|  |  |  |  |  |
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| **Table S8. List of canonical pathways associated with the identified gene co-expression modules in B cells of primary Sjögren's syndrome.** | | | | |
| Ingenuity Canonical Pathways | -log(p-value) | Ratio | module | Molecules |
| Tec Kinase Signaling | 5.16 | 0.0485 | yellow | FYN,PIK3C2B,PIK3CA,HCK,PLCG1,GNG3,PRKD3,TNFRSF10A |
| Prolactin Signaling | 4.74 | 0.0659 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1,SOCS5,PRKD3 |
| Protein Kinase A Signaling | 4.74 | 0.0289 | yellow | AKAP2,DUSP5,H3F3A/H3F3B,YWHAH,SMAD3,PPP1R14A,PLCG1,UBASH3B,LEF1,GNG3,PRKD3 |
| Molecular Mechanisms of Cancer | 4.67 | 0.0284 | yellow | FYN,PIK3C2B,PIK3CA,ARHGEF7,SMAD3,CTNNA1,CDK6,BMPR2,LEF1,MAP2K3,PRKD3 |
| FAK Signaling | 4.36 | 0.0566 | yellow | PIK3C2B,FYN,PIK3CA,ARHGEF7,PLCG1,CAPN7 |
| Virus Entry via Endocytic Pathways | 4.1 | 0.0508 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1,AP1B1,PRKD3 |
| Fc Epsilon RI Signaling | 3.97 | 0.048 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1,MAP2K3,PRKD3 |
| Non-Small Cell Lung Cancer Signaling | 3.79 | 0.0588 | yellow | PIK3C2B,FHIT,PIK3CA,CDK6,PLCG1 |
| Growth Hormone Signaling | 3.77 | 0.0581 | yellow | PIK3C2B,PIK3CA,PLCG1,SOCS5,PRKD3 |
| ERK/MAPK Signaling | 3.67 | 0.0348 | yellow | FYN,PIK3C2B,PIK3CA,H3F3A/H3F3B,YWHAH,PPP1R14A,PLCG1 |
| CTLA4 Signaling in Cytotoxic T Lymphocytes | 3.55 | 0.0521 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1,AP1B1 |
| HER-2 Signaling in Breast Cancer | 3.55 | 0.0521 | yellow | PIK3C2B,PIK3CA,CDK6,PLCG1,PRKD3 |
| Integrin Signaling | 3.52 | 0.0329 | yellow | PIK3C2B,FYN,PIK3CA,MPRIP,ARHGEF7,PLCG1,CAPN7 |
| ErbB Signaling | 3.37 | 0.0476 | yellow | PIK3C2B,PIK3CA,PLCG1,MAP2K3,PRKD3 |
| Phospholipase C Signaling | 3.36 | 0.031 | yellow | FYN,MPRIP,ARHGEF7,PLCG1,PPP1R14A,GNG3,PRKD3 |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 3.26 | 0.026 | yellow | PIK3C2B,PIK3CA,TRAF3IP2,IL15,PLCG1,LEF1,MAP2K3,PRKD3 |
| UVB-Induced MAPK Signaling | 3.15 | 0.0597 | yellow | PIK3C2B,PIK3CA,H3F3A/H3F3B,PRKD3 |
| Glioma Signaling | 3.09 | 0.0413 | yellow | PIK3C2B,PIK3CA,CDK6,PLCG1,PRKD3 |
| Thrombopoietin Signaling | 3.03 | 0.0556 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Endometrial Cancer Signaling | 3.03 | 0.0556 | yellow | PIK3C2B,PIK3CA,CTNNA1,LEF1 |
| Natural Killer Cell Signaling | 3.02 | 0.04 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1,PRKD3 |
| CCR3 Signaling in Eosinophils | 2.93 | 0.0382 | yellow | PIK3C2B,PIK3CA,MPRIP,GNG3,PRKD3 |
| GP6 Signaling Pathway | 2.92 | 0.0379 | yellow | PIK3C2B,FYN,PIK3CA,PRKD3,RASGRP2 |
| ErbB4 Signaling | 2.9 | 0.0513 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| 14-3-3-mediated Signaling | 2.86 | 0.0368 | yellow | PIK3C2B,PIK3CA,YWHAH,PLCG1,PRKD3 |
| p70S6K Signaling | 2.82 | 0.036 | yellow | PIK3C2B,PIK3CA,YWHAH,PLCG1,PRKD3 |
| P2Y Purigenic Receptor Signaling Pathway | 2.82 | 0.036 | yellow | PIK3C2B,PIK3CA,PLCG1,GNG3,PRKD3 |
| Clathrin-mediated Endocytosis Signaling | 2.8 | 0.029 | yellow | PIK3C2B,PIK3CA,AAK1,HIP1,AP1B1,HIP1R |
| Thrombin Signaling | 2.79 | 0.0288 | yellow | PIK3C2B,PIK3CA,MPRIP,PLCG1,GNG3,PRKD3 |
| Human Embryonic Stem Cell Pluripotency | 2.79 | 0.0355 | yellow | PIK3C2B,PIK3CA,SMAD3,BMPR2,LEF1 |
| IL-15 Signaling | 2.78 | 0.0476 | yellow | PIK3C2B,PIK3CA,IL15,PLCG1 |
| Neurotrophin/TRK Signaling | 2.78 | 0.0476 | yellow | PIK3C2B,PIK3CA,PLCG1,MAP2K3 |
| Breast Cancer Regulation by Stathmin1 | 2.78 | 0.0287 | yellow | PIK3C2B,PIK3CA,ARHGEF7,PPP1R14A,GNG3,PRKD3 |
| Small Cell Lung Cancer Signaling | 2.73 | 0.046 | yellow | PIK3C2B,FHIT,PIK3CA,CDK6 |
| Erythropoietin Signaling | 2.71 | 0.0455 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Hereditary Breast Cancer Signaling | 2.7 | 0.0338 | yellow | PIK3C2B,PIK3CA,GADD45B,CDK6,SMARCA4 |
| Macropinocytosis Signaling | 2.69 | 0.0449 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Role of NFAT in Cardiac Hypertrophy | 2.66 | 0.0271 | yellow | PIK3C2B,PIK3CA,PLCG1,MAP2K3,GNG3,PRKD3 |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 2.64 | 0.0435 | yellow | FYN,HCK,PLCG1,PRKD3 |
| FGF Signaling | 2.64 | 0.0435 | yellow | PIK3C2B,PIK3CA,PLCG1,MAP2K3 |
| IL-17 Signaling | 2.62 | 0.043 | yellow | PIK3C2B,PIK3CA,TRAF3IP2,MAP2K3 |
| Reelin Signaling in Neurons | 2.6 | 0.0426 | yellow | PIK3C2B,FYN,PIK3CA,HCK |
| VEGF Family Ligand-Receptor Interactions | 2.6 | 0.0426 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Superpathway of Inositol Phosphate Compounds | 2.59 | 0.0263 | yellow | PIK3C2B,FYN,DUSP5,PIK3CA,PLCG1,PPP1R14A |
| LPS-stimulated MAPK Signaling | 2.59 | 0.0421 | yellow | PIK3C2B,PIK3CA,MAP2K3,PRKD3 |
| Acute Myeloid Leukemia Signaling | 2.55 | 0.0412 | yellow | PIK3C2B,PIK3CA,MAP2K3,LEF1 |
| Gαq Signaling | 2.55 | 0.0312 | yellow | PIK3C2B,PIK3CA,PLCG1,GNG3,PRKD3 |
| Glioblastoma Multiforme Signaling | 2.46 | 0.0298 | yellow | PIK3C2B,PIK3CA,CDK6,PLCG1,LEF1 |
| T Cell Exhaustion Signaling Pathway | 2.44 | 0.0294 | yellow | PIK3C2B,PIK3CA,SMAD3,BMPR2,PLCG1 |
| Huntington's Disease Signaling | 2.42 | 0.0243 | yellow | PIK3C2B,PIK3CA,GNG3,HIP1,CAPN7,PRKD3 |
| Dendritic Cell Maturation | 2.35 | 0.0281 | yellow | PIK3C2B,PIK3CA,IL15,PLCG1,CD58 |
| Mouse Embryonic Stem Cell Pluripotency | 2.34 | 0.036 | yellow | PIK3C2B,PIK3CA,BMPR2,LEF1 |
| Chronic Myeloid Leukemia Signaling | 2.33 | 0.0357 | yellow | PIK3C2B,PIK3CA,SMAD3,CDK6 |
| Role of NFAT in Regulation of the Immune Response | 2.32 | 0.0276 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1,GNG3 |
| p53 Signaling | 2.32 | 0.0354 | yellow | PIK3C2B,PIK3CA,GADD45B,TNFRSF10A |
| IGF-1 Signaling | 2.32 | 0.0354 | yellow | PIK3C2B,PIK3CA,YWHAH,SOCS5 |
| T Cell Receptor Signaling | 2.3 | 0.0351 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1 |
| Apelin Cardiomyocyte Signaling Pathway | 2.3 | 0.0351 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 2.28 | 0.0345 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 2.23 | 0.0263 | yellow | PIK3C2B,PIK3CA,SMAD3,MAP2K3,LEF1 |
| HGF Signaling | 2.22 | 0.0333 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Phagosome Formation | 2.21 | 0.0331 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Ephrin A Signaling | 2.21 | 0.0484 | yellow | PIK3C2B,FYN,PIK3CA |
| 3-phosphoinositide Biosynthesis | 2.2 | 0.0258 | yellow | PIK3C2B,FYN,DUSP5,PIK3CA,PPP1R14A |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 2.19 | 0.0256 | yellow | PIK3C2B,PIK3CA,PLCG1,PPP1R14A,PRKD3 |
| CD28 Signaling in T Helper Cells | 2.17 | 0.0323 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1 |
| Apelin Endothelial Signaling Pathway | 2.17 | 0.0323 | yellow | PIK3C2B,PIK3CA,SMAD3,PRKD3 |
| fMLP Signaling in Neutrophils | 2.13 | 0.0312 | yellow | PIK3C2B,PIK3CA,GNG3,PRKD3 |
| Role of Tissue Factor in Cancer | 2.13 | 0.0312 | yellow | PIK3C2B,FYN,PIK3CA,HCK |
| Renin-Angiotensin Signaling | 2.11 | 0.031 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Axonal Guidance Signaling | 2.1 | 0.0168 | yellow | PIK3C2B,FYN,PIK3CA,ADAM28,ARHGEF7,PLCG1,GNG3,PRKD3 |
