMAD2/SMAD3:SMAD4 HETEROTRIMER REGULATES TRANSCRIPTION | 32 | 0.2773595 | 0.2773595 | 0.0117073 | 0.54801863 | 1 | 6319 tags=41%, list=13%, signal=47% |
| REACTOME_BASIGIN | REACTOME_BASIGIN INTERACTIONS | 25 | 0.27693093 | 0.27693093 | 0.0404858 | 0.5486556 | 1 | 25618 tags=80%, list=52%, signal=168% |
| REACTOME_O-GLYCOSYLATION OF TSR DOMAIN-CONTAINING | REACTOME_O-GLYCOSYLATION OF TSR DOMAIN-CONTAINING PROTEINS | 39 | 0.2767691 | 0.2767691 | 0.0071795 | 0.5482207 | 1 | 6546 tags=41%, list=13%, signal=47% |
| REACTOME_TNFR1-MEDIATED CERAMIDE PRODUCTION | REACTOME_TNFR1-MEDIATED CERAMIDE PRODUCTION | 6 | 0.27662945 | 0.27662945 | 0.6653307 | 0.54765534 | 1 | 10938 tags=50%, list=22%, signal=64% |

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| REACTOME_CONSTITUTIVE SIGNALING BY LIGAND-RESPONSIVE EGFR CANCER | REACTOME_CONSTITUTIVE SIGNALING BY LIGAND-RESPONSIVE EGFR CANCER VARIANTS | 19 | 0.27660775 | 0.27660775 | 0.0961338 | 0.5466043 | 1 | 7077 tags=42%, list=14%, signal=49% |
| REACTOME_SIGNALING BY EGFR IN CANCER | REACTOME_SIGNALING BY EGFR IN CANCER | 19 | 0.27660775 | 0.27660775 | 0.1126761 | 0.54546076 | 1 | 7077 tags=42%, list=14%, signal=49% |
| REACTOME_SIGNALING BY LIGAND-RESPONSIVE EGFR VARIANTS IN CANCER | REACTOME_SIGNALING BY LIGAND-RESPONSIVE EGFR VARIANTS IN CANCER | 19 | 0.27660775 | 0.27660775 | 0.0869141 | 0.544322 | 1 | 7077 tags=42%, list=14%, signal=49% |
| REACTOME_ARYL HYDROCARBON RECEPTOR | REACTOME_ARYL HYDROCARBON RECEPTOR SIGNALLING | 7 | 0.2765636 | 0.2765636 | 0.5693359 | 0.54337424 | 1 | 7444 tags=43%, list=15%, signal=51% |
| REACTOME_GENERATION OF SECOND MESSENGER | REACTOME_GENERATION OF SECOND MESSENGER MOLECULES | 34 | 0.27598825 | 0.27598825 | 0.0088583 | 0.54474473 | 1 | 19618 tags=68%, list=40%, signal=113% |
| REACTOME_DEFECTIVE B3GALT CAUSES PETERS-PLUS SYNDROME (PPS) | REACTOME_DEFECTIVE B3GALT CAUSES PETERS-PLUS SYNDROME (PPS) | 37 | 0.2757842 | 0.2757842 | 0.0088933 | 0.54449314 | 1 | 12973 tags=54%, list=26%, signal=73% |
| REACTOME_TELOMERE C-STRAND (LAGGING STRAND) | REACTOME_TELOMERE C-STRAND (LAGGING STRAND) SYNTHESIS | 24 | 0.2755546 | 0.2755546 | 0.0433498 | 0.5443826 | 1 | 15076 tags=58%, list=31%, signal=84% |
| REACTOME_REGULATION OF PYRUVATE DEHYDROGENASE (PDH) COMPLEX | REACTOME_REGULATION OF PYRUVATE DEHYDROGENASE (PDH) COMPLEX | 15 | 0.27529454 | 0.27529454 | 0.1756098 | 0.5443478 | 1 | 12638 tags=53%, list=26%, signal=72% |
| REACTOME_CATION-COUPLED CHLORIDE COTRANSPORTERS | REACTOME_CATION-COUPLED CHLORIDE COTRANSPORTERS | 7 | 0.27460274 | 0.27460274 | 0.5625 | 0.5460637 | 1 | 545 tags=29%, list=1%, signal=29% |
| REACTOME_FICOLINS BIND TO REPETITIVE CARBOHYDRATE STRUCTURES ON THE TARGET CELL SURFACE | REACTOME_FICOLINS BIND TO REPETITIVE CARBOHYDRATE STRUCTURES ON THE TARGET CELL SURFACE | 5 | 0.27422386 | 0.27422386 | 0.7517803 | 0.54651946 | 1 | 6159 tags=40%, list=13%, signal=46% |
| REACTOME_ION INFLUX/EFFLUX AT HOST-PATHOGEN INTERFACE | REACTOME_ION INFLUX/EFFLUX AT HOST-PATHOGEN INTERFACE | 4 | 0.27405488 | 0.27405488 | 0.8305253 | 0.546125 | 1 | 35546 tags=100%, list=73%, signal=365% |
| REACTOME_TFAP2 (AP-2) FAMILY REGULATES TRANSCRIPTION OF GROWTH FACTORS AND THEIR RECEPTORS | REACTOME_TFAP2 (AP-2) FAMILY REGULATES TRANSCRIPTION OF GROWTH FACTORS AND THEIR RECEPTORS | 13 | 0.27396855 | 0.27396855 | 0.2317881 | 0.5453385 | 1 | 16720 tags=62%, list=34%, signal=93% |
| REACTOME_APOPTOTIC CLEAVAGE OF CELLULAR | REACTOME_APOPTOTIC CLEAVAGE OF CELLULAR PROTEINS | 37 | 0.27364534 | 0.27364534 | 0.0069238 | 0.5456442 | 1 | 3814 tags=35%, list=8%, signal=38% |
| REACTOME_GLYCOGEN METABOLISM | REACTOME_GLYCOGEN METABOLISM | 27 | 0.27327776 | 0.27327776 | 0.0240848 | 0.5460979 | 1 | 2947 tags=33%, list=6%, signal=35% |
| REACTOME_FCGR ACTIVATION | REACTOME_FCGR ACTIVATION | 89 | 0.2724404 | 0.2724404 | 0 | 0.5486019 | 1 | 25195 tags=79%, list=51%, signal=162% |
| REACTOME_ATTENUATION | REACTOME_ATTENUATION PHASE | 26 | 0.27197203 | 0.27197203 | 0.0284035 | 0.54950166 | 1 | 14938 tags=58%, list=31%, signal=83% |
| REACTOME_DOWNREGULATION OF ERBB2:ERBB3 SIGNALING | REACTOME_DOWNREGULATION OF ERBB2:ERBB3 SIGNALING | 13 | 0.27185187 | 0.27185187 | 0.2345906 | 0.54892075 | 1 | 5524 tags=38%, list=11%, signal=43% |
| REACTOME_PHASE 3 - RAPID REPOLARISATION | REACTOME_PHASE 3 - RAPID REPOLARISATION | 8 | 0.27174357 | 0.27174357 | 0.5055388 | 0.5482534 | 1 | 23419 tags=75%, list=48%, signal=144% |
| REACTOME_DOWNREGULATION OF ERBB4 SIGNALING | REACTOME_DOWNREGULATION OF ERBB4 SIGNALING | 8 | 0.27110526 | 0.27110526 | 0.5315228 | 0.5499185 | 1 | 11209 tags=50%, list=23%, signal=65% |
| REACTOME_INTRA-GOLGI | REACTOME_INTRA-GOLGI TRAFFIC | 44 | 0.27082488 | 0.27082488 | 0.0020161 | 0.5499557 | 1 | 14571 tags=57%, list=30%, signal=81% |
| REACTOME_SYNTHESIS OF SUBSTRATES IN N-GLYCAN BIOSYTHESIS | REACTOME_SYNTHESIS OF SUBSTRATES IN N-GLYCAN BIOSYTHESIS | 63 | 0.2708206 | 0.2708206 | 0 | 0.54886997 | 1 | 10072 tags=48%, list=21%, signal=60% |
| REACTOME_REGULATION OF COMPLEMENT CASCADE | REACTOME_REGULATION OF COMPLEMENT CASCADE | 121 | 0.27009073 | 0.27009073 | 0 | 0.5507581 | 1 | 32939 tags=94%, list=67%, signal=287% |
| REACTOME_NOTCH2 INTRACELLULAR DOMAIN REGULATES TRANSCRIPTION | REACTOME_NOTCH2 INTRACELLULAR DOMAIN REGULATES TRANSCRIPTION | 12 | 0.2697877 | 0.2697877 | 0.2865672 | 0.55092525 | 1 | 15355 tags=58%, list=31%, signal=85% |
| REACTOME_RHO GTPASES ACTIVATE NADPH OXIDASES | REACTOME_RHO GTPASES ACTIVATE NADPH OXIDASES | 13 | 0.26926064 | 0.26926064 | 0.2414487 | 0.5520265 | 1 | 20717 tags=69%, list=42%, signal=120% |

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| REACTOME_BICARBONATE TRANSPORTERS | REACTOME_BICARBONATE TRANSPORTERS | 10 | 0.26833826 | 0.26833826 | 0.3830898 | 0.5547749 | 1 | 1552 tags=30%, list=3%, signal=31% |
| REACTOME_METABOLIC DISORDERS OF BIOLOGICAL OXIDATION ENZYMES | REACTOME_METABOLIC DISORDERS OF BIOLOGICAL OXIDATION ENZYMES | 6 | 0.26832658 | 0.26832658 | 0.7105263 | 0.55372846 | 1 | 35827 tags=100%, list=73%, signal=373% |
| REACTOME_DEFECTIVE CYP11A1 CAUSES ADRENAL INSUFFICIENCY, CONGENITAL, WITH 46,XY SEX REVERSAL | REACTOME_DEFECTIVE CYP11A1 CAUSES ADRENAL INSUFFICIENCY, CONGENITAL, WITH 46,XY SEX REVERSAL (AICSR) | 4 | 0.2683156 | 0.2683156 | 0.860396 | 0.5526799 | 1 | 35827 tags=100%, list=73%, signal=373% |
| REACTOME_ELECTRON TRANSPORT FROM NADPH TO REACTOME_BIOSYNTHESIS OF THE N-GLYCAN PRECURSOR (DOLICHOL LIPID-LINKED OLIGOSACCHARIDE, LLO) AND TRANSFER TO A NASCENT | REACTOME_ELECTRON TRANSPORT FROM NADPH TO FERREDOXIN | 3 | 0.26831016 | 0.26831016 | 0.9412361 | 0.5516113 | 1 | 35827 tags=100%, list=73%, signal=373% |
| REACTOME_NEPHRIN FAMILY INTERACTIONS | REACTOME_BIOSYNTHESIS OF THE N-GLYCAN PRECURSOR (DOLICHOL LIPID-LINKED OLIGOSACCHARIDE, LLO) AND TRANSFER TO A NASCENT PROTEIN | 78 | 0.26760536 | 0.26760536 | 9.94E-04 | 0.5535588 | 1 | 3866 tags=35%, list=8%, signal=38% |
| REACTOME_RECYCLING OF EIF2:GDP | REACTOME_NEPHRIN FAMILY INTERACTIONS | 22 | 0.26699984 | 0.26699984 | 0.0653218 | 0.55512196 | 1 | 2511 tags=32%, list=5%, signal=34% |
| REACTOME_CELL-CELL COMMUNICATION | REACTOME_RECYCLING OF EIF2:GDP | 8 | 0.26681578 | 0.26681578 | 0.5262626 | 0.5548495 | 1 | 11419 tags=50%, list=23%, signal=65% |
| REACTOME_CREATION OF C4 AND C2 ACTIVATORS | REACTOME_CELL-CELL COMMUNICATION | 121 | 0.266668 | 0.266668 | 0 | 0.55438644 | 1 | 6398 tags=40%, list=13%, signal=46% |
| REACTOME_REMOVAL OF AMINOTERMINAL PROPEPTIDES FROM GAMMA-CARBOXYLATED PROTEINS | REACTOME_CREATION OF C4 AND C2 ACTIVATORS | 91 | 0.2661428 | 0.2661428 | 0 | 0.55565304 | 1 | 25195 tags=78%, list=51%, signal=160% |
| REACTOME_LYSOSOME VESICLE BIOGENESIS | REACTOME_REMOVAL OF AMINOTERMINAL PROPEPTIDES FROM GAMMA-CARBOXYLATED PROTEINS | 10 | 0.26607087 | 0.26607087 | 0.4031311 | 0.5548687 | 1 | 1663 tags=30%, list=3%, signal=31% |
| REACTOME_PHENYLALANINE AND TYROSINE CATABOLISM | REACTOME_LYSOSOME VESICLE BIOGENESIS | 35 | 0.26591048 | 0.26591048 | 0.0133745 | 0.55446416 | 1 | 6574 tags=40%, list=13%, signal=46% |
| REACTOME_NICOTINATE METABOLISM | REACTOME_PHENYLALANINE AND TYROSINE CATABOLISM | 11 | 0.26563343 | 0.26563343 | 0.3648781 | 0.55455357 | 1 | 9252 tags=45%, list=19%, signal=56% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF GENES INVOLVED IN CYTOCHROME C RELEASE | REACTOME_NICOTINATE METABOLISM | 31 | 0.26537192 | 0.26537192 | 0.0225641 | 0.5545783 | 1 | 7547 tags=42%, list=15%, signal=50% |
| REACTOME_CIRCADIAN CLOCK | REACTOME_TP53 REGULATES TRANSCRIPTION OF GENES INVOLVED IN CYTOCHROME C RELEASE | 20 | 0.2647921 | 0.2647921 | 0.0923226 | 0.555979 | 1 | 18866 tags=65%, list=39%, signal=106% |
| REACTOME_ASTROCYTIC GLUTAMATE-GLUTAMINE UPTAKE AND METABOLISM | REACTOME_CIRCADIAN CLOCK | 69 | 0.26473698 | 0.26473698 | 0 | 0.5551289 | 1 | 5505 tags=38%, list=11%, signal=42% |
| REACTOME_NEUROTRANSMITTER UPTAKE AND METABOLISM IN GLIAL CELLS | REACTOME_ASTROCYTIC GLUTAMATE-GLUTAMINE UPTAKE AND METABOLISM | 4 | 0.2639754 | 0.2639754 | 0.8773006 | 0.5573486 | 1 | 11557 tags=50%, list=24%, signal=65% |
| REACTOME_PCNA-DEPENDENT LONG PATCH BASE EXCISION REPAIR | REACTOME_NEUROTRANSMITTER UPTAKE AND METABOLISM IN GLIAL CELLS | 4 | 0.2639754 | 0.2639754 | 0.8384845 | 0.5562706 | 1 | 11557 tags=50%, list=24%, signal=65% |
| REACTOME_ELEVATION OF CYTOSOLIC CA2+ LEVELS | REACTOME_PCNA-DEPENDENT LONG PATCH BASE EXCISION REPAIR | 21 | 0.26362783 | 0.26362783 | 0.0901961 | 0.5566774 | 1 | 15076 tags=57%, list=31%, signal=83% |
| REACTOME_ACYL CHAIN REMODELLING OF PC | REACTOME_ELEVATION OF CYTOSOLIC CA2+ LEVELS | 16 | 0.2635562 | 0.2635562 | 0.1674926 | 0.5558915 | 1 | 14641 tags=56%, list=30%, signal=80% |
| REACTOME_ADHERENS JUNCTIONS INTERACTIONS | REACTOME_ACYL CHAIN REMODELLING OF PC | 27 | 0.2630933 | 0.2630933 | 0.0468594 | 0.5569238 | 1 | 12513 tags=52%, list=26%, signal=70% |
| | REACTOME_ADHERENS JUNCTIONS INTERACTIONS | 31 | 0.26282734 | 0.26282734 | 0.0281974 | 0.5570977 | 1 | 6092 tags=39%, list=12%, signal=44% |

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| REACTOME_ZINC EFFLUX AND COMPARTMENTALIZATION BY THE SLC30 FAMILY | REACTOME_ZINC EFFLUX AND COMPARTMENTALIZATION BY THE SLC30 FAMILY | 7 | 0.262715 | 0.262715 | 0.6169154 | 0.55651456 | 1 | 8122 tags=43%, list=17%, signal=51% |
| REACTOME_METABOLISM OF FAT-SOLUBLE VITAMINS | REACTOME_METABOLISM OF FAT-SOLUBLE VITAMINS | 48 | 0.26236236 | 0.26236236 | 0.0020367 | 0.55695564 | 1 | 6547 tags=40%, list=13%, signal=46% |
| REACTOME_IRF3-MEDIATED INDUCTION OF TYPE I IFN | REACTOME_IRF3-MEDIATED INDUCTION OF TYPE I IFN | 12 | 0.26225325 | 0.26225325 | 0.3382789 | 0.55635124 | 1 | 7563 tags=42%, list=15%, signal=49% |
| REACTOME_CREB PHOSPHORYLATION THROUGH THE ACTIVATION OF ADENYLATE CYCLASE | REACTOME_CREB PHOSPHORYLATION THROUGH THE ACTIVATION OF ADENYLATE CYCLASE | 7 | 0.26189798 | 0.26189798 | 0.6359127 | 0.55680704 | 1 | 15157 tags=57%, list=31%, signal=83% |
| REACTOME_REGULATION OF GLUCOKINASE BY GLUCOKINASE REGULATORY PROTEIN | REACTOME_REGULATION OF GLUCOKINASE BY GLUCOKINASE REGULATORY PROTEIN | 31 | 0.26136586 | 0.26136586 | 0.0282132 | 0.55795354 | 1 | 4584 tags=35%, list=9%, signal=39% |
| REACTOME_REGULATION OF IFNG SIGNALING | REACTOME_REGULATION OF IFNG SIGNALING | 14 | 0.26081184 | 0.26081184 | 0.2557443 | 0.55930835 | 1 | 1222 tags=29%, list=2%, signal=29% |
| REACTOME_WNT5A-DEPENDENT INTERNALIZATION OF FZD4 | REACTOME_WNT5A-DEPENDENT INTERNALIZATION OF FZD4 | 15 | 0.26060608 | 0.26060608 | 0.2400398 | 0.5591063 | 1 | 13357 tags=53%, list=27%, signal=73% |
| REACTOME_CD22 MEDIATED BCR REGULATION | REACTOME_CD22 MEDIATED BCR REGULATION | 65 | 0.25988203 | 0.25988203 | 0 | 0.56118786 | 1 | 29476 tags=86%, list=60%, signal=216% |
| REACTOME_COMPLEMENT CASCADE | REACTOME_COMPLEMENT CASCADE | 132 | 0.25979316 | 0.25979316 | 0 | 0.5605626 | 1 | 32939 tags=93%, list=67%, signal=284% |
| REACTOME_EXTENSION OF TELOMERES | REACTOME_EXTENSION OF TELOMERES | 30 | 0.25891152 | 0.25891152 | 0.0326087 | 0.56334364 | 1 | 15076 tags=57%, list=31%, signal=82% |
| REACTOME_LOSS OF FUNCTION OF SMAD4 IN CANCER | REACTOME_LOSS OF FUNCTION OF SMAD4 IN CANCER | 3 | 0.258847 | 0.258847 | 0.9607251 | 0.56253666 | 1 | 3647 tags=33%, list=7%, signal=36% |
| REACTOME_SMAD4 MH2 DOMAIN MUTANTS IN CANCER | REACTOME_SMAD4 MH2 DOMAIN MUTANTS IN CANCER | 3 | 0.258847 | 0.258847 | 0.9739218 | 0.56148124 | 1 | 3647 tags=33%, list=7%, signal=36% |
| REACTOME_EGFR DOWNREGULATION | REACTOME_EGFR DOWNREGULATION | 25 | 0.25875765 | 0.25875765 | 0.0498961 | 0.5608509 | 1 | 8880 tags=44%, list=18%, signal=54% |
| REACTOME_ACYL CHAIN REMODELLING OF PE | REACTOME_ACYL CHAIN REMODELLING OF PE | 29 | 0.25865874 | 0.25865874 | 0.0512295 | 0.56023574 | 1 | 12668 tags=52%, list=26%, signal=70% |
| REACTOME_COMMON PATHWAY OF FIBRIN CLOT FORMATION | REACTOME_COMMON PATHWAY OF FIBRIN CLOT FORMATION | 22 | 0.25834692 | 0.25834692 | 0.1035176 | 0.5605394 | 1 | 27417 tags=82%, list=56%, signal=186% |
| REACTOME_CLEC7A (DECTIN-1) INDUCES NFAT ACTIVATION | REACTOME_CLEC7A (DECTIN-1) INDUCES NFAT ACTIVATION | 11 | 0.25779676 | 0.25779676 | 0.3817635 | 0.5618556 | 1 | 14087 tags=55%, list=29%, signal=77% |
| REACTOME_HDR THROUGH MMEJ (ALT-NHEJ) | REACTOME_HDR THROUGH MMEJ (ALT-NHEJ) | 10 | 0.2576039 | 0.2576039 | 0.4438928 | 0.5616447 | 1 | 16767 tags=60%, list=34%, signal=91% |
| REACTOME_RUNX3 REGULATES WNT SIGNALING | REACTOME_RUNX3 REGULATES WNT SIGNALING | 9 | 0.2574693 | 0.2574693 | 0.5010482 | 0.5611517 | 1 | 3716 tags=33%, list=8%, signal=36% |
| REACTOME_BMAL1:CLOCK,NPAS 2 ACTIVATES CIRCADIAN GENE EXPRESSION | REACTOME_BMAL1:CLOCK,NPAS2 ACTIVATES CIRCADIAN GENE EXPRESSION | 46 | 0.25735933 | 0.25735933 | 0.0049652 | 0.56057584 | 1 | 5505 tags=37%, list=11%, signal=42% |
| REACTOME_TRAFFICKING AND PROCESSING OF ENDOSOMAL | REACTOME_TRAFFICKING AND PROCESSING OF ENDOSOMAL | 13 | 0.25719544 | 0.25719544 | 0.3088843 | 0.5602639 | 1 | 10008 tags=46%, list=20%, signal=58% |
| REACTOME_CLEAVAGE OF THE DAMAGED PURINE | REACTOME_CLEAVAGE OF THE DAMAGED PURINE | 3 | 0.2561306 | 0.2561306 | 0.9642857 | 0.5638821 | 1 | 3780 tags=33%, list=8%, signal=36% |
| REACTOME_DEPURINATION | REACTOME_DEPURINATION | 3 | 0.2561306 | 0.2561306 | 0.9625247 | 0.5628437 | 1 | 3780 tags=33%, list=8%, signal=36% |
| REACTOME_RECOGNITION AND ASSOCIATION OF DNA GLYCOSYLASE WITH SITE CONTAINING AN AFFECTED PURINE | REACTOME_RECOGNITION AND ASSOCIATION OF DNA GLYCOSYLASE WITH SITE CONTAINING AN AFFECTED PURINE | 3 | 0.2561306 | 0.2561306 | 0.9719439 | 0.56180906 | 1 | 3780 tags=33%, list=8%, signal=36% |
| REACTOME_SCAVENGING OF HEME FROM PLASMA | REACTOME_SCAVENGING OF HEME FROM PLASMA | 87 | 0.25599816 | 0.25599816 | 0 | 0.5613695 | 1 | 25195 tags=77%, list=51%, signal=158% |

