
A
Positive correlation
GO:0001775: cell activation
GO:0050865: regulation of cell activation
R-HSA-1280215: Cytokine Signaling in Immune system
GO:0050778: positive regulation of immune response
GO:0001819: positive regulation of cytokine production
R-HSA-1280218: Adaptive Immune System
GO:0006954: inflammatory response
R-HSA-6798695: Neutrophil degranulation
GO:0045087: innate immune response
GO:0031347: regulation of defense response
GO:0002697: regulation of immune effector process
GO:0002683: negative regulation of immune system process
R-HSA-72312: rRNA processing
GO:0042254: ribosome biogenesis
GO:0010942: positive regulation of cell death
GO:0050900: leukocyte migration
GO:0009617: response to bacterium
GO:0055082: cellular chemical homeostasis
WP5115: Network map of SARS-CoV-2 signaling pathway
hsa05169: Epstein-Barr virus infection
hsa04659: Th17 cell differentiation
GO:0043549: regulation of kinase activity
GO:0040017: positive regulation of locomotion
GO:2001233: regulation of apoptotic signaling pathway
GO:0050864: regulation of B cell activation
WP4217: Ebola virus pathway in host
M54: PID IL12 2PATHWAY
R-HSA-109582: Hemostasis
hsa04145: Phagosome
hsa04060: Cytokine-cytokine receptor interaction
hsa05132: Salmonella infection
GO:0030162: regulation of proteolysis
hsa04064: NF-kappa B signaling pathway
R-HSA-202403: TCR signaling
WP4754: IL-18 signaling pathway
GO:0030029: actin filament-based process
R-HSA-6785807: Interleukin-4 and Interleukin-13 signaling
GO:2000106: regulation of leukocyte apoptotic process
GO:0006897: endocytosis
GO:0034976: response to endoplasmic reticulum stress
GO:0043086: negative regulation of catalytic activity
GO:0031341: regulation of cell killing
GO:0046634: regulation of alpha-beta T cell activation
GO:0008285: negative regulation of cell population proliferation
GO:0009615: response to virus
GO:0046631: alpha-beta T cell activation
hsa04514: Cell adhesion molecules
GO:0071496: cellular response to external stimulus
WP3888: VEGFA-VEGFR2 signaling pathway
GO:0050777: negative regulation of immune response
GO:0009725: response to hormone
WP69: T-cell receptor (TCR) signaling pathway
R-HSA-877300: Interferon gamma signaling
GO:0080135: regulation of cellular response to stress
GO:0051223: regulation of protein transport
GO:0009611: response to wounding
GO:0097190: apoptotic signaling pathway
GO:0008283: cell population proliferation
hsa04380: Osteoclast differentiation
GO:0051345: positive regulation of hydrolase activity
GO:0043122: regulation of I-kappaB kinase/NF-kappaB signaling
hsa04210: Apoptosis
GO:0048002: antigen processing and presentation of peptide antigen
GO:0061024: membrane organization
GO:0030163: protein catabolic process
hsa05417: Lipid and atherosclerosis
GO:0010506: regulation of autophagy
GO:0040008: regulation of growth
hsa04640: Hematopoietic cell lineage
M124: PID CXCR4 PATHWAY
GO:0050730: regulation of peptidyl-tyrosine phosphorylation
R-HSA-5357801: Programmed Cell Death
GO:0043368: positive T cell selection
R-HSA-5213460: RIPK1-mediated regulated necrosis
R-HSA-9012999: RHO GTPase cycle
GO:0009896: positive regulation of catabolic process
M145: PID P53 DOWNSTREAM PATHWAY
R-HSA-382551: Transport of small molecules
GO:0007167: enzyme linked receptor protein signaling pathway
R-HSA-5653656: Vesicle-mediated transport
GO:0006914: autophagy
GO:0030099: myeloid cell differentiation
GO:2000377: regulation of reactive oxygen species metabolic process
GO:0006979: response to oxidative stress
GO:1903707: negative regulation of hemopoiesis
GO:0050854: regulation of antigen receptor-mediated
hsa05134: Legionellosis
GO:2001236: regulation of extrinsic apoptotic signaling pathway
GO:0010035: response to inorganic substance
GO:0045862: positive regulation of proteolysis
GO:0032970: regulation of actin filament-based process
WP3945: TYROBP causal network in microglia
GO:0070482: response to oxygen levels
GO:0010817: regulation of hormone levels
GO:0071674: mononuclear cell migration
GO:0007159: leukocyte cell-cell adhesion
M183: PID IL6 7 PATHWAY
GO:0120161: regulation of cold-induced thermogenesis
GO:0001525: angiogenesis
GO:0002274: myeloid leukocyte activation
0
10
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40
50
60
-log10(P)
B
Negative correlation