| Leukocyte Extravasation Signaling | 2.09 | 0.0243 | yellow | PIK3C2B,PIK3CA,CTNNA1,PLCG1,PRKD3 |
| Melatonin Signaling | 2.06 | 0.0429 | yellow | PLCG1,MAP2K3,PRKD3 |
| Role of IL-17A in Arthritis | 2.06 | 0.0429 | yellow | PIK3C2B,PIK3CA,MAP2K3 |
| EGF Signaling | 2.06 | 0.0429 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| Th2 Pathway | 2 | 0.0288 | yellow | PIK3C2B,PIK3CA,BHLHE41,BMPR2 |
| CREB Signaling in Neurons | 2 | 0.023 | yellow | PIK3C2B,PIK3CA,PLCG1,GNG3,PRKD3 |
| Role of JAK1 and JAK3 in γc Cytokine Signaling | 1.97 | 0.0395 | yellow | PIK3C2B,PIK3CA,IL15 |
| Insulin Receptor Signaling | 1.96 | 0.028 | yellow | PIK3C2B,FYN,PIK3CA,PPP1R14A |
| Myc Mediated Apoptosis Signaling | 1.95 | 0.039 | yellow | PIK3C2B,PIK3CA,YWHAH |
| CD40 Signaling | 1.9 | 0.0375 | yellow | PIK3C2B,PIK3CA,MAP2K3 |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 1.9 | 0.0218 | yellow | PIK3C2B,PIK3CA,BMPR2,MAP2K3,LEF1 |
| IL-17A Signaling in Airway Cells | 1.9 | 0.0375 | yellow | PIK3C2B,PIK3CA,TRAF3IP2 |
| GM-CSF Signaling | 1.9 | 0.0375 | yellow | PIK3C2B,PIK3CA,HCK |
| Type II Diabetes Mellitus Signaling | 1.88 | 0.0265 | yellow | PIK3C2B,PIK3CA,SOCS5,PRKD3 |
| Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes | 1.86 | 0.0361 | yellow | FYN,SMAD3,PLCG1 |
| G Protein Signaling Mediated by Tubby | 1.85 | 0.0667 | yellow | PLCG1,GNG3 |
| Antiproliferative Role of Somatostatin Receptor 2 | 1.85 | 0.0357 | yellow | PIK3C2B,PIK3CA,GNG3 |
| GDNF Family Ligand-Receptor Interactions | 1.85 | 0.0357 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| HIPPO signaling | 1.85 | 0.0357 | yellow | YWHAH,SMAD3,PPP1R14A |
| Cardiac Hypertrophy Signaling | 1.84 | 0.0211 | yellow | PIK3C2B,PIK3CA,PLCG1,MAP2K3,GNG3 |
| Endocannabinoid Cancer Inhibition Pathway | 1.83 | 0.0256 | yellow | PIK3C2B,PIK3CA,MAP2K3,LEF1 |
| Opioid Signaling Pathway | 1.83 | 0.0209 | yellow | FYN,HCK,MAP2K3,AP1B1,PRKD3 |
| PKCθ Signaling in T Lymphocytes | 1.82 | 0.0255 | yellow | PIK3C2B,FYN,PIK3CA,PLCG1 |
| Leptin Signaling in Obesity | 1.81 | 0.0345 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| CCR5 Signaling in Macrophages | 1.79 | 0.0341 | yellow | PLCG1,GNG3,PRKD3 |
| IL-7 Signaling Pathway | 1.79 | 0.0341 | yellow | PIK3C2B,FYN,PIK3CA |
| Factors Promoting Cardiogenesis in Vertebrates | 1.78 | 0.0337 | yellow | BMPR2,LEF1,PRKD3 |
| α-Adrenergic Signaling | 1.77 | 0.0333 | yellow | PLCG1,GNG3,PRKD3 |
| IL-3 Signaling | 1.77 | 0.0333 | yellow | PIK3C2B,PIK3CA,PRKD3 |
| Colorectal Cancer Metastasis Signaling | 1.76 | 0.0201 | yellow | PIK3C2B,PIK3CA,SMAD3,LEF1,GNG3 |
| JAK/Stat Signaling | 1.75 | 0.033 | yellow | PIK3C2B,PIK3CA,SOCS5 |
| eNOS Signaling | 1.74 | 0.0241 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| TGF-β Signaling | 1.73 | 0.0323 | yellow | SMAD3,BMPR2,MAP2K3 |
| Aldosterone Signaling in Epithelial Cells | 1.72 | 0.0237 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| NF-κB Activation by Viruses | 1.71 | 0.0316 | yellow | PIK3C2B,PIK3CA,PRKD3 |
| CXCR4 Signaling | 1.7 | 0.0234 | yellow | PIK3C2B,PIK3CA,GNG3,PRKD3 |
| Th1 and Th2 Activation Pathway | 1.7 | 0.0234 | yellow | PIK3C2B,PIK3CA,BHLHE41,BMPR2 |
| PPARα/RXRα Activation | 1.68 | 0.023 | yellow | SMAD3,PLCG1,BMPR2,MAP2K3 |
| Germ Cell-Sertoli Cell Junction Signaling | 1.68 | 0.023 | yellow | PIK3C2B,PIK3CA,CTNNA1,MAP2K3 |
| PDGF Signaling | 1.67 | 0.0306 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| Prostate Cancer Signaling | 1.64 | 0.0297 | yellow | PIK3C2B,PIK3CA,LEF1 |
| Melanocyte Development and Pigmentation Signaling | 1.59 | 0.0286 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| RAR Activation | 1.58 | 0.0214 | yellow | PIK3CA,SMAD3,PRKD3,SMARCA4 |
| PAK Signaling | 1.56 | 0.0278 | yellow | PIK3C2B,PIK3CA,ARHGEF7 |
| VEGF Signaling | 1.56 | 0.0278 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells | 1.56 | 0.0278 | yellow | PLCG1,GNG3,PRKD3 |
| Endothelin-1 Signaling | 1.54 | 0.0208 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Role of p14/p19ARF in Tumor Suppression | 1.54 | 0.0455 | yellow | PIK3C2B,PIK3CA |
| Nitric Oxide Signaling in the Cardiovascular System | 1.54 | 0.0273 | yellow | PIK3C2B,PIK3CA,PRKD3 |
| UVA-Induced MAPK Signaling | 1.53 | 0.027 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| FAT10 Cancer Signaling Pathway | 1.52 | 0.0444 | yellow | SMAD3,BMPR2 |
| Amyotrophic Lateral Sclerosis Signaling | 1.52 | 0.0268 | yellow | PIK3C2B,PIK3CA,CAPN7 |
| NRF2-mediated Oxidative Stress Response | 1.51 | 0.0203 | yellow | PIK3C2B,PIK3CA,MAP2K3,PRKD3 |
| nNOS Signaling in Neurons | 1.5 | 0.0435 | yellow | CAPN7,PRKD3 |
| iCOS-iCOSL Signaling in T Helper Cells | 1.49 | 0.0261 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| IL-9 Signaling | 1.49 | 0.0426 | yellow | PIK3C2B,PIK3CA |
| Gap Junction Signaling | 1.49 | 0.02 | yellow | PIK3C2B,PIK3CA,PLCG1,PRKD3 |
| Osteoarthritis Pathway | 1.49 | 0.02 | yellow | SMAD3,CTNNA1,BMPR2,LEF1 |
| mTOR Signaling | 1.48 | 0.0199 | yellow | PIK3C2B,PIK3CA,PRR5L,PRKD3 |
| Adrenomedullin signaling pathway | 1.47 | 0.0198 | yellow | PIK3C2B,PIK3CA,PLCG1,MAP2K3 |
| IL-8 Signaling | 1.46 | 0.0197 | yellow | PIK3C2B,PIK3CA,GNG3,PRKD3 |
| Paxillin Signaling | 1.46 | 0.0254 | yellow | PIK3C2B,PIK3CA,ARHGEF7 |
| G Beta Gamma Signaling | 1.45 | 0.0252 | yellow | PLCG1,GNG3,PRKD3 |
| Pancreatic Adenocarcinoma Signaling | 1.43 | 0.0246 | yellow | PIK3C2B,PIK3CA,SMAD3 |
| Synaptic Long Term Potentiation | 1.42 | 0.0244 | yellow | PLCG1,PPP1R14A,PRKD3 |
| Sphingosine-1-phosphate Signaling | 1.42 | 0.0244 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| NGF Signaling | 1.42 | 0.0244 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| PTEN Signaling | 1.42 | 0.0244 | yellow | PIK3CA,YWHAH,BMPR2 |
| HIF1α Signaling | 1.41 | 0.0242 | yellow | SLC2A5,PIK3C2B,PIK3CA |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 1.38 | 0.0236 | yellow | PIK3C2B,PIK3CA,BMPR2 |
| Docosahexaenoic Acid (DHA) Signaling | 1.38 | 0.037 | yellow | PIK3C2B,PIK3CA |
| Endocannabinoid Developing Neuron Pathway | 1.38 | 0.0234 | yellow | PIK3C2B,PIK3CA,MAP2K3 |
| AMPK Signaling | 1.37 | 0.0183 | yellow | PIK3C2B,PIK3CA,MAP2K3,SMARCA4 |
| Calcium-induced T Lymphocyte Apoptosis | 1.36 | 0.0364 | yellow | PLCG1,PRKD3 |
| PI3K Signaling in B Lymphocytes | 1.35 | 0.0229 | yellow | FYN,PIK3CA,PLCG1 |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 1.34 | 0.0227 | yellow | PIK3C2B,PIK3CA,PRKD3 |
| Actin Cytoskeleton Signaling | 1.33 | 0.0179 | yellow | PIK3C2B,PIK3CA,MPRIP,ARHGEF7 |
| Apelin Pancreas Signaling Pathway | 1.32 | 0.0345 | yellow | PIK3C2B,PIK3CA |
| Androgen Signaling | 1.32 | 0.0222 | yellow | SMAD3,GNG3,PRKD3 |
| IL-6 Signaling | 1.31 | 0.0221 | yellow | PIK3C2B,PIK3CA,MAP2K3 |
| Regulation of Cellular Mechanics by Calpain Protease | 1.29 | 0.0333 | yellow | CDK6,CAPN7 |
| HMGB1 Signaling | 1.29 | 0.0216 | yellow | PIK3C2B,PIK3CA,MAP2K3 |