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| REACTOME_NEGATIVE REGULATION OF TCF-DEPENDENT SIGNALING BY WNT | REACTOME_NEGATIVE REGULATION OF TCF-DEPENDENT SIGNALING BY WNT LIGAND ANTAGONISTS | 14 | 0.2559192 | 0.2559192 | 0.2631058 | 0.56065726 | 1 | 4959 tags=36%, list=10%, signal=40% |
| REACTOME_NADE MODULATES DEATH SIGNALLING | REACTOME_NADE MODULATES DEATH SIGNALLING | 6 | 0.25545186 | 0.25545186 | 0.7376238 | 0.5616175 | 1 | 3814 tags=33%, list=8%, signal=36% |
| REACTOME_ACTIVATED TAK1 MEDIATES P38 MAPK | REACTOME_ACTIVATED TAK1 MEDIATES P38 MAPK ACTIVATION | 19 | 0.2548039 | 0.2548039 | 0.1298315 | 0.56340915 | 1 | 2990 tags=32%, list=6%, signal=34% |
| REACTOME_REGULATION OF TLR BY ENDOGENOUS LIGAND | REACTOME_REGULATION OF TLR BY ENDOGENOUS LIGAND | 16 | 0.2532585 | 0.2532585 | 0.2520492 | 0.5691655 | 1 | 24326 tags=75%, list=50%, signal=149% |
| REACTOME_RETINOID METABOLISM AND TRANSPORT | REACTOME_RETINOID METABOLISM AND TRANSPORT | 44 | 0.2528627 | 0.2528627 | 0.0048309 | 0.5698803 | 1 | 6547 tags=39%, list=13%, signal=45% |
| REACTOME_GLYCOGEN BREAKDOWN | REACTOME_GLYCOGEN BREAKDOWN (GLYCOGENOLYSIS) | 16 | 0.2523762 | 0.2523762 | 0.2346939 | 0.5709547 | 1 | 2947 tags=31%, list=6%, signal=33% |
| REACTOME_TETRAHYDROBIOPT ERIN (BH4) SYNTHESIS, RECYCLING, SALVAGE AND | REACTOME_TETRAHYDROBIOPTERIN (BH4) SYNTHESIS, RECYCLING, SALVAGE AND REGULATION | 10 | 0.25159842 | 0.25159842 | 0.473 | 0.57329327 | 1 | 7268 tags=40%, list=15%, signal=47% |
| REACTOME_REGULATION OF PTEN LOCALIZATION | REACTOME_REGULATION OF PTEN LOCALIZATION | 9 | 0.25145483 | 0.25145483 | 0.5403226 | 0.5728931 | 1 | 9451 tags=44%, list=19%, signal=55% |
| REACTOME_ROLE OF PHOSPHOLIPIDS IN | REACTOME_ROLE OF PHOSPHOLIPIDS IN PHAGOCYTOSIS | 102 | 0.25065643 | 0.25065643 | 0 | 0.5754253 | 1 | 25195 tags=76%, list=51%, signal=157% |
| REACTOME_RELEASE OF HH-NP FROM THE SECRETING CELL | REACTOME_RELEASE OF HH-NP FROM THE SECRETING CELL | 8 | 0.25054383 | 0.25054383 | 0.6097319 | 0.574904 | 1 | 6095 tags=38%, list=12%, signal=43% |
| REACTOME_FORMATION OF FIBRIN CLOT (CLOTTING | REACTOME_FORMATION OF FIBRIN CLOT (CLOTTING CASCADE) | 38 | 0.25020844 | 0.25020844 | 0.0153061 | 0.57543015 | 1 | 10951 tags=47%, list=22%, signal=61% |
| REACTOME_BILE SALT AND ORGANIC ANION SLC TRANSPORTERS | REACTOME_BILE SALT AND ORGANIC ANION SLC TRANSPORTERS | 14 | 0.25015834 | 0.25015834 | 0.2945892 | 0.5746008 | 1 | 12236 tags=50%, list=25%, signal=67% |
| REACTOME_LECTIN PATHWAY OF COMPLEMENT ACTIVATION | REACTOME_LECTIN PATHWAY OF COMPLEMENT ACTIVATION | 8 | 0.24923657 | 0.24923657 | 0.6438632 | 0.57768977 | 1 | 6159 tags=38%, list=13%, signal=43% |
| REACTOME_UREA CYCLE | REACTOME_UREA CYCLE | 10 | 0.24921867 | 0.24921867 | 0.495229 | 0.5767321 | 1 | 2488 tags=30%, list=5%, signal=32% |
| REACTOME_CLATHRIN DERIVED VESICLE BUDDING | REACTOME_CLATHRIN DERIVED VESICLE BUDDING | 72 | 0.24906144 | 0.24906144 | 0 | 0.5764233 | 1 | 10944 tags=47%, list=22%, signal=61% |
| REACTOME_TRANS-GOLGI NETWORK VESICLE BUDDING | REACTOME_TRANS-GOLGI NETWORK VESICLE BUDDING | 72 | 0.24906144 | 0.24906144 | 0 | 0.57539576 | 1 | 10944 tags=47%, list=22%, signal=61% |
| REACTOME_SHC-RELATED EVENTS TRIGGERED BY IGF1R | REACTOME_SHC-RELATED EVENTS TRIGGERED BY IGF1R | 9 | 0.24856333 | 0.24856333 | 0.5447236 | 0.576553 | 1 | 4152 tags=33%, list=8%, signal=36% |
| REACTOME_NEGATIVE REGULATORS OF DDX58/IFIH1 SIGNALING | REACTOME_NEGATIVE REGULATORS OF DDX58/IFIH1 SIGNALING | 34 | 0.24838278 | 0.24838278 | 0.0220662 | 0.57636786 | 1 | 3687 tags=32%, list=8%, signal=35% |
| REACTOME_RAF-INDEPENDENT MAPK1/3 ACTIVATION | REACTOME_RAF-INDEPENDENT MAPK1/3 ACTIVATION | 23 | 0.2481358 | 0.2481358 | 0.1149425 | 0.5764811 | 1 | 30433 tags=87%, list=62%, signal=230% |
| REACTOME_OPSINS | REACTOME_OPSINS | 7 | 0.24786556 | 0.24786556 | 0.7130178 | 0.5766536 | 1 | 15844 tags=57%, list=32%, signal=84% |
| REACTOME_MYD88-INDEPENDENT TLR3/TLR4 | REACTOME_MYD88-INDEPENDENT TLR3/TLR4 CASCADE | 100 | 0.24781437 | 0.24781437 | 0 | 0.57586014 | 1 | 4048 tags=33%, list=8%, signal=36% |
| REACTOME_TRIF-MEDIATED TLR3/TLR4 SIGNALING | REACTOME_TRIF-MEDIATED TLR3/TLR4 SIGNALING | 100 | 0.24781437 | 0.24781437 | 0 | 0.57484454 | 1 | 4048 tags=33%, list=8%, signal=36% |
| REACTOME_TOLL LIKE RECEPTOR 3 (TLR3) CASCADE | REACTOME_TOLL LIKE RECEPTOR 3 (TLR3) CASCADE | 100 | 0.24781437 | 0.24781437 | 0 | 0.5738325 | 1 | 4048 tags=33%, list=8%, signal=36% |
| REACTOME_SIGNALING BY TGF-BETA RECEPTOR COMPLEX | REACTOME_SIGNALING BY TGF-BETA RECEPTOR COMPLEX | 73 | 0.24764983 | 0.24764983 | 9.84E-04 | 0.5735693 | 1 | 6672 tags=38%, list=14%, signal=44% |
| REACTOME_NUCLEOTIDE-BINDING DOMAIN, LEUCINE RICH REPEAT CONTAINING RECEPTOR (NLR) SIGNALING PATHWAYS | REACTOME_NUCLEOTIDE-BINDING DOMAIN, LEUCINE RICH REPEAT CONTAINING RECEPTOR (NLR) SIGNALING PATHWAYS | 47 | 0.24731922 | 0.24731922 | 0.0048309 | 0.5740517 | 1 | 7695 tags=40%, list=16%, signal=48% |
| REACTOME_NEGATIVE REGULATION OF MET ACTIVITY | REACTOME_NEGATIVE REGULATION OF MET ACTIVITY | 21 | 0.24730305 | 0.24730305 | 0.1200397 | 0.57312846 | 1 | 8880 tags=43%, list=18%, signal=52% |

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|---|---|-----|------------|------------|-----------|------------|---|--|
| REACTOME_GOLGI CISTERNAE PERICENTRIOLAR STACK REORGANIZATION | REACTOME_GOLGI CISTERNAE PERICENTRIOLAR STACK REORGANIZATION | 14 | 0.24728814 | 0.24728814 | 0.2921811 | 0.5721988 | 1 | 22869 tags=71%, list=47%, signal=134% |
| REACTOME_SYNTHESIS OF PROSTAGLANDINS (PG) AND THROMBOXANES (TX) | REACTOME_SYNTHESIS OF PROSTAGLANDINS (PG) AND THROMBOXANES (TX) | 15 | 0.24721146 | 0.24721146 | 0.2893924 | 0.5715363 | 1 | 7484 tags=40%, list=15%, signal=47% |
| REACTOME_NUCLEOTIDE | REACTOME_NUCLEOTIDE SALVAGE | 23 | 0.24719146 | 0.24719146 | 0.1082164 | 0.5706227 | 1 | 11319 tags=48%, list=23%, signal=62% |
| REACTOME_HSF1 ACTIVATION | REACTOME_HSF1 ACTIVATION | 29 | 0.24677481 | 0.24677481 | 0.0477137 | 0.57147634 | 1 | 14938 tags=55%, list=31%, signal=79% |
| REACTOME_GAMMA-CARBOXYLATION OF PROTEIN PRECURSORS | REACTOME_GAMMA-CARBOXYLATION OF PROTEIN PRECURSORS | 10 | 0.24603207 | 0.24603207 | 0.4940594 | 0.5737237 | 1 | 2644 tags=30%, list=5%, signal=32% |
| REACTOME_ERBB2 REGULATES CELL MOTILITY | REACTOME_ERBB2 REGULATES CELL MOTILITY | 15 | 0.24599253 | 0.24599253 | 0.2650841 | 0.57288164 | 1 | 1015 tags=27%, list=2%, signal=27% |
| REACTOME_SEMET INCORPORATION INTO PROTEINS | REACTOME_SEMET INCORPORATION INTO PROTEINS | 11 | 0.24588019 | 0.24588019 | 0.4444445 | 0.5723862 | 1 | 10219 tags=45%, list=21%, signal=57% |
| REACTOME_ACYL CHAIN REMODELLING OF PG | REACTOME_ACYL CHAIN REMODELLING OF PG | 18 | 0.24541852 | 0.24541852 | 0.172 | 0.57347876 | 1 | 12469 tags=50%, list=25%, signal=67% |
| REACTOME_EPHB-MEDIATED FORWARD SIGNALING | REACTOME_EPHB-MEDIATED FORWARD SIGNALING | 42 | 0.2453822 | 0.2453822 | 0.0136187 | 0.5726487 | 1 | 10145 tags=45%, list=21%, signal=57% |
| REACTOME_REGULATION OF LIPID METABOLISM BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR ALPHA | REACTOME_REGULATION OF LIPID METABOLISM BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR ALPHA (PPARALPHA) | 121 | 0.2452324 | 0.2452324 | 0 | 0.57227373 | 1 | 7445 tags=40%, list=15%, signal=47% |
| REACTOME_LIPID PARTICLE ORGANIZATION | REACTOME_LIPID PARTICLE ORGANIZATION | 6 | 0.24493967 | 0.24493967 | 0.7736585 | 0.57255524 | 1 | 36972 tags=100%, list=76%, signal=408% |
| REACTOME_THE NLRP3 INFLAMMASOME | REACTOME_THE NLRP3 INFLAMMASOME | 12 | 0.24489479 | 0.24489479 | 0.3767396 | 0.5717445 | 1 | 20654 tags=67%, list=42%, signal=115% |
| REACTOME_SEMAPHORIN INTERACTIONS | REACTOME_SEMAPHORIN INTERACTIONS | 67 | 0.24488044 | 0.24488044 | 0 | 0.5708258 | 1 | 7757 tags=40%, list=16%, signal=48% |
| REACTOME_BINDING AND UPTAKE OF LIGANDS BY SCAVENGER RECEPTORS | REACTOME_BINDING AND UPTAKE OF LIGANDS BY SCAVENGER RECEPTORS | 116 | 0.24462858 | 0.24462858 | 0 | 0.57101923 | 1 | 25195 tags=76%, list=51%, signal=156% |
| REACTOME_SYNTHESIS OF PIPS AT THE ER MEMBRANE | REACTOME_SYNTHESIS OF PIPS AT THE ER MEMBRANE | 5 | 0.24389297 | 0.24389297 | 0.8801611 | 0.5733009 | 1 | 17437 tags=60%, list=36%, signal=93% |
| REACTOME_TRAF6 MEDIATED INDUCTION OF PROINFLAMMATORY CYTOKINES | REACTOME_TRAF6 MEDIATED INDUCTION OF PROINFLAMMATORY CYTOKINES | 83 | 0.24302141 | 0.24302141 | 0 | 0.5761061 | 1 | 4048 tags=33%, list=8%, signal=35% |
| REACTOME_DEFECTIVE B4GALT1 CAUSES B4GALT1-CDG | REACTOME_DEFECTIVE B4GALT1 CAUSES B4GALT1-CDG (CDG-2D) | 7 | 0.24255492 | 0.24255492 | 0.71139 | 0.5771926 | 1 | 37089 tags=100%, list=76%, signal=412% |
| REACTOME_DEFECTIVE CHST6 CAUSES MCDC1 | REACTOME_DEFECTIVE CHST6 CAUSES MCDC1 | 7 | 0.24255492 | 0.24255492 | 0.7241379 | 0.5762126 | 1 | 37089 tags=100%, list=76%, signal=412% |
| REACTOME_DEFECTIVE ST3GAL3 CAUSES MCT12 AND | REACTOME_DEFECTIVE ST3GAL3 CAUSES MCT12 AND EIEE15 | 7 | 0.24255492 | 0.24255492 | 0.7376238 | 0.575236 | 1 | 37089 tags=100%, list=76%, signal=412% |
| REACTOME_AXONAL GROWTH STIMULATION | REACTOME_AXONAL GROWTH STIMULATION | 4 | 0.24158514 | 0.24158514 | 0.9268051 | 0.57849807 | 1 | 412 tags=25%, list=1%, signal=25% |
| REACTOME_FORMATION OF THE EDITOSOME | REACTOME_FORMATION OF THE EDITOSOME | 7 | 0.24132936 | 0.24132936 | 0.7359438 | 0.5786689 | 1 | 30154 tags=86%, list=62%, signal=223% |
| REACTOME_MRNA EDITING: C TO U CONVERSION | REACTOME_MRNA EDITING: C TO U CONVERSION | 7 | 0.24132936 | 0.24132936 | 0.7051282 | 0.57769305 | 1 | 30154 tags=86%, list=62%, signal=223% |
| REACTOME_SHC1 EVENTS IN ERBB2 SIGNALING | REACTOME_SHC1 EVENTS IN ERBB2 SIGNALING | 22 | 0.2409965 | 0.2409965 | 0.1502392 | 0.5782344 | 1 | 1558 tags=27%, list=3%, signal=28% |
| REACTOME_GLUONEOGENESIS | REACTOME_GLUONEOGENESIS | 33 | 0.24024807 | 0.24024807 | 0.0352823 | 0.58055145 | 1 | 10500 tags=45%, list=21%, signal=58% |
| REACTOME_TGF-BETA RECEPTOR SIGNALING | REACTOME_TGF-BETA RECEPTOR SIGNALING ACTIVATES SMADS | 32 | 0.2388751 | 0.2388751 | 0.037037 | 0.585508 | 1 | 6672 tags=38%, list=14%, signal=43% |
| REACTOME_CELL-CELL JUNCTION ORGANIZATION | REACTOME_CELL-CELL JUNCTION ORGANIZATION | 62 | 0.23866071 | 0.23866071 | 0.0010163 | 0.5854925 | 1 | 10441 tags=45%, list=21%, signal=57% |

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|---|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_TRANSPORT OF RIBONUCLEOPROTEINS INTO THE HOST NUCLEUS | REACTOME_TRANSPORT OF RIBONUCLEOPROTEINS INTO THE HOST NUCLEUS | 31 | 0.23828341 | 0.23828341 | 0.0573123 | 0.58613485 | 1 | 4134 tags=32%, list=8%, signal=35% |
| REACTOME_PROCESSING OF INTRONLESS PRE-MRNAS | REACTOME_PROCESSING OF INTRONLESS PRE-MRNAS | 19 | 0.23820668 | 0.23820668 | 0.2056452 | 0.58549464 | 1 | 19265 tags=63%, list=39%, signal=104% |
| REACTOME_VLDL CLEARANCE | REACTOME_VLDL CLEARANCE | 6 | 0.23819251 | 0.23819251 | 0.814096 | 0.5845938 | 1 | 4659 tags=33%, list=10%, signal=37% |
| REACTOME_GLUCOSE | REACTOME_GLUCOSE METABOLISM | 90 | 0.23797329 | 0.23797329 | 0 | 0.58451897 | 1 | 7410 tags=39%, list=15%, signal=46% |
| REACTOME_EPHA-MEDIATED GROWTH CONE COLLAPSE | REACTOME_EPHA-MEDIATED GROWTH CONE COLLAPSE | 34 | 0.23796594 | 0.23796594 | 0.0254065 | 0.58357584 | 1 | 7077 tags=38%, list=14%, signal=45% |
| REACTOME_CHYLOMICRON CLEARANCE | REACTOME_CHYLOMICRON CLEARANCE | 5 | 0.23764297 | 0.23764297 | 0.8960396 | 0.58401763 | 1 | 7950 tags=40%, list=16%, signal=48% |
| REACTOME_PEPTIDE HORMONE BIOSYNTHESIS | REACTOME_PEPTIDE HORMONE BIOSYNTHESIS | 12 | 0.23728204 | 0.23728204 | 0.4368635 | 0.5846737 | 1 | 4705 tags=33%, list=10%, signal=37% |
| REACTOME_FERTILIZATION | REACTOME_FERTILIZATION | 26 | 0.23717126 | 0.23717126 | 0.0938144 | 0.58424026 | 1 | 29824 tags=85%, list=61%, signal=216% |
| REACTOME_REPRODUCTION | REACTOME_REPRODUCTION | 26 | 0.23717126 | 0.23717126 | 0.0885312 | 0.5832762 | 1 | 29824 tags=85%, list=61%, signal=216% |
| REACTOME_FCERI MEDIATED CA+2 MOBILIZATION | REACTOME_FCERI MEDIATED CA+2 MOBILIZATION | 102 | 0.23625684 | 0.23625684 | 0 | 0.5863765 | 1 | 29739 tags=84%, list=61%, signal=214% |
| REACTOME_TRAF6 MEDIATED IRF7 ACTIVATION IN TLR7/8 OR 9 SIGNALING | REACTOME_TRAF6 MEDIATED IRF7 ACTIVATION IN TLR7/8 OR 9 SIGNALING | 11 | 0.2350537 | 0.2350537 | 0.4736318 | 0.590628 | 1 | 10749 tags=45%, list=22%, signal=58% |
| REACTOME_TRANSCRIPTIONAL ACTIVITY OF SMAD2/SMAD3:SMAD4 | REACTOME_TRANSCRIPTIONAL ACTIVITY OF SMAD2/SMAD3:SMAD4 | 44 | 0.23477556 | 0.23477556 | 0.0119403 | 0.5908679 | 1 | 6319 tags=36%, list=13%, signal=42% |
| REACTOME_FGFRL1 MODULATION OF FGFR1 | REACTOME_FGFRL1 MODULATION OF FGFR1 SIGNALING | 13 | 0.23428603 | 0.23428603 | 0.3889458 | 0.59214324 | 1 | 14896 tags=54%, list=30%, signal=77% |
| REACTOME_SIGNALING BY REACTOME_DEPOLYMERISATION OF THE NUCLEAR LAMINA | REACTOME_SIGNALING BY NOTCH REACTOME_DEPOLYMERISATION OF THE NUCLEAR LAMINA | 113 | 0.23423755 | 0.23423755 | 0 | 0.59138227 | 1 | 8922 tags=42%, list=18%, signal=51% |
| REACTOME_COPII (COAT PROTEIN 2) MEDIATED VESICLE TRANSPORT | REACTOME_COPII (COAT PROTEIN 2) MEDIATED VESICLE TRANSPORT | 14 | 0.23349884 | 0.23349884 | 0.3874756 | 0.5937327 | 1 | 16549 tags=57%, list=34%, signal=86% |
| REACTOME_ACTIVATION OF E2F1 TARGET GENES AT G1/S | REACTOME_ACTIVATION OF E2F1 TARGET GENES AT G1/S | 68 | 0.23193021 | 0.23193021 | 0 | 0.5997067 | 1 | 5220 tags=34%, list=11%, signal=38% |
| REACTOME_G1/S-SPECIFIC TRANSCRIPTION | REACTOME_G1/S-SPECIFIC TRANSCRIPTION | 28 | 0.23167033 | 0.23167033 | 0.0898204 | 0.5999436 | 1 | 7898 tags=39%, list=16%, signal=47% |
| REACTOME_ERK/MAPK TARGETS | REACTOME_ERK/MAPK TARGETS | 28 | 0.23167033 | 0.23167033 | 0.0850851 | 0.598968 | 1 | 7898 tags=39%, list=16%, signal=47% |
| REACTOME_CENTROSOME MATURATION | REACTOME_CENTROSOME MATURATION | 22 | 0.23150307 | 0.23150307 | 0.1888889 | 0.59875625 | 1 | 6474 tags=36%, list=13%, signal=42% |
| REACTOME_RECRUITMENT OF MITOTIC CENTROSOME PROTEINS AND COMPLEXES | REACTOME_RECRUITMENT OF MITOTIC CENTROSOME PROTEINS AND COMPLEXES | 80 | 0.23131585 | 0.23131585 | 0 | 0.5985999 | 1 | 16846 tags=58%, list=34%, signal=88% |
| REACTOME_THE CANONICAL RETINOID CYCLE IN RODS (TWILIGHT VISION) | REACTOME_THE CANONICAL RETINOID CYCLE IN RODS (TWILIGHT VISION) | 80 | 0.23131585 | 0.23131585 | 0 | 0.59763134 | 1 | 16846 tags=58%, list=34%, signal=88% |
| REACTOME_CD28 DEPENDENT PI3K/AKT SIGNALING | REACTOME_CD28 DEPENDENT PI3K/AKT SIGNALING | 23 | 0.2309513 | 0.2309513 | 0.1465863 | 0.59833145 | 1 | 7856 tags=39%, list=16%, signal=47% |
| REACTOME_SCAVENGING BY CLASS B RECEPTORS | REACTOME_SCAVENGING BY CLASS B RECEPTORS | 22 | 0.23093934 | 0.23093934 | 0.161689 | 0.59742016 | 1 | 17630 tags=59%, list=36%, signal=92% |
| REACTOME_IRAK4 DEFICIENCY (TLR2/4) | REACTOME_IRAK4 DEFICIENCY (TLR2/4) | 6 | 0.23055346 | 0.23055346 | 0.8394161 | 0.5981262 | 1 | 5033 tags=33%, list=10%, signal=37% |
| REACTOME_MYD88 DEFICIENCY (TLR2/4) | REACTOME_MYD88 DEFICIENCY (TLR2/4) | 11 | 0.23050027 | 0.23050027 | 0.5257937 | 0.59738934 | 1 | 24326 tags=73%, list=50%, signal=144% |
| REACTOME_NUCLEAR PORE COMPLEX (NPC) DISASSEMBLY | REACTOME_NUCLEAR PORE COMPLEX (NPC) DISASSEMBLY | 11 | 0.23050027 | 0.23050027 | 0.5043902 | 0.5964305 | 1 | 24326 tags=73%, list=50%, signal=144% |
| REACTOME_DOWNREGULATION OF SMAD2/3:SMAD4 TRANSCRIPTIONAL ACTIVITY | REACTOME_DOWNREGULATION OF SMAD2/3:SMAD4 TRANSCRIPTIONAL ACTIVITY | 35 | 0.23000205 | 0.23000205 | 0.0353288 | 0.5977316 | 1 | 4134 tags=31%, list=8%, signal=34% |
| | | 23 | 0.22995365 | 0.22995365 | 0.1415753 | 0.5969758 | 1 | 3647 tags=30%, list=7%, signal=33% |

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|---|---|-----|------------|------------|-----------|------------|---|--------------------------------------|
| REACTOME_IRAK2 MEDIATED ACTIVATION OF TAK1 COMPLEX UPON TLR7/8 OR 9 STIMULATION | REACTOME_IRAK2 MEDIATED ACTIVATION OF TAK1 COMPLEX UPON TLR7/8 OR 9 STIMULATION | 16 | 0.2298834 | 0.2298834 | 0.3441624 | 0.5963209 | 1 | 4048 tags=31%, list=8%, signal=34% |
| REACTOME_BUTYROPHILIN (BTN) FAMILY INTERACTIONS | REACTOME_BUTYROPHILIN (BTN) FAMILY INTERACTIONS | 12 | 0.22984293 | 0.22984293 | 0.4603175 | 0.59554 | 1 | 13230 tags=50%, list=27%, signal=68% |
| REACTOME_PPARG ACTIVATES GENE EXPRESSION | REACTOME_PPARG ACTIVATES GENE EXPRESSION | 118 | 0.22984202 | 0.22984202 | 0 | 0.5945948 | 1 | 7445 tags=38%, list=15%, signal=45% |
| REACTOME_ACTIVATION OF GENE EXPRESSION BY SREBF | REACTOME_ACTIVATION OF GENE EXPRESSION BY SREBF (SREBP) | 42 | 0.22949329 | 0.22949329 | 0.0227273 | 0.5952159 | 1 | 6259 tags=36%, list=13%, signal=41% |
| REACTOME_ER-PHAGOSOME PATHWAY | REACTOME_ER-PHAGOSOME PATHWAY | 83 | 0.2293901 | 0.2293901 | 9.99E-04 | 0.5947214 | 1 | 17693 tags=59%, list=36%, signal=92% |
| REACTOME_INTERFERON | REACTOME_INTERFERON SIGNALING | 194 | 0.22923732 | 0.22923732 | 0 | 0.594492 | 1 | 10525 tags=44%, list=21%, signal=56% |
| REACTOME_NUCLEAR IMPORT OF REV PROTEIN | REACTOME_NUCLEAR IMPORT OF REV PROTEIN | 33 | 0.22838746 | 0.22838746 | 0.0517578 | 0.5974049 | 1 | 6629 tags=36%, list=14%, signal=42% |
| REACTOME_EXPORT OF VIRAL RIBONUCLEOPROTEINS FROM NUCLEUS | REACTOME_EXPORT OF VIRAL RIBONUCLEOPROTEINS FROM NUCLEUS | 32 | 0.22820106 | 0.22820106 | 0.0553907 | 0.5972385 | 1 | 4134 tags=31%, list=8%, signal=34% |
| REACTOME_NUCLEAR EVENTS (KINASE AND TRANSCRIPTION FACTOR ACTIVATION) | REACTOME_NUCLEAR EVENTS (KINASE AND TRANSCRIPTION FACTOR ACTIVATION) | 25 | 0.22787903 | 0.22787903 | 0.1384768 | 0.5977263 | 1 | 6474 tags=36%, list=13%, signal=41% |
| REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 HD+PEST DOMAIN MUTANTS | REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 HD+PEST DOMAIN MUTANTS | 57 | 0.22734344 | 0.22734344 | 9.81E-04 | 0.59921867 | 1 | 11215 tags=46%, list=23%, signal=59% |
| REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 PEST DOMAIN MUTANTS | REACTOME_CONSTITUTIVE SIGNALING BY NOTCH1 PEST DOMAIN MUTANTS | 57 | 0.22734344 | 0.22734344 | 0.0050403 | 0.59827656 | 1 | 11215 tags=46%, list=23%, signal=59% |
| REACTOME_SIGNALING BY NOTCH1 HD+PEST DOMAIN MUTANTS IN CANCER | REACTOME_SIGNALING BY NOTCH1 HD+PEST DOMAIN MUTANTS IN CANCER | 57 | 0.22734344 | 0.22734344 | 0.0058537 | 0.5973373 | 1 | 11215 tags=46%, list=23%, signal=59% |
| REACTOME_SIGNALING BY NOTCH1 PEST DOMAIN MUTANTS IN CANCER | REACTOME_SIGNALING BY NOTCH1 PEST DOMAIN MUTANTS IN CANCER | 57 | 0.22734344 | 0.22734344 | 0.0050201 | 0.5964011 | 1 | 11215 tags=46%, list=23%, signal=59% |
| REACTOME_SIGNALING BY NOTCH1 IN CANCER | REACTOME_SIGNALING BY NOTCH1 IN CANCER | 57 | 0.22734344 | 0.22734344 | 0.0060302 | 0.5954677 | 1 | 11215 tags=46%, list=23%, signal=59% |
| REACTOME_PLATELET AGGREGATION (PLUG FORMATION) | REACTOME_PLATELET AGGREGATION (PLUG FORMATION) | 36 | 0.22729874 | 0.22729874 | 0.0383858 | 0.59474635 | 1 | 13360 tags=50%, list=27%, signal=69% |
| REACTOME_NUCLEOBASE CATABOLISM | REACTOME_NUCLEOBASE CATABOLISM | 36 | 0.22691667 | 0.22691667 | 0.0507614 | 0.5954889 | 1 | 6578 tags=36%, list=13%, signal=42% |
| REACTOME_VPX CARGO-TARGETING TO CILIUM | REACTOME_VPX CARGO-TARGETING TO CILIUM | 21 | 0.2261292 | 0.2261292 | 0.2213198 | 0.5979896 | 1 | 12248 tags=48%, list=25%, signal=63% |
| REACTOME_RECRUITMENT OF NUMA TO MITOTIC CENTROSOMES | REACTOME_RECRUITMENT OF NUMA TO MITOTIC CENTROSOMES | 79 | 0.22592267 | 0.22592267 | 0.00199 | 0.5979668 | 1 | 16846 tags=57%, list=34%, signal=87% |
| REACTOME_RECOGNITION OF DNA DAMAGE BY PCNA-CONTAINING REPLICATION COMPLEX | REACTOME_RECOGNITION OF DNA DAMAGE BY PCNA-CONTAINING REPLICATION COMPLEX | 30 | 0.22566333 | 0.22566333 | 0.1007905 | 0.5981964 | 1 | 16703 tags=57%, list=34%, signal=86% |
| REACTOME_SIGNALING BY ERBB2 | REACTOME_SIGNALING BY ERBB2 | 50 | 0.22522947 | 0.22522947 | 0.0148305 | 0.5991615 | 1 | 5630 tags=34%, list=11%, signal=38% |
| REACTOME_SIGNALING BY BRAF AND RAF FUSIONS | REACTOME_SIGNALING BY BRAF AND RAF FUSIONS | 58 | 0.22487226 | 0.22487226 | 0.0059701 | 0.5997875 | 1 | 10951 tags=45%, list=22%, signal=58% |
| REACTOME_ANTIGEN PROCESSING-CROSS PRESENTATION | REACTOME_ANTIGEN PROCESSING-CROSS PRESENTATION | 99 | 0.22483048 | 0.22483048 | 0 | 0.59900767 | 1 | 17699 tags=59%, list=36%, signal=92% |
| REACTOME_NEUTROPHIL DEGRANULATION | REACTOME_NEUTROPHIL DEGRANULATION | 474 | 0.22426558 | 0.22426558 | 0 | 0.6006854 | 1 | 11334 tags=45%, list=23%, signal=58% |
| REACTOME_AURKA ACTIVATION BY TPX2 | REACTOME_AURKA ACTIVATION BY TPX2 | 72 | 0.22335365 | 0.22335365 | 0.0019743 | 0.6038068 | 1 | 12881 tags=49%, list=26%, signal=66% |
| REACTOME_AKT PHOSPHORYLATES TARGETS IN THE CYTOSOL | REACTOME_AKT PHOSPHORYLATES TARGETS IN THE CYTOSOL | 14 | 0.22285552 | 0.22285552 | 0.4436475 | 0.6050608 | 1 | 10075 tags=43%, list=21%, signal=54% |

