```
GO:0016569: covalent chromatin modification
                                    GO:0046649: lymphocyte activation
                                    GO:0006913: nucleocytoplasmic transport
                                    GO:0006914: autophagy
                                    GO:0046488: phosphatidylinositol metabolic process
                                    R-HSA-1059683: Interleukin-6 signaling
                                    GO:0006405: RNA export from nucleus
                                    WP395: IL-4 signaling pathway
                                    R-HSA-8878171: Transcriptional regulation by RUNX1
                                    GO:0035303: regulation of dephosphorylation
                                    GO:1903047: mitotic cell cycle process
                                    GO:0002262: myeloid cell homeostasis
                                    hsa04120: Ubiquitin mediated proteolysis
                                    R-HSA-3108232: SUMO E3 ligases SUMOylate target proteins
                                    R-HSA-194315: Signaling by Rho GTPases
                                    M124: PID CXCR4 PATHWAY
                                    GO:0051129: negative regulation of cellular component organization
                                    GO:0000226: microtubule cytoskeleton organization
                                    GO:0006511: ubiquitin-dependent protein catabolic process
                                    GO:0017015: regulation of transforming growth factor beta receptor signaling pathway
                                    M261: PID P53 REGULATION PATHWAY
                                    GO:0051656: establishment of organelle localization
                                    GO:0045815: positive regulation of gene expression, epigenetic
                                    GO:0080135: regulation of cellular response to stress
                                    GO:0002764: immune response-regulating signaling pathway
                                    GO:0009895: negative regulation of catabolic process
                                    GO:0031122: cytoplasmic microtubule organization
                                    GO:0060968: regulation of gene silencing
                                    WP2261: Glioblastoma signaling pathways
                                    M136: PID FOXO PATHWAY
                                    GO:0045596: negative regulation of cell differentiation
                                    M101: PID HDAC CLASSI PATHWAY
                                    GO:0032870: cellular response to hormone stimulus
                                    WP4754: IL-18 signaling pathway
                                    GO:0033044: regulation of chromosome organization
                                    GO:0051493: regulation of cytoskeleton organization
                                    GO:0006401: RNA catabolic process
                                    GO:1902275: regulation of chromatin organization
                                    WP4217: Ebola virus pathway in host
                                    R-HSA-8939243: RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known
                                    GO:0018105: peptidyl-serine phosphorylation
                                    R-HSA-201556: Signaling by ALK
                                    GO:0072539: T-helper 17 cell differentiation
                                    R-HSA-5653656: Vesicle-mediated transport
                                    GO:0010256: endomembrane system organization
                                    GO:0031648: protein destabilization
                                    GO:0045936: negative regulation of phosphate metabolic process
                                    GO:0043414: macromolecule methylation
                                    CORUM:7557: LGR4-RSPO supercomplex
                                    GO:0006109: regulation of carbohydrate metabolic process
                                    GO:0071407: cellular response to organic cyclic compound
                                    ko04659: Th17 cell differentiation
                                    CORUM:6290: Ubiquitin E3 ligase (DDB1, DYRK2, EDD, VPRBP)
                                    GO:0006333: chromatin assembly or disassembly GO:0007173: epidermal growth factor receptor signaling pathway
                                    R-HSA-69278: Cell Cycle, Mitotic
                                    GO:0022613: ribonucleoprotein complex biogenesis
                                    WP437: EGF/EGFR signaling pathway
                                    M113: PID NFAT 3PATHWAY
                                    GO:0006338: chromatin remodeling
                                    GO:0001655: urogenital system development
                                    GO:0016579: protein deubiquitination
                                    R-HSA-9013424: RHOV GTPase cycle
                                    GO:0010815: bradykinin catabolic process
                                    ko03013: RNA transport
                                    GO:0030335: positive regulation of cell migration
                                    GO:0032886: regulation of microtubule-based process
                                    M186: PID PDGFRB PATHWAY
                                    GO:0010171: body morphogenesis
                                    WP2857: Mesodermal commitment pathway
                                    GO:0062197: cellular response to chemical stress
                                    R-HSA-5633007: Regulation of TP53 Activity
                                    GO:0016055: Wnt signaling pathway
                                    GO:0009299: mRNA transcription
                                    R-HSA-2559584: Formation of Senescence-Associated Heterochromatin Foci (SAHF)
                                    GO:0006984: ER-nucleus signaling pathway
                                    GO:0001776: leukocyte homeostasis
                                    R-HSA-6798695: Neutrophil degranulation
                                     GO:00/0482: response to oxygen levels
                                    GO:0016032: viral process
                                    WP2038: Microtubule cytoskeleton regulation
                                    M237: PID VEGFR1 2 PATHWAY
                                    GO:0060322: head development
                                    R-HSA-177929: Signaling by EGFR
                                    GO:1900181: negative regulation of protein localization to nucleus
                                    R-HSA-8939242: RUNX1 regulates transcription of genes involved in differentiation of keratinocytes
                                    R-HSA-199992: trans-Golgi Network Vesicle Budding
                                    GO:0016925: protein sumoylation
                                    GO:0048511: rhythmic process
                                    GO:0043299: leukocyte degranulation
                                    GO:0032011: ARF protein signal transduction
                                    GO:0043555: regulation of translation in response to stress
                                    R-HSA-9662834: CD163 mediating an anti-inflammatory response
                                    GO:0034214: protein hexamerization
                                    GO:0022604: regulation of cell morphogenesis
                                    R-HSA-2262752: Cellular responses to stress
                                    M00130: Inositol phosphate metabolism, PI => PIP2 => Ins(1,4,5)P3 => Ins(1,3,4,5)P4
                                    GO:0001817: regulation of cytokine production
                                    GO:0043087: regulation of GTPase activity
                                    R-HSA-9679191: Potential therapeutics for SARS
         8
                 10
                           12
6
-log10(P)
```