| Cardiac β-adrenergic Signaling | 1.29 | 0.0216 | yellow | AKAP2,PPP1R14A,GNG3 |
| Gα12/13 Signaling | 1.27 | 0.0213 | yellow | PIK3C2B,PIK3CA,TBXA2R |
| Glucocorticoid Receptor Signaling | 1.27 | 0.0148 | yellow | PIK3C2B,PIK3CA,YWHAH,SMAD3,SMARCA4 |
| Melanoma Signaling | 1.26 | 0.0317 | yellow | PIK3C2B,PIK3CA |
| Epithelial Adherens Junction Signaling | 1.25 | 0.0208 | yellow | CTNNA1,BMPR2,LEF1 |
| Pyridoxal 5'-phosphate Salvage Pathway | 1.25 | 0.0312 | yellow | CDK6,MAP2K3 |
| IL-12 Signaling and Production in Macrophages | 1.24 | 0.0205 | yellow | PIK3C2B,PIK3CA,PRKD3 |
| Cell Cycle: G1/S Checkpoint Regulation | 1.22 | 0.0303 | yellow | SMAD3,CDK6 |
| Ovarian Cancer Signaling | 1.21 | 0.0201 | yellow | PIK3C2B,PIK3CA,LEF1 |
| CNTF Signaling | 1.21 | 0.0299 | yellow | PIK3C2B,PIK3CA |
| Signaling by Rho Family GTPases | 1.2 | 0.0161 | yellow | PIK3C2B,PIK3CA,ARHGEF7,GNG3 |
| Lymphotoxin β Receptor Signaling | 1.19 | 0.029 | yellow | PIK3C2B,PIK3CA |
| D-myo-inositol-5-phosphate Metabolism | 1.18 | 0.0195 | yellow | DUSP5,PLCG1,PPP1R14A |
| Hematopoiesis from Multipotent Stem Cells | 1.16 | 0.0833 | yellow | IL15 |
| Guanosine Nucleotides Degradation III | 1.16 | 0.0833 | yellow | NT5E |
| Pregnenolone Biosynthesis | 1.16 | 0.0833 | yellow | MICAL3 |
| IL-2 Signaling | 1.16 | 0.0278 | yellow | PIK3C2B,PIK3CA |
| SPINK1 General Cancer Pathway | 1.16 | 0.0278 | yellow | PIK3C2B,PIK3CA |
| Regulation of eIF4 and p70S6K Signaling | 1.15 | 0.019 | yellow | PIK3C2B,PIK3CA,AGO2 |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 1.15 | 0.0189 | yellow | PLCG1,PPP1R14A,PRKD3 |
| Relaxin Signaling | 1.14 | 0.0188 | yellow | PIK3C2B,PIK3CA,GNG3 |
| MSP-RON Signaling Pathway | 1.13 | 0.027 | yellow | PIK3C2B,PIK3CA |
| Chemokine Signaling | 1.13 | 0.027 | yellow | MPRIP,PLCG1 |
| Urate Biosynthesis/Inosine 5'-phosphate Degradation | 1.12 | 0.0769 | yellow | NT5E |
| ErbB2-ErbB3 Signaling | 1.11 | 0.0263 | yellow | PIK3C2B,PIK3CA |
| Role of PI3K/AKT Signaling in the Pathogenesis of Influenza | 1.11 | 0.026 | yellow | PIK3C2B,PIK3CA |
| Wnt/β-catenin Signaling | 1.1 | 0.018 | yellow | SOX4,BMPR2,LEF1 |
| Glioma Invasiveness Signaling | 1.1 | 0.0256 | yellow | PIK3C2B,PIK3CA |
| Xenobiotic Metabolism Signaling | 1.08 | 0.0146 | yellow | PIK3C2B,PIK3CA,MAP2K3,PRKD3 |
| Acute Phase Response Signaling | 1.06 | 0.0173 | yellow | PIK3CA,MAP2K3,SOCS5 |
| Adenosine Nucleotides Degradation II | 1.06 | 0.0667 | yellow | NT5E |
| Histidine Degradation VI | 1.06 | 0.0667 | yellow | MICAL3 |
| G-Protein Coupled Receptor Signaling | 1.06 | 0.0144 | yellow | PIK3C2B,FYN,PIK3CA,TBXA2R |
| Estrogen-Dependent Breast Cancer Signaling | 1.04 | 0.0238 | yellow | PIK3C2B,PIK3CA |
| Angiopoietin Signaling | 1.03 | 0.0235 | yellow | PIK3C2B,PIK3CA |
| NF-κB Signaling | 1.02 | 0.0167 | yellow | PIK3C2B,PIK3CA,BMPR2 |
| FcγRIIB Signaling in B Lymphocytes | 1.02 | 0.023 | yellow | PIK3C2B,PIK3CA |
| Renal Cell Carcinoma Signaling | 1.02 | 0.023 | yellow | PIK3C2B,PIK3CA |
| Ubiquinol-10 Biosynthesis (Eukaryotic) | 1.01 | 0.0588 | yellow | MICAL3 |
| FLT3 Signaling in Hematopoietic Progenitor Cells | 1.01 | 0.0227 | yellow | PIK3C2B,PIK3CA |
| Purine Nucleotides Degradation II (Aerobic) | 0.987 | 0.0556 | yellow | NT5E |
| B Cell Receptor Signaling | 0.987 | 0.016 | yellow | PIK3C2B,PIK3CA,MAP2K3 |
| Neuregulin Signaling | 0.983 | 0.022 | yellow | PLCG1,PRKD3 |
| IL-1 Signaling | 0.983 | 0.022 | yellow | MAP2K3,GNG3 |
| Neuroinflammation Signaling Pathway | 0.979 | 0.0134 | yellow | PIK3C2B,PIK3CA,BMPR2,PLCG1 |
| IL-4 Signaling | 0.975 | 0.0217 | yellow | PIK3C2B,PIK3CA |
| Cardiomyocyte Differentiation via BMP Receptors | 0.967 | 0.0526 | yellow | BMPR2 |
| GADD45 Signaling | 0.967 | 0.0526 | yellow | GADD45B |
| Salvage Pathways of Pyrimidine Ribonucleotides | 0.959 | 0.0213 | yellow | CDK6,MAP2K3 |
| ILK Signaling | 0.955 | 0.0155 | yellow | PIK3C2B,PIK3CA,LEF1 |
| PEDF Signaling | 0.951 | 0.0211 | yellow | PIK3C2B,PIK3CA |
| Apoptosis Signaling | 0.951 | 0.0211 | yellow | PLCG1,CAPN7 |
| Lipid Antigen Presentation by CD1 | 0.943 | 0.05 | yellow | AP1B1 |
| Systemic Lupus Erythematosus Signaling | 0.932 | 0.0152 | yellow | PIK3C2B,PIK3CA,PLCG1 |
| NAD Salvage Pathway II | 0.924 | 0.0476 | yellow | NT5E |
| Ceramide Signaling | 0.914 | 0.02 | yellow | PIK3C2B,PIK3CA |
| TR/RXR Activation | 0.914 | 0.02 | yellow | PIK3C2B,PIK3CA |
| Type I Diabetes Mellitus Signaling | 0.9 | 0.0196 | yellow | MAP2K3,SOCS5 |
| RANK Signaling in Osteoclasts | 0.9 | 0.0196 | yellow | PIK3C2B,PIK3CA |
| Antioxidant Action of Vitamin C | 0.9 | 0.0196 | yellow | SLC2A5,PLCG1 |
| Gαs Signaling | 0.886 | 0.0192 | yellow | HCK,GNG3 |
| Cholecystokinin/Gastrin-mediated Signaling | 0.879 | 0.019 | yellow | MAP2K3,PRKD3 |
| SAPK/JNK Signaling | 0.866 | 0.0187 | yellow | PIK3C2B,PIK3CA |
| EIF2 Signaling | 0.854 | 0.014 | yellow | PIK3C2B,PIK3CA,AGO2 |
| CDP-diacylglycerol Biosynthesis I | 0.854 | 0.04 | yellow | AGPAT5 |
| Antiproliferative Role of TOB in T Cell Signaling | 0.839 | 0.0385 | yellow | SMAD3 |
| p38 MAPK Signaling | 0.83 | 0.0177 | yellow | H3F3A/H3F3B,MAP2K3 |
| D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis | 0.821 | 0.037 | yellow | PLCG1 |
| Phosphatidylglycerol Biosynthesis II (Non-plastidic) | 0.821 | 0.037 | yellow | AGPAT5 |
| Telomerase Signaling | 0.81 | 0.0172 | yellow | PIK3C2B,PIK3CA |
| Sperm Motility | 0.81 | 0.0172 | yellow | PLCG1,PRKD3 |
| IL-15 Production | 0.807 | 0.0357 | yellow | IL15 |
| Thyroid Hormone Metabolism II (via Conjugation and/or Degradation) | 0.793 | 0.0345 | yellow | LARGE1 |
| Gαi Signaling | 0.793 | 0.0168 | yellow | TBXA2R,GNG3 |
| DNA Methylation and Transcriptional Repression Signaling | 0.78 | 0.0333 | yellow | H3F3A/H3F3B |
| Th1 Pathway | 0.777 | 0.0164 | yellow | PIK3C2B,PIK3CA |
| Rac Signaling | 0.772 | 0.0163 | yellow | PIK3C2B,PIK3CA |
| Cellular Effects of Sildenafil (Viagra) | 0.754 | 0.0159 | yellow | MPRIP,PLCG1 |
| Inhibition of Angiogenesis by TSP1 | 0.754 | 0.0312 | yellow | FYN |
| Role of JAK2 in Hormone-like Cytokine Signaling | 0.754 | 0.0312 | yellow | SOCS5 |
| PI3K/AKT Signaling | 0.75 | 0.0157 | yellow | PIK3CA,YWHAH |
| Adipogenesis pathway | 0.745 | 0.0156 | yellow | SMAD3,BMPR2 |
| Circadian Rhythm Signaling | 0.742 | 0.0303 | yellow | BHLHE41 |
| Iron homeostasis signaling pathway | 0.728 | 0.0153 | yellow | SMAD3,BMPR2 |
| STAT3 Pathway | 0.724 | 0.0152 | yellow | BMPR2,SOCS5 |
| IL-17A Signaling in Fibroblasts | 0.719 | 0.0286 | yellow | TRAF3IP2 |
| Estrogen Receptor Signaling | 0.719 | 0.015 | yellow | H3F3A/H3F3B,SMARCA4 |
| Aryl Hydrocarbon Receptor Signaling | 0.71 | 0.0148 | yellow | CDK6,SMARCA4 |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0.706 | 0.0147 | yellow | DUSP5,PPP1R14A |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0.706 | 0.0147 | yellow | DUSP5,PPP1R14A |
| Corticotropin Releasing Hormone Signaling | 0.699 | 0.0146 | yellow | PLCG1,PRKD3 |
| Notch Signaling | 0.699 | 0.027 | yellow | MAML3 |