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|--|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_MAPK TARGETS/ NUCLEAR EVENTS MEDIATED BY MAP KINASES | REACTOME_MAPK TARGETS/ NUCLEAR EVENTS MEDIATED BY MAP KINASES | 31 | 0.22274241 | 0.22274241 | 0.0798817 | 0.60463727 | 1 | 6474 tags=35%, list=13%, signal=41% |
| REACTOME_CYTOSOLIC SENSORS OF PATHOGEN- REACTOME_SPHINGOLIPID METABOLISM | REACTOME_CYTOSOLIC SENSORS OF PATHOGEN-ASSOCIATED DNA REACTOME_SPHINGOLIPID METABOLISM | 68 | 0.22264989 | 0.22264989 | 9.95E-04 | 0.60413104 | 1 | 7834 tags=38%, list=16%, signal=45% |
| REACTOME_TNFR2 NON- CANONICAL NF-KB PATHWAY | REACTOME_TNFR2 NON-CANONICAL NF- KB PATHWAY | 90 | 0.22239728 | 0.22239728 | 0 | 0.60432595 | 1 | 5451 tags=33%, list=11%, signal=37% |
| REACTOME_CDO IN REACTOME_MYOGENESIS | REACTOME_CDO IN MYOGENESIS REACTOME_MYOGENESIS | 98 | 0.2223674 | 0.2223674 | 0 | 0.6035315 | 1 | 8119 tags=39%, list=17%, signal=46% |
| REACTOME_MOLYBDENUM COFACTOR BIOSYNTHESIS | REACTOME_MOLYBDENUM COFACTOR BIOSYNTHESIS | 29 | 0.2223298 | 0.2223298 | 0.1117479 | 0.6027765 | 1 | 7692 tags=38%, list=16%, signal=45% |
| REACTOME_CELLULAR HEXOSE TRANSPORT | REACTOME_CELLULAR HEXOSE TRANSPORT | 29 | 0.2223298 | 0.2223298 | 0.1154219 | 0.60185766 | 1 | 7692 tags=38%, list=16%, signal=45% |
| REACTOME_ACTIVATED TLR4 SIGNALLING | REACTOME_ACTIVATED TLR4 SIGNALLING | 6 | 0.2223187 | 0.2223187 | 0.865458 | 0.60099554 | 1 | 13597 tags=50%, list=28%, signal=69% |
| REACTOME_PLATELET ACTIVATION, SIGNALING AND REACTOME_PAUSING AND RECOVERY OF TAT-MEDIATED HIV ELONGATION | REACTOME_PLATELET ACTIVATION, SIGNALING AND AGGREGATION REACTOME_PAUSING AND RECOVERY OF TAT-MEDIATED HIV ELONGATION | 22 | 0.22227435 | 0.22227435 | 0.1901544 | 0.6002853 | 1 | 4700 tags=32%, list=10%, signal=35% |
| REACTOME_TAT-MEDIATED HIV ELONGATION ARREST AND RECOVERY | REACTOME_TAT-MEDIATED HIV ELONGATION ARREST AND RECOVERY | 115 | 0.22217791 | 0.22217791 | 0 | 0.5997934 | 1 | 4048 tags=30%, list=8%, signal=33% |
| REACTOME_MET RECEPTOR RECYCLING | REACTOME_MET RECEPTOR RECYCLING | 275 | 0.22214605 | 0.22214605 | 0 | 0.5990131 | 1 | 6454 tags=35%, list=13%, signal=40% |
| REACTOME_TFAP2A ACTS AS A TRANSCRIPTIONAL REPRESSOR DURING RETINOIC ACID INDUCED CELL DIFFERENTIATION | REACTOME_TFAP2A ACTS AS A TRANSCRIPTIONAL REPRESSOR DURING RETINOIC ACID INDUCED CELL DIFFERENTIATION | 27 | 0.22199896 | 0.22199896 | 0.129285 | 0.5987477 | 1 | 7270 tags=37%, list=15%, signal=43% |
| REACTOME_NRAGE SIGNALS DEATH THROUGH JNK | REACTOME_NRAGE SIGNALS DEATH THROUGH JNK | 27 | 0.22199896 | 0.22199896 | 0.1230159 | 0.5978432 | 1 | 7270 tags=37%, list=15%, signal=43% |
| REACTOME_POU5F1 (OCT4), SOX2, NANOG ACTIVATE GENES RELATED TO PROLIFERATION | REACTOME_POU5F1 (OCT4), SOX2, NANOG ACTIVATE GENES RELATED TO PROLIFERATION | 10 | 0.2215504 | 0.2215504 | 0.6334341 | 0.598873 | 1 | 8739 tags=40%, list=18%, signal=49% |
| REACTOME_SIGNALING BY CYTOSOLIC FGFR1 FUSION | REACTOME_SIGNALING BY CYTOSOLIC FGFR1 FUSION MUTANTS | 5 | 0.22017974 | 0.22017974 | 0.9195737 | 0.6040217 | 1 | 28391 tags=80%, list=58%, signal=190% |
| REACTOME_DNA REPLICATION INITIATION | REACTOME_DNA REPLICATION INITIATION | 59 | 0.2198971 | 0.2198971 | 0.0061665 | 0.6043967 | 1 | 15802 tags=54%, list=32%, signal=80% |
| REACTOME_TELOMERE C- STRAND SYNTHESIS INITIATION | REACTOME_TELOMERE C-STRAND SYNTHESIS INITIATION | 13 | 0.21943161 | 0.21943161 | 0.465641 | 0.60554314 | 1 | 557 tags=23%, list=1%, signal=23% |
| REACTOME_VPR-MEDIATED NUCLEAR IMPORT OF PICS | REACTOME_VPR-MEDIATED NUCLEAR IMPORT OF PICS | 18 | 0.2189443 | 0.2189443 | 0.3065476 | 0.6068245 | 1 | 5604 tags=33%, list=11%, signal=38% |
| REACTOME_INLB-MEDIATED ENTRY OF LISTERIA MONOCYTOGENES INTO HOST CELL | REACTOME_INLB-MEDIATED ENTRY OF LISTERIA MONOCYTOGENES INTO HOST CELL | 8 | 0.21883489 | 0.21883489 | 0.7694672 | 0.6064164 | 1 | 13768 tags=50%, list=28%, signal=70% |
| REACTOME_REGULATION OF PTEN GENE TRANSCRIPTION | REACTOME_REGULATION OF PTEN GENE TRANSCRIPTION | 8 | 0.21883489 | 0.21883489 | 0.8011869 | 0.60551 | 1 | 13768 tags=50%, list=28%, signal=70% |
| REACTOME_ASSOCIATION OF TRIC/CCT WITH TARGET PROTEINS DURING BIOSYNTHESIS | REACTOME_ASSOCIATION OF TRIC/CCT WITH TARGET PROTEINS DURING BIOSYNTHESIS | 33 | 0.21872965 | 0.21872965 | 0.063745 | 0.60507405 | 1 | 4134 tags=30%, list=8%, signal=33% |
| REACTOME_TIE2 SIGNALING | REACTOME_TIE2 SIGNALING | 15 | 0.21869256 | 0.21869256 | 0.4158607 | 0.6043324 | 1 | 8880 tags=40%, list=18%, signal=49% |
| REACTOME_GRB2 EVENTS IN ERBB2 SIGNALING | REACTOME_GRB2 EVENTS IN ERBB2 SIGNALING | 61 | 0.21868135 | 0.21868135 | 0.0039604 | 0.6034791 | 1 | 4556 tags=31%, list=9%, signal=34% |
| | | 39 | 0.21861011 | 0.21861011 | 0.041958 | 0.6028697 | 1 | 10647 tags=44%, list=22%, signal=56% |
| | | 18 | 0.21841311 | 0.21841311 | 0.3029126 | 0.60280174 | 1 | 5630 tags=33%, list=11%, signal=38% |
| | | 16 | 0.21823224 | 0.21823224 | 0.3834661 | 0.60268843 | 1 | 1558 tags=25%, list=3%, signal=26% |

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|--|--|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_GPVI-MEDIATED ACTIVATION CASCADE | REACTOME_GPVI-MEDIATED ACTIVATION CASCADE | 53 | 0.21821323 | 0.21821323 | 0.0107422 | 0.6018977 | 1 | 22585 tags=68%, list=46%, signal=126% |
| REACTOME_REGULATION OF ACTIN DYNAMICS FOR PHAGOCYTIC CUP FORMATION | REACTOME_REGULATION OF ACTIN DYNAMICS FOR PHAGOCYTIC CUP FORMATION | 138 | 0.21792665 | 0.21792665 | 0 | 0.60225576 | 1 | 25195 tags=73%, list=51%, signal=150% |
| REACTOME_TRANSPORT OF MATURE MRNAS DERIVED FROM INTRONLESS TRANSCRIPTS | REACTOME_TRANSPORT OF MATURE MRNAS DERIVED FROM INTRONLESS TRANSCRIPTS | 42 | 0.21779463 | 0.21779463 | 0.0370732 | 0.6019584 | 1 | 9163 tags=40%, list=19%, signal=50% |
| REACTOME_RESOLUTION OF AP SITES VIA THE MULTIPLE-NUCLEOTIDE PATCH REPLACEMENT PATHWAY | REACTOME_RESOLUTION OF AP SITES VIA THE MULTIPLE-NUCLEOTIDE PATCH REPLACEMENT PATHWAY | 25 | 0.21766244 | 0.21766244 | 0.1652004 | 0.6017 | 1 | 16767 tags=56%, list=34%, signal=85% |
| REACTOME_SIGNALING BY HIGH-KINASE ACTIVITY BRAF | REACTOME_SIGNALING BY HIGH-KINASE ACTIVITY BRAF MUTANTS | 34 | 0.21765763 | 0.21765763 | 0.0682927 | 0.60083973 | 1 | 10951 tags=44%, list=22%, signal=57% |
| REACTOME_LOSS OF NLP FROM MITOTIC CENTROSOMES | REACTOME_LOSS OF NLP FROM MITOTIC CENTROSOMES | 69 | 0.217589 | 0.217589 | 0 | 0.60026646 | 1 | 16326 tags=55%, list=33%, signal=83% |
| REACTOME_LOSS OF PROTEINS REQUIRED FOR INTERPHASE MICROTUBULE ORGANIZATION FROM THE CENTROSOME | REACTOME_LOSS OF PROTEINS REQUIRED FOR INTERPHASE MICROTUBULE ORGANIZATION FROM THE CENTROSOME | 69 | 0.217589 | 0.217589 | 0.0040568 | 0.5993863 | 1 | 16326 tags=55%, list=33%, signal=83% |
| REACTOME_SIGNALING BY RETINOIC ACID | REACTOME_SIGNALING BY RETINOIC ACID | 43 | 0.21677315 | 0.21677315 | 0.0341709 | 0.6020451 | 1 | 9891 tags=42%, list=20%, signal=52% |
| REACTOME_SYNTHESIS OF PIPS AT THE GOLGI MEMBRANE | REACTOME_SYNTHESIS OF PIPS AT THE GOLGI MEMBRANE | 18 | 0.21670492 | 0.21670492 | 0.2950655 | 0.60148376 | 1 | 19315 tags=61%, list=39%, signal=101% |
| REACTOME_RHO GTPASES ACTIVATE CIT | REACTOME_RHO GTPASES ACTIVATE CIT | 19 | 0.21635552 | 0.21635552 | 0.326572 | 0.60209703 | 1 | 7449 tags=37%, list=15%, signal=43% |
| REACTOME_HISTIDINE, LYSINE, PHENYLALANINE, TYROSINE, PROLINE AND TRYPTOPHAN CATABOLISM | REACTOME_HISTIDINE, LYSINE, PHENYLALANINE, TYROSINE, PROLINE AND TRYPTOPHAN CATABOLISM | 46 | 0.21548131 | 0.21548131 | 0.0200803 | 0.6050752 | 1 | 10747 tags=43%, list=22%, signal=56% |
| REACTOME_P75 NTR RECEPTOR-MEDIATED SIGNALLING | REACTOME_P75 NTR RECEPTOR-MEDIATED SIGNALLING | 96 | 0.2136846 | 0.2136846 | 0 | 0.61211705 | 1 | 14549 tags=51%, list=30%, signal=72% |
| REACTOME_DEADENYLATION OF MRNA | REACTOME_DEADENYLATION OF MRNA | 24 | 0.21335214 | 0.21335214 | 0.2007952 | 0.6127406 | 1 | 5879 tags=33%, list=12%, signal=38% |
| REACTOME_ONCOGENIC MAPK SIGNALING | REACTOME_ONCOGENIC MAPK SIGNALING | 71 | 0.21325897 | 0.21325897 | 9.87E-04 | 0.6122489 | 1 | 10951 tags=44%, list=22%, signal=56% |
| REACTOME_TRANSCRIPTIONAL REGULATION BY RUNX3 | REACTOME_TRANSCRIPTIONAL REGULATION BY RUNX3 | 108 | 0.21318413 | 0.21318413 | 0 | 0.6116824 | 1 | 17693 tags=57%, list=36%, signal=90% |
| REACTOME_COENZYME A BIOSYNTHESIS | REACTOME_COENZYME A BIOSYNTHESIS | 8 | 0.21294707 | 0.21294707 | 0.8055832 | 0.6118375 | 1 | 1815 tags=25%, list=4%, signal=26% |
| REACTOME_GAP-FILLING DNA REPAIR SYNTHESIS AND LIGATION IN GG-NER | REACTOME_GAP-FILLING DNA REPAIR SYNTHESIS AND LIGATION IN GG-NER | 25 | 0.21219452 | 0.21219452 | 0.1819096 | 0.614318 | 1 | 15076 tags=52%, list=31%, signal=75% |
| REACTOME_OTHER SEMAPHORIN INTERACTIONS | REACTOME_OTHER SEMAPHORIN INTERACTIONS | 19 | 0.21186078 | 0.21186078 | 0.3320197 | 0.6149147 | 1 | 7669 tags=37%, list=16%, signal=44% |
| REACTOME_PYRUVATE METABOLISM | REACTOME_PYRUVATE METABOLISM | 28 | 0.21154752 | 0.21154752 | 0.1275304 | 0.61536264 | 1 | 7134 tags=36%, list=15%, signal=42% |
| REACTOME_TRAF6 MEDIATED INDUCTION OF TAK1 COMPLEX | REACTOME_TRAF6 MEDIATED INDUCTION OF TAK1 COMPLEX | 17 | 0.21149936 | 0.21149936 | 0.3898477 | 0.6146749 | 1 | 4048 tags=29%, list=8%, signal=32% |
| REACTOME_SYNTHESIS OF GLYCOSYLPHOSPHATIDYLINOSITOL (GPI) | REACTOME_SYNTHESIS OF GLYCOSYLPHOSPHATIDYLINOSITOL (GPI) | 16 | 0.2113386 | 0.2113386 | 0.4246988 | 0.61454934 | 1 | 17197 tags=56%, list=35%, signal=87% |
| REACTOME_TRAF6 MEDIATED INDUCTION OF NFKB AND MAP KINASES UPON TLR7/8 OR 9 ACTIVATION | REACTOME_TRAF6 MEDIATED INDUCTION OF NFKB AND MAP KINASES UPON TLR7/8 OR 9 ACTIVATION | 92 | 0.21118334 | 0.21118334 | 0 | 0.6143658 | 1 | 4048 tags=29%, list=8%, signal=32% |

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|---|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_POLB-DEPENDENT LONG PATCH BASE EXCISION REPAIR | REACTOME_POLB-DEPENDENT LONG PATCH BASE EXCISION REPAIR | 8 | 0.21091723 | 0.21091723 | 0.7985758 | 0.6146747 | 1 | 8035 tags=38%, list=16%, signal=45% |
| REACTOME_CELL DEATH SIGNALLING VIA NRAGE, NRIF AND NADE | REACTOME_CELL DEATH SIGNALLING VIA NRAGE, NRIF AND NADE | 75 | 0.21091567 | 0.21091567 | 0.0039216 | 0.613798 | 1 | 15802 tags=53%, list=32%, signal=79% |
| REACTOME_TRIGLYCERIDE CATABOLISM | REACTOME_TRIGLYCERIDE CATABOLISM | 24 | 0.21080741 | 0.21080741 | 0.2134831 | 0.6133974 | 1 | 20285 tags=63%, list=41%, signal=107% |
| REACTOME_METABOLISM OF INGESTED SEMET, SEC, MESEC INTO H2SE | REACTOME_METABOLISM OF INGESTED SEMET, SEC, MESEC INTO H2SE | 8 | 0.21077168 | 0.21077168 | 0.811608 | 0.6127001 | 1 | 26404 tags=75%, list=54%, signal=163% |
| REACTOME_INTRINSIC PATHWAY OF FIBRIN CLOT FORMATION | REACTOME_INTRINSIC PATHWAY OF FIBRIN CLOT FORMATION | 21 | 0.21054676 | 0.21054676 | 0.2736521 | 0.6128348 | 1 | 10679 tags=43%, list=22%, signal=55% |
| REACTOME_METHYLATION | REACTOME_METHYLATION | 14 | 0.21041453 | 0.21041453 | 0.5010374 | 0.6125121 | 1 | 17679 tags=57%, list=36%, signal=89% |
| REACTOME_CD209 (DC-SIGN) SIGNALING | REACTOME_CD209 (DC-SIGN) SIGNALING | 21 | 0.21014495 | 0.21014495 | 0.264151 | 0.6128288 | 1 | 15362 tags=52%, list=31%, signal=76% |
| REACTOME_ERBB2 ACTIVATES PTK6 SIGNALING | REACTOME_ERBB2 ACTIVATES PTK6 SIGNALING | 13 | 0.2100755 | 0.2100755 | 0.5474227 | 0.6122736 | 1 | 1015 tags=23%, list=2%, signal=24% |
| REACTOME_ASPARAGINE N-LINKED GLYCOSYLATION | REACTOME_ASPARAGINE N-LINKED GLYCOSYLATION | 286 | 0.20999297 | 0.20999297 | 0 | 0.6117315 | 1 | 7411 tags=36%, list=15%, signal=42% |
| REACTOME_GRB2:SOS PROVIDES LINKAGE TO MAPK SIGNALING FOR INTEGRINS | REACTOME_GRB2:SOS PROVIDES LINKAGE TO MAPK SIGNALING FOR INTEGRINS | 15 | 0.20995575 | 0.20995575 | 0.449 | 0.6110143 | 1 | 2779 tags=27%, list=6%, signal=28% |
| REACTOME_PLASMA LIPOPROTEIN REMODELING | REACTOME_PLASMA LIPOPROTEIN REMODELING | 32 | 0.209829 | 0.209829 | 0.0923695 | 0.610695 | 1 | 5033 tags=31%, list=10%, signal=35% |
| REACTOME_HDR THROUGH HOMOLOGOUS RECOMBINATION (HRR) | REACTOME_HDR THROUGH HOMOLOGOUS RECOMBINATION (HRR) | 65 | 0.20980966 | 0.20980966 | 0.0072314 | 0.60992134 | 1 | 18365 tags=58%, list=38%, signal=93% |
| REACTOME_ERKS ARE INACTIVATED | REACTOME_ERKS ARE INACTIVATED | 13 | 0.20934008 | 0.20934008 | 0.5503489 | 0.6110787 | 1 | 1051 tags=23%, list=2%, signal=24% |
| REACTOME_INACTIVATION OF CDC42 AND RAC | REACTOME_INACTIVATION OF CDC42 AND RAC | 9 | 0.20914246 | 0.20914246 | 0.7619048 | 0.61111337 | 1 | 16963 tags=56%, list=35%, signal=85% |
| REACTOME_IKK COMPLEX RECRUITMENT MEDIATED BY RIP1 | REACTOME_IKK COMPLEX RECRUITMENT MEDIATED BY RIP1 | 24 | 0.20907743 | 0.20907743 | 0.2058824 | 0.610547 | 1 | 4048 tags=29%, list=8%, signal=32% |
| REACTOME_APEX1-INDEPENDENT RESOLUTION OF AP SITES VIA THE SINGLE NUCLEOTIDE REPLACEMENT PATHWAY | REACTOME_APEX1-INDEPENDENT RESOLUTION OF AP SITES VIA THE SINGLE NUCLEOTIDE REPLACEMENT PATHWAY | 7 | 0.20881166 | 0.20881166 | 0.8657172 | 0.6108825 | 1 | 3766 tags=29%, list=8%, signal=31% |
| REACTOME_PARADOXICAL ACTIVATION OF RAF SIGNALING BY KINASE INACTIVE BRAF | REACTOME_PARADOXICAL ACTIVATION OF RAF SIGNALING BY KINASE INACTIVE BRAF | 38 | 0.20867985 | 0.20867985 | 0.0626896 | 0.6105861 | 1 | 3963 tags=29%, list=8%, signal=31% |
| REACTOME_SIGNALING BY MODERATE KINASE ACTIVITY BRAF MUTANTS | REACTOME_SIGNALING BY MODERATE KINASE ACTIVITY BRAF MUTANTS | 38 | 0.20867985 | 0.20867985 | 0.077381 | 0.60973215 | 1 | 3963 tags=29%, list=8%, signal=31% |
| REACTOME_COSTIMULATION BY THE CD28 FAMILY | REACTOME_COSTIMULATION BY THE CD28 FAMILY | 72 | 0.20763537 | 0.20763537 | 0.003 | 0.6135485 | 1 | 18410 tags=58%, list=38%, signal=93% |
| REACTOME_MAP KINASE ACTIVATION IN TLR CASCADE | REACTOME_MAP KINASE ACTIVATION IN TLR CASCADE | 63 | 0.20761934 | 0.20761934 | 0.006135 | 0.6127543 | 1 | 3836 tags=29%, list=8%, signal=31% |
| REACTOME_COBALAMIN (CBL, VITAMIN B12) TRANSPORT AND METABOLISM | REACTOME_COBALAMIN (CBL, VITAMIN B12) TRANSPORT AND METABOLISM | 21 | 0.20759101 | 0.20759101 | 0.2919075 | 0.61204106 | 1 | 15487 tags=52%, list=32%, signal=77% |
| REACTOME_L1CAM INTERACTIONS | REACTOME_L1CAM INTERACTIONS | 100 | 0.20752582 | 0.20752582 | 0 | 0.61146307 | 1 | 6996 tags=35%, list=14%, signal=41% |
| REACTOME_ANTIGEN ACTIVATES B CELL RECEPTOR (BCR) LEADING TO GENERATION OF SECOND MESSENGERS | REACTOME_ANTIGEN ACTIVATES B CELL RECEPTOR (BCR) LEADING TO GENERATION OF SECOND MESSENGERS | 97 | 0.20747136 | 0.20747136 | 9.89E-04 | 0.61085105 | 1 | 29739 tags=81%, list=61%, signal=207% |