GO:0031175: neuron projection development
GO:0034330: cell junction organization
GO:0001655: urogenital system development
GO:0031344: regulation of cell projection organization
GO:1905114: cell surface receptor signaling pathway
GO:0048598: embryonic morphogenesis
GO:0060322: head development
M5884: external encapsulating structure-NABA CORE MATRISOME
GO:0007423: sensory organ development
hsa04340: Hedgehog signaling pathway
GO:0001501: skeletal system development
hsa04310: Wnt signaling pathway
GO:0050803: regulation of synapse structure or activity
GO:0007167: enzyme linked receptor protein signaling pathway
GO:0007389: pattern specification process
GO:0099537: trans-synaptic signaling
GO:0098609: cell-cell adhesion
GO:0035107: appendage morphogenesis
R-HSA-1474290: Collagen formation
GO:0001568: blood vessel development
GO:0006468: protein phosphorylation
GO:0007017: microtubule-based process
GO:0001503: ossification
R-HSA-6794362: Protein-protein interactions at synapses
R-HSA-112316: Neuronal System
GO:0048589: developmental growth
WP5053: Development of ureteric collection system
GO:2000027: regulation of animal organ morphogenesis
WP2857: Mesodermal commitment pathway
GO:0006325: chromatin organization
GO:0030029: actin filament-based process
GO:0051668: localization within membrane
GO:0022604: regulation of cell morphogenesis
GO:0007610: behavior
GO:0060485: mesenchyme development
hsa05168: Herpes simplex virus 1 infection
GO:0051129: negative regulation of cellular component organization
GO:0021510: spinal cord development
GO:0030031: cell projection assembly
GO:0009100: glycoprotein metabolic process
GO:0031345: negative regulation of cell projection organization
GO:0060341: regulation of cellular localization
GO:0044089: positive regulation of cellular component biogenesis
GO:0048706: embryonic skeletal system development
R-HSA-3781865: Diseases of glycosylation
GO:0030001: metal ion transport
GO:0099054: presynapse assembly
GO:0060541: respiratory system development
GO:0051056: regulation of small GTPase mediated signal transduction
WP4803: Ciliopathies
R-HSA-9006934: Signaling by Receptor Tyrosine Kinases
GO:0048608: reproductive structure development
GO:0007185: transmembrane receptor protein tyrosine phosphatase
GO:0099111: microtubule-based transport
GO:0003205: cardiac chamber development
GO:0043087: regulation of GTPase activity
R-HSA-8849932: Synaptic adhesion-like molecules
GO:0090102: cochlea development
GO:0032412: regulation of ion transmembrane transporter activity
GO:0099504: synaptic vesicle cycle
GO:0060021: roof of mouth development
GO:0090287: regulation of cellular response to growth factor stimulus
R-HSA-2243919: Crosslinking of collagen fibrils
GO:0032330: regulation of chondrocyte differentiation
GO:0051301: cell division
GO:0007163: establishment or maintenance of cell polarity
GO:1903530: regulation of secretion by cell
GO:0007369: gastrulation
GO:0030177: positive regulation of Wnt signaling pathway
GO:0001894: tissue homeostasis
GO:0045667: regulation of osteoblast differentiation
GO:0040008: regulation of growth
GO:0060627: regulation of vesicle-mediated transport
WP3967: miR-509-3p alteration of YAP1/ECM axis
GO:0060840: artery development
GO:0042391: regulation of membrane potential
GO:2001223: negative regulation of neuron migration
GO:0099173: postsynapse organization
GO:0045216: cell-cell junction organization
R-HSA-9012999: RHO GTPase cycle
GO:0050773: regulation of dendrite development
M219: PID HEDGEHOG GLI PATHWAY
R-HSA-3769402: Deactivation of the beta-catenin transactivating complex
GO:0021953: central nervous system neuron differentiation
GO:0099175: regulation of postsynapse organization
GO:0008038: neuron recognition
GO:0009855: determination of bilateral symmetry
GO:0018200: peptidyl-glutamic acid modification
GO:0016570: histone modification
GO:0070848: response to growth factor
R-HSA-372790: Signaling by GPCR
R-HSA-8939243: RUNX1 interacts with co-factors
GO:0060976: coronary vasculature development
GO:0050905: neuromuscular process
M211: PID HEDGEHOG 2PATHWAY
GO:0032964: collagen biosynthetic process
GO:0061061: muscle structure development
M77: PID WNT SIGNALING PATHWAY
R-HSA-4791275: Signaling by WNT in cancer
GO:0009954: proximal/distal pattern formation
0
5
10
15
20
25
30
-log10(P)