| nNOS Signaling in Skeletal Muscle Cells | 0.668 | 0.025 | yellow | SNTB1 |
| Role of PKR in Interferon Induction and Antiviral Response | 0.66 | 0.0244 | yellow | MAP2K3 |
| Mechanisms of Viral Exit from Host Cells | 0.66 | 0.0244 | yellow | PRKD3 |
| Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza | 0.66 | 0.0244 | yellow | IL15 |
| Role of IL-17F in Allergic Inflammatory Airway Diseases | 0.66 | 0.0244 | yellow | TRAF3IP2 |
| 3-phosphoinositide Degradation | 0.642 | 0.0133 | yellow | DUSP5,PPP1R14A |
| Nicotine Degradation III | 0.64 | 0.0233 | yellow | LARGE1 |
| Triacylglycerol Biosynthesis | 0.64 | 0.0233 | yellow | AGPAT5 |
| Thyroid Cancer Signaling | 0.623 | 0.0222 | yellow | LEF1 |
| Cancer Drug Resistance By Drug Efflux | 0.614 | 0.0217 | yellow | PIK3CA |
| UVC-Induced MAPK Signaling | 0.599 | 0.0208 | yellow | PRKD3 |
| Nicotine Degradation II | 0.592 | 0.0204 | yellow | LARGE1 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 0.592 | 0.0204 | yellow | YWHAH |
| Transcriptional Regulatory Network in Embryonic Stem Cells | 0.583 | 0.02 | yellow | H3F3A/H3F3B |
| Melatonin Degradation I | 0.583 | 0.02 | yellow | LARGE1 |
| Amyloid Processing | 0.583 | 0.02 | yellow | CAPN7 |
| GNRH Signaling | 0.575 | 0.012 | yellow | MAP2K3,PRKD3 |
| CD27 Signaling in Lymphocytes | 0.569 | 0.0192 | yellow | MAP2K3 |
| Role of Cytokines in Mediating Communication between Immune Cells | 0.569 | 0.0192 | yellow | IL15 |
| Semaphorin Signaling in Neurons | 0.569 | 0.0192 | yellow | FYN |
| RhoGDI Signaling | 0.55 | 0.0115 | yellow | ARHGEF7,GNG3 |
| Sertoli Cell-Sertoli Cell Junction Signaling | 0.55 | 0.0115 | yellow | CTNNA1,MAP2K3 |
| Serotonin Degradation | 0.548 | 0.0182 | yellow | LARGE1 |
| Superpathway of Melatonin Degradation | 0.548 | 0.0182 | yellow | LARGE1 |
| SPINK1 Pancreatic Cancer Pathway | 0.548 | 0.0182 | yellow | SMAD3 |
| Ephrin Receptor Signaling | 0.547 | 0.0114 | yellow | FYN,GNG3 |
| Cell Cycle Control of Chromosomal Replication | 0.542 | 0.0179 | yellow | CDK6 |
| Synaptic Long Term Depression | 0.541 | 0.0113 | yellow | PLCG1,PRKD3 |
| Phospholipases | 0.535 | 0.0175 | yellow | PLCG1 |
| Retinoic acid Mediated Apoptosis Signaling | 0.523 | 0.0169 | yellow | TNFRSF10A |
| Wnt/Ca+ pathway | 0.51 | 0.0164 | yellow | PLCG1 |
| Eicosanoid Signaling | 0.499 | 0.0159 | yellow | TBXA2R |
| Remodeling of Epithelial Adherens Junctions | 0.493 | 0.0156 | yellow | CTNNA1 |
| ERK5 Signaling | 0.478 | 0.0149 | yellow | YWHAH |
| Basal Cell Carcinoma Signaling | 0.472 | 0.0147 | yellow | LEF1 |
| IL-10 Signaling | 0.467 | 0.0145 | yellow | MAP2K3 |
| TREM1 Signaling | 0.462 | 0.0143 | yellow | PLCG1 |
| Caveolar-mediated Endocytosis Signaling | 0.457 | 0.0141 | yellow | FYN |
| Role of Wnt/GSK-3β Signaling in the Pathogenesis of Influenza | 0.452 | 0.0139 | yellow | LEF1 |
| Ephrin B Signaling | 0.452 | 0.0139 | yellow | GNG3 |
| GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell | 0.452 | 0.0139 | yellow | PLCG1 |
| Agrin Interactions at Neuromuscular Junction | 0.447 | 0.0137 | yellow | ARHGEF7 |
| Role of MAPK Signaling in the Pathogenesis of Influenza | 0.442 | 0.0135 | yellow | MAP2K3 |
| Toll-like Receptor Signaling | 0.442 | 0.0135 | yellow | MAP2K3 |
| Dopamine Receptor Signaling | 0.433 | 0.0132 | yellow | PPP1R14A |
| VDR/RXR Activation | 0.429 | 0.013 | yellow | PRKD3 |
| Communication between Innate and Adaptive Immune Cells | 0.425 | 0.0128 | yellow | IL15 |
| Altered T Cell and B Cell Signaling in Rheumatoid Arthritis | 0.425 | 0.0128 | yellow | IL15 |
| cAMP-mediated signaling | 0.417 | 0.00909 | yellow | AKAP2,TBXA2R |
| Role of BRCA1 in DNA Damage Response | 0.416 | 0.0125 | yellow | SMARCA4 |
| Cyclins and Cell Cycle Regulation | 0.416 | 0.0125 | yellow | CDK6 |
| BMP signaling pathway | 0.416 | 0.0125 | yellow | BMPR2 |
| Regulation of Actin-based Motility by Rho | 0.4 | 0.0119 | yellow | MPRIP |
| Crosstalk between Dendritic Cells and Natural Killer Cells | 0.396 | 0.0118 | yellow | IL15 |
| Death Receptor Signaling | 0.37 | 0.0109 | yellow | TNFRSF10A |
| GABA Receptor Signaling | 0.367 | 0.0108 | yellow | AP1B1 |
| ATM Signaling | 0.356 | 0.0104 | yellow | GADD45B |
| NER Pathway | 0.35 | 0.0102 | yellow | H3F3A/H3F3B |
| CDK5 Signaling | 0.331 | 0.00962 | yellow | PPP1R14A |
| Sirtuin Signaling Pathway | 0.309 | 0.00733 | yellow | H3F3A/H3F3B,GADD45B |
| RhoA Signaling | 0.292 | 0.00847 | yellow | MPRIP |
| Cdc42 Signaling | 0.284 | 0.00826 | yellow | MPRIP |
| Hepatic Cholestasis | 0.21 | 0.00633 | yellow | PRKD3 |
| Tight Junction Signaling | 0.199 | 0.00606 | yellow | CTNNA1 |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation | 0 | 0.00549 | yellow | SMAD3 |
| Oxidative Phosphorylation | 14.6 | 0.439 | turquoise | COX7B,SDHB,NDUFA9,ATP5PD,NDUFA7,ATP5F1D,UQCRH,COX6C,COX5B,COX8A,ATP5MG,NDUFB8,NDUFA1,NDUFA2,NDUFB3,ATP5F1E,NDUFB10,NDUFS6,NDUFAB1,ATP5ME,ATP5MC3,NDUFS4,SDHA,ATP5PF,ATP5MC2,COX17,COX6B1,NDUFB4,ATP5F1A,NDUFA13,UQCRB,NDUFS5,ATP5F1C,NDUFB11,ATP5F1B,NDUFA11,NDUFA6,NDUFB7,COX5A,COX7A2,UQCRC1,UQCRQ,NDUFB2 |
| Mitochondrial Dysfunction | 11.3 | 0.327 | turquoise | FURIN,NDUFA9,ATP5F1D,COX8A,ATP5MG,NDUFB8,NDUFA1,NDUFB3,NDUFB10,NDUFS6,ATP5MC3,ATP5PF,ATP5MC2,ATP5F1A,NDUFS5,ATP5F1C,PRDX3,NDUFB11,ATP5F1B,NDUFA6,TXN2,NDUFB7,BACE2,VDAC1,NDUFB2,HSD17B10,COX7B,SDHB,ATP5PD,NDUFA7,UQCRH,PRDX5,COX6C,COX5B,ATP5F1E,NDUFA2,NDUFAB1,ATP5ME,NDUFS4,SDHA,NDUFB4,COX17,COX6B1,GLRX2,VDAC3,NDUFA13,UQCRB,NDUFA11,COX7A2,COX5A,UQCRC1,UQCRQ |
| B Cell Development | 7.2 | 0.556 | turquoise | HLA-DOA,CD19,SPN,IGH,HLA-B,IL7,IL7R,CD80,HLA-DMA,IGLC1,HLA-DMB,IGHM,HLA-DOB,CD86,IGHD |
| Phagosome Formation | 6.36 | 0.289 | turquoise | FCAR,PIK3CA,PIK3R5,FCGR2B,RHOH,IGHG3,PIK3C3,RHOU,PRKCE,PLCB1,IRS2,RHOF,FRS2,FCGR3A/FCGR3B,FCGR1B,FCER2,CR2,ITGB1,C5AR1,FCGR2A,PLCL2,TLR2,MARCKS,TLR4,CR1,CLEC7A,ITGAM,PRKCI,GAB1,PRKCD,PIK3R6,FCER1G,FNBP1,PRKCB,ITGAX |
| Germ Cell-Sertoli Cell Junction Signaling | 5.59 | 0.247 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,MAPK1,PIK3R5,AFDN,LIMK2,MAP3K5,TUBB,RHOH,LIMK1,TGFBR2,PTK2,KEAP1,PIK3C3,RHOU,TGFB2,IRS2,TUBA1C,VCL,RHOF,FRS2,ACTN1,ITGB1,MAP3K14,MAP3K9,TUBB3,PXN,CFL1,TUBB4B,TUBG1,TUBA4A,RRAS2,GAB1,PIK3R6,ZYX,ACTN4,ACTG1,TNF,FNBP1,CTNND1 |
| Role of NFAT in Regulation of the Immune Response | 5.5 | 0.243 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,HLA-DOA,CAMK4,MAPK1,NFATC3,CD4,SOS2,HLA-B,PIK3R5,CSNK1A1,FCGR2B,HLA-DMA,PIK3C3,HLA-DMB,PLCB1,IRS2,GNG5,FRS2,FCGR3A/FCGR3B,FCGR1B,GNAS,FCGR2A,CSNK1G3,TRGV9,CHP1,GNAQ,ITPR1,NFATC4,CALM1 (includes others),GNAI3,RRAS2,GAB1,CD80,LAT,PIK3R6,FCER1G,LYN,CD86,HLA-DOB,MEF2C,LCP2 |
| Integrin Signaling | 5.32 | 0.23 | turquoise | RAP2B,MPRIP,MAPK1,ARF1,SOS2,PTK2,NCK2,ARF4,ITGAV,CAV1,IRS2,FRS2,CAPN5,TTN,ITGAM,GAB1,ARPC2,PIK3R6,ZYX,CAPN2,ACTN4,ACTG1,FNBP1,CAPN3,RAP1B,RAP2A,PIK3CA,ARPC1B,ARHGEF7,PIK3R5,RHOH,ITGB7,BRAF,ACTR3,PIK3C3,RHOU,VCL,RHOF,ACTN1,MYL12A,ITGB1,PXN,ARPC5L,ITGAL,RRAS2,CAPNS1,LIMS1,ARPC4,ITGAX |