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|---|--|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_RA BIOSYNTHESIS PATHWAY | REACTOME_RA BIOSYNTHESIS PATHWAY | 22 | 0.20716214 | 0.20716214 | 0.2644466 | 0.61139363 | 1 | 9891 tags=41%, list=20%, signal=51% |
| REACTOME_NRIF SIGNALS CELL DEATH FROM THE NUCLEUS | REACTOME_NRIF SIGNALS CELL DEATH FROM THE NUCLEUS | 15 | 0.20693907 | 0.20693907 | 0.4907317 | 0.6115472 | 1 | 6191 tags=33%, list=13%, signal=38% |
| REACTOME_ACETYLCHOLINE BINDING AND DOWNSTREAM EVENTS | REACTOME_ACETYLCHOLINE BINDING AND DOWNSTREAM EVENTS | 14 | 0.20684972 | 0.20684972 | 0.5436508 | 0.61109215 | 1 | 7361 tags=36%, list=15%, signal=42% |
| REACTOME_ACTIVATION OF NICOTINIC ACETYLCHOLINE RECEPTORS | REACTOME_ACTIVATION OF NICOTINIC ACETYLCHOLINE RECEPTORS | 14 | 0.20684972 | 0.20684972 | 0.505988 | 0.6102481 | 1 | 7361 tags=36%, list=15%, signal=42% |
| REACTOME_POSTSYNAPTIC NICOTINIC ACETYLCHOLINE RECEPTORS | REACTOME_POSTSYNAPTIC NICOTINIC ACETYLCHOLINE RECEPTORS | 14 | 0.20684972 | 0.20684972 | 0.5024438 | 0.6094064 | 1 | 7361 tags=36%, list=15%, signal=42% |
| REACTOME_MAP2K AND MAPK ACTIVATION | REACTOME_MAP2K AND MAPK ACTIVATION | 38 | 0.20667687 | 0.20667687 | 0.0646817 | 0.6093413 | 1 | 4061 tags=29%, list=8%, signal=32% |
| REACTOME_NEP/NS2 INTERACTS WITH THE CELLULAR EXPORT MACHINERY | REACTOME_NEP/NS2 INTERACTS WITH THE CELLULAR EXPORT MACHINERY | 31 | 0.20600492 | 0.20600492 | 0.1031434 | 0.61148894 | 1 | 4134 tags=29%, list=8%, signal=32% |
| REACTOME_GOLGI ASSOCIATED VESICLE BIOGENESIS | REACTOME_GOLGI ASSOCIATED VESICLE BIOGENESIS | 56 | 0.20527922 | 0.20527922 | 0.0143296 | 0.61388785 | 1 | 10944 tags=43%, list=22%, signal=55% |
| REACTOME_HOST INTERACTIONS WITH INFLUENZA | REACTOME_HOST INTERACTIONS WITH INFLUENZA FACTORS | 42 | 0.20515573 | 0.20515573 | 0.0439122 | 0.61356056 | 1 | 5118 tags=31%, list=10%, signal=35% |
| REACTOME_MXD88 DEPENDENT CASCADE INITIATED ON | REACTOME_MXD88 DEPENDENT CASCADE INITIATED ON ENDOSOME | 94 | 0.20493574 | 0.20493574 | 9.99E-04 | 0.6136908 | 1 | 4048 tags=29%, list=8%, signal=31% |
| REACTOME_TOLL LIKE RECEPTOR 7/8 (TLR7/8) | REACTOME_TOLL LIKE RECEPTOR 7/8 (TLR7/8) CASCADE | 94 | 0.20493574 | 0.20493574 | 9.70E-04 | 0.61285126 | 1 | 4048 tags=29%, list=8%, signal=31% |
| REACTOME_IMMUNOREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON-LYMPHOID CELL | REACTOME_IMMUNOREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON-LYMPHOID CELL | 199 | 0.20485389 | 0.20485389 | 0 | 0.61236954 | 1 | 25195 tags=72%, list=51%, signal=147% |
| REACTOME_GENE AND PROTEIN EXPRESSION BY JAK-STAT SIGNALING AFTER INTERLEUKIN-12 STIMULATION | REACTOME_GENE AND PROTEIN EXPRESSION BY JAK-STAT SIGNALING AFTER INTERLEUKIN-12 STIMULATION | 37 | 0.20484598 | 0.20484598 | 0.0683168 | 0.61157167 | 1 | 20414 tags=62%, list=42%, signal=107% |
| REACTOME_TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRONLESS TRANSCRIPT | REACTOME_TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRONLESS TRANSCRIPT | 41 | 0.2046474 | 0.2046474 | 0.0491968 | 0.61159736 | 1 | 17455 tags=56%, list=36%, signal=87% |
| REACTOME_COMPETING ENDOGENOUS RNAS (CERNAS) REGULATE PTEN TRANSLATION | REACTOME_COMPETING ENDOGENOUS RNAS (CERNAS) REGULATE PTEN TRANSLATION | 8 | 0.20429918 | 0.20429918 | 0.8214634 | 0.61238545 | 1 | 8359 tags=38%, list=17%, signal=45% |
| REACTOME_RUNX1 REGULATES GENES INVOLVED IN MEGAKARYOCYTE DIFFERENTIATION AND | REACTOME_RUNX1 REGULATES GENES INVOLVED IN MEGAKARYOCYTE DIFFERENTIATION AND PLATELET FUNCTION | 64 | 0.20419349 | 0.20419349 | 0.0070423 | 0.6119884 | 1 | 12201 tags=45%, list=25%, signal=60% |
| REACTOME_GLYCOPROTEIN HORMONES | REACTOME_GLYCOPROTEIN HORMONES | 10 | 0.20393218 | 0.20393218 | 0.7261331 | 0.6123117 | 1 | 4705 tags=30%, list=10%, signal=33% |
| REACTOME_TRYPTOPHAN CATABOLISM | REACTOME_TRYPTOPHAN CATABOLISM | 14 | 0.20350967 | 0.20350967 | 0.5351239 | 0.6133587 | 1 | 25012 tags=71%, list=51%, signal=146% |
| REACTOME_TOLL LIKE RECEPTOR 9 (TLR9) CASCADE | REACTOME_TOLL LIKE RECEPTOR 9 (TLR9) CASCADE | 98 | 0.20342971 | 0.20342971 | 0 | 0.6128814 | 1 | 4048 tags=29%, list=8%, signal=31% |
| REACTOME_SUMOYLATION OF TRANSCRIPTION FACTORS | REACTOME_SUMOYLATION OF TRANSCRIPTION FACTORS | 20 | 0.20324855 | 0.20324855 | 0.3352999 | 0.6128387 | 1 | 9637 tags=40%, list=20%, signal=50% |
| REACTOME_ALPHA-LINOLENIC (OMEGA3) AND LINOLEIC (OMEGA6) ACID METABOLISM | REACTOME_ALPHA-LINOLENIC (OMEGA3) AND LINOLEIC (OMEGA6) ACID METABOLISM | 13 | 0.20319277 | 0.20319277 | 0.554337 | 0.61228603 | 1 | 8885 tags=38%, list=18%, signal=47% |

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|---|--|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_ALPHA-LINOLENIC ACID (ALA) METABOLISM | REACTOME_ALPHA-LINOLENIC ACID (ALA) METABOLISM | 13 | 0.20319277 | 0.20319277 | 0.5733064 | 0.6114608 | 1 | 8885 tags=38%, list=18%, signal=47% |
| REACTOME_THROMBOXANE SIGNALLING THROUGH TP RECEPTOR | REACTOME_THROMBOXANE SIGNALLING THROUGH TP RECEPTOR | 23 | 0.20318373 | 0.20318373 | 0.2540816 | 0.61066455 | 1 | 9215 tags=39%, list=19%, signal=48% |
| REACTOME_ENDOGENOUS STEROLS | REACTOME_ENDOGENOUS STEROLS | 27 | 0.20287271 | 0.20287271 | 0.1928721 | 0.61123693 | 1 | 8206 tags=37%, list=17%, signal=44% |
| REACTOME_INITIATION OF NUCLEAR ENVELOPE | REACTOME_INITIATION OF NUCLEAR ENVELOPE REFORMATION | 12 | 0.20221949 | 0.20221949 | 0.6432806 | 0.613288 | 1 | 2341 tags=25%, list=5%, signal=26% |
| REACTOME_NUCLEAR ENVELOPE REASSEMBLY | REACTOME_NUCLEAR ENVELOPE REASSEMBLY | 12 | 0.20221949 | 0.20221949 | 0.6286008 | 0.6124659 | 1 | 2341 tags=25%, list=5%, signal=26% |
| REACTOME_ORGANIC CATION/ANION/ZWITTERION TRANSPORT | REACTOME_ORGANIC CATION/ANION/ZWITTERION TRANSPORT | 14 | 0.20200814 | 0.20200814 | 0.545005 | 0.612578 | 1 | 7598 tags=36%, list=16%, signal=42% |
| REACTOME_MYD88:MAL CASCADE INITIATED ON PLASMA | REACTOME_MYD88:MAL CASCADE INITIATED ON PLASMA MEMBRANE | 95 | 0.20191056 | 0.20191056 | 0 | 0.6121624 | 1 | 4048 tags=28%, list=8%, signal=31% |
| REACTOME_TOLL LIKE RECEPTOR 2 (TLR2) CASCADE | REACTOME_TOLL LIKE RECEPTOR 2 (TLR2) CASCADE | 95 | 0.20191056 | 0.20191056 | 0 | 0.6113452 | 1 | 4048 tags=28%, list=8%, signal=31% |
| REACTOME_TOLL LIKE RECEPTOR TLR1:TLR2 CASCADE | REACTOME_TOLL LIKE RECEPTOR TLR1:TLR2 CASCADE | 95 | 0.20191056 | 0.20191056 | 9.49E-04 | 0.61052996 | 1 | 4048 tags=28%, list=8%, signal=31% |
| REACTOME_TOLL LIKE RECEPTOR TLR6:TLR2 CASCADE | REACTOME_TOLL LIKE RECEPTOR TLR6:TLR2 CASCADE | 95 | 0.20191056 | 0.20191056 | 0.0031881 | 0.6097171 | 1 | 4048 tags=28%, list=8%, signal=31% |
| REACTOME_SIGNALING BY REACTOME_NUCLEAR RECEPTOR TRANSCRIPTION | REACTOME_SIGNALING BY NOTCH1 REACTOME_NUCLEAR RECEPTOR TRANSCRIPTION PATHWAY | 72 | 0.2017907 | 0.2017907 | 0.004065 | 0.609409 | 1 | 11215 tags=43%, list=23%, signal=56% |
| REACTOME_MYD88 CASCADE INITIATED ON PLASMA | REACTOME_MYD88 CASCADE INITIATED ON PLASMA MEMBRANE | 51 | 0.20119947 | 0.20119947 | 0.0336301 | 0.6112269 | 1 | 4559 tags=29%, list=9%, signal=32% |
| REACTOME_TOLL LIKE RECEPTOR 10 (TLR10) CASCADE | REACTOME_TOLL LIKE RECEPTOR 10 (TLR10) CASCADE | 85 | 0.20113364 | 0.20113364 | 9.63E-04 | 0.610718 | 1 | 3993 tags=28%, list=8%, signal=31% |
| REACTOME_TOLL LIKE RECEPTOR 5 (TLR5) CASCADE | REACTOME_TOLL LIKE RECEPTOR 5 (TLR5) CASCADE | 85 | 0.20113364 | 0.20113364 | 0.0020263 | 0.6099091 | 1 | 3993 tags=28%, list=8%, signal=31% |
| REACTOME_INTERLEUKIN-12 FAMILY SIGNALING | REACTOME_TOLL LIKE RECEPTOR 10 (TLR10) CASCADE | 85 | 0.20113364 | 0.20113364 | 0.002947 | 0.6091024 | 1 | 3993 tags=28%, list=8%, signal=31% |
| REACTOME_VITAMIN C (ASCORBATE) METABOLISM | REACTOME_INTERLEUKIN-12 FAMILY SIGNALING | 56 | 0.20092678 | 0.20092678 | 0.0162437 | 0.6091641 | 1 | 34765 tags=91%, list=71%, signal=314% |
| REACTOME_RHO GTPASE CYCLE | REACTOME_VITAMIN C (ASCORBATE) METABOLISM | 8 | 0.20058928 | 0.20058928 | 0.8377581 | 0.6098457 | 1 | 2420 tags=25%, list=5%, signal=26% |
| REACTOME_TOLL LIKE RECEPTOR 4 (TLR4) CASCADE | REACTOME_RHO GTPASE CYCLE | 139 | 0.20057012 | 0.20057012 | 0 | 0.6091298 | 1 | 12751 tags=46%, list=26%, signal=62% |
| REACTOME_REGULATION OF TP53 ACTIVITY THROUGH | REACTOME_TOLL LIKE RECEPTOR 4 (TLR4) CASCADE | 126 | 0.20048529 | 0.20048529 | 0 | 0.6087183 | 1 | 7695 tags=36%, list=16%, signal=42% |
| REACTOME_REGULATION OF HSF1-MEDIATED HEAT SHOCK | REACTOME_REGULATION OF TP53 ACTIVITY THROUGH ACETYLATION | 30 | 0.19988765 | 0.19988765 | 0.1524574 | 0.61046207 | 1 | 24493 tags=70%, list=50%, signal=140% |
| REACTOME_TRIGLYCERIDE BIOSYNTHESIS | REACTOME_REGULATION OF HSF1-MEDIATED HEAT SHOCK RESPONSE | 81 | 0.19983311 | 0.19983311 | 0.001998 | 0.60989404 | 1 | 4134 tags=28%, list=8%, signal=31% |
| REACTOME_ACTIVATION OF THE PRE-REPLICATIVE COMPLEX | REACTOME_TRIGLYCERIDE BIOSYNTHESIS | 14 | 0.19967932 | 0.19967932 | 0.5184079 | 0.60975945 | 1 | 35692 tags=93%, list=73%, signal=342% |
| REACTOME_CYTOKINE SIGNALING IN IMMUNE SYSTEM | REACTOME_ACTIVATION OF THE PRE-REPLICATIVE COMPLEX | 32 | 0.19948706 | 0.19948706 | 0.1375661 | 0.6098376 | 1 | 14720 tags=50%, list=30%, signal=71% |
| REACTOME_INTERACTIONS OF REV WITH HOST CELLULAR | REACTOME_CYTOKINE SIGNALING IN IMMUNE SYSTEM | 900 | 0.19887434 | 0.19887434 | 0 | 0.61164993 | 1 | 10951 tags=42%, list=22%, signal=53% |
| REACTOME_HEDGEHOG 'ON' STATE | REACTOME_INTERACTIONS OF REV WITH HOST CELLULAR PROTEINS | 36 | 0.19807613 | 0.19807613 | 0.1056676 | 0.6143297 | 1 | 6629 tags=33%, list=14%, signal=39% |
| REACTOME_FREE FATTY ACID RECEPTORS | REACTOME_HEDGEHOG 'ON' STATE | 85 | 0.19773637 | 0.19773637 | 0.0010417 | 0.61503464 | 1 | 13376 tags=47%, list=27%, signal=65% |
| REACTOME_RHO GTPASES ACTIVATE KTN1 | REACTOME_FREE FATTY ACID RECEPTORS | 5 | 0.19750817 | 0.19750817 | 0.9692155 | 0.6152658 | 1 | 29501 tags=80%, list=60%, signal=201% |
| | REACTOME_RHO GTPASES ACTIVATE KTN1 | 11 | 0.19743954 | 0.19743954 | 0.7129001 | 0.61475843 | 1 | 8139 tags=36%, list=17%, signal=44% |

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|---|---|-----|------------|------------|-----------|------------|---|--|
| REACTOME_CHYLOMICRON REMODELING | REACTOME_CHYLOMICRON REMODELING | 10 | 0.19723216 | 0.19723216 | 0.7638749 | 0.61488307 | 1 | 5033 tags=30%, list=10%, signal=33% |
| REACTOME_FATTY ACYL-COA BIOSYNTHESIS | REACTOME_FATTY ACYL-COA BIOSYNTHESIS | 37 | 0.19705074 | 0.19705074 | 0.1010204 | 0.61484516 | 1 | 8885 tags=38%, list=18%, signal=46% |
| REACTOME_APOPTOTIC EXECUTION PHASE | REACTOME_APOPTOTIC EXECUTION PHASE | 51 | 0.196802 | 0.196802 | 0.0269231 | 0.6151448 | 1 | 3814 tags=27%, list=8%, signal=30% |
| REACTOME_HIV ELONGATION ARREST AND RECOVERY | REACTOME_HIV ELONGATION ARREST AND RECOVERY | 29 | 0.19645011 | 0.19645011 | 0.1961962 | 0.6159152 | 1 | 7270 tags=34%, list=15%, signal=40% |
| REACTOME_PAUSING AND RECOVERY OF HIV ELONGATION | REACTOME_PAUSING AND RECOVERY OF HIV ELONGATION | 29 | 0.19645011 | 0.19645011 | 0.182721 | 0.6151194 | 1 | 7270 tags=34%, list=15%, signal=40% |
| REACTOME_TRANSPORT OF THE SLBP DEPENDANT MATURE | REACTOME_TRANSPORT OF THE SLBP DEPENDANT MATURE MRNA | 35 | 0.1964439 | 0.1964439 | 0.1286008 | 0.61435723 | 1 | 7175 tags=34%, list=15%, signal=40% |
| REACTOME_DOPAMINE | REACTOME_DOPAMINE RECEPTORS | 5 | 0.19609885 | 0.19609885 | 0.9611273 | 0.61503774 | 1 | 39363 tags=100%, list=80%, signal=510% |
| REACTOME_CELLULAR RESPONSE TO HEAT STRESS | REACTOME_CELLULAR RESPONSE TO HEAT STRESS | 97 | 0.19584675 | 0.19584675 | 0.0010142 | 0.6153469 | 1 | 3553 tags=27%, list=7%, signal=29% |
| REACTOME_NS1 MEDIATED EFFECTS ON HOST PATHWAYS | REACTOME_NS1 MEDIATED EFFECTS ON HOST PATHWAYS | 40 | 0.19561575 | 0.19561575 | 0.0796813 | 0.61557454 | 1 | 5118 tags=30%, list=10%, signal=33% |
| REACTOME_N-GLYCAN ANTENNAE ELONGATION IN THE MEDIAL/TRANS-GOLGI | REACTOME_N-GLYCAN ANTENNAE ELONGATION IN THE MEDIAL/TRANS-GOLGI | 26 | 0.19432828 | 0.19432828 | 0.2418236 | 0.6205534 | 1 | 13088 tags=46%, list=27%, signal=63% |
| REACTOME_STRIATED MUSCLE CONTRACTION | REACTOME_STRIATED MUSCLE CONTRACTION | 34 | 0.19389188 | 0.19389188 | 0.1469388 | 0.62166846 | 1 | 3473 tags=26%, list=7%, signal=28% |
| REACTOME_NUCLEAR SIGNALING BY ERBB4 | REACTOME_NUCLEAR SIGNALING BY ERBB4 | 25 | 0.19364119 | 0.19364119 | 0.2540323 | 0.62198275 | 1 | 6191 tags=32%, list=13%, signal=37% |
| REACTOME_SYNTHESIS OF VERY LONG-CHAIN FATTY ACYL- | REACTOME_SYNTHESIS OF VERY LONG-CHAIN FATTY ACYL-COAS | 24 | 0.19361834 | 0.19361834 | 0.2625128 | 0.621293 | 1 | 8885 tags=38%, list=18%, signal=46% |
| REACTOME_INTERACTIONS OF VPR WITH HOST CELLULAR | REACTOME_INTERACTIONS OF VPR WITH HOST CELLULAR PROTEINS | 36 | 0.19347195 | 0.19347195 | 0.1163491 | 0.62109095 | 1 | 4134 tags=28%, list=8%, signal=30% |
| REACTOME_CELL SURFACE INTERACTIONS AT THE VASCULAR WALL | REACTOME_CELL SURFACE INTERACTIONS AT THE VASCULAR WALL | 211 | 0.19326219 | 0.19326219 | 0 | 0.6211872 | 1 | 25618 tags=72%, list=52%, signal=149% |
| REACTOME_SIGNAL REGULATORY PROTEIN FAMILY | REACTOME_SIGNAL REGULATORY PROTEIN FAMILY INTERACTIONS | 13 | 0.19325997 | 0.19325997 | 0.6403326 | 0.6204017 | 1 | 35737 tags=92%, list=73%, signal=342% |
| REACTOME_SIGNALING BY RAS MUTANTS | REACTOME_SIGNALING BY RAS MUTANTS | 48 | 0.19318609 | 0.19318609 | 0.0558276 | 0.6199697 | 1 | 10951 tags=42%, list=22%, signal=54% |
| REACTOME_EARLY PHASE OF HIV LIFE CYCLE | REACTOME_EARLY PHASE OF HIV LIFE CYCLE | 14 | 0.19308086 | 0.19308086 | 0.5890688 | 0.6196916 | 1 | 8035 tags=36%, list=16%, signal=43% |
| REACTOME_NUCLEAR ENVELOPE BREAKDOWN | REACTOME_NUCLEAR ENVELOPE BREAKDOWN | 51 | 0.19272083 | 0.19272083 | 0.0396432 | 0.62042695 | 1 | 17455 tags=55%, list=36%, signal=85% |
| REACTOME_ANCHORING OF THE BASAL BODY TO THE PLASMA MEMBRANE | REACTOME_ANCHORING OF THE BASAL BODY TO THE PLASMA MEMBRANE | 97 | 0.1927127 | 0.1927127 | 0.003009 | 0.6196901 | 1 | 16326 tags=53%, list=33%, signal=79% |
| REACTOME_TRANSCRIPTIONAL ACTIVATION OF MITOCHONDRIAL BIOGENESIS | REACTOME_TRANSCRIPTIONAL ACTIVATION OF MITOCHONDRIAL BIOGENESIS | 53 | 0.19232269 | 0.19232269 | 0.0303327 | 0.62061876 | 1 | 5374 tags=30%, list=11%, signal=34% |
| REACTOME_DETOXIFICATION OF REACTIVE OXYGEN SPECIES | REACTOME_DETOXIFICATION OF REACTIVE OXYGEN SPECIES | 37 | 0.19225606 | 0.19225606 | 0.1061508 | 0.62011725 | 1 | 21030 tags=62%, list=43%, signal=109% |
| REACTOME_RRNA MODIFICATION IN THE NUCLEUS | REACTOME_RRNA MODIFICATION IN THE NUCLEUS AND CYTOSOL | 61 | 0.19210568 | 0.19210568 | 0.0212551 | 0.62001103 | 1 | 13080 tags=46%, list=27%, signal=63% |
| REACTOME_EPHRIN SIGNALING | REACTOME_EPHRIN SIGNALING | 19 | 0.19165267 | 0.19165267 | 0.437811 | 0.6211928 | 1 | 6081 tags=32%, list=12%, signal=36% |
| REACTOME_FCGAMMA RECEPTOR (FCGR) DEPENDENT | REACTOME_FCGAMMA RECEPTOR (FCGR) DEPENDENT PHAGOCYTOSIS | 163 | 0.19158761 | 0.19158761 | 0 | 0.62067825 | 1 | 25195 tags=71%, list=51%, signal=145% |
| REACTOME_COPI-DEPENDENT GOLGI-TO-ER RETROGRADE | REACTOME_COPI-DEPENDENT GOLGI-TO-ER RETROGRADE TRAFFIC | 82 | 0.1914277 | 0.1914277 | 0.0091556 | 0.620591 | 1 | 10944 tags=41%, list=22%, signal=53% |