| IL-4 Signaling | 5.19 | 0.293 | turquoise | RAP1B,RAP2B,RAP2A,IL4R,PIK3CA,HLA-DOA,IRF4,IL13RA1,NFATC3,IGH,HLA-B,SOS2,PIK3R5,NFATC4,HMGA1,OCRL,NR3C1,RRAS2,GAB1,HLA-DMA,PIK3C3,HLA-DMB,PIK3R6,HLA-DOB,IRS2,FRS2,FCER2 |
| T Cell Exhaustion Signaling Pathway | 5.08 | 0.241 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,HLA-DOA,MAPK1,GZMB,NFATC3,SMAD3,TGFBR3,HAVCR2,HLA-B,PIK3R5,TBX21,TGFBR2,VEGFA,HLA-DMA,PIK3C3,HLA-DMB,PRDM1,IRS2,FRS2,BTLA,IRF4,TRGV9,IL6R,MGAT5,ACVR1,NFATC4,IFNAR2,STAT4,RRAS2,GAB1,CD80,FOXO1,PIK3R6,FCER1G,CD86,HLA-DOB,TCF7,FOXP1 |
| Remodeling of Epithelial Adherens Junctions | 4.99 | 0.328 | turquoise | TUBA1B,TUBB3,ARPC1B,TUBB4B,ARPC5L,TUBG1,TUBA4A,TUBB,CLIP1,MAPRE2,ACTR3,ARPC2,ZYX,TUBA1C,VCL,ACTN4,ACTG1,ACTN1,DNM2,ARPC4,CTNND1 |
| Glioma Signaling | 4.97 | 0.264 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,PA2G4,CAMK1D,MAPK1,IDH3G,SOS2,CDK4,PIK3R5,CDKN2C,CAMK2D,PIK3C3,PRKCE,IRS2,FRS2,E2F2,RBL2,TFDP1,MDM2,CALM1 (includes others),RRAS2,PRKCI,GAB1,PRKCD,E2F7,PIK3R6,IDH2,PDGFD,PRKCB |
| Unfolded protein response | 4.94 | 0.345 | turquoise | P4HB,ERN1,HSPA9,XBP1,CEBPD,CANX,DNAJC3,CEBPB,MAP3K5,HSPA5,MBTPS2,SEL1L,HSPA8,HSP90B1,PDIA6,EDEM1,VCP,ERO1B,CEBPA |
| Phospholipase C Signaling | 4.92 | 0.221 | turquoise | RAP2B,MPRIP,MYL6,MAPK1,NFATC3,SOS2,PLCB1,PLD3,TRGV9,CREB3,CREBBP,ITPR1,CREB5,PLA2G6,MARCKS,PRKCD,LAT,ARHGEF18,ARHGEF10,FNBP1,LCP2,RAP1B,PEBP1,RAP2A,CAMK4,ARHGEF7,FCGR2B,RHOH,HMOX1,IGHG3,AHNAK,RHOU,PRKCE,RHOF,GNG5,MYL12A,ITGB1,HDAC9,GNAS,FCGR2A,CHP1,GNAQ,NFATC4,CALM1 (includes others),PRKCI,RRAS2,FCER1G,LYN,MEF2C,PRKCB |
| B Cell Receptor Signaling | 4.74 | 0.23 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MAPK1,NFATC3,SOS2,PIK3R5,MAP3K5,FCGR2B,OCRL,PTK2,PAX5,IGHG3,CAMK2D,PIK3C3,CD22,IGHM,IRS2,FRS2,IGHD,MAP3K9,MAP3K14,CD19,CFL1,FCGR2A,IGHE,CREB3,CREBBP,NFATC4,CREB5,CALM1 (includes others),RRAS2,GAB1,FOXO1,VAV3,PAG1,PIK3R6,LYN,MEF2C,IGHA1,PRKCB |
| Sirtuin Signaling Pathway | 4.71 | 0.209 | turquoise | TUBA1B,TIMM13,NDUFA9,MAPK1,ATP5F1D,NDUFB8,NDUFA1,LDHB,NDUFB3,NDUFB10,NDUFS6,TUBA1C,PGK1,ATP5PF,PFKFB3,CXCL8,ATP5F1A,HIST1H3C,TIMM8B,AGTRAP,ATG13,NDUFS5,ATP5F1C,NDUFB11,ATP5F1B,XRCC6,NDUFA6,NDUFB7,IDH2,VDAC1,TNF,NDUFB2,GABPB1,SDHB,NDUFA7,DUSP6,ATP5F1E,NDUFA2,GADD45A,PGAM1,ATG4A,NAMPT,GOT2,NDUFAB1,NDUFS4,SDHA,NDUFB4,ARNTL,SLC25A4,TUBA4A,GLUD1,SOD1,VDAC3,NDUFA13,FOXO1,NDUFA11,LDHA |
| Graft-versus-Host Disease Signaling | 4.65 | 0.385 | turquoise | HLA-DOA,GZMB,TRGV9,HLA-B,FAS,PRF1,CD80,IL1RN,HLA-DMA,HLA-DMB,FCER1G,HLA-DOB,IL1B,CD86,TNF |
| Autoimmune Thyroid Disease Signaling | 4.61 | 0.4 | turquoise | HLA-DOA,GZMB,TRGV9,HLA-B,FAS,PRF1,IGHG3,CD80,HLA-DMA,HLA-DMB,FCER1G,TSHR,HLA-DOB,CD86 |
| Dendritic Cell Maturation | 4.57 | 0.23 | turquoise | PIK3CA,HLA-DOA,MAPK1,IL32,HLA-B,PIK3R5,FCGR2B,IGHG3,HLA-DMA,CD1A,PIK3C3,HLA-DMB,PLCB1,IRS2,COL18A1,TNFRSF1B,FRS2,FCGR3A/FCGR3B,FCGR1B,MAP3K14,FCGR2A,TYROBP,TRGV9,CREB3,CREBBP,CD58,PLCL2,CREB5,TLR2,STAT4,TLR4,GAB1,CD80,IL1RN,PIK3R6,FCER1G,CD86,IL1B,HLA-DOB,IRF8,TNF |
| iCOS-iCOSL Signaling in T Helper Cells | 4.57 | 0.261 | turquoise | HLA-DOA,PIK3CA,CAMK4,NFATC3,CD4,HLA-B,PIK3R5,CAMK2D,HLA-DMA,PIK3C3,HLA-DMB,IRS2,FRS2,ICOSLG/LOC102723996,IL2RB,TRGV9,CHP1,ITPR1,NFATC4,CALM1 (includes others),GAB1,CD80,LAT,FCER1G,PIK3R6,CD86,HLA-DOB,PLEKHA1,PLEKHA2,LCP2 |
| Glioma Invasiveness Signaling | 4.55 | 0.295 | turquoise | RAP2B,RAP1B,RAP2A,TIMP3,PIK3CA,MAPK1,HMMR,PIK3R5,PLAUR,RHOH,PTK2,RRAS2,GAB1,TIMP1,PIK3C3,PIK3R6,ITGAV,RHOU,IRS2,RHOF,FRS2,FNBP1,TIMP2 |
| fMLP Signaling in Neutrophils | 4.43 | 0.25 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,ARPC1B,MAPK1,NFATC3,PIK3R5,ACTR3,PIK3C3,PRKCE,PLCB1,IRS2,GNG5,FRS2,GNAS,ARPC5L,CHP1,ITPR1,NFATC4,FPR1,CALM1 (includes others),GNAI3,RRAS2,PRKCI,GAB1,ARPC2,PRKCD,PIK3R6,ARPC4,PRKCB |
| T Helper Cell Differentiation | 4.43 | 0.312 | turquoise | IL4R,HLA-DOA,TRGV9,IL21R,HLA-B,IL6R,TBX21,TGFBR2,STAT4,CD80,HLA-DMA,HLA-DMB,FCER1G,HLA-DOB,CD86,CXCR5,TNFRSF1B,GATA3,TNF,ICOSLG/LOC102723996 |
| Rac Signaling | 4.39 | 0.252 | turquoise | RAP2B,RAP1B,RAP2A,ABI2,PIK3CA,ARPC1B,MAPK1,PIK3R5,PIP4K2B,LIMK2,PIP5K1B,LIMK1,PTK2,IQGAP2,ACTR3,CYFIP2,PIK3C3,IRS2,FRS2,ITGB1,TIAM1,CFL1,ARPC5L,RRAS2,PRKCI,GAB1,CYFIP1,ARPC2,PIK3R6,SH3RF1,ARPC4 |
| Actin Cytoskeleton Signaling | 4.37 | 0.214 | turquoise | RAP2B,RAP1B,RAP2A,ABI2,PIK3CA,MPRIP,ARPC1B,MYL6,MAPK1,ARHGEF7,SOS2,PIK3R5,LIMK2,PIP5K1B,MYH11,LIMK1,PTK2,DIAPH1,IQGAP2,ACTR3,CYFIP2,FLNA,PIK3C3,IRS2,VCL,SSH2,FRS2,ACTN1,MYL12A,ITGB1,PXN,TIAM1,CFL1,ARPC5L,FGF9,RDX,TTN,RRAS2,GAB1,CYFIP1,VAV3,ARPC2,PIK3R6,CD14,ACTN4,PDGFD,ACTG1,ARPC4 |
| Primary Immunodeficiency Signaling | 4.35 | 0.366 | turquoise | IL7R,CD19,IGHG3,DCLRE1C,CD4,IGH,IGLC1,IGLL1/IGLL5,ADA,CIITA,IGHM,TNFRSF13B,IGHA1,CD8A,IGHD |
| Aryl Hydrocarbon Receptor Signaling | 4.34 | 0.244 | turquoise | MAPK1,CDK4,RARG,PTGES3,FAS,ARNT,CHEK1,NR2F1,CCNA2,NCOA7,HSP90B1,GSTM2,ALDH1A1,HSP90AB1,TGFB2,AHR,GSTK1,GSTM1,MGST1,RBL2,TFDP1,MDM2,NCOA3,CYP1B1,GSTO1,CCND2,MGST2,IL1B,NRIP1,RXRA,TNF,ESR2,ESR1 |
| Th1 and Th2 Activation Pathway | 4.28 | 0.228 | turquoise | PIK3CA,HLA-DOA,NFATC3,KLRD1,CD4,TGFBR3,HAVCR2,HLA-B,PIK3R5,CXCR3,CD8A,TBX21,TGFBR2,NFIL3,HLA-DMA,PIK3C3,HLA-DMB,IRS2,STAT5B,FRS2,ICOSLG/LOC102723996,IL2RB,CCR1,RUNX3,IL4R,CXCR4,BHLHE41,IL6R,ACVR1,NFATC4,STAT4,NOTCH4,GAB1,CD80,GFI1,PIK3R6,CD86,HLA-DOB,GATA3 |
| Allograft Rejection Signaling | 4.14 | 0.368 | turquoise | HLA-DOA,GZMB,TRGV9,HLA-B,FAS,PRF1,IGHG3,CD80,HLA-DMA,HLA-DMB,FCER1G,HLA-DOB,CD86,TNF |
| Communication between Innate and Adaptive Immune Cells | 4.06 | 0.282 | turquoise | CXCL8,IGHE,CD4,TRGV9,HLA-B,CCL5,CD8A,CCL3,TNFRSF17,TLR2,TLR4,IGHG3,CD80,IL1RN,FCER1G,IL1B,IGHM,CD86,TNFRSF13B,IGHA1,TNF,IGHD |
| Role of Tissue Factor in Cancer | 4.04 | 0.242 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,PIK3R5,LIMK2,LIMK1,VEGFA,ARRB1,PIK3C3,ITGAV,PLCB1,IRS2,STAT5B,FRS2,ITGB1,CXCL8,P4HB,CFL1,GNAQ,PLAUR,HBEGF,RPS6KA6,RRAS2,GAB1,PDIA6,PIK3R6,LYN,IL1B,RPS6KA4 |
| Virus Entry via Endocytic Pathways | 3.94 | 0.246 | turquoise | RAP2B,RAP1B,RAP2A,FLNB,PIK3CA,HLA-B,PIK3R5,ITGB7,CD55,FLNA,PIK3C3,CAV1,PRKCE,IRS2,FRS2,DNM2,ITGB1,AP1S2,ITGAL,AP2S1,PRKCI,RRAS2,GAB1,AP3B1,PRKCD,PIK3R6,TFRC,ACTG1,PRKCB |
| Paxillin Signaling | 3.94 | 0.246 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,ARF1,ARHGEF7,SOS2,PIK3R5,PTPN12,ITGB7,NCK2,PTK2,PIK3C3,ITGAV,IRS2,VCL,FRS2,ACTN1,ITGB1,PXN,ITGAL,ITGAM,RRAS2,GAB1,PIK3R6,ACTN4,ACTG1,ITGAX |
| CD28 Signaling in T Helper Cells | 3.92 | 0.242 | turquoise | HLA-DOA,PIK3CA,CAMK4,ARPC1B,NFATC3,CD4,HLA-B,PIK3R5,ACTR3,HLA-DMA,PIK3C3,HLA-DMB,IRS2,FRS2,ARPC5L,TRGV9,CHP1,ITPR1,NFATC4,CALM1 (includes others),GAB1,CD80,ARPC2,LAT,FCER1G,PIK3R6,HLA-DOB,CD86,ARPC4,LCP2 |
| IL-8 Signaling | 3.86 | 0.212 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,PIK3R5,LIMK2,RHOH,LIMK1,IRAK1,PTK2,BRAF,VEGFA,HMOX1,PIK3C3,RHOU,ITGAV,PRKCE,IRS2,RHOF,GNG5,FRS2,LASP1,CR2,CXCL8,PLD3,GNAS,FLT1,HBEGF,CSTB,GNAI3,ITGAM,PRKCI,CCND2,RRAS2,GAB1,PRKCD,PIK3R6,PTGS2,FNBP1,PRKCB,IRAK2,ITGAX |
| Natural Killer Cell Signaling | 3.85 | 0.24 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,KLRD1,SOS2,PIK3R5,OCRL,CD300A,SH2D1A,PIK3C3,PRKCE,IRS2,HCST,FRS2,FCGR3A/FCGR3B,TYROBP,FCGR2A,SH3BP2,PRKCI,RRAS2,GAB1,VAV3,PRKCD,LAT,FCER1G,PIK3R6,LCP2,PRKCB |
| Calcium-induced T Lymphocyte Apoptosis | 3.79 | 0.309 | turquoise | HLA-DOA,CAMK4,CD4,TRGV9,HLA-B,CHP1,ITPR1,CALM1 (includes others),PRKCI,HLA-DMA,PRKCD,HLA-DMB,FCER1G,PRKCE,HLA-DOB,CAPN2,PRKCB |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 3.74 | 0.192 | turquoise | RAP2B,MAPK1,NFATC3,IL32,CSNK1A1,VEGFA,CAMK2D,WNT7B,PLCB1,IRS2,TRAF5,FRS2,CXCL8,MAP3K14,MIF,CREBBP,IL6R,CREB3,PLCL2,CREB5,IL7,TLR2,GAB1,IL1RN,PRKCD,PIK3R6,PDGFD,TNF,RAP1B,RAP2A,PIK3CA,CAMK4,PIK3R5,CEBPD,FZD1,CCL5,IRAK1,TRADD,IGHG3,PIK3C3,CEBPA,PRKCE,TNFRSF1B,FCGR3A/FCGR3B,C5AR1,DAAM1,CHP1,GNAQ,NFATC4,CEBPB,IL16,CALM1 (includes others),TLR4,RRAS2,PRKCI,WNT10A,IL1B,IRAK2,PRKCB |
| Th1 Pathway | 3.67 | 0.238 | turquoise | HLA-DOA,PIK3CA,NFATC3,KLRD1,HAVCR2,CD4,HLA-B,PIK3R5,CXCR3,CD8A,TBX21,NFIL3,HLA-DMA,PIK3C3,HLA-DMB,IRS2,FRS2,ICOSLG/LOC102723996,RUNX3,IL6R,NFATC4,STAT4,NOTCH4,CD80,GAB1,PIK3R6,HLA-DOB,CD86,GATA3 |
| Hypoxia Signaling in the Cardiovascular System | 3.64 | 0.278 | turquoise | P4HB,UBE2Q1,UBE2N,CREBBP,CREB3,MDM2,UBE2W,CREB5,ARNT,VEGFA,HSP90B1,UBE2L3,UBE2J1,UBE2H,HSP90AB1,UBE2G1,UBE2E2,LDHA,UBE2Q2,UBE2C |
| NRF2-mediated Oxidative Stress Response | 3.54 | 0.208 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,USP14,MAPK1,PRDX1,PPIB,PIK3R5,GCLC,DNAJC3,MAP3K5,HMOX1,GSTM2,KEAP1,PIK3C3,VCP,PRKCE,IRS2,TXN,FKBP5,FRS2,GSTK1,GSTM1,MGST1,CREBBP,DNAJC1,SOD1,GSTO1,PRKCI,RRAS2,MGST2,GAB1,PRKCD,DNAJB11,RBX1,PIK3R6,ABCC4,ACTG1,DNAJC7,PRKCB |
| Xenobiotic Metabolism Signaling | 3.54 | 0.193 | turquoise | RAP2B,MAPK1,CAMK1D,GCLC,ARNT,ALDH1A1,GSTM2,CAMK2D,KEAP1,HS3ST1,IRS2,FRS2,AHR,GSTK1,MAP3K14,MAP3K9,MGST1,CREBBP,GAB1,SMOX,RBX1,PRKCD,PIK3R6,RXRA,NDST1,TNF,RAP1B,RAP2A,PIK3CA,CAMK4,PIK3R5,MAP3K5,FMO5,PTGES3,HMOX1,HSP90B1,HSP90AB1,PIK3C3,PRKCE,CITED2,ABCB1,GSTM1,SRA1,GSTO1,CYP1B1,PRKCI,RRAS2,MGST2,SULT1A1,IL1B,NRIP1,DNAJC7,PRKCB |
| Protein Ubiquitination Pathway | 3.49 | 0.195 | turquoise | PSMA7,HLA-B,FBXW7,DNAJC3,ELOB,HSPA5,ELOC,PSMA2,PSMC2,BIRC3,UBE2Q2,PSMA6,UBE2Q1,HSPA9,PSME2,HSPA8,PSMB7,UBE2L3,UBE2H,PSMB2,RBX1,UBE2G1,PSMA5,ANAPC5,HSPB11,UBE2C,PSMB3,USP14,PSMB10,USP53,UBE2N,UBE2W,UCHL1,HSP90B1,HSP90AB1,STUB1,HSPE1,PSMA3,PSMD14,PSMD13,DNAJC1,MDM2,PSMA1,PSMB6,PSMD8,USP44,UBE2J1,HSCB,DNAJB11,UBE2E2,DNAJC7 |
| Chemokine Signaling | 3.47 | 0.27 | turquoise | RAP2B,RAP1B,RAP2A,MPRIP,CAMK4,MAPK1,CFL1,CAMK1D,CXCR4,GNAQ,LIMK2,CCL5,LIMK1,PTK2,CALM1 (includes others),GNAI3,RRAS2,CAMK2D,PLCB1,PRKCB |
| VEGF Signaling | 3.44 | 0.241 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,ARNT,PTK2,VEGFA,EIF1,PIK3C3,IRS2,VCL,FRS2,ACTN1,PXN,YWHAE,FLT1,RRAS2,GAB1,FOXO1,PIK3R6,ACTN4,ACTG1,PRKCB |
| Prolactin Signaling | 3.43 | 0.253 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,CREBBP,SOS2,PIK3R5,CEBPB,NR3C1,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,SOCS2,IRS2,TCF7,STAT5B,FRS2,PRKCB |
| Epithelial Adherens Junction Signaling | 3.41 | 0.222 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,ARPC1B,MYL6,TGFBR3,AFDN,MYH11,TUBB,CLIP1,TGFBR2,ACTR3,KEAP1,TGFB2,TUBA1C,VCL,ACTN1,TUBB3,ARPC5L,TUBB4B,TUBG1,ACVR1,TUBA4A,NOTCH4,RRAS2,ARPC2,ZYX,ACTN4,ACTG1,ARPC4,CTNND1 |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 3.36 | 0.25 | turquoise | PXN,PLD3,MAPK1,ARPC1B,FCGR2A,ARPC5L,FYB1,NCK2,HMOX1,PLA2G6,PRKCI,ACTR3,ARPC2,PRKCD,VAV3,LYN,PRKCE,RAB11A,ACTG1,LCP2,ARPC4,FCGR3A/FCGR3B,PRKCB |
| Th2 Pathway | 3.35 | 0.223 | turquoise | HLA-DOA,PIK3CA,TGFBR3,CD4,HLA-B,PIK3R5,TBX21,TGFBR2,HLA-DMA,PIK3C3,HLA-DMB,IRS2,STAT5B,FRS2,ICOSLG/LOC102723996,IL2RB,CCR1,RUNX3,IL4R,CXCR4,BHLHE41,ACVR1,STAT4,NOTCH4,CD80,GAB1,GFI1,PIK3R6,HLA-DOB,CD86,GATA3 |
| mTOR Signaling | 3.35 | 0.204 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,RPS3A,MAPK1,RPS27,PIK3R5,FKBP1A,EIF4G1,RHOH,RPS11,VEGFA,HMOX1,RPS20,PIK3C3,RHOU,EIF3A,PRKCE,IRS2,RHOF,RPS17,FRS2,EIF4B,PLD3,RPS8,EIF3E,EIF3M,ATG13,RPS6KA6,PRKCI,RRAS2,GAB1,EIF4A3,PRKCD,RPS27L,PIK3R6,PRR5,RPS6KA4,FNBP1,PRKCB |
| Role of JAK1 and JAK3 in γc Cytokine Signaling | 3.31 | 0.263 | turquoise | RAP2B,RAP1B,RAP2A,IL4R,PIK3CA,IL15RA,MAPK1,IL9R,IL21R,PIK3R5,IL7,IL7R,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,STAT5B,FRS2,IL2RB |
| Regulation of Cellular Mechanics by Calpain Protease | 3.29 | 0.283 | turquoise | RAP2B,RAP1B,ITGB1,CAPN5,RAP2A,PXN,MAPK1,CDK4,PTK2,CCNA2,CAPNS1,RRAS2,CAPN2,VCL,ACTN4,ACTN1,CAPN3 |
| Hematopoiesis from Pluripotent Stem Cells | 3.29 | 0.343 | turquoise | CXCL8,IGHG3,TRGV9,IGH,CD4,IGLC1,FCER1G,IGHM,IGHA1,CD8A,IL7,IGHD |
| Breast Cancer Regulation by Stathmin1 | 3.28 | 0.201 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,CAMK4,CAMK1D,MAPK1,ARHGEF7,SOS2,PIK3R5,LIMK2,TUBB,LIMK1,CAMK2D,PIK3C3,PLCB1,PRKCE,IRS2,TUBA1C,GNG5,FRS2,E2F2,TUBB3,GNAS,TUBB4B,TUBG1,GNAQ,TUBA4A,ITPR1,CALM1 (includes others),GNAI3,PPP1R3D,PRKCI,RRAS2,GAB1,PRKCD,E2F7,PIK3R6,ARHGEF18,ARHGEF10,PRKCB |
| Cholecystokinin/Gastrin-mediated Signaling | 3.26 | 0.238 | turquoise | RAP1B,RAP2B,RAP2A,PXN,MAPK1,SOS2,GNAQ,EPHA4,ITPR1,RHOH,PTK2,PRKCI,RRAS2,IL1RN,PRKCD,RHOU,PRKCE,PLCB1,IL1B,MEF2C,PTGS2,RHOF,TNF,FNBP1,PRKCB |
| 14-3-3-mediated Signaling | 3.18 | 0.221 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,MAPK1,PIK3R5,MAP3K5,TUBB,PIK3C3,PLCB1,PRKCE,TUBA1C,IRS2,FRS2,TUBB3,YWHAE,TUBB4B,TUBG1,TUBA4A,VIM,PLCL2,PRKCI,RRAS2,FOXO1,GAB1,PRKCD,PIK3R6,TNF,PRKCB |
| Macropinocytosis Signaling | 3.17 | 0.247 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3CA,PIK3R5,RAB34,CSF1R,ITGB7,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,CD14,IRS2,ACTN4,PDGFD,FRS2,PRKCB |
| NF-κB Activation by Viruses | 3.15 | 0.242 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,MAP3K14,PIK3CA,MAPK1,CD4,PIK3R5,ITGAL,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,ITGAV,PRKCE,IRS2,CXCR5,FRS2,CR2,PRKCB |
| Neuroinflammation Signaling Pathway | 3.13 | 0.185 | turquoise | HLA-DOA,MAPK1,NFATC3,TGFBR3,HLA-B,IDE,CX3CR1,TGFBR2,IRS2,BIRC3,FRS2,CXCL8,CD200,CREBBP,IL6R,CREB3,TBK1,CREB5,TLR2,PLA2G6,GAB1,PIK3R6,GLUL,CD86,CFLAR,BACE2,TNF,PIK3CA,PYCARD,GRIA1,PIK3R5,FZD1,CCL5,CCL3,FAS,IRAK1,HMOX1,HLA-DMA,PIK3C3,HLA-DMB,TGFB2,NLRP3,TYROBP,CHP1,ACVR1,GABBR1,NFATC4,CSF1R,BIRC5,TLR4,CD80,HLA-DOB,IL1B,PTGS2,IRAK2 |
| PAK Signaling | 3.06 | 0.231 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,MYL6,MAPK1,ARHGEF7,SOS2,PIK3R5,LIMK2,LIMK1,PTK2,NCK2,PIK3C3,IRS2,FRS2,MYL12A,ITGB1,PXN,CFL1,RRAS2,GAB1,PIK3R6,PDGFD,TNF |
| PKCθ Signaling in T Lymphocytes | 3.05 | 0.21 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,HLA-DOA,MAPK1,NFATC3,CD4,SOS2,HLA-B,PIK3R5,MAP3K5,CAMK2D,HLA-DMA,PIK3C3,HLA-DMB,IRS2,FRS2,MAP3K9,MAP3K14,TRGV9,CHP1,NFATC4,RRAS2,GAB1,CD80,VAV3,LAT,PIK3R6,FCER1G,CD86,HLA-DOB,LCP2 |
| Tec Kinase Signaling | 2.96 | 0.206 | turquoise | PIK3CA,GTF2I,PIK3R5,RHOH,FAS,PTK2,PIK3C3,RHOU,PRKCE,IRS2,STAT5B,RHOF,GNG5,FRS2,ITGB1,GNAS,TRGV9,IGH,GNAQ,STAT4,TLR4,GNAI3,PRKCI,GAB1,VAV3,PRKCD,TNFRSF25,PIK3R6,FCER1G,LYN,ACTG1,TNF,FNBP1,PRKCB |