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|---|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_SUMOYLATION OF DNA DAMAGE RESPONSE AND REPAIR PROTEINS | REACTOME_SUMOYLATION OF DNA DAMAGE RESPONSE AND REPAIR PROTEINS | 76 | 0.19061305 | 0.19061305 | 0.0118812 | 0.6233621 | 1 | 18384 tags=57%, list=38%, signal=90% |
| REACTOME_BH3-ONLY PROTEINS ASSOCIATE WITH AND INACTIVATE ANTI-APOPTOTIC | REACTOME_BH3-ONLY PROTEINS ASSOCIATE WITH AND INACTIVATE ANTI-APOPTOTIC BCL-2 MEMBERS | 8 | 0.19005454 | 0.19005454 | 0.8687068 | 0.6250303 | 1 | 15177 tags=50%, list=31%, signal=72% |
| REACTOME_CITRIC ACID CYCLE (TCA CYCLE) | REACTOME_CITRIC ACID CYCLE (TCA CYCLE) | 19 | 0.18891497 | 0.18891497 | 0.464497 | 0.6293805 | 1 | 6215 tags=32%, list=13%, signal=36% |
| REACTOME_DOWNREGULATION OF TGF-BETA RECEPTOR | REACTOME_DOWNREGULATION OF TGF-BETA RECEPTOR SIGNALING | 26 | 0.18854399 | 0.18854399 | 0.2689162 | 0.6302131 | 1 | 5838 tags=31%, list=12%, signal=35% |
| REACTOME_REV-MEDIATED NUCLEAR EXPORT OF HIV RNA | REACTOME_REV-MEDIATED NUCLEAR EXPORT OF HIV RNA | 34 | 0.18825729 | 0.18825729 | 0.1561866 | 0.63074136 | 1 | 6629 tags=32%, list=14%, signal=37% |
| REACTOME_REGULATION OF FZD BY UBIQUITINATION | REACTOME_REGULATION OF FZD BY UBIQUITINATION | 21 | 0.18811296 | 0.18811296 | 0.4089069 | 0.6305979 | 1 | 11777 tags=43%, list=24%, signal=56% |
| REACTOME_SYNTHESIS OF PA | REACTOME_SYNTHESIS OF PA | 39 | 0.18696053 | 0.18696053 | 0.1190717 | 0.63481396 | 1 | 13451 tags=46%, list=27%, signal=64% |
| REACTOME_SIGNAL | REACTOME_SIGNAL AMPLIFICATION | 32 | 0.18690608 | 0.18690608 | 0.180198 | 0.6342525 | 1 | 9215 tags=38%, list=19%, signal=46% |
| REACTOME_THROMBIN SIGNALING THROUGH PROTEINASE ACTIVATED RECEPTORS (PARS) | REACTOME_THROMBIN SIGNALING THROUGH PROTEINASE ACTIVATED RECEPTORS (PARS) | 32 | 0.18690608 | 0.18690608 | 0.1971545 | 0.6334636 | 1 | 9215 tags=38%, list=19%, signal=46% |
| REACTOME_POST-CHAPERONIN TUBULIN FOLDING PATHWAY | REACTOME_POST-CHAPERONIN TUBULIN FOLDING PATHWAY | 22 | 0.18554516 | 0.18554516 | 0.3804453 | 0.6387284 | 1 | 10949 tags=41%, list=22%, signal=53% |
| REACTOME_REGULATION OF PLK1 ACTIVITY AT G2/M | REACTOME_REGULATION OF PLK1 ACTIVITY AT G2/M TRANSITION | 87 | 0.18551962 | 0.18551962 | 0.0078355 | 0.63804746 | 1 | 12881 tags=45%, list=26%, signal=61% |
| REACTOME_RHO GTPASES ACTIVATE WASPS AND WAVES | REACTOME_RHO GTPASES ACTIVATE WASPS AND WAVES | 36 | 0.18523553 | 0.18523553 | 0.1570248 | 0.6385075 | 1 | 4537 tags=28%, list=9%, signal=31% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF DNA REPAIR GENES | REACTOME_TP53 REGULATES TRANSCRIPTION OF DNA REPAIR GENES | 58 | 0.18485296 | 0.18485296 | 0.035122 | 0.6394572 | 1 | 12064 tags=43%, list=25%, signal=57% |
| REACTOME_FANCONI ANEMIA PATHWAY | REACTOME_FANCONI ANEMIA PATHWAY | 36 | 0.184376 | 0.184376 | 0.1481113 | 0.64078283 | 1 | 23621 tags=67%, list=48%, signal=129% |
| REACTOME_DISASSEMBLY OF THE DESTRUCTION COMPLEX AND RECRUITMENT OF AXIN TO THE MEMBRANE | REACTOME_DISASSEMBLY OF THE DESTRUCTION COMPLEX AND RECRUITMENT OF AXIN TO THE MEMBRANE | 31 | 0.18386318 | 0.18386318 | 0.238477 | 0.6423547 | 1 | 6797 tags=32%, list=14%, signal=37% |
| REACTOME_PKA ACTIVATION | REACTOME_PKA ACTIVATION | 16 | 0.1837065 | 0.1837065 | 0.6087805 | 0.64226264 | 1 | 3248 tags=25%, list=7%, signal=27% |
| REACTOME_CD28 CO- | REACTOME_CD28 CO-STIMULATION | 35 | 0.18291438 | 0.18291438 | 0.1829026 | 0.6450965 | 1 | 17630 tags=54%, list=36%, signal=85% |
| REACTOME_PYRUVATE METABOLISM AND CITRIC ACID (TCA) CYCLE | REACTOME_PYRUVATE METABOLISM AND CITRIC ACID (TCA) CYCLE | 49 | 0.1809954 | 0.1809954 | 0.0733198 | 0.65293294 | 1 | 7134 tags=33%, list=15%, signal=38% |
| REACTOME_METABOLISM OF NUCLEOTIDES | REACTOME_METABOLISM OF NUCLEOTIDES | 102 | 0.18093166 | 0.18093166 | 0.0050302 | 0.6524365 | 1 | 9400 tags=37%, list=19%, signal=46% |
| REACTOME_TRANSCRIPTIONAL REGULATION BY THE AP-2 (TFAP2) FAMILY OF TRANSCRIPTION FACTORS | REACTOME_TRANSCRIPTIONAL REGULATION BY THE AP-2 (TFAP2) FAMILY OF TRANSCRIPTION FACTORS | 36 | 0.18071537 | 0.18071537 | 0.1549439 | 0.652562 | 1 | 12919 tags=44%, list=26%, signal=60% |
| REACTOME_TRANSPORT OF THE SLBP INDEPENDENT MATURE | REACTOME_TRANSPORT OF THE SLBP INDEPENDENT MATURE MRNA | 34 | 0.18038306 | 0.18038306 | 0.1757451 | 0.65324825 | 1 | 4134 tags=26%, list=8%, signal=29% |
| REACTOME_SUMOYLATION OF DNA REPLICATION PROTEINS | REACTOME_SUMOYLATION OF DNA REPLICATION PROTEINS | 45 | 0.18024895 | 0.18024895 | 0.1170635 | 0.65306807 | 1 | 18384 tags=56%, list=38%, signal=89% |
| REACTOME_UPTAKE AND ACTIONS OF BACTERIAL TOXINS | REACTOME_UPTAKE AND ACTIONS OF BACTERIAL TOXINS | 29 | 0.18019313 | 0.18019313 | 0.2914172 | 0.65252155 | 1 | 9754 tags=38%, list=20%, signal=47% |
| REACTOME_TP53 REGULATES TRANSCRIPTION OF ADDITIONAL CELL CYCLE GENES WHOSE EXACT ROLE IN THE P53 PATHWAY REMAIN UNCERTAIN | REACTOME_TP53 REGULATES TRANSCRIPTION OF ADDITIONAL CELL CYCLE GENES WHOSE EXACT ROLE IN THE P53 PATHWAY REMAIN UNCERTAIN | 20 | 0.17998774 | 0.17998774 | 0.4557823 | 0.65265083 | 1 | 5879 tags=30%, list=12%, signal=34% |

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|---|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_TRANSCRIPTIONAL REGULATION OF WHITE ADIPOCYTE DIFFERENTIATION | REACTOME_TRANSCRIPTIONAL REGULATION OF WHITE ADIPOCYTE DIFFERENTIATION | 83 | 0.17942297 | 0.17942297 | 0.01002 | 0.65436465 | 1 | 5387 tags=29%, list=11%, signal=32% |
| REACTOME_SIGNALING BY INTERLEUKINS | REACTOME_SIGNALING BY INTERLEUKINS | 687 | 0.17913449 | 0.17913449 | 0 | 0.65491956 | 1 | 10951 tags=40%, list=22%, signal=51% |
| REACTOME_TOLL-LIKE RECEPTORS CASCADES | REACTOME_TOLL-LIKE RECEPTORS CASCADES | 152 | 0.1789082 | 0.1789082 | 0 | 0.655176 | 1 | 7695 tags=34%, list=16%, signal=40% |
| REACTOME_SYNTHESIS OF PIPS AT THE EARLY ENDOSOME | REACTOME_SYNTHESIS OF PIPS AT THE EARLY ENDOSOME MEMBRANE | 16 | 0.17864384 | 0.17864384 | 0.6290323 | 0.6555626 | 1 | 24918 tags=69%, list=51%, signal=140% |
| REACTOME_PCP/CE PATHWAY | REACTOME_PCP/CE PATHWAY | 91 | 0.17863518 | 0.17863518 | 0.007992 | 0.6548081 | 1 | 16558 tags=52%, list=34%, signal=78% |
| REACTOME_SYNTHESIS OF LEUKOTRIENES (LT) AND EOXINS | REACTOME_SYNTHESIS OF LEUKOTRIENES (LT) AND EOXINS (EX) | 21 | 0.17800617 | 0.17800617 | 0.4747475 | 0.6567849 | 1 | 16935 tags=52%, list=35%, signal=80% |
| REACTOME_TBC/RABGAPS | REACTOME_TBC/RABGAPS | 45 | 0.17711684 | 0.17711684 | 0.1155779 | 0.66005325 | 1 | 6568 tags=31%, list=13%, signal=36% |
| REACTOME_G ALPHA (12/13) SIGNALLING EVENTS | REACTOME_G ALPHA (12/13) SIGNALLING EVENTS | 87 | 0.17666459 | 0.17666459 | 0.0111902 | 0.66126907 | 1 | 12751 tags=44%, list=26%, signal=59% |
| REACTOME_NOTCH1 INTRACELLULAR DOMAIN REGULATES TRANSCRIPTION | REACTOME_NOTCH1 INTRACELLULAR DOMAIN REGULATES TRANSCRIPTION | 47 | 0.17650293 | 0.17650293 | 0.0880881 | 0.6612204 | 1 | 12201 tags=43%, list=25%, signal=57% |
| REACTOME_FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT/TRIC | REACTOME_FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT/TRIC | 25 | 0.17646097 | 0.17646097 | 0.3642931 | 0.6605905 | 1 | 10949 tags=40%, list=22%, signal=51% |
| REACTOME_POST-ELONGATION PROCESSING OF INTRONLESS PRE-MRNA | REACTOME_POST-ELONGATION PROCESSING OF INTRONLESS PRE-MRNA | 28 | 0.17630324 | 0.17630324 | 0.2910373 | 0.6605212 | 1 | 21100 tags=61%, list=43%, signal=107% |
| REACTOME_PROCESSING OF CAPPED INTRONLESS PRE-MRNA | REACTOME_PROCESSING OF CAPPED INTRONLESS PRE-MRNA | 28 | 0.17630324 | 0.17630324 | 0.3106893 | 0.6597263 | 1 | 21100 tags=61%, list=43%, signal=107% |
| REACTOME_REGULATION OF RUNX3 EXPRESSION AND ACTIVITY | REACTOME_REGULATION OF RUNX3 EXPRESSION AND ACTIVITY | 54 | 0.17587084 | 0.17587084 | 0.0639594 | 0.6608591 | 1 | 17693 tags=54%, list=36%, signal=84% |
| REACTOME_SYNTHESIS OF IP3 AND IP4 IN THE CYTOSOL | REACTOME_SYNTHESIS OF IP3 AND IP4 IN THE CYTOSOL | 26 | 0.17504288 | 0.17504288 | 0.3550107 | 0.66374475 | 1 | 8382 tags=35%, list=17%, signal=42% |
| REACTOME_TRP CHANNELS | REACTOME_TRP CHANNELS | 25 | 0.1735758 | 0.1735758 | 0.4048096 | 0.6696438 | 1 | 16966 tags=52%, list=35%, signal=80% |
| REACTOME_MAPK6/MAPK4 SIGNALING | REACTOME_MAPK6/MAPK4 SIGNALING | 88 | 0.17304175 | 0.17304175 | 9.96E-04 | 0.67135364 | 1 | 17693 tags=53%, list=36%, signal=83% |
| REACTOME_TRNA MODIFICATION IN THE NUCLEUS AND CYTOSOL | REACTOME_TRNA MODIFICATION IN THE NUCLEUS AND CYTOSOL | 43 | 0.17226139 | 0.17226139 | 0.1372162 | 0.6741192 | 1 | 6375 tags=30%, list=13%, signal=35% |
| REACTOME_RETROGRADE TRANSPORT AT THE TRANS-GOLGI-NETWORK | REACTOME_RETROGRADE TRANSPORT AT THE TRANS-GOLGI-NETWORK | 49 | 0.1719595 | 0.1719595 | 0.0954774 | 0.67474914 | 1 | 14571 tags=47%, list=30%, signal=67% |
| REACTOME_ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 1 | REACTOME_ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 1 | 25 | 0.17187168 | 0.17187168 | 0.4228395 | 0.67434597 | 1 | 9215 tags=36%, list=19%, signal=44% |
| REACTOME_HOMOLOGY DIRECTED REPAIR | REACTOME_HOMOLOGY DIRECTED REPAIR | 118 | 0.17176585 | 0.17176585 | 9.79E-04 | 0.6740035 | 1 | 18581 tags=55%, list=38%, signal=89% |
| REACTOME_TRANSCRIPTION OF E2F TARGETS UNDER NEGATIVE CONTROL BY DREAM COMPLEX | REACTOME_TRANSCRIPTION OF E2F TARGETS UNDER NEGATIVE CONTROL BY DREAM COMPLEX | 19 | 0.17154889 | 0.17154889 | 0.5656155 | 0.67419946 | 1 | 7065 tags=32%, list=14%, signal=37% |
| REACTOME_SIGNALING BY HEDGEHOG | REACTOME_SIGNALING BY HEDGEHOG | 136 | 0.1713793 | 0.1713793 | 0.001007 | 0.6742128 | 1 | 13953 tags=46%, list=28%, signal=64% |
| REACTOME_THE ROLE OF GTSE1 IN G2/M PROGRESSION AFTER G2 CHECKPOINT | REACTOME_THE ROLE OF GTSE1 IN G2/M PROGRESSION AFTER G2 CHECKPOINT | 59 | 0.17110445 | 0.17110445 | 0.0544355 | 0.67466 | 1 | 20678 tags=59%, list=42%, signal=103% |
| REACTOME_INTERLEUKIN-1 FAMILY SIGNALING | REACTOME_INTERLEUKIN-1 FAMILY SIGNALING | 94 | 0.17088279 | 0.17088279 | 0.0083074 | 0.67486113 | 1 | 17693 tags=53%, list=36%, signal=83% |
| REACTOME_REPRESSION OF WNT TARGET GENES | REACTOME_REPRESSION OF WNT TARGET GENES | 14 | 0.17083411 | 0.17083411 | 0.7619522 | 0.6742898 | 1 | 2129 tags=21%, list=4%, signal=22% |
| REACTOME_EFFECTS OF PIP2 HYDROLYSIS | REACTOME_EFFECTS OF PIP2 HYDROLYSIS | 27 | 0.17053701 | 0.17053701 | 0.3580875 | 0.674829 | 1 | 15229 tags=48%, list=31%, signal=70% |

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|---|---|------|------------|------------|-----------|------------|---|--------------------------------------|
| REACTOME_SYNTHESIS OF DNA | REACTOME_SYNTHESIS OF DNA | 99 | 0.17030185 | 0.17030185 | 0.0030519 | 0.67514706 | 1 | 19869 tags=58%, list=41%, signal=97% |
| REACTOME_KINESINS | REACTOME_KINESINS | 43 | 0.17028767 | 0.17028767 | 0.1589069 | 0.67440933 | 1 | 8749 tags=35%, list=18%, signal=42% |
| REACTOME_ACTIVATION OF NF-KAPPAB IN B CELLS | REACTOME_ACTIVATION OF NF-KAPPAB IN B CELLS | 66 | 0.17018694 | 0.17018694 | 0.0433031 | 0.67408895 | 1 | 19869 tags=58%, list=41%, signal=97% |
| REACTOME_MHC CLASS II ANTIGEN PRESENTATION | REACTOME_MHC CLASS II ANTIGEN PRESENTATION | 105 | 0.16957295 | 0.16957295 | 0.0081716 | 0.67610073 | 1 | 10367 tags=38%, list=21%, signal=48% |
| REACTOME_VIRAL MESSENGER RNA SYNTHESIS | REACTOME_VIRAL MESSENGER RNA SYNTHESIS | 43 | 0.1693089 | 0.1693089 | 0.1565907 | 0.67653674 | 1 | 4242 tags=26%, list=9%, signal=28% |
| REACTOME_EGFR INTERACTS WITH PHOSPHOLIPASE C-GAMMA | REACTOME_EGFR INTERACTS WITH PHOSPHOLIPASE C-GAMMA | 34 | 0.169058 | 0.169058 | 0.2547835 | 0.6769248 | 1 | 3248 tags=24%, list=7%, signal=25% |
| REACTOME_PKA ACTIVATION IN GLUCAGON SIGNALLING | REACTOME_PKA ACTIVATION IN GLUCAGON SIGNALLING | 17 | 0.16899928 | 0.16899928 | 0.6443089 | 0.6763964 | 1 | 3248 tags=24%, list=7%, signal=25% |
| REACTOME_PKA-MEDIATED PHOSPHORYLATION OF CREB | REACTOME_PKA-MEDIATED PHOSPHORYLATION OF CREB | 17 | 0.16899928 | 0.16899928 | 0.6564103 | 0.6756034 | 1 | 3248 tags=24%, list=7%, signal=25% |
| REACTOME_DEACTIVATION OF THE BETA-CATENIN TRANSACTIVATING COMPLEX | REACTOME_DEACTIVATION OF THE BETA-CATENIN TRANSACTIVATING COMPLEX | 42 | 0.16813837 | 0.16813837 | 0.168932 | 0.67872983 | 1 | 6929 tags=31%, list=14%, signal=36% |
| REACTOME_DNA DOUBLE STRAND BREAK RESPONSE | REACTOME_DNA DOUBLE STRAND BREAK RESPONSE | 59 | 0.1675265 | 0.1675265 | 0.0679012 | 0.6807684 | 1 | 10894 tags=39%, list=22%, signal=50% |
| REACTOME_ORC1 REMOVAL FROM CHROMATIN | REACTOME_ORC1 REMOVAL FROM CHROMATIN | 70 | 0.16745065 | 0.16745065 | 0.0371859 | 0.6803058 | 1 | 17693 tags=53%, list=36%, signal=83% |
| REACTOME_SWITCHING OF ORIGINS TO A POST-REPLICATIVE STATE | REACTOME_SWITCHING OF ORIGINS TO A POST-REPLICATIVE STATE | 70 | 0.16745065 | 0.16745065 | 0.0333333 | 0.679512 | 1 | 17693 tags=53%, list=36%, signal=83% |
| REACTOME_SUMO E3 LIGASES SUMOYLATE TARGET PROTEINS | REACTOME_SUMO E3 LIGASES SUMOYLATE TARGET PROTEINS | 112 | 0.16686158 | 0.16686158 | 0.0019157 | 0.6813761 | 1 | 16767 tags=51%, list=34%, signal=77% |
| REACTOME_PI3K EVENTS IN ERBB2 SIGNALING | REACTOME_PI3K EVENTS IN ERBB2 SIGNALING | 16 | 0.16680498 | 0.16680498 | 0.672888 | 0.68081784 | 1 | 1015 tags=19%, list=2%, signal=19% |
| REACTOME_HOST INTERACTIONS OF HIV FACTORS | REACTOME_HOST INTERACTIONS OF HIV FACTORS | 127 | 0.16663107 | 0.16663107 | 0.0010183 | 0.6808053 | 1 | 17693 tags=53%, list=36%, signal=82% |
| REACTOME_ASYMMETRIC LOCALIZATION OF PCP | REACTOME_ASYMMETRIC LOCALIZATION OF PCP PROTEINS | 63 | 0.16584194 | 0.16584194 | 0.0493827 | 0.6836172 | 1 | 19869 tags=57%, list=41%, signal=96% |
| REACTOME_HDR THROUGH HOMOLOGOUS RECOMBINATION (HR) OR SINGLE STRAND ANNEALING (SSA) | REACTOME_HDR THROUGH HOMOLOGOUS RECOMBINATION (HR) OR SINGLE STRAND ANNEALING (SSA) | 112 | 0.16552594 | 0.16552594 | 0.002907 | 0.68428534 | 1 | 18581 tags=54%, list=38%, signal=88% |
| REACTOME_PLATELET CALCIUM HOMEOSTASIS | REACTOME_PLATELET CALCIUM HOMEOSTASIS | 28 | 0.16535038 | 0.16535038 | 0.3899497 | 0.68427914 | 1 | 14641 tags=46%, list=30%, signal=66% |
| REACTOME_FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET | REACTOME_FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION | 140 | 0.16462877 | 0.16462877 | 0.0019881 | 0.686792 | 1 | 8749 tags=34%, list=18%, signal=42% |
| REACTOME_METABOLISM OF VITAMINS AND COFACTORS | REACTOME_METABOLISM OF VITAMINS AND COFACTORS | 180 | 0.16311538 | 0.16311538 | 0 | 0.6929649 | 1 | 7547 tags=32%, list=15%, signal=37% |
| REACTOME_IMMUNE SYSTEM | REACTOME_IMMUNE SYSTEM | 2213 | 0.1629798 | 0.1629798 | 0 | 0.6927681 | 1 | 10567 tags=37%, list=22%, signal=45% |
| REACTOME_TCR SIGNALING | REACTOME_TCR SIGNALING | 118 | 0.16238791 | 0.16238791 | 0.003 | 0.6947047 | 1 | 19869 tags=57%, list=41%, signal=95% |
| REACTOME_REGULATION OF MRNA STABILITY BY PROTEINS THAT BIND AU-RICH ELEMENTS | REACTOME_REGULATION OF MRNA STABILITY BY PROTEINS THAT BIND AU-RICH ELEMENTS | 88 | 0.16214658 | 0.16214658 | 0.025974 | 0.69507205 | 1 | 14887 tags=47%, list=30%, signal=67% |
| REACTOME_DNA DOUBLE-STRAND BREAK REPAIR | REACTOME_DNA DOUBLE-STRAND BREAK REPAIR | 146 | 0.1620836 | 0.1620836 | 0 | 0.6945904 | 1 | 18581 tags=54%, list=38%, signal=87% |
| REACTOME_DOWNSTREAM TCR SIGNALING | REACTOME_DOWNSTREAM TCR SIGNALING | 97 | 0.16153023 | 0.16153023 | 0.011022 | 0.69638044 | 1 | 19869 tags=57%, list=41%, signal=95% |
| REACTOME_SIGNALING BY REACTOME_ASSEMBLY OF THE PRE-REPLICATIVE COMPLEX | REACTOME_SIGNALING BY ERBB4 REACTOME_ASSEMBLY OF THE PRE-REPLICATIVE COMPLEX | 43 | 0.16152431 | 0.16152431 | 0.1979695 | 0.69560814 | 1 | 8039 tags=33%, list=16%, signal=39% |
| REACTOME_POST NMDA RECEPTOR ACTIVATION EVENTS | REACTOME_POST NMDA RECEPTOR ACTIVATION EVENTS | 67 | 0.16124853 | 0.16124853 | 0.0462366 | 0.6960464 | 1 | 17693 tags=52%, list=36%, signal=82% |
| | | 35 | 0.16106683 | 0.16106683 | 0.2834171 | 0.6961157 | 1 | 3310 tags=23%, list=7%, signal=24% |

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|--|--|------|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_FORMATION OF THE BETA-CATENIN:TCF TRANSACTIVATING COMPLEX | REACTOME_FORMATION OF THE BETA-CATENIN:TCF TRANSACTIVATING COMPLEX | 61 | 0.160838 | 0.160838 | 0.0626808 | 0.6964105 | 1 | 12201 tags=41%, list=25%, signal=55% |
| REACTOME_Glutathione conjugation | REACTOME_Glutathione conjugation | 35 | 0.15943184 | 0.15943184 | 0.3115079 | 0.7022076 | 1 | 3390 tags=23%, list=7%, signal=25% |
| REACTOME_CDK-MEDIATED PHOSPHORYLATION AND REMOVAL OF CDC6 | REACTOME_CDK-MEDIATED PHOSPHORYLATION AND REMOVAL OF CDC6 | 50 | 0.15880197 | 0.15880197 | 0.1600408 | 0.7043601 | 1 | 17693 tags=52%, list=36%, signal=81% |
| REACTOME_SUMOYLATION OF RNA BINDING PROTEINS | REACTOME_SUMOYLATION OF RNA BINDING PROTEINS | 46 | 0.15872289 | 0.15872289 | 0.1819106 | 0.7039214 | 1 | 2879 tags=22%, list=6%, signal=23% |
| REACTOME_POST-TRANSLATIONAL PROTEIN MODIFICATION | REACTOME_POST-TRANSLATIONAL PROTEIN MODIFICATION | 1327 | 0.15847869 | 0.15847869 | 0 | 0.70425695 | 1 | 7209 tags=30%, list=15%, signal=34% |
| REACTOME_REGULATION OF APOPTOSIS | REACTOME_REGULATION OF APOPTOSIS | 52 | 0.15803847 | 0.15803847 | 0.1325536 | 0.7054041 | 1 | 17693 tags=52%, list=36%, signal=81% |
| REACTOME_AUF1 (HNRNP D0) BINDS AND DESTABILIZES MRNA | REACTOME_AUF1 (HNRNP D0) BINDS AND DESTABILIZES MRNA | 54 | 0.15733187 | 0.15733187 | 0.1138614 | 0.7079125 | 1 | 17693 tags=52%, list=36%, signal=81% |
| REACTOME_RECRUITMENT AND ATM-MEDIATED PHOSPHORYLATION OF REPAIR AND SIGNALING PROTEINS AT DNA DOUBLE STRAND BREAKS | REACTOME_RECRUITMENT AND ATM-MEDIATED PHOSPHORYLATION OF REPAIR AND SIGNALING PROTEINS AT DNA DOUBLE STRAND BREAKS | 58 | 0.15699044 | 0.15699044 | 0.1019368 | 0.70870197 | 1 | 10894 tags=38%, list=22%, signal=49% |
| REACTOME_DEGRADATION OF REACTOME_PACKAGING OF TELOMERE ENDS | REACTOME_DEGRADATION OF DVL REACTOME_PACKAGING OF TELOMERE ENDS | 56 | 0.1566762 | 0.1566762 | 0.1237425 | 0.7093791 | 1 | 17693 tags=52%, list=36%, signal=81% |
| REACTOME_SYNTHESIS OF (16-20)-HYDROXYEICOSATETRAENOIC ACIDS (HETE) | REACTOME_SYNTHESIS OF (16-20)-HYDROXYEICOSATETRAENOIC ACIDS (HETE) | 33 | 0.1563289 | 0.1563289 | 0.3460076 | 0.71022326 | 1 | 30928 tags=79%, list=63%, signal=214% |
| REACTOME_TRANSPORT TO THE GOLGI AND SUBSEQUENT MODIFICATION | REACTOME_TRANSPORT TO THE GOLGI AND SUBSEQUENT MODIFICATION | 9 | 0.1561039 | 0.1561039 | 0.9641077 | 0.7104686 | 1 | 14119 tags=44%, list=29%, signal=62% |
| REACTOME_PERK REGULATES GENE EXPRESSION | REACTOME_PERK REGULATES GENE EXPRESSION | 167 | 0.15566997 | 0.15566997 | 0.001003 | 0.7117581 | 1 | 7356 tags=31%, list=15%, signal=36% |
| REACTOME_MET ACTIVATES PI3K/AKT SIGNALING | REACTOME_MET ACTIVATES PI3K/AKT SIGNALING | 28 | 0.15539369 | 0.15539369 | 0.4872549 | 0.71228296 | 1 | 9882 tags=36%, list=20%, signal=45% |
| REACTOME_FcERI MEDIATED NF-KB ACTIVATION | REACTOME_FcERI MEDIATED NF-KB ACTIVATION | 6 | 0.15485747 | 0.15485747 | 0.9959391 | 0.7139793 | 1 | 8739 tags=33%, list=18%, signal=41% |
| REACTOME_HEDGEHOG LIGAND BIOGENESIS | REACTOME_HEDGEHOG LIGAND BIOGENESIS | 151 | 0.15477985 | 0.15477985 | 0.005123 | 0.7135574 | 1 | 25195 tags=67%, list=51%, signal=137% |
| REACTOME_PROGRAMMED CELL DEATH | REACTOME_PROGRAMMED CELL DEATH | 64 | 0.15446675 | 0.15446675 | 0.0909091 | 0.71423596 | 1 | 17693 tags=52%, list=36%, signal=81% |
| REACTOME_GLYCEROPHOSPHOLIPID BIOSYNTHESIS | REACTOME_GLYCEROPHOSPHOLIPID BIOSYNTHESIS | 169 | 0.15418413 | 0.15418413 | 0 | 0.714748 | 1 | 17972 tags=52%, list=37%, signal=82% |
| REACTOME_ACTIVATION OF THE TFAP2 (AP-2) FAMILY OF TRANSCRIPTION FACTORS | REACTOME_ACTIVATION OF THE TFAP2 (AP-2) FAMILY OF TRANSCRIPTION FACTORS | 129 | 0.15365061 | 0.15365061 | 0.0030151 | 0.7164516 | 1 | 11474 tags=39%, list=23%, signal=50% |
| REACTOME_CELLULAR RESPONSE TO HYPOXIA | REACTOME_CELLULAR RESPONSE TO HYPOXIA | 12 | 0.15284221 | 0.15284221 | 0.8959366 | 0.7194929 | 1 | 12919 tags=42%, list=26%, signal=57% |
| REACTOME_REGULATION OF HYPOXIA-INDUCIBLE FACTOR (HIF) BY OXYGEN | REACTOME_REGULATION OF HYPOXIA-INDUCIBLE FACTOR (HIF) BY OXYGEN | 72 | 0.15275334 | 0.15275334 | 0.0636183 | 0.7191186 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_REMOVAL OF LICENSING FACTORS FROM REACTOME_DAG AND IP3 | REACTOME_REMOVAL OF LICENSING FACTORS FROM ORIGINS REACTOME_DAG AND IP3 SIGNALING | 72 | 0.15275334 | 0.15275334 | 0.0814664 | 0.7183142 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_CYTOSOLIC SULFONATION OF SMALL MOLECULES | REACTOME_CYTOSOLIC SULFONATION OF SMALL MOLECULES | 72 | 0.15275334 | 0.15275334 | 0.0661841 | 0.71751165 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_G0 AND EARLY G1 | REACTOME_G0 AND EARLY G1 | 32 | 0.15249614 | 0.15249614 | 0.4092742 | 0.7178915 | 1 | 3248 tags=22%, list=7%, signal=23% |
| | | 24 | 0.15232883 | 0.15232883 | 0.5659068 | 0.7178828 | 1 | 23147 tags=63%, list=47%, signal=118% |
| | | 27 | 0.152073 | 0.152073 | 0.5071428 | 0.71827114 | 1 | 7065 tags=30%, list=14%, signal=35% |