| Nur77 Signaling in T Lymphocytes | 2.94 | 0.292 | turquoise | HDAC9,HLA-DOA,CAMK4,TRGV9,CHP1,HLA-B,CALM1 (includes others),CD80,HLA-DMA,HLA-DMB,FCER1G,HLA-DOB,CD86,RXRA |
| Systemic Lupus Erythematosus Signaling | 2.91 | 0.197 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MAPK1,NFATC3,SOS2,TXNL4A,HLA-B,PIK3R5,FCGR2B,SNRPN,IGHG3,PIK3C3,CD22,IGHM,IRS2,FRS2,FCGR3A/FCGR3B,SNRPA1,FCGR1B,FCGR2A,IGH,TRGV9,IL6R,NFATC4,RRAS2,GAB1,CD80,IL1RN,CD72,LAT,PIK3R6,FCER1G,LYN,CD86,IL1B,TNF |
| IL-7 Signaling Pathway | 2.84 | 0.239 | turquoise | PIK3CA,MAPK1,IGH,SOS2,PIK3R5,IL7,BAK1,IL7R,PTK2,PAX5,FOXO1,GAB1,PIK3C3,PIK3R6,LYN,IGHM,IRS2,CXCR5,STAT5B,FRS2,MCL1 |
| Chronic Myeloid Leukemia Signaling | 2.82 | 0.223 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,MAPK1,PA2G4,SMAD3,SOS2,CDK4,PIK3R5,TGFBR2,PIK3C3,TGFB2,IRS2,STAT5B,FRS2,E2F2,HDAC9,RBL2,TFDP1,MDM2,RRAS2,GAB1,E2F7,PIK3R6 |
| FAK Signaling | 2.82 | 0.226 | turquoise | RAP2B,RAP1B,ITGB1,CAPN5,RAP2A,PIK3CA,PXN,MAPK1,ARHGEF7,HMMR,SOS2,PIK3R5,PTK2,RRAS2,CAPNS1,GAB1,PIK3C3,PIK3R6,IRS2,CAPN2,VCL,ACTG1,FRS2,CAPN3 |
| CCR3 Signaling in Eosinophils | 2.79 | 0.214 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MPRIP,MAPK1,PIK3R5,LIMK2,LIMK1,PIK3C3,PRKCE,PLCB1,IRS2,GNG5,FRS2,GNAS,CFL1,ITPR1,CALM1 (includes others),PLA2G6,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,PRKCB |
| PI3K Signaling in B Lymphocytes | 2.79 | 0.214 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,CAMK4,MAPK1,NFATC3,ATF5,FCGR2B,CAMK2D,PLCB1,IRS2,CR2,IL4R,CD19,CHP1,PLCL2,ITPR1,NFATC4,CALM1 (includes others),TLR4,PRKCI,RRAS2,VAV3,LYN,PLEKHA1,PLEKHA2,PRKCB |
| SPINK1 General Cancer Pathway | 2.76 | 0.25 | turquoise | RAP2B,RAP1B,GZMA,MT2A,RAP2A,MT1G,PIK3CA,MAPK1,MT1X,IL6R,PIK3R5,MT1E,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,FRS2 |
| HGF Signaling | 2.72 | 0.217 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,MAP3K5,PTK2,ETS2,PIK3C3,PRKCE,IRS2,FRS2,ITGB1,MAP3K14,MAP3K9,PXN,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,PTGS2,ELK3,PRKCB |
| CXCR4 Signaling | 2.69 | 0.199 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MYL6,MAPK1,CD4,PIK3R5,RHOH,PTK2,PIK3C3,RHOU,PLCB1,PRKCE,IRS2,RHOF,GNG5,FRS2,MYL12A,PXN,GNAS,CXCR4,GNAQ,ITPR1,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,LYN,ELMO1,FNBP1,PRKCB |
| Actin Nucleation by ARP-WASP Complex | 2.66 | 0.258 | turquoise | ITGB1,RAP1B,RAP2B,RAP2A,ARPC1B,ARPC5L,SOS2,RHOH,NCK2,RRAS2,ACTR3,ARPC2,RHOU,RHOF,ARPC4,FNBP1 |
| Leukocyte Extravasation Signaling | 2.59 | 0.189 | turquoise | RAP1B,CD99,PIK3CA,SPN,MYL6,MAPK1,PIK3R5,AFDN,RHOH,PTK2,TIMP1,PIK3C3,PRKCE,MMP11,IRS2,VCL,FRS2,ACTN1,TIMP2,ITGB1,TIMP3,PXN,ARHGAP6,CXCR4,RDX,ITGAL,SELPLG,GNAI3,ITGAM,PRKCI,GAB1,RASGRP1,VAV3,PRKCD,PIK3R6,ACTN4,ACTG1,CTNND1,PRKCB |
| PPAR Signaling | 2.59 | 0.224 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K14,SRA1,MAPK1,CREBBP,SOS2,NR2F1,HSP90B1,RRAS2,HSP90AB1,IL1RN,IL1B,PTGS2,NRIP1,PDGFD,TNFRSF1B,RXRA,STAT5B,TNF,CITED2 |
| ILK Signaling | 2.58 | 0.192 | turquoise | FLNB,PIK3CA,MYL6,MAPK1,PIK3R5,MYH11,RHOH,ITGB7,VEGFA,PTK2,NCK2,FLNA,PIK3C3,RHOU,IRS2,VCL,RHOF,FRS2,ACTN1,DSP,NACA,ITGB1,PXN,CFL1,CREB3,CREBBP,VIM,CREB5,GAB1,LIMS1,PIK3R6,RPS6KA4,ACTN4,PTGS2,ACTG1,TNF,FNBP1 |
| Clathrin-mediated Endocytosis Signaling | 2.55 | 0.188 | turquoise | PIK3CA,ARPC1B,PICALM,APOA2,PIK3R5,SH3GLB1,ITGB7,VEGFA,LYZ,ARRB1,SNX9,ACTR3,PIK3C3,AAK1,SERPINA1,IRS2,S100A8,LDLRAP1,SH3KBP1,FRS2,DNM2,ITGB1,ARPC5L,AP1S2,FGF9,CHP1,MDM2,AP2S1,HSPA8,LDLR,GAB1,AP3B1,ARPC2,PIK3R6,RAB11A,TFRC,PDGFD,ACTG1,ARPC4 |
| Glycolysis I | 2.54 | 0.364 | turquoise | PGK1,ENO1,GPI,TPI1,PGAM1,PKM,GAPDH,ALDOA |
| TREM1 Signaling | 2.49 | 0.243 | turquoise | ITGB1,CXCL8,TREM1,NLRP3,MAPK1,TYROBP,CIITA,FCGR2B,CCL3,IRAK1,TLR2,TLR4,IL1B,CD86,STAT5B,TNF,ITGAX |
| FLT3 Signaling in Hematopoietic Progenitor Cells | 2.47 | 0.227 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,CREB5,STAT4,RPS6KA6,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,RPS6KA4,STAT5B,FRS2 |
| Fc Epsilon RI Signaling | 2.46 | 0.208 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,IGH,SOS2,PIK3R5,OCRL,PLA2G6,RRAS2,PRKCI,GAB1,PRKCD,VAV3,PIK3C3,LAT,FCER1G,PIK3R6,LYN,PRKCE,IRS2,TNF,FRS2,LCP2,PRKCB |
| Caveolar-mediated Endocytosis Signaling | 2.42 | 0.239 | turquoise | ITGB1,COPZ1,FLNB,HLA-B,CD48,FLOT1,ITGAL,ITGB7,COPG1,CD55,ITGAM,FLNA,ITGAV,CAV1,ACTG1,DNM2,ITGAX |
| Prostate Cancer Signaling | 2.42 | 0.218 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,TFDP1,PA2G4,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,MDM2,CREB5,HSP90B1,RRAS2,GAB1,HSP90AB1,FOXO1,PIK3C3,PIK3R6,IRS2,FRS2 |
| T Cell Receptor Signaling | 2.38 | 0.211 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MAPK1,NFATC3,CD4,SOS2,PIK3R5,NFATC4,CD8A,CALM1 (includes others),RRAS2,GAB1,PAG1,RASGRP1,PIK3C3,VAV3,LAT,PIK3R6,IRS2,FRS2,LCP2 |
| Type I Diabetes Mellitus Signaling | 2.36 | 0.216 | turquoise | MAP3K14,HLA-DOA,MAPK1,GZMB,TRGV9,HLA-B,MAP3K5,FAS,IRAK1,TRADD,PRF1,CD80,HLA-DMA,HLA-DMB,FCER1G,IL1B,HLA-DOB,SOCS2,BID,CD86,TNFRSF1B,TNF |
| Thrombopoietin Signaling | 2.36 | 0.236 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,RRAS2,PRKCI,GAB1,MAPK1,PRKCD,PIK3C3,PIK3R6,PIK3R5,PRKCE,IRS2,STAT5B,FRS2,PRKCB |
| HER-2 Signaling in Breast Cancer | 2.35 | 0.219 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3CA,SOS2,PIK3R5,MDM2,MAP3K5,ITGB7,PRKCI,RRAS2,GAB1,FOXO1,PRKCD,PIK3C3,PIK3R6,PRKCE,IRS2,FRS2,PRKCB |
| IL-3 Signaling | 2.35 | 0.222 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,CHP1,PIK3R5,CSF2RB,PRKCI,RRAS2,FOXO1,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,IRS2,STAT5B,FRS2,PRKCB |
| Altered T Cell and B Cell Signaling in Rheumatoid Arthritis | 2.35 | 0.231 | turquoise | MAP3K14,HLA-DOA,TRGV9,HLA-B,FAS,TNFRSF17,TLR2,TLR4,CD80,HLA-DMA,IL1RN,HLA-DMB,FCER1G,IL1B,HLA-DOB,CD86,TNFRSF13B,TNF |
| Estrogen-Dependent Breast Cancer Signaling | 2.35 | 0.226 | turquoise | RAP2B,RAP1B,HSD17B10,RAP2A,PIK3CA,MAPK1,CREBBP,CREB3,PIK3R5,CREB5,HSD17B8,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,STAT5B,FRS2,ESR1 |
| Molecular Mechanisms of Cancer | 2.31 | 0.165 | turquoise | RAP2B,MAPK1,SMAD3,SOS2,CDKN2C,PTK2,TGFBR2,CAMK2D,WNT7B,PLCB1,IRS2,HIPK2,FRS2,BIRC3,E2F2,TFDP1,CREBBP,BMP8B,AURKA,CCND2,GAB1,RABIF,PRKCD,PIK3R6,ARHGEF18,CFLAR,ARHGEF10,FNBP1,RAP1B,RAP2A,PIK3CA,PA2G4,ARHGEF7,CDK4,PIK3R5,MAP3K5,FZD1,RHOH,FAS,CHEK1,BRAF,CDK5,BMPR1A,PIK3C3,TGFB2,RHOU,PRKCE,BID,RHOF,ITGB1,GNAS,GNAQ,MDM2,BAK1,GNAI3,PRKCI,RRAS2,FOXO1,WNT10A,RASGRP1,E2F7,BMP6,CTNND1,PRKCB |
| Acute Myeloid Leukemia Signaling | 2.3 | 0.216 | turquoise | RAP2B,RAP1B,CSF3R,RAP2A,PIK3CA,MAPK1,IDH3G,SOS2,PIK3R5,CSF1R,BRAF,CSF2RB,RRAS2,GAB1,PIK3C3,PIK3R6,CEBPA,IRS2,IDH2,STAT5B,FRS2 |
| Non-Small Cell Lung Cancer Signaling | 2.29 | 0.224 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,TFDP1,PA2G4,MAPK1,SOS2,PIK3R5,CDK4,ITPR1,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,RXRA,FRS2,RASSF1 |
| EIF2 Signaling | 2.26 | 0.181 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,RPS3A,MAPK1,RPS27,ATF5,SOS2,PIK3R5,EIF4G1,HSPA5,RPL7,RPS11,VEGFA,EIF1,RPL13,RPS20,PIK3C3,EIF3A,IRS2,RPS17,FRS2,EIF2AK1,RPL3,RPS8,AGO2,RPL23,EIF3E,EIF3M,WARS,RRAS2,GAB1,EIF4A3,RPL26L1,RPS27L,PIK3R6,RPL10,RPLP0 |
| GM-CSF Signaling | 2.23 | 0.225 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,CSF2RB,CAMK2D,RRAS2,GAB1,PIK3C3,PIK3R6,LYN,IRS2,STAT5B,FRS2,PRKCB |
| Heme Degradation | 2.2 | 0.75 | turquoise | HMOX1,BLVRA,HMOX2 |
| Melanoma Signaling | 2.18 | 0.238 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,CDK4,PIK3R5,MDM2,BRAF,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,FRS2 |
| Renal Cell Carcinoma Signaling | 2.17 | 0.218 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,CREBBP,SOS2,PIK3R5,ELOB,ELOC,ARNT,VEGFA,RRAS2,GAB1,RBX1,PIK3C3,PIK3R6,IRS2,FRS2 |
| CDP-diacylglycerol Biosynthesis I | 2.15 | 0.32 | turquoise | ABHD5,LPCAT2,CDS1,LPCAT4,MBOAT1,GPAT3,AGPAT3,CDS2 |
| Regulation of eIF4 and p70S6K Signaling | 2.14 | 0.19 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,RPS3A,EIF4EBP2,MAPK1,RPS27,SOS2,PIK3R5,PAIP2,EIF4G1,RPS11,EIF1,RPS20,PIK3C3,EIF3A,IRS2,RPS17,FRS2,ITGB1,RPS8,AGO2,EIF3E,EIF3M,RRAS2,GAB1,EIF4A3,RPS27L,PIK3R6 |
| Semaphorin Signaling in Neurons | 2.14 | 0.25 | turquoise | DPYSL2,PTK2,ITGB1,SEMA3A,CDK5,CFL1,MAPK1,RHOU,LIMK2,RHOF,RHOH,FNBP1,LIMK1 |
| STAT3 Pathway | 2.13 | 0.197 | turquoise | RAP1B,RAP2B,RAP2A,IL15RA,MAPK1,TGFBR3,IL21R,TGFBR2,VEGFA,IL7R,BMPR1A,TGFB2,SOCS2,IL2RB,MAP3K9,IL4R,IL5RA,IL13RA1,FLT1,IL9R,IL6R,NDUFA13,CSF2RB,RRAS2,IL1B,BMP6 |
| GP6 Signaling Pathway | 2.13 | 0.197 | turquoise | RAP1B,COL19A1,PIK3CA,COL9A1,CAMK4,COL4A3,PIK3R5,ITPR1,LAMC1,PTK2,CALM1 (includes others),PRKCI,GAB1,PRKCD,PIK3C3,LAT,FCER1G,PIK3R6,LYN,PRKCE,COL4A4,IRS2,COL18A1,FRS2,LCP2,PRKCB |
| VEGF Family Ligand-Receptor Interactions | 2.13 | 0.213 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,FLT1,SOS2,PIK3R5,VEGFA,PLA2G6,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,IRS2,FRS2,PRKCB |
| Huntington's Disease Signaling | 2.11 | 0.174 | turquoise | SDHB,PIK3CA,ATP5F1D,MAPK1,SOS2,PIK3R5,HSPA5,VTI1B,ATP5F1E,CDK5,PIK3C3,PLCB1,PRKCE,IRS2,GNG5,FRS2,NAPA,DNM2,POLR2L,CAPN5,SDHA,ATP5PF,HDAC9,ATP5F1A,CREB3,CREBBP,HSPA9,PSME2,GNAQ,ITPR1,CREB5,HSPA8,ATP5F1C,PRKCI,CAPNS1,GAB1,ATP5F1B,PRKCD,PIK3R6,PSME4,CAPN2,CAPN3,PRKCB |
| SAPK/JNK Signaling | 2.11 | 0.206 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K9,PIK3CA,NFATC3,TRGV9,SOS2,PIK3R5,MAP3K5,MINK1,TRADD,RRAS2,GAB1,GADD45A,PIK3C3,PIK3R6,FCER1G,IRS2,DUSP4,GNG5,FRS2 |
| eNOS Signaling | 2.09 | 0.187 | turquoise | PIK3CA,CAMK4,PIK3R5,HSPA5,VEGFA,AQP3,CCNA2,HSP90B1,HSP90AB1,STUB1,PIK3C3,CAV1,PRKCE,IRS2,FRS2,DNM2,GNAS,FLT1,HSPA9,GNAQ,ITPR1,HSPA8,CALM1 (includes others),AQP9,PRKCI,GAB1,PRKCD,PIK3R6,ESR1,ESR2,PRKCB |
| LPS-stimulated MAPK Signaling | 2.08 | 0.211 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K14,PIK3CA,MAPK1,PIK3R5,MAP3K5,TLR4,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,CD14,IRS2,FRS2,PRKCB |
| NF-κB Signaling | 2.07 | 0.183 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,TGFBR3,UBE2N,PIK3R5,IRAK1,TNFRSF17,TGFBR2,BRAF,TRADD,BMPR1A,PIK3C3,IRS2,TRAF5,TNFRSF1B,FRS2,MAP3K14,FLT1,TRGV9,CREBBP,TBK1,TLR2,TLR4,RRAS2,GAB1,IL1RN,PIK3R6,FCER1G,IL1B,TNF,PRKCB |
| Cdc42 Signaling | 2.05 | 0.198 | turquoise | ITGB1,HLA-DOA,MPRIP,MAPK1,CFL1,MYL6,ARPC1B,ARPC5L,TRGV9,HLA-B,LIMK2,CLIP1,LIMK1,DIAPH1,IQGAP2,ACTR3,PRKCI,HLA-DMA,ARPC2,HLA-DMB,FCER1G,HLA-DOB,ARPC4,MYL12A |
| Endoplasmic Reticulum Stress Pathway | 2.04 | 0.333 | turquoise | HSP90B1,ERN1,XBP1,DNAJC3,MAP3K5,HSPA5,MBTPS2 |
| Salvage Pathways of Pyrimidine Deoxyribonucleotides | 2.01 | 0.5 | turquoise | APOBEC3B,TYMP,APOBEC3G,APOBEC3A |
| IL-15 Signaling | 2 | 0.214 | turquoise | RAP2B,RAP1B,RAP2A,CXCL8,PIK3CA,IL15RA,MAPK1,PIK3R5,PTK2,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,STAT5B,TNF,FRS2,IL2RB |
| Neurotrophin/TRK Signaling | 2 | 0.214 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SPRY1,CREBBP,CREB3,SOS2,PIK3R5,MAP3K5,CREB5,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,FRS2 |
| ErbB4 Signaling | 1.99 | 0.218 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,PRKCI,RRAS2,GAB1,PIK3C3,PRKCD,PIK3R6,PRKCE,IRS2,FRS2,PRKCB |
| Aldosterone Signaling in Epithelial Cells | 1.98 | 0.183 | turquoise | ICMT,PIK3CA,MAPK1,SOS2,PIK3R5,DNAJC3,PIP4K2B,PIP5K1B,HSPA5,HSP90B1,HSP90AB1,PIK3C3,HSPE1,PRKCE,PLCB1,IRS2,FRS2,HSPA9,DNAJC1,PLCL2,ITPR1,HSPA8,PRKCI,GAB1,HSCB,PRKCD,DNAJB11,HSPB11,PIK3R6,DNAJC7,PRKCB |
| MIF-mediated Glucocorticoid Regulation | 1.96 | 0.281 | turquoise | TLR4,PLA2G6,LY96,MIF,MAPK1,CD14,CD74,PTGS2,NR3C1 |
| JAK/Stat Signaling | 1.96 | 0.209 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,PIAS2,MAPK1,SOS2,GNAQ,PIK3R5,CEBPB,STAT4,RRAS2,GAB1,PIK3C3,PIK3R6,SOCS2,IRS2,STAT5B,FRS2 |
| Crosstalk between Dendritic Cells and Natural Killer Cells | 1.95 | 0.212 | turquoise | IL15RA,TYROBP,KLRD1,CD69,HLA-B,ITGAL,FAS,TLR4,CSF2RB,PRF1,CAMK2D,CD80,CD226,CD86,TNFRSF1B,ACTG1,TNF,IL2RB |
| Phosphatidylglycerol Biosynthesis II (Non-plastidic) | 1.94 | 0.296 | turquoise | ABHD5,LPCAT2,CDS1,LPCAT4,MBOAT1,GPAT3,AGPAT3,CDS2 |
| Apelin Endothelial Signaling Pathway | 1.92 | 0.194 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,GNAS,CAMK4,MAPK1,SMAD3,PIK3R5,ARNT,GNAI3,CALM1 (includes others),RRAS2,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,PLCB1,IRS2,MEF2C,FRS2,PRKCB |
| Choline Biosynthesis III | 1.85 | 0.385 | turquoise | HMOX1,CEPT1,PLD3,CHPT1,PCYT1A |
| Gap Junction Signaling | 1.85 | 0.175 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,MAPK1,GRIA1,SOS2,CSNK1A1,PIK3R5,TUBB,PIK3C3,CAV1,PLCB1,PRKCE,IRS2,TUBA1C,FRS2,TUBB3,GNAS,TUBB4B,CSNK1G3,TUBG1,GNAQ,TUBA4A,ITPR1,PLCL2,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,ACTG1,PRKCB |
| p70S6K Signaling | 1.85 | 0.187 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,PIK3C3,PLCB1,PRKCE,IRS2,EEF2K,FRS2,CD19,IL4R,YWHAE,GNAQ,PLCL2,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,LYN,PRKCB |
| p53 Signaling | 1.83 | 0.195 | turquoise | HDAC9,PIK3CA,TP63,RRM2B,PERP,PIK3R5,CDK4,MDM2,BIRC5,FAS,CHEK1,TP53I3,SCO2,MDM4,CCND2,GAB1,GADD45A,PIK3C3,PIK3R6,IRS2,HIPK2,FRS2 |
| Thrombin Signaling | 1.82 | 0.173 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MPRIP,CAMK4,CAMK1D,MYL6,MAPK1,PIK3R5,RHOH,PTK2,CAMK2D,PIK3C3,RHOU,PLCB1,PRKCE,IRS2,RHOF,GNG5,FRS2,MYL12A,GNAS,GNAQ,ITPR1,PLCL2,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,GATA3,ARHGEF10,FNBP1,PRKCB |
| Gαq Signaling | 1.82 | 0.181 | turquoise | PIK3CA,CAMK4,MAPK1,NFATC3,PIK3R5,RHOH,HMOX1,PIK3C3,RHOU,PLCB1,PRKCE,IRS2,RHOF,GNG5,FRS2,GNAS,PLD3,CHP1,GNAQ,ITPR1,NFATC4,CALM1 (includes others),PRKCI,GAB1,PRKCD,CALCR,PIK3R6,FNBP1,PRKCB |
| Gluconeogenesis I | 1.81 | 0.304 | turquoise | PGK1,ENO1,GPI,PGAM1,ALDOA,GAPDH,MDH2 |
| Pathogenesis of Multiple Sclerosis | 1.8 | 0.444 | turquoise | CCR1,CXCR3,CCL5,CCL3 |
| Erythropoietin Signaling | 1.8 | 0.205 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,PRKCI,RRAS2,GAB1,PIK3C3,PRKCD,PIK3R6,PRKCE,IRS2,STAT5B,FRS2,PRKCB |
| Protein Kinase A Signaling | 