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|--|--|------|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_ER TO GOLGI ANTEROGRADE TRANSPORT | REACTOME_ER TO GOLGI ANTEROGRADE TRANSPORT | 136 | 0.15194653 | 0.15194653 | 0.0069652 | 0.718073 | 1 | 6261 tags=28%, list=13%, signal=32% |
| REACTOME_APOPTOSIS | REACTOME_APOPTOSIS | 166 | 0.15152787 | 0.15152787 | 0.0020346 | 0.7192581 | 1 | 17972 tags=52%, list=37%, signal=82% |
| REACTOME_INTERCONVERSION OF NUCLEOTIDE DI- AND TRIPHOSPHATES | REACTOME_INTERCONVERSION OF NUCLEOTIDE DI- AND TRIPHOSPHATES | 32 | 0.15127955 | 0.15127955 | 0.3897959 | 0.7195847 | 1 | 7898 tags=31%, list=16%, signal=37% |
| REACTOME_HEDGEHOG 'OFF' STATE | REACTOME_HEDGEHOG 'OFF' STATE | 99 | 0.15123796 | 0.15123796 | 0.0152439 | 0.7189687 | 1 | 17833 tags=52%, list=36%, signal=81% |
| REACTOME_TRIGLYCERIDE METABOLISM | REACTOME_TRIGLYCERIDE METABOLISM | 38 | 0.15092196 | 0.15092196 | 0.3280633 | 0.71973175 | 1 | 20963 tags=58%, list=43%, signal=101% |
| REACTOME_CILIUM ASSEMBLY | REACTOME_CILIUM ASSEMBLY | 187 | 0.1503117 | 0.1503117 | 0 | 0.7218668 | 1 | 13091 tags=42%, list=27%, signal=57% |
| REACTOME_INTRA-GOLGI AND RETROGRADE GOLGI-TO-ER TRAFFIC | REACTOME_INTRA-GOLGI AND RETROGRADE GOLGI-TO-ER TRAFFIC | 185 | 0.15001275 | 0.15001275 | 9.90E-04 | 0.7224751 | 1 | 10944 tags=37%, list=22%, signal=48% |
| REACTOME_SUMOYLATION | REACTOME_SUMOYLATION | 118 | 0.14943688 | 0.14943688 | 0.008 | 0.724475 | 1 | 16767 tags=49%, list=34%, signal=75% |
| REACTOME_CROSS-PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS | REACTOME_CROSS-PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS (ENDOSOMES) | 49 | 0.14899302 | 0.14899302 | 0.1952895 | 0.72581947 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_REGULATION OF ACTIVATED PAK-2P34 BY PROTEASOME MEDIATED DEGRADATION | REACTOME_REGULATION OF ACTIVATED PAK-2P34 BY PROTEASOME MEDIATED DEGRADATION | 49 | 0.14899302 | 0.14899302 | 0.203668 | 0.7250201 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_HOMOLOGOUS DNA PAIRING AND STRAND EXCHANGE | REACTOME_HOMOLOGOUS DNA PAIRING AND STRAND EXCHANGE | 42 | 0.14885296 | 0.14885296 | 0.2958877 | 0.724875 | 1 | 18365 tags=52%, list=38%, signal=84% |
| REACTOME_ONCOGENE INDUCED SENESCENCE | REACTOME_ONCOGENE INDUCED SENESCENCE | 31 | 0.14852856 | 0.14852856 | 0.4576772 | 0.725574 | 1 | 2208 tags=19%, list=5%, signal=20% |
| REACTOME_BASE EXCISION REPAIR | REACTOME_BASE EXCISION REPAIR | 38 | 0.14845641 | 0.14845641 | 0.3366734 | 0.7251114 | 1 | 5621 tags=26%, list=11%, signal=30% |
| REACTOME_RESOLUTION OF ABASIC SITES (AP SITES) | REACTOME_RESOLUTION OF ABASIC SITES (AP SITES) | 38 | 0.14845641 | 0.14845641 | 0.3253968 | 0.72431636 | 1 | 5621 tags=26%, list=11%, signal=30% |
| REACTOME_C-TYPE LECTIN RECEPTORS (CLRS) | REACTOME_C-TYPE LECTIN RECEPTORS (CLRS) | 141 | 0.14837793 | 0.14837793 | 0.0019512 | 0.72388697 | 1 | 17758 tags=51%, list=36%, signal=80% |
| REACTOME_INFLAMMASOMES | REACTOME_INFLAMMASOMES | 17 | 0.14830986 | 0.14830986 | 0.7782139 | 0.7234016 | 1 | 7141 tags=29%, list=15%, signal=34% |
| REACTOME_DEPOSITION OF NEW CENPA-CONTAINING NUCLEOSOMES AT THE CENTROMERE | REACTOME_DEPOSITION OF NEW CENPA-CONTAINING NUCLEOSOMES AT THE CENTROMERE | 52 | 0.14820234 | 0.14820234 | 0.1631274 | 0.7231317 | 1 | 31357 tags=79%, list=64%, signal=219% |
| REACTOME_NUCLEOSOME ASSEMBLY | REACTOME_NUCLEOSOME ASSEMBLY | 52 | 0.14820234 | 0.14820234 | 0.1565041 | 0.72234225 | 1 | 31357 tags=79%, list=64%, signal=219% |
| REACTOME_DISEASES OF SIGNAL TRANSDUCTION | REACTOME_DISEASES OF SIGNAL TRANSDUCTION | 356 | 0.14819399 | 0.14819399 | 0 | 0.72159255 | 1 | 10951 tags=37%, list=22%, signal=47% |
| REACTOME_DNA REPLICATION | REACTOME_DNA REPLICATION | 107 | 0.14812464 | 0.14812464 | 0.0234834 | 0.7210996 | 1 | 16558 tags=49%, list=34%, signal=73% |
| REACTOME_HH MUTANTS THAT DON'T UNDERGO AUTOCATALYTIC PROCESSING ARE DEGRADED BY ERAD | REACTOME_HH MUTANTS THAT DON'T UNDERGO AUTOCATALYTIC PROCESSING ARE DEGRADED BY ERAD | 55 | 0.14789686 | 0.14789686 | 0.1767677 | 0.72141564 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_HH MUTANTS ABROGATE LIGAND SECRETION | REACTOME_HH MUTANTS ABROGATE LIGAND SECRETION | 57 | 0.14758359 | 0.14758359 | 0.1620513 | 0.7221274 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_INNATE IMMUNE SYSTEM | REACTOME_INNATE IMMUNE SYSTEM | 1394 | 0.1474198 | 0.1474198 | 0 | 0.72212654 | 1 | 11427 tags=38%, list=23%, signal=48% |
| REACTOME_REGULATION OF PTEN MRNA TRANSLATION | REACTOME_REGULATION OF PTEN MRNA TRANSLATION | 13 | 0.14734057 | 0.14734057 | 0.8932927 | 0.72170454 | 1 | 4086 tags=23%, list=8%, signal=25% |
| REACTOME_DEGRADATION OF GLI1 BY THE PROTEASOME | REACTOME_DEGRADATION OF GLI1 BY THE PROTEASOME | 59 | 0.1472919 | 0.1472919 | 0.1349125 | 0.72115564 | 1 | 17693 tags=51%, list=36%, signal=80% |
| REACTOME_METABOLISM OF WATER-SOLUBLE VITAMINS AND COFACTORS | REACTOME_METABOLISM OF WATER-SOLUBLE VITAMINS AND COFACTORS | 123 | 0.14703141 | 0.14703141 | 0.0062893 | 0.72160506 | 1 | 7547 tags=30%, list=15%, signal=35% |
| REACTOME_HEMOSTASIS | REACTOME_HEMOSTASIS | 684 | 0.14644608 | 0.14644608 | 0 | 0.7235838 | 1 | 8749 tags=32%, list=18%, signal=39% |

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|---|---|-----------|--------------------------|--------------------------|----------------|------------------------|--------|---|
| REACTOME_CONSTITUTIVE SIGNALING BY AKT1 E17K IN CANCER | REACTOME_CONSTITUTIVE SIGNALING BY AKT1 E17K IN CANCER | 25 | 0.14574173 | 0.14574173 | 0.611002 | 0.7262173 | 1 | 14411 tags=44%, list=29%, signal=62% |
| REACTOME_REGULATION OF DNA REPLICATION | REACTOME_REGULATION OF DNA REPLICATION | 75 | 0.14552942 | 0.14552942 | 0.0625621 | 0.7264237 | 1 | 17693 tags=51%, list=36%, signal=79% |
| REACTOME_AXON GUIDANCE | REACTOME_AXON GUIDANCE | 555 | 0.14538394 | 0.14538394 | 0 | 0.72634673 | 1 | 7077 tags=29%, list=14%, signal=33% |
| REACTOME_INTRAFLAGELLAR TRANSPORT | REACTOME_INTRAFLAGELLAR TRANSPORT | 41 | 0.14532794 | 0.14532794 | 0.3357216 | 0.7258359 | 1 | 10803 tags=37%, list=22%, signal=47% |
| REACTOME_S PHASE | REACTOME_S PHASE | 138 | 0.14527453 | 0.14527453 | 0.0049164 | 0.7253025 | 1 | 17743 tags=51%, list=36%, signal=79% |
| REACTOME_CHAPERONIN-MEDIATED PROTEIN FOLDING | REACTOME_CHAPERONIN-MEDIATED PROTEIN FOLDING | 95 | 0.1450734 | 0.1450734 | 0.0339157 | 0.7254069 | 1 | 10949 tags=37%, list=22%, signal=47% |
| REACTOME_METABOLISM OF REACTOME_ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS | REACTOME_METABOLISM OF LIPIDS REACTOME_ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS | 733 37 | 0.14474992 0.14401361 | 0.14474992 0.14401361 | 0 0.3914767 | 0.7261285 0.7288602 | 1 1 | 7580 tags=30%, list=15%, signal=35% 11480 tags=38%, list=23%, signal=49% |
| REACTOME_ANTIVIRAL MECHANISM BY IFN-STIMULATED | REACTOME_ANTIVIRAL MECHANISM BY IFN-STIMULATED GENES | 73 | 0.14400372 | 0.14400372 | 0.1036168 | 0.7281259 | 1 | 18447 tags=52%, list=38%, signal=83% |
| REACTOME_ISG15 ANTIVIRAL MECHANISM | REACTOME_ISG15 ANTIVIRAL MECHANISM | 73 | 0.14400372 | 0.14400372 | 0.0987167 | 0.7273471 | 1 | 18447 tags=52%, list=38%, signal=83% |
| REACTOME_CLEC7A (DECTIN-1) SIGNALING | REACTOME_CLEC7A (DECTIN-1) SIGNALING | 99 | 0.14398147 | 0.14398147 | 0.0306748 | 0.72666967 | 1 | 17693 tags=51%, list=36%, signal=79% |
| REACTOME_SPRY REGULATION OF FGF SIGNALING | REACTOME_SPRY REGULATION OF FGF SIGNALING | 16 | 0.1436061 | 0.1436061 | 0.8529412 | 0.7277334 | 1 | 35814 tags=88%, list=73%, signal=326% |
| REACTOME_G2/M TRANSITION | REACTOME_G2/M TRANSITION | 181 | 0.14357756 | 0.14357756 | 0 | 0.72707665 | 1 | 17883 tags=51%, list=37%, signal=80% |
| REACTOME_MITOTIC G2-G2/M PHASES | REACTOME_MITOTIC G2-G2/M PHASES | 183 | 0.1434925 | 0.1434925 | 0 | 0.7266975 | 1 | 17883 tags=51%, list=37%, signal=80% |
| REACTOME_SIGNALING BY ROBO RECEPTOR | REACTOME_SIGNALING BY ROBO RECEPTOR | 32 | 0.14308469 | 0.14308469 | 0.4833006 | 0.72791535 | 1 | 8299 tags=31%, list=17%, signal=38% |
| REACTOME_PTEN REGULATION | REACTOME_PTEN REGULATION | 142 | 0.14211178 | 0.14211178 | 0.0059642 | 0.73173076 | 1 | 17888 tags=51%, list=37%, signal=80% |
| REACTOME_DIGESTION | REACTOME_DIGESTION | 22 | 0.14178368 | 0.14178368 | 0.7159329 | 0.73253024 | 1 | 39799 tags=95%, list=81%, signal=510% |
| REACTOME_MITOTIC PROMETAPHASE | REACTOME_MITOTIC PROMETAPHASE | 181 | 0.140902 | 0.140902 | 0 | 0.7360072 | 1 | 17743 tags=50%, list=36%, signal=79% |
| REACTOME_DNA REPLICATION PRE-INITIATION | REACTOME_DNA REPLICATION PRE-INITIATION | 84 | 0.1405744 | 0.1405744 | 0.0472362 | 0.7368732 | 1 | 18193 tags=51%, list=37%, signal=81% |
| REACTOME_M/G1 TRANSITION | REACTOME_M/G1 TRANSITION | 84 | 0.1405744 | 0.1405744 | 0.053554 | 0.73609346 | 1 | 18193 tags=51%, list=37%, signal=81% |
| REACTOME_SIGNALING BY VEGF | REACTOME_SIGNALING BY VEGF | 331 | 0.14010817 | 0.14010817 | 0 | 0.7374899 | 1 | 16558 tags=48%, list=34%, signal=72% |
| REACTOME_REGULATION OF SIGNALING BY CBL | REACTOME_REGULATION OF SIGNALING BY CBL | 18 | 0.13997793 | 0.13997793 | 0.814664 | 0.7372836 | 1 | 17630 tags=50%, list=36%, signal=78% |
| REACTOME_PLC-GAMMA1 SIGNALLING | REACTOME_PLC-GAMMA1 SIGNALLING | 34 | 0.13962579 | 0.13962579 | 0.4683664 | 0.738176 | 1 | 3248 tags=21%, list=7%, signal=22% |
| REACTOME_NIK-->NONCANONICAL NF-KB | REACTOME_NIK-->NONCANONICAL NF-KB SIGNALING | 58 | 0.13880426 | 0.13880426 | 0.1886051 | 0.74129134 | 1 | 17693 tags=50%, list=36%, signal=78% |
| REACTOME_FBXL7 DOWN-REGULATES AURKA DURING MITOTIC ENTRY AND IN EARLY MITOSIS | REACTOME_FBXL7 DOWN-REGULATES AURKA DURING MITOTIC ENTRY AND IN EARLY MITOSIS | 54 | 0.1387929 | 0.1387929 | 0.2332016 | 0.74057305 | 1 | 17693 tags=50%, list=36%, signal=78% |
| REACTOME_SCF-BETA-TRCP MEDIATED DEGRADATION OF | REACTOME_SCF-BETA-TRCP MEDIATED DEGRADATION OF EMI1 | 54 | 0.1387929 | 0.1387929 | 0.2243461 | 0.7397944 | 1 | 17693 tags=50%, list=36%, signal=78% |
| REACTOME_KSRP (KHSRP) BINDS AND DESTABILIZES MRNA | REACTOME_KSRP (KHSRP) BINDS AND DESTABILIZES MRNA | 17 | 0.1378618 | 0.1378618 | 0.8620343 | 0.74334556 | 1 | 13413 tags=41%, list=27%, signal=57% |
| REACTOME_DECTIN-2 FAMILY | REACTOME_DECTIN-2 FAMILY | 28 | 0.13739096 | 0.13739096 | 0.6272991 | 0.7447658 | 1 | 17758 tags=50%, list=36%, signal=78% |
| REACTOME_TRANSPORT OF BILE SALTS AND ORGANIC ACIDS, METAL IONS AND AMINE | REACTOME_TRANSPORT OF BILE SALTS AND ORGANIC ACIDS, METAL IONS AND AMINE COMPOUNDS | 85 | 0.13692236 | 0.13692236 | 0.0791583 | 0.74617565 | 1 | 10588 tags=35%, list=22%, signal=45% |
| REACTOME_SIGNALING BY NGF | REACTOME_SIGNALING BY NGF | 545 | 0.13686493 | 0.13686493 | 0 | 0.7456583 | 1 | 12958 tags=40%, list=26%, signal=54% |
| REACTOME_TELOMERE MAINTENANCE | REACTOME_TELOMERE MAINTENANCE | 63 | 0.13670656 | 0.13670656 | 0.1624016 | 0.74561757 | 1 | 15076 tags=44%, list=31%, signal=64% |

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|---|---|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_TRNA PROCESSING IN THE NUCLEUS | REACTOME_TRNA PROCESSING IN THE NUCLEUS | 58 | 0.1359297 | 0.1359297 | 0.1805274 | 0.7485804 | 1 | 4326 tags=22%, list=9%, signal=25% |
| REACTOME_CONDENSATION OF PROPHASE CHROMOSOMES | REACTOME_CONDENSATION OF PROPHASE CHROMOSOMES | 43 | 0.13590592 | 0.13590592 | 0.3631011 | 0.7479152 | 1 | 30928 tags=77%, list=63%, signal=208% |
| REACTOME_SIGNALING BY RHO GTPASES | REACTOME_SIGNALING BY RHO GTPASES | 391 | 0.13461123 | 0.13461123 | 0 | 0.7532782 | 1 | 11744 tags=37%, list=24%, signal=49% |
| REACTOME_SUMOYLATION OF CHROMATIN ORGANIZATION PROTEINS | REACTOME_SUMOYLATION OF CHROMATIN ORGANIZATION PROTEINS | 57 | 0.1343213 | 0.1343213 | 0.2303207 | 0.75385755 | 1 | 2879 tags=19%, list=6%, signal=20% |
| REACTOME_IMPORT OF PALMITOYL-COA INTO THE MITOCHONDRIAL MATRIX | REACTOME_IMPORT OF PALMITOYL-COA INTO THE MITOCHONDRIAL MATRIX | 12 | 0.13412698 | 0.13412698 | 0.9611273 | 0.7540432 | 1 | 21996 tags=58%, list=45%, signal=106% |
| REACTOME_FORMATION OF HIV-1 ELONGATION COMPLEX CONTAINING HIV-1 TAT | REACTOME_FORMATION OF HIV-1 ELONGATION COMPLEX CONTAINING HIV-1 TAT | 39 | 0.13366392 | 0.13366392 | 0.4717899 | 0.7554281 | 1 | 7270 tags=28%, list=15%, signal=33% |
| REACTOME_HIV TRANSCRIPTION ELONGATION | REACTOME_HIV TRANSCRIPTION ELONGATION | 39 | 0.13366392 | 0.13366392 | 0.4580078 | 0.7546437 | 1 | 7270 tags=28%, list=15%, signal=33% |
| REACTOME_TAT-MEDIATED ELONGATION OF THE HIV-1 TRANSCRIPT | REACTOME_TAT-MEDIATED ELONGATION OF THE HIV-1 TRANSCRIPT | 39 | 0.13366392 | 0.13366392 | 0.4605769 | 0.75386083 | 1 | 7270 tags=28%, list=15%, signal=33% |
| REACTOME_DNA METHYLATION | REACTOME_DNA METHYLATION | 34 | 0.13314305 | 0.13314305 | 0.5423228 | 0.7555342 | 1 | 30928 tags=76%, list=63%, signal=207% |
| REACTOME_REGULATION OF RAS BY GAPS | REACTOME_REGULATION OF RAS BY GAPS | 67 | 0.13169356 | 0.13169356 | 0.1866538 | 0.76165855 | 1 | 19869 tags=54%, list=41%, signal=90% |
| REACTOME_DECTIN-1 MEDIATED NONCANONICAL NF-KB | REACTOME_DECTIN-1 MEDIATED NONCANONICAL NF-KB SIGNALING | 61 | 0.13060579 | 0.13060579 | 0.2313278 | 0.76606786 | 1 | 17693 tags=49%, list=36%, signal=77% |
| REACTOME_RHO GTPASES ACTIVATE FORMINS | REACTOME_RHO GTPASES ACTIVATE FORMINS | 119 | 0.1305857 | 0.1305857 | 0.0359343 | 0.7653754 | 1 | 13371 tags=40%, list=27%, signal=55% |
| REACTOME_FORMATION OF RNA POL II ELONGATION COMPLEX | REACTOME_FORMATION OF RNA POL II ELONGATION COMPLEX | 54 | 0.1303312 | 0.1303312 | 0.2796117 | 0.7658201 | 1 | 6319 tags=26%, list=13%, signal=30% |
| REACTOME_RNA POLYMERASE II TRANSCRIPTION ELONGATION | REACTOME_RNA POLYMERASE II TRANSCRIPTION ELONGATION | 54 | 0.1303312 | 0.1303312 | 0.2857143 | 0.7650306 | 1 | 6319 tags=26%, list=13%, signal=30% |
| REACTOME_DEGRADATION OF GLI2 BY THE PROTEASOME | REACTOME_DEGRADATION OF GLI2 BY THE PROTEASOME | 59 | 0.13032229 | 0.13032229 | 0.2303823 | 0.7642791 | 1 | 17693 tags=49%, list=36%, signal=77% |
| REACTOME_GLI3 IS PROCESSED TO GLI3R BY THE PROTEASOME | REACTOME_GLI3 IS PROCESSED TO GLI3R BY THE PROTEASOME | 59 | 0.13032229 | 0.13032229 | 0.2340842 | 0.7634929 | 1 | 17693 tags=49%, list=36%, signal=77% |
| REACTOME_VEGFA-VEGFR2 PATHWAY | REACTOME_VEGFA-VEGFR2 PATHWAY | 323 | 0.13017058 | 0.13017058 | 0 | 0.7634159 | 1 | 16558 tags=47%, list=34%, signal=70% |
| REACTOME_SIGNALING BY PDGF | REACTOME_SIGNALING BY PDGF | 451 | 0.12990381 | 0.12990381 | 0 | 0.76384497 | 1 | 12588 tags=39%, list=26%, signal=51% |
| REACTOME_AUTODEGRADATION OF THE E3 UBIQUITIN LIGASE | REACTOME_AUTODEGRADATION OF THE E3 UBIQUITIN LIGASE COP1 | 51 | 0.12897028 | 0.12897028 | 0.3349609 | 0.7675277 | 1 | 17693 tags=49%, list=36%, signal=77% |
| REACTOME_VIF-MEDIATED DEGRADATION OF APOBEC3G | REACTOME_VIF-MEDIATED DEGRADATION OF APOBEC3G | 51 | 0.12897028 | 0.12897028 | 0.3343284 | 0.7667413 | 1 | 17693 tags=49%, list=36%, signal=77% |
| REACTOME_VPU MEDIATED DEGRADATION OF CD4 | REACTOME_VPU MEDIATED DEGRADATION OF CD4 | 51 | 0.12897028 | 0.12897028 | 0.3258537 | 0.76595646 | 1 | 17693 tags=49%, list=36%, signal=77% |
| REACTOME_EPIGENETIC REGULATION OF GENE | REACTOME_EPIGENETIC REGULATION OF GENE EXPRESSION | 117 | 0.1289346 | 0.1289346 | 0.0467381 | 0.76535 | 1 | 12952 tags=39%, list=26%, signal=53% |
| REACTOME_HDMS DEMETHYLATE HISTONES | REACTOME_HDMS DEMETHYLATE HISTONES | 27 | 0.12887053 | 0.12887053 | 0.7293087 | 0.76487356 | 1 | 10014 tags=33%, list=20%, signal=42% |
| REACTOME_TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM | REACTOME_TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM | 82 | 0.12884821 | 0.12884821 | 0.1090555 | 0.7642023 | 1 | 9226 tags=32%, list=19%, signal=39% |
| REACTOME_MEMBRANE TRAFFICKING | REACTOME_MEMBRANE TRAFFICKING | 614 | 0.12877911 | 0.12877911 | 0 | 0.7637413 | 1 | 6851 tags=27%, list=14%, signal=31% |
| REACTOME_TRANSCRIPTIONAL REGULATION BY RUNX1 | REACTOME_TRANSCRIPTIONAL REGULATION BY RUNX1 | 206 | 0.12866412 | 0.12866412 | 9.79E-04 | 0.7634985 | 1 | 12741 tags=39%, list=26%, signal=52% |

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|---|---|-----|------------|------------|-----------|------------|---|--|
| REACTOME_DIGESTION AND ABSORPTION | REACTOME_DIGESTION AND ABSORPTION | 26 | 0.12860912 | 0.12860912 | 0.753878 | 0.76300657 | 1 | 42670 tags=100%, list=87%, signal=777% |
| REACTOME_SIGNALING BY | REACTOME_SIGNALING BY FGFR1 | 50 | 0.12829193 | 0.12829193 | 0.3359684 | 0.76370627 | 1 | 1558 tags=16%, list=3%, signal=17% |
| REACTOME_SIGNALING BY SCF- | REACTOME_SIGNALING BY SCF-KIT | 411 | 0.1280941 | 0.1280941 | 0 | 0.76390547 | 1 | 13437 tags=40%, list=27%, signal=55% |
| REACTOME_RNA POLYMERASE II PRE-TRANSCRIPTION EVENTS | REACTOME_RNA POLYMERASE II PRE-TRANSCRIPTION EVENTS | 76 | 0.12802067 | 0.12802067 | 0.1589267 | 0.76347804 | 1 | 7270 tags=28%, list=15%, signal=32% |
| REACTOME_COPI-MEDIATED ANTEROGRADE TRANSPORT | REACTOME_COPI-MEDIATED ANTEROGRADE TRANSPORT | 83 | 0.1275523 | 0.1275523 | 0.1278119 | 0.7649213 | 1 | 13232 tags=40%, list=27%, signal=54% |
| REACTOME_PHASE I - FUNCTIONALIZATION OF COMPOUNDS | REACTOME_PHASE I - FUNCTIONALIZATION OF COMPOUNDS | 106 | 0.12753063 | 0.12753063 | 0.0542714 | 0.7642597 | 1 | 7626 tags=28%, list=16%, signal=33% |
| REACTOME_INTERLEUKIN-17 SIGNALING | REACTOME_INTERLEUKIN-17 SIGNALING | 300 | 0.12710881 | 0.12710881 | 0 | 0.76546776 | 1 | 10951 tags=35%, list=22%, signal=45% |
| REACTOME_CLASS I MHC MEDIATED ANTIGEN PROCESSING & PRESENTATION | REACTOME_CLASS I MHC MEDIATED ANTIGEN PROCESSING & PRESENTATION | 367 | 0.12635598 | 0.12635598 | 0 | 0.76830244 | 1 | 11870 tags=37%, list=24%, signal=48% |
| REACTOME_DISEASE | REACTOME_DISEASE | 836 | 0.12542656 | 0.12542656 | 0 | 0.77195793 | 1 | 7785 tags=28%, list=16%, signal=33% |
| REACTOME_ABC-FAMILY PROTEINS MEDIATED | REACTOME_ABC-FAMILY PROTEINS MEDIATED TRANSPORT | 103 | 0.12507984 | 0.12507984 | 0.0685773 | 0.77278715 | 1 | 8149 tags=29%, list=17%, signal=35% |
| REACTOME_INTERLEUKIN-7 SIGNALING | REACTOME_INTERLEUKIN-7 SIGNALING | 274 | 0.12473932 | 0.12473932 | 0 | 0.7736933 | 1 | 17693 tags=49%, list=36%, signal=76% |
| REACTOME_ACTIVATION OF HOX GENES DURING | REACTOME_ACTIVATION OF HOX GENES DURING DIFFERENTIATION | 90 | 0.12375562 | 0.12375562 | 0.0959446 | 0.77763695 | 1 | 18977 tags=51%, list=39%, signal=83% |
| REACTOME_ACTIVATION OF ANTERIOR HOX GENES IN HINDBRAIN DEVELOPMENT DURING EARLY | REACTOME_ACTIVATION OF ANTERIOR HOX GENES IN HINDBRAIN DEVELOPMENT DURING EARLY EMBRYOGENESIS | 90 | 0.12375562 | 0.12375562 | 0.1126214 | 0.77685535 | 1 | 18977 tags=51%, list=39%, signal=83% |
| REACTOME_DOWNSTREAM SIGNALING EVENTS OF B CELL RECEPTOR (BCR) | REACTOME_DOWNSTREAM SIGNALING EVENTS OF B CELL RECEPTOR (BCR) | 279 | 0.12353016 | 0.12353016 | 0 | 0.77716976 | 1 | 12588 tags=38%, list=26%, signal=51% |
| REACTOME_PHOSPHOLIPID METABOLISM | REACTOME_PHOSPHOLIPID METABOLISM | 212 | 0.12223013 | 0.12223013 | 0.002045 | 0.78259164 | 1 | 7436 tags=27%, list=15%, signal=32% |
| REACTOME_DAP12 | REACTOME_DAP12 INTERACTIONS | 442 | 0.12220477 | 0.12220477 | 0 | 0.78193074 | 1 | 14896 tags=43%, list=30%, signal=61% |
| REACTOME_DEFECTIVE CFTR CAUSES CYSTIC FIBROSIS | REACTOME_DEFECTIVE CFTR CAUSES CYSTIC FIBROSIS | 60 | 0.12212284 | 0.12212284 | 0.2876579 | 0.7815365 | 1 | 17693 tags=48%, list=36%, signal=76% |
| REACTOME_VISUAL PHOTOTRANSDUCTION | REACTOME_VISUAL PHOTOTRANSDUCTION | 98 | 0.12161727 | 0.12161727 | 0.0811359 | 0.7831764 | 1 | 6547 tags=26%, list=13%, signal=29% |
| REACTOME_CDT1 ASSOCIATION WITH THE CDC6:ORC:ORIGIN COMPLEX | REACTOME_CDT1 ASSOCIATION WITH THE CDC6:ORC:ORIGIN COMPLEX | 58 | 0.12154243 | 0.12154243 | 0.3298647 | 0.78277713 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_M PHASE | REACTOME_M PHASE | 344 | 0.12102712 | 0.12102712 | 0 | 0.7844737 | 1 | 17743 tags=48%, list=36%, signal=75% |
| REACTOME_TERMINATION OF TRANSLESION DNA SYNTHESIS | REACTOME_TERMINATION OF TRANSLESION DNA SYNTHESIS | 31 | 0.12044134 | 0.12044134 | 0.7175197 | 0.7865051 | 1 | 11480 tags=35%, list=23%, signal=46% |
| REACTOME_CELL CYCLE, | REACTOME_CELL CYCLE, MITOTIC | 485 | 0.12038592 | 0.12038592 | 0 | 0.78595215 | 1 | 17888 tags=48%, list=37%, signal=76% |
| REACTOME_DEGRADATION OF | REACTOME_DEGRADATION OF AXIN | 54 | 0.12025394 | 0.12025394 | 0.3594059 | 0.78578115 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_FORMATION OF HIV ELONGATION COMPLEX IN THE ABSENCE OF HIV TAT | REACTOME_FORMATION OF HIV ELONGATION COMPLEX IN THE ABSENCE OF HIV TAT | 41 | 0.11989925 | 0.11989925 | 0.5864136 | 0.7867292 | 1 | 7270 tags=27%, list=15%, signal=31% |
| REACTOME_SCF(SKP2)-MEDIATED DEGRADATION OF | REACTOME_SCF(SKP2)-MEDIATED DEGRADATION OF P27/P21 | 59 | 0.11976798 | 0.11976798 | 0.3537207 | 0.786558 | 1 | 19869 tags=53%, list=41%, signal=88% |
| REACTOME_NGF SIGNALLING VIA TRKA FROM THE PLASMA MEMBRANE | REACTOME_NGF SIGNALLING VIA TRKA FROM THE PLASMA MEMBRANE | 462 | 0.11970925 | 0.11970925 | 0 | 0.7860648 | 1 | 13376 tags=39%, list=27%, signal=53% |
| REACTOME_UBIQUITIN MEDIATED DEGRADATION OF PHOSPHORYLATED CDC25A | REACTOME_UBIQUITIN MEDIATED DEGRADATION OF PHOSPHORYLATED CDC25A | 52 | 0.11953604 | 0.11953604 | 0.4455348 | 0.7861363 | 1 | 17693 tags=48%, list=36%, signal=75% |

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|--|--|------|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_P53-INDEPENDENT DNA DAMAGE RESPONSE | REACTOME_P53-INDEPENDENT DNA DAMAGE RESPONSE | 52 | 0.11953604 | 0.11953604 | 0.4121757 | 0.78535795 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_P53-INDEPENDENT G1/S DNA DAMAGE CHECKPOINT | REACTOME_P53-INDEPENDENT G1/S DNA DAMAGE CHECKPOINT | 52 | 0.11953604 | 0.11953604 | 0.4074074 | 0.7845812 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_CELLULAR SENESENCE | REACTOME_CELLULAR SENESENCE | 161 | 0.11942001 | 0.11942001 | 0.01417 | 0.7843876 | 1 | 10898 tags=34%, list=22%, signal=44% |
| REACTOME_G1/S TRANSITION | REACTOME_G1/S TRANSITION | 127 | 0.11926412 | 0.11926412 | 0.045954 | 0.78435916 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_HDACS DEACETYLATE HISTONES | REACTOME_HDACS DEACETYLATE HISTONES | 59 | 0.119262 | 0.119262 | 0.3277662 | 0.78359264 | 1 | 17404 tags=47%, list=36%, signal=74% |
| REACTOME_METABOLISM OF STEROIDS | REACTOME_METABOLISM OF STEROIDS | 146 | 0.11908399 | 0.11908399 | 0.0310982 | 0.7836217 | 1 | 6259 tags=25%, list=13%, signal=28% |
| REACTOME_PEROXISOMAL LIPID METABOLISM | REACTOME_PEROXISOMAL LIPID METABOLISM | 29 | 0.11879062 | 0.11879062 | 0.7671756 | 0.78425616 | 1 | 6005 tags=24%, list=12%, signal=27% |
| REACTOME_REGULATION OF ORNITHINE DECARBOXYLASE | REACTOME_REGULATION OF ORNITHINE DECARBOXYLASE (ODC) | 50 | 0.11876109 | 0.11876109 | 0.4542714 | 0.7836366 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_UBIQUITIN-DEPENDENT DEGRADATION OF | REACTOME_UBIQUITIN-DEPENDENT DEGRADATION OF CYCLIN D | 50 | 0.11876109 | 0.11876109 | 0.4462312 | 0.7828669 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_UBIQUITIN-DEPENDENT DEGRADATION OF | REACTOME_UBIQUITIN-DEPENDENT DEGRADATION OF CYCLIN D1 | 50 | 0.11876109 | 0.11876109 | 0.4736842 | 0.7820986 | 1 | 17693 tags=48%, list=36%, signal=75% |
| REACTOME_TRANSCRIPTIONAL REGULATION BY TP53 | REACTOME_TRANSCRIPTIONAL REGULATION BY TP53 | 355 | 0.11861234 | 0.11861234 | 0 | 0.78205913 | 1 | 8440 tags=29%, list=17%, signal=35% |
| REACTOME_FORMATION OF THE CORNIFIED ENVELOPE | REACTOME_FORMATION OF THE CORNIFIED ENVELOPE | 65 | 0.11855907 | 0.11855907 | 0.3026052 | 0.7815399 | 1 | 7761 tags=28%, list=16%, signal=33% |
| REACTOME_RNA POLYMERASE I PROMOTER OPENING | REACTOME_RNA POLYMERASE I PROMOTER OPENING | 32 | 0.11842215 | 0.11842215 | 0.7121662 | 0.7814053 | 1 | 30928 tags=75%, list=63%, signal=203% |
| REACTOME_NEGATIVE REGULATION OF MAPK | REACTOME_NEGATIVE REGULATION OF MAPK PATHWAY | 40 | 0.11825754 | 0.11825754 | 0.5890547 | 0.7814301 | 1 | 1558 tags=15%, list=3%, signal=15% |
| REACTOME_G-PROTEIN BETA:GAMMA SIGNALLING | REACTOME_G-PROTEIN BETA:GAMMA SIGNALLING | 51 | 0.11823153 | 0.11823153 | 0.4519231 | 0.78077763 | 1 | 5737 tags=24%, list=12%, signal=27% |
| REACTOME_PI3K/AKT SIGNALING IN CANCER | REACTOME_PI3K/AKT SIGNALING IN CANCER | 90 | 0.11820177 | 0.11820177 | 0.1336684 | 0.7801685 | 1 | 14896 tags=42%, list=30%, signal=61% |
| REACTOME_DNA DAMAGE/TELOMERE STRESS INDUCED SENESENCE | REACTOME_DNA DAMAGE/TELOMERE STRESS INDUCED SENESENCE | 61 | 0.11788231 | 0.11788231 | 0.2947799 | 0.7809195 | 1 | 13499 tags=39%, list=28%, signal=54% |
| REACTOME_SIGNALING BY EGFR | REACTOME_SIGNALING BY EGFR | 439 | 0.11772945 | 0.11772945 | 0 | 0.78089464 | 1 | 11909 tags=36%, list=24%, signal=47% |
| REACTOME_RAB GEFS EXCHANGE GTP FOR GDP ON | REACTOME_RAB GEFS EXCHANGE GTP FOR GDP ON RABS | 90 | 0.1176914 | 0.1176914 | 0.1497006 | 0.7803251 | 1 | 15465 tags=43%, list=32%, signal=63% |
| REACTOME_TRANSPORT OF VITAMINS, NUCLEOSIDES, AND RELATED MOLECULES | REACTOME_TRANSPORT OF VITAMINS, NUCLEOSIDES, AND RELATED MOLECULES | 39 | 0.11760828 | 0.11760828 | 0.5934718 | 0.7799607 | 1 | 4289 tags=21%, list=9%, signal=22% |
| REACTOME_BETA-CATENIN INDEPENDENT WNT SIGNALING | REACTOME_BETA-CATENIN INDEPENDENT WNT SIGNALING | 140 | 0.11718893 | 0.11718893 | 0.0404449 | 0.7811953 | 1 | 15612 tags=44%, list=32%, signal=64% |
| REACTOME_DNA DAMAGE BYPASS | REACTOME_DNA DAMAGE BYPASS | 47 | 0.11694647 | 0.11694647 | 0.5040984 | 0.781549 | 1 | 17198 tags=47%, list=35%, signal=72% |
| REACTOME_INTERLEUKIN-19,20,22,24,26,28 AND 29 | REACTOME_INTERLEUKIN-19,20,22,24,26,28 AND 29 SIGNALING | 256 | 0.11678435 | 0.11678435 | 0.001 | 0.7815507 | 1 | 10951 tags=34%, list=22%, signal=44% |
| REACTOME_DOWNSTREAM SIGNAL TRANSDUCTION | REACTOME_DOWNSTREAM SIGNAL TRANSDUCTION | 427 | 0.11658027 | 0.11658027 | 0 | 0.78178805 | 1 | 13376 tags=39%, list=27%, signal=53% |
| REACTOME_MAPK FAMILY SIGNALING CASCADES | REACTOME_MAPK FAMILY SIGNALING CASCADES | 283 | 0.11634982 | 0.11634982 | 9.79E-04 | 0.78212816 | 1 | 11810 tags=36%, list=24%, signal=47% |
| REACTOME_SIGNAL TRANSDUCTION | REACTOME_SIGNAL TRANSDUCTION | 2434 | 0.11630812 | 0.11630812 | 0 | 0.7815568 | 1 | 11928 tags=35%, list=24%, signal=44% |
| REACTOME_GAB1 SIGNALLOSOME | REACTOME_GAB1 SIGNALLOSOME | 260 | 0.11617981 | 0.11617981 | 0.0020305 | 0.7813989 | 1 | 17693 tags=48%, list=36%, signal=74% |
| REACTOME_HIV LIFE CYCLE | REACTOME_HIV LIFE CYCLE | 143 | 0.11594164 | 0.11594164 | 0.0276923 | 0.7817837 | 1 | 8035 tags=28%, list=16%, signal=33% |
| REACTOME_PROCESSING OF DNA DOUBLE-STRAND BREAK | REACTOME_PROCESSING OF DNA DOUBLE-STRAND BREAK ENDS | 80 | 0.11571546 | 0.11571546 | 0.2310838 | 0.78209627 | 1 | 11480 tags=35%, list=23%, signal=46% |
| REACTOME_MRNA SPLICING - MAJOR PATHWAY | REACTOME_MRNA SPLICING - MAJOR PATHWAY | 180 | 0.11566511 | 0.11566511 | 0.0149254 | 0.78158826 | 1 | 11222 tags=34%, list=23%, signal=45% |

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|--|--|------|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_CELLULAR RESPONSES TO STRESS | REACTOME_CELLULAR RESPONSES TO STRESS | 382 | 0.11517048 | 0.11517048 | 0 | 0.7830389 | 1 | 8119 tags=28%, list=17%, signal=33% |
| REACTOME_METABOLISM OF PROTEINS | REACTOME_METABOLISM OF PROTEINS | 1976 | 0.11445591 | 0.11445591 | 0 | 0.78565395 | 1 | 7209 tags=26%, list=15%, signal=29% |
| REACTOME_SENESCENCE-ASSOCIATED SECRETORY PHENOTYPE (SASP) | REACTOME_SENESCENCE-ASSOCIATED SECRETORY PHENOTYPE (SASP) | 79 | 0.11443364 | 0.11443364 | 0.234714 | 0.7850109 | 1 | 6801 tags=25%, list=14%, signal=29% |
| REACTOME_VESICLE-MEDIATED TRANSPORT | REACTOME_VESICLE-MEDIATED TRANSPORT | 727 | 0.11425342 | 0.11425342 | 0 | 0.7850608 | 1 | 8901 tags=29%, list=18%, signal=35% |
| REACTOME_MEIOTIC SYNAPSIS | REACTOME_MEIOTIC SYNAPSIS | 59 | 0.1142451 | 0.1142451 | 0.3932039 | 0.78435206 | 1 | 30928 tags=75%, list=63%, signal=202% |
| REACTOME_DEVELOPMENTAL BIOLOGY | REACTOME_DEVELOPMENTAL BIOLOGY | 1000 | 0.11401054 | 0.11401054 | 0 | 0.78465253 | 1 | 7800 tags=27%, list=16%, signal=32% |
| REACTOME_PIP3 ACTIVATES AKT SIGNALING | REACTOME_PIP3 ACTIVATES AKT SIGNALING | 257 | 0.11394609 | 0.11394609 | 0.0010593 | 0.7842124 | 1 | 17693 tags=47%, list=36%, signal=74% |
| REACTOME_LATE PHASE OF HIV LIFE CYCLE | REACTOME_LATE PHASE OF HIV LIFE CYCLE | 130 | 0.11334557 | 0.11334557 | 0.0643863 | 0.7861972 | 1 | 7270 tags=26%, list=15%, signal=31% |
| REACTOME_CONSTITUTIVE SIGNALING BY ABERRANT PI3K IN CANCER | REACTOME_CONSTITUTIVE SIGNALING BY ABERRANT PI3K IN CANCER | 65 | 0.1129731 | 0.1129731 | 0.3644401 | 0.7871362 | 1 | 12554 tags=37%, list=26%, signal=50% |
| REACTOME_G ALPHA (Q) SIGNALLING EVENTS | REACTOME_G ALPHA (Q) SIGNALLING EVENTS | 192 | 0.11269578 | 0.11269578 | 0.0108374 | 0.78764266 | 1 | 9294 tags=30%, list=19%, signal=37% |
| REACTOME_RHO GTPASE EFFECTORS | REACTOME_RHO GTPASE EFFECTORS | 262 | 0.11231678 | 0.11231678 | 0.002064 | 0.7886644 | 1 | 17890 tags=48%, list=37%, signal=75% |
| REACTOME_PI3K/AKT | REACTOME_PI3K/AKT ACTIVATION | 260 | 0.11231313 | 0.11231313 | 0.001002 | 0.787927 | 1 | 17693 tags=47%, list=36%, signal=74% |
| REACTOME_G BETA:GAMMA SIGNALLING THROUGH | REACTOME_G BETA:GAMMA SIGNALLING THROUGH PI3KGAMMA | 48 | 0.11209081 | 0.11209081 | 0.537092 | 0.78824794 | 1 | 5737 tags=23%, list=12%, signal=26% |
| REACTOME_DISORDERS OF TRANSMEMBRANE | REACTOME_DISORDERS OF TRANSMEMBRANE TRANSPORTERS | 74 | 0.11178175 | 0.11178175 | 0.3145246 | 0.78894824 | 1 | 17693 tags=47%, list=36%, signal=74% |
| REACTOME_POSITIVE EPIGENETIC REGULATION OF | REACTOME_POSITIVE EPIGENETIC REGULATION OF RNA EXPRESSION | 75 | 0.11169701 | 0.11169701 | 0.2855721 | 0.7886012 | 1 | 14777 tags=41%, list=30%, signal=59% |
| REACTOME_RNA POLYMERASE I TRANSCRIPTION INITIATION | REACTOME_RNA POLYMERASE I TRANSCRIPTION INITIATION | 47 | 0.11169191 | 0.11169191 | 0.5572968 | 0.78787446 | 1 | 12246 tags=36%, list=25%, signal=48% |
| REACTOME_PEPTIDE LIGAND-BINDING RECEPTORS | REACTOME_PEPTIDE LIGAND-BINDING RECEPTORS | 188 | 0.11087988 | 0.11087988 | 0.0253807 | 0.79088056 | 1 | 11520 tags=35%, list=24%, signal=45% |
| REACTOME_CELLULAR RESPONSES TO EXTERNAL | REACTOME_CELLULAR RESPONSES TO EXTERNAL STIMULI | 459 | 0.11061188 | 0.11061188 | 0 | 0.7913759 | 1 | 7755 tags=27%, list=16%, signal=32% |
| REACTOME_ADAPTIVE IMMUNE SYSTEM | REACTOME_ADAPTIVE IMMUNE SYSTEM | 961 | 0.11059002 | 0.11059002 | 0 | 0.79073006 | 1 | 14103 tags=40%, list=29%, signal=55% |
| REACTOME_ORGANELLE BIOGENESIS AND MAINTENANCE | REACTOME_ORGANELLE BIOGENESIS AND MAINTENANCE | 278 | 0.10999464 | 0.10999464 | 0.003996 | 0.79274744 | 1 | 12257 tags=36%, list=25%, signal=48% |
| REACTOME_G2/M CHECKPOINTS | REACTOME_G2/M CHECKPOINTS | 149 | 0.10928422 | 0.10928422 | 0.0550363 | 0.7952446 | 1 | 16682 tags=45%, list=34%, signal=68% |
| REACTOME_GAP-FILLING DNA REPAIR SYNTHESIS AND LIGATION IN TC-NER | REACTOME_GAP-FILLING DNA REPAIR SYNTHESIS AND LIGATION IN TC-NER | 64 | 0.10898359 | 0.10898359 | 0.3850051 | 0.7958672 | 1 | 8441 tags=28%, list=17%, signal=34% |
| REACTOME_DAP12 SIGNALING | REACTOME_DAP12 SIGNALING | 430 | 0.10834163 | 0.10834163 | 0 | 0.7980836 | 1 | 14896 tags=41%, list=30%, signal=59% |
| REACTOME_METABOLISM | REACTOME_METABOLISM | 2073 | 0.10830744 | 0.10830744 | 0 | 0.79748935 | 1 | 7628 tags=26%, list=16%, signal=29% |
| REACTOME_SIGNALLING TO | REACTOME_SIGNALLING TO ERKS | 256 | 0.10824383 | 0.10824383 | 0.0049554 | 0.79702914 | 1 | 11367 tags=34%, list=23%, signal=44% |
| REACTOME_DNA REPAIR | REACTOME_DNA REPAIR | 289 | 0.10786337 | 0.10786337 | 0.0031381 | 0.79806256 | 1 | 18977 tags=49%, list=39%, signal=80% |
| REACTOME_DUAL INCISION IN GG-NER | REACTOME_DUAL INCISION IN GG-NER | 41 | 0.10680975 | 0.10680975 | 0.6821121 | 0.80214125 | 1 | 15076 tags=41%, list=31%, signal=60% |
| REACTOME_PRC2 METHYLATES HISTONES AND DNA | REACTOME_PRC2 METHYLATES HISTONES AND DNA | 42 | 0.10653135 | 0.10653135 | 0.7028451 | 0.8026518 | 1 | 30928 tags=74%, list=63%, signal=200% |
| REACTOME_DEUBIQUITINATION | REACTOME_DEUBIQUITINATION | 265 | 0.10644145 | 0.10644145 | 0.0052966 | 0.80232126 | 1 | 8119 tags=27%, list=17%, signal=32% |
| REACTOME_MRNA SPLICING | REACTOME_MRNA SPLICING | 191 | 0.10628861 | 0.10628861 | 0.0237859 | 0.8022706 | 1 | 11222 tags=34%, list=23%, signal=43% |
| REACTOME_FATTY ACID METABOLISM | REACTOME_FATTY ACID METABOLISM | 176 | 0.10565336 | 0.10565336 | 0.0301455 | 0.8043917 | 1 | 9033 tags=29%, list=18%, signal=35% |

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|---|---|-----|------------|------------|-----------|------------|---|--|
| REACTOME_CHROMOSOME MAINTENANCE | REACTOME_CHROMOSOME MAINTENANCE | 88 | 0.10555206 | 0.10555206 | 0.2522523 | 0.8040948 | 1 | 29338 tags=70%, list=60%, signal=175% |
| REACTOME_SPHINGOLIPID DE NOVO BIOSYNTHESIS | REACTOME_SPHINGOLIPID DE NOVO BIOSYNTHESIS | 44 | 0.10551149 | 0.10551149 | 0.6693069 | 0.8035202 | 1 | 3740 tags=18%, list=8%, signal=20% |
| REACTOME_PI5P, PP2A AND IER3 REGULATE PI3K/AKT SIGNALING | REACTOME_PI5P, PP2A AND IER3 REGULATE PI3K/AKT SIGNALING | 94 | 0.10549702 | 0.10549702 | 0.2280355 | 0.80284196 | 1 | 12554 tags=36%, list=26%, signal=49% |
| REACTOME_METABOLISM OF NON-CODING RNA | REACTOME_METABOLISM OF NON-CODING RNA | 52 | 0.10515061 | 0.10515061 | 0.5884146 | 0.80367845 | 1 | 17455 tags=46%, list=36%, signal=72% |
| REACTOME_SNRNP ASSEMBLY | REACTOME_SNRNP ASSEMBLY | 52 | 0.10515061 | 0.10515061 | 0.5991903 | 0.8029309 | 1 | 17455 tags=46%, list=36%, signal=72% |
| REACTOME_RNA POLYMERASE I TRANSCRIPTION TERMINATION | REACTOME_RNA POLYMERASE I TRANSCRIPTION TERMINATION | 31 | 0.1047876 | 0.1047876 | 0.8366081 | 0.8038922 | 1 | 12246 tags=35%, list=25%, signal=47% |
| REACTOME_RESOLUTION OF SISTER CHROMATID COHESION | REACTOME_RESOLUTION OF SISTER CHROMATID COHESION | 105 | 0.1045095 | 0.1045095 | 0.2045455 | 0.8044288 | 1 | 17743 tags=47%, list=36%, signal=73% |
| REACTOME_CELL CYCLE | REACTOME_CELL CYCLE | 589 | 0.10450535 | 0.10450535 | 0 | 0.8037011 | 1 | 17888 tags=47%, list=37%, signal=73% |
| REACTOME_STABILIZATION OF REACTOME_SIGNALING BY THE B CELL RECEPTOR (BCR) | REACTOME_STABILIZATION OF P53 REACTOME_SIGNALING BY THE B CELL RECEPTOR (BCR) | 56 | 0.10441589 | 0.10441589 | 0.5625 | 0.80335945 | 1 | 20249 tags=52%, list=41%, signal=88% |
| REACTOME_APC/C:CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC/C:CDH1 TARGETED PROTEINS IN LATE MITOSIS/EARLY G1 | REACTOME_APC/C:CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC/C:CDH1 TARGETED PROTEINS IN LATE MITOSIS/EARLY G1 | 369 | 0.10386639 | 0.10386639 | 0 | 0.80512315 | 1 | 17908 tags=47%, list=37%, signal=73% |
| REACTOME_TCF DEPENDENT SIGNALING IN RESPONSE TO REACTOME_SLC-MEDIATED TRANSMEMBRANE TRANSPORT | REACTOME_TCF DEPENDENT SIGNALING IN RESPONSE TO WNT REACTOME_SLC-MEDIATED TRANSMEMBRANE TRANSPORT | 71 | 0.10357875 | 0.10357875 | 0.3849903 | 0.8057116 | 1 | 17693 tags=46%, list=36%, signal=73% |
| REACTOME_POLO-LIKE KINASE MEDIATED EVENTS | REACTOME_POLO-LIKE KINASE MEDIATED EVENTS | 201 | 0.10301334 | 0.10301334 | 0.01998 | 0.8075861 | 1 | 13977 tags=39%, list=29%, signal=54% |
| REACTOME_HIV INFECTION | REACTOME_HIV INFECTION | 245 | 0.10262432 | 0.10262432 | 0.0110887 | 0.8085989 | 1 | 10588 tags=32%, list=22%, signal=40% |
| REACTOME_MITOTIC PROPHASE | REACTOME_MITOTIC PROPHASE | 16 | 0.10249443 | 0.10249443 | 0.9881423 | 0.8084496 | 1 | 43947 tags=100%, list=90%, signal=975% |
| REACTOME_OXYGEN-DEPENDENT PROLINE HYDROXYLATION OF HYPOXIA-INDUCIBLE FACTOR ALPHA | REACTOME_OXYGEN-DEPENDENT PROLINE HYDROXYLATION OF HYPOXIA-INDUCIBLE FACTOR ALPHA | 224 | 0.10249329 | 0.10249329 | 0.0145349 | 0.80770874 | 1 | 8119 tags=27%, list=17%, signal=32% |
| REACTOME_VEGFR2 MEDIATED CELL PROLIFERATION | REACTOME_VEGFR2 MEDIATED CELL PROLIFERATION | 110 | 0.1022841 | 0.1022841 | 0.1883495 | 0.8079171 | 1 | 18149 tags=47%, list=37%, signal=75% |
| REACTOME_ERCC6 (CSB) AND EHMT2 (G9A) POSITIVELY REGULATE RRNA EXPRESSION | REACTOME_ERCC6 (CSB) AND EHMT2 (G9A) POSITIVELY REGULATE RRNA EXPRESSION | 63 | 0.10226807 | 0.10226807 | 0.4822335 | 0.8072502 | 1 | 19869 tags=51%, list=41%, signal=85% |
| REACTOME_SIGNALLING TO RAS | REACTOME_SIGNALLING TO RAS | 251 | 0.10182885 | 0.10182885 | 0.0110331 | 0.8085002 | 1 | 13376 tags=37%, list=27%, signal=51% |
| REACTOME_CYCLIN A:CDK2-ASSOCIATED EVENTS AT S PHASE ENTRY | REACTOME_CYCLIN A:CDK2-ASSOCIATED EVENTS AT S PHASE ENTRY | 45 | 0.10177162 | 0.10177162 | 0.7026749 | 0.8080167 | 1 | 30928 tags=73%, list=63%, signal=199% |
| REACTOME_MAPK1/MAPK3 SIGNALING | REACTOME_MAPK1/MAPK3 SIGNALING | 249 | 0.10168458 | 0.10168458 | 0.0102987 | 0.8076756 | 1 | 11367 tags=33%, list=23%, signal=43% |
| REACTOME_PROCESSING OF CAPPED INTRON-CONTAINING PRE-MRNA | REACTOME_PROCESSING OF CAPPED INTRON-CONTAINING PRE-MRNA | 80 | 0.10130536 | 0.10130536 | 0.3753878 | 0.80861074 | 1 | 17693 tags=46%, list=36%, signal=72% |
| REACTOME_UB-SPECIFIC PROCESSING PROTEASES | REACTOME_UB-SPECIFIC PROCESSING PROTEASES | 244 | 0.10060182 | 0.10060182 | 0.0217166 | 0.8111162 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_NEGATIVE REGULATION OF THE PI3K/AKT NETWORK | REACTOME_NEGATIVE REGULATION OF THE PI3K/AKT NETWORK | 243 | 0.10051238 | 0.10051238 | 0.0145833 | 0.81078964 | 1 | 11222 tags=33%, list=23%, signal=42% |
| REACTOME_TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRON-CONTAINING TRANSCRIPT | REACTOME_TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRON-CONTAINING TRANSCRIPT | 188 | 0.099972 | 0.099972 | 0.0484027 | 0.8125168 | 1 | 17782 tags=46%, list=36%, signal=72% |
| REACTOME_PROLONGED ERK ACTIVATION EVENTS | REACTOME_PROLONGED ERK ACTIVATION EVENTS | 101 | 0.09953895 | 0.09953895 | 0.277666 | 0.8137426 | 1 | 12588 tags=36%, list=26%, signal=48% |
| | | 73 | 0.09937866 | 0.09937866 | 0.4120553 | 0.8137138 | 1 | 9226 tags=29%, list=19%, signal=35% |
| | | 245 | 0.09927574 | 0.09927574 | 0.0096432 | 0.81344503 | 1 | 10951 tags=32%, list=22%, signal=41% |

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|---|---|-----|------------|------------|-----------|------------|---|--------------------------------------|
| REACTOME_NCAM SIGNALING FOR NEURITE OUT-GROWTH | REACTOME_NCAM SIGNALING FOR NEURITE OUT-GROWTH | 271 | 0.09881721 | 0.09881721 | 0.0099108 | 0.81473917 | 1 | 11810 tags=34%, list=24%, signal=44% |
| REACTOME_GASTRIN-CREB SIGNALLING PATHWAY VIA PKC AND MAPK | REACTOME_GASTRIN-CREB SIGNALLING PATHWAY VIA PKC AND MAPK | 436 | 0.09830628 | 0.09830628 | 9.88E-04 | 0.8162959 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN DIFFERENTIATION OF HSCS | REACTOME_RUNX1 REGULATES TRANSCRIPTION OF GENES INVOLVED IN DIFFERENTIATION OF HSCS | 98 | 0.0980197 | 0.0980197 | 0.2813765 | 0.8168317 | 1 | 17693 tags=46%, list=36%, signal=72% |
| REACTOME_FRS2-MEDIATED ACTIVATION | REACTOME_FRS2-MEDIATED ACTIVATION | 243 | 0.09780305 | 0.09780305 | 0.022022 | 0.81701726 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_SIGNALING BY REACTOME_INTERLEUKIN-2 FAMILY SIGNALING | REACTOME_SIGNALING BY LEPTIN REACTOME_INTERLEUKIN-2 FAMILY SIGNALING | 246 | 0.09759275 | 0.09759275 | 0.0130522 | 0.81719446 | 1 | 11367 tags=33%, list=23%, signal=43% |
| REACTOME_SEPARATION OF SISTER CHROMATIDS | REACTOME_SEPARATION OF SISTER CHROMATIDS | 259 | 0.09730806 | 0.09730806 | 0.0159521 | 0.8176994 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_UCH PROTEINASES | REACTOME_UCH PROTEINASES | 168 | 0.09628239 | 0.09628239 | 0.0809191 | 0.82153124 | 1 | 17743 tags=46%, list=36%, signal=72% |
| REACTOME_RET SIGNALING | REACTOME_RET SIGNALING | 94 | 0.09627147 | 0.09627147 | 0.3517636 | 0.82084316 | 1 | 17693 tags=46%, list=36%, signal=71% |
| REACTOME_ARACHIDONIC ACID METABOLISM | REACTOME_ARACHIDONIC ACID METABOLISM | 263 | 0.09623858 | 0.09623858 | 0.014437 | 0.8202369 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_CYCLIN E ASSOCIATED EVENTS DURING | REACTOME_CYCLIN E ASSOCIATED EVENTS DURING G1/S TRANSITION | 59 | 0.09621813 | 0.09621813 | 0.5997994 | 0.81958866 | 1 | 8572 tags=27%, list=18%, signal=33% |
| REACTOME_ROLE OF LAT2/NTAL/LAB ON CALCIUM MOBILIZATION | REACTOME_ROLE OF LAT2/NTAL/LAB ON CALCIUM MOBILIZATION | 81 | 0.0955881 | 0.0955881 | 0.418 | 0.8216258 | 1 | 17693 tags=46%, list=36%, signal=71% |
| REACTOME_INTERLEUKIN-3, 5 AND GM-CSF SIGNALING | REACTOME_INTERLEUKIN-3, 5 AND GM-CSF SIGNALING | 337 | 0.0952089 | 0.0952089 | 0.0050813 | 0.8225873 | 1 | 21232 tags=53%, list=43%, signal=93% |
| REACTOME_ARMS-MEDIATED ACTIVATION | REACTOME_ARMS-MEDIATED ACTIVATION | 264 | 0.09502418 | 0.09502418 | 0.015 | 0.8227275 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_SIGNALING TO P38 VIA RIT AND RIN | REACTOME_SIGNALING TO P38 VIA RIT AND RIN | 242 | 0.09498125 | 0.09498125 | 0.0256663 | 0.82219046 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_REGULATION OF PTEN STABILITY AND ACTIVITY | REACTOME_REGULATION OF PTEN STABILITY AND ACTIVITY | 242 | 0.09498125 | 0.09498125 | 0.0241935 | 0.8214511 | 1 | 10951 tags=32%, list=22%, signal=41% |
| REACTOME_P53-DEPENDENT G1 DNA DAMAGE RESPONSE | REACTOME_P53-DEPENDENT G1 DNA DAMAGE RESPONSE | 68 | 0.09465365 | 0.09465365 | 0.5361744 | 0.8221687 | 1 | 17693 tags=46%, list=36%, signal=71% |
| REACTOME_P53-DEPENDENT G1/S DNA DAMAGE CHECKPOINT | REACTOME_P53-DEPENDENT G1/S DNA DAMAGE CHECKPOINT | 65 | 0.09425673 | 0.09425673 | 0.5909548 | 0.82321787 | 1 | 20249 tags=51%, list=41%, signal=86% |
| REACTOME_G1/S DNA DAMAGE CHECKPOINTS | REACTOME_G1/S DNA DAMAGE CHECKPOINTS | 65 | 0.09425673 | 0.09425673 | 0.5936571 | 0.82247955 | 1 | 20249 tags=51%, list=41%, signal=86% |
| REACTOME_MITOTIC ANAPHASE | REACTOME_MITOTIC ANAPHASE | 67 | 0.09403063 | 0.09403063 | 0.5477099 | 0.82271767 | 1 | 20249 tags=51%, list=41%, signal=86% |
| REACTOME_POST-ELONGATION PROCESSING OF INTRON-CONTAINING PRE-MRNA | REACTOME_POST-ELONGATION PROCESSING OF INTRON-CONTAINING PRE-MRNA | 178 | 0.09301301 | 0.09301301 | 0.0918367 | 0.8263691 | 1 | 17743 tags=46%, list=36%, signal=71% |
| REACTOME_MRNA 3'-END PROCESSING | REACTOME_MRNA 3'-END PROCESSING | 57 | 0.09236857 | 0.09236857 | 0.7118812 | 0.82845414 | 1 | 9226 tags=28%, list=19%, signal=35% |
| REACTOME_GRB2 EVENTS IN EGFR SIGNALING | REACTOME_GRB2 EVENTS IN EGFR SIGNALING | 57 | 0.09236857 | 0.09236857 | 0.7112887 | 0.8277138 | 1 | 9226 tags=28%, list=19%, signal=35% |
| REACTOME_RAF/MAP KINASE CASCADE | REACTOME_RAF/MAP KINASE CASCADE | 238 | 0.09190281 | 0.09190281 | 0.0417515 | 0.8289345 | 1 | 10951 tags=32%, list=22%, signal=40% |
| REACTOME_SHC1 EVENTS IN EGFR SIGNALING | REACTOME_SHC1 EVENTS IN EGFR SIGNALING | 238 | 0.09190281 | 0.09190281 | 0.024728 | 0.82819504 | 1 | 10951 tags=32%, list=22%, signal=40% |
| REACTOME_SOS-MEDIATED SIGNALLING | REACTOME_SOS-MEDIATED SIGNALLING | 238 | 0.09190281 | 0.09190281 | 0.0372233 | 0.8274569 | 1 | 10951 tags=32%, list=22%, signal=40% |
| REACTOME_APC/C-MEDIATED DEGRADATION OF CELL CYCLE PROTEINS | REACTOME_APC/C-MEDIATED DEGRADATION OF CELL CYCLE PROTEINS | 238 | 0.09190281 | 0.09190281 | 0.0421569 | 0.82672006 | 1 | 10951 tags=32%, list=22%, signal=40% |
| | | 85 | 0.0912511 | 0.0912511 | 0.4421769 | 0.82879275 | 1 | 18581 tags=47%, list=38%, signal=76% |

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|--|--|-----|------------|------------|-----------|------------|---|---------------------------------------|
| REACTOME_REGULATION OF MITOTIC CELL CYCLE | REACTOME_REGULATION OF MITOTIC CELL CYCLE | 85 | 0.0912511 | 0.0912511 | 0.4485219 | 0.828056 | 1 | 18581 tags=47%, list=38%, signal=76% |
| REACTOME_METABOLISM OF POLYAMINES | REACTOME_METABOLISM OF POLYAMINES | 84 | 0.09117723 | 0.09117723 | 0.4753623 | 0.8276129 | 1 | 17693 tags=45%, list=36%, signal=71% |
| REACTOME_B-WICH COMPLEX POSITIVELY REGULATES RRNA EXPRESSION | REACTOME_B-WICH COMPLEX POSITIVELY REGULATES RRNA EXPRESSION | 60 | 0.09107114 | 0.09107114 | 0.6513292 | 0.82735544 | 1 | 13499 tags=37%, list=28%, signal=51% |
| REACTOME_MITOTIC METAPHASE AND ANAPHASE | REACTOME_MITOTIC METAPHASE AND ANAPHASE | 179 | 0.09046336 | 0.09046336 | 0.1130604 | 0.829201 | 1 | 17743 tags=45%, list=36%, signal=71% |
| REACTOME_MITOTIC G1-G1/S PHASES | REACTOME_MITOTIC G1-G1/S PHASES | 145 | 0.08967141 | 0.08967141 | 0.1684518 | 0.83193505 | 1 | 16558 tags=43%, list=34%, signal=64% |
| REACTOME_CLASS A/1 (RHODOPSIN-LIKE RECEPTORS) | REACTOME_CLASS A/1 (RHODOPSIN-LIKE RECEPTORS) | 320 | 0.08907615 | 0.08907615 | 0.0107738 | 0.8337646 | 1 | 6530 tags=22%, list=13%, signal=25% |
| REACTOME_ACTIVATION OF APC/C AND APC/C:CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS | REACTOME_ACTIVATION OF APC/C AND APC/C:CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS | 75 | 0.08766756 | 0.08766756 | 0.5880567 | 0.8391659 | 1 | 19869 tags=49%, list=41%, signal=83% |
| REACTOME_SIGNALING BY WNT | REACTOME_SIGNALING BY WNT | 292 | 0.08752456 | 0.08752456 | 0.0254324 | 0.8390464 | 1 | 11837 tags=33%, list=24%, signal=43% |
| REACTOME_INTERLEUKIN RECEPTOR SHC SIGNALING | REACTOME_INTERLEUKIN RECEPTOR SHC SIGNALING | 248 | 0.08725584 | 0.08725584 | 0.0456853 | 0.83943546 | 1 | 10951 tags=31%, list=22%, signal=40% |
| REACTOME_OXIDATIVE STRESS INDUCED SENESCENCE | REACTOME_OXIDATIVE STRESS INDUCED SENESCENCE | 91 | 0.08706219 | 0.08706219 | 0.4853516 | 0.8395257 | 1 | 17267 tags=44%, list=35%, signal=68% |
| REACTOME_CHROMATIN MODIFYING ENZYMES | REACTOME_CHROMATIN MODIFYING ENZYMES | 238 | 0.08677158 | 0.08677158 | 0.0551724 | 0.84005195 | 1 | 8115 tags=25%, list=17%, signal=30% |
| REACTOME_CHROMATIN ORGANIZATION | REACTOME_CHROMATIN ORGANIZATION | 238 | 0.08677158 | 0.08677158 | 0.0583333 | 0.8393125 | 1 | 8115 tags=25%, list=17%, signal=30% |
| REACTOME_AMPLIFICATION OF SIGNAL FROM UNATTACHED KINETOCHORES VIA A MAD2 INHIBITORY SIGNAL | REACTOME_AMPLIFICATION OF SIGNAL FROM UNATTACHED KINETOCHORES VIA A MAD2 INHIBITORY SIGNAL | 92 | 0.08653775 | 0.08653775 | 0.464497 | 0.8395838 | 1 | 17591 tags=45%, list=36%, signal=69% |
| REACTOME_AMPLIFICATION OF SIGNAL FROM THE KINETOCHORES | REACTOME_AMPLIFICATION OF SIGNAL FROM THE KINETOCHORES | 92 | 0.08653775 | 0.08653775 | 0.4501953 | 0.8388461 | 1 | 17591 tags=45%, list=36%, signal=69% |
| REACTOME_ABC TRANSPORTER DISORDERS | REACTOME_ABC TRANSPORTER DISORDERS | 67 | 0.08651941 | 0.08651941 | 0.6423712 | 0.8381914 | 1 | 17693 tags=45%, list=36%, signal=70% |
| REACTOME_AMYLOID FIBER FORMATION | REACTOME_AMYLOID FIBER FORMATION | 69 | 0.08622234 | 0.08622234 | 0.6702439 | 0.8387336 | 1 | 5718 tags=20%, list=12%, signal=23% |
| REACTOME_KERATINIZATION | REACTOME_KERATINIZATION | 171 | 0.08597071 | 0.08597071 | 0.1581582 | 0.8390596 | 1 | 33029 tags=76%, list=67%, signal=233% |
| REACTOME_FC EPSILON RECEPTOR (FCER1) SIGNALING | REACTOME_FC EPSILON RECEPTOR (FCER1) SIGNALING | 519 | 0.0848435 | 0.0848435 | 0.0019608 | 0.84303117 | 1 | 20324 tags=50%, list=42%, signal=84% |
| REACTOME_CLEAVAGE OF GROWING TRANSCRIPT IN THE TERMINATION REGION | REACTOME_CLEAVAGE OF GROWING TRANSCRIPT IN THE TERMINATION REGION | 66 | 0.08365544 | 0.08365544 | 0.7018634 | 0.8472203 | 1 | 12230 tags=33%, list=25%, signal=44% |
| REACTOME_POST-ELONGATION PROCESSING OF THE TRANSCRIPT | REACTOME_POST-ELONGATION PROCESSING OF THE TRANSCRIPT | 66 | 0.08365544 | 0.08365544 | 0.7288136 | 0.8464797 | 1 | 12230 tags=33%, list=25%, signal=44% |
| REACTOME_RNA POLYMERASE II TRANSCRIPTION TERMINATION | REACTOME_RNA POLYMERASE II TRANSCRIPTION TERMINATION | 66 | 0.08365544 | 0.08365544 | 0.7212787 | 0.84574044 | 1 | 12230 tags=33%, list=25%, signal=44% |
| REACTOME_NEGATIVE EPIGENETIC REGULATION OF RNA EXPRESSION | REACTOME_NEGATIVE EPIGENETIC REGULATION OF RNA EXPRESSION | 78 | 0.08334868 | 0.08334868 | 0.6390593 | 0.84630275 | 1 | 12246 tags=33%, list=25%, signal=44% |
| REACTOME_BIOLOGICAL OXIDATIONS | REACTOME_BIOLOGICAL OXIDATIONS | 215 | 0.08180418 | 0.08180418 | 0.1056676 | 0.85195166 | 1 | 7626 tags=24%, list=16%, signal=28% |
| REACTOME_APC/C:CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS | REACTOME_APC/C:CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS | 74 | 0.08080855 | 0.08080855 | 0.7220039 | 0.855291 | 1 | 19869 tags=49%, list=41%, signal=82% |
| REACTOME_INSULIN RECEPTOR SIGNALLING CASCADE | REACTOME_INSULIN RECEPTOR SIGNALLING CASCADE | 291 | 0.07977558 | 0.07977558 | 0.0480962 | 0.85872036 | 1 | 1837 tags=12%, list=4%, signal=12% |

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| REACTOME_RHO GTPASES ACTIVATE PKNS | REACTOME_RHO GTPASES ACTIVATE PKNS | 63 | 0.07924696 | 0.07924696 | 0.8168168 | 0.86009264 | 1 | 14777 tags=38%, list=30%, signal=54% |
| REACTOME_APC/C:CDC20 MEDIATED DEGRADATION OF | REACTOME_APC/C:CDC20 MEDIATED DEGRADATION OF SECURIN | 66 | 0.07915513 | 0.07915513 | 0.7778865 | 0.85971844 | 1 | 19869 tags=48%, list=41%, signal=81% |
| REACTOME_FCERI MEDIATED MAPK ACTIVATION | REACTOME_FCERI MEDIATED MAPK ACTIVATION | 332 | 0.07894721 | 0.07894721 | 0.0306122 | 0.8597906 | 1 | 21232 tags=51%, list=43%, signal=90% |
| REACTOME_TRANSCRIPTIONAL REGULATION BY SMALL RNAS | REACTOME_TRANSCRIPTIONAL REGULATION BY SMALL RNAS | 73 | 0.07828716 | 0.07828716 | 0.72167 | 0.861703 | 1 | 18977 tags=47%, list=39%, signal=76% |
| REACTOME_IRS-MEDIATED SIGNALLING | REACTOME_IRS-MEDIATED SIGNALLING | 288 | 0.07750217 | 0.07750217 | 0.0558882 | 0.8640499 | 1 | 1837 tags=11%, list=4%, signal=12% |
| REACTOME_SIGNALING BY TYPE 1 INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR (IGF1R) | REACTOME_SIGNALING BY TYPE 1 INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR (IGF1R) | 293 | 0.07713287 | 0.07713287 | 0.0472441 | 0.86474866 | 1 | 10951 tags=30%, list=22%, signal=38% |
| REACTOME_REGULATION OF APC/C ACTIVATORS BETWEEN G1/S AND EARLY ANAPHASE | REACTOME_REGULATION OF APC/C ACTIVATORS BETWEEN G1/S AND EARLY ANAPHASE | 79 | 0.07632379 | 0.07632379 | 0.7099792 | 0.86727977 | 1 | 18581 tags=46%, list=38%, signal=73% |
| REACTOME_GPCR LIGAND | REACTOME_GPCR LIGAND BINDING | 451 | 0.07574237 | 0.07574237 | 0.0099404 | 0.8688629 | 1 | 6530 tags=21%, list=13%, signal=24% |
| REACTOME_RNA POLYMERASE I TRANSCRIPTION | REACTOME_RNA POLYMERASE I TRANSCRIPTION | 80 | 0.07500511 | 0.07500511 | 0.7277277 | 0.8709809 | 1 | 12246 tags=33%, list=25%, signal=43% |
| REACTOME_CELL CYCLE CHECKPOINTS | REACTOME_CELL CYCLE CHECKPOINTS | 270 | 0.07237223 | 0.07237223 | 0.118593 | 0.8803273 | 1 | 17693 tags=43%, list=36%, signal=67% |
| REACTOME_RNA POLYMERASE I PROMOTER CLEARANCE | REACTOME_RNA POLYMERASE I PROMOTER CLEARANCE | 78 | 0.07050771 | 0.07050771 | 0.7992203 | 0.88646805 | 1 | 12246 tags=32%, list=25%, signal=43% |
| REACTOME_NORC NEGATIVELY REGULATES RRNA EXPRESSION | REACTOME_NORC NEGATIVELY REGULATES RRNA EXPRESSION | 75 | 0.06998978 | 0.06998978 | 0.8228856 | 0.8875867 | 1 | 12246 tags=32%, list=25%, signal=43% |
| REACTOME_POST- TRANSLATIONAL MODIFICATION: SYNTHESIS OF GPI-ANCHORED | REACTOME_POST-TRANSLATIONAL MODIFICATION: SYNTHESIS OF GPI- ANCHORED PROTEINS | 92 | 0.05890001 | 0.05890001 | 0.8786982 | 0.92497164 | 1 | 12555 tags=32%, list=26%, signal=42% |
| REACTOME_ANTIMICROBIAL PEPTIDES | REACTOME_ANTIMICROBIAL PEPTIDES | 75 | 0.0585914 | 0.0585914 | 0.949495 | 0.92515135 | 1 | 23902 tags=55%, list=49%, signal=107% |
| REACTOME_MEIOSIS | REACTOME_MEIOSIS | 87 | 0.05810317 | 0.05810317 | 0.9057171 | 0.92587537 | 1 | 30928 tags=69%, list=63%, signal=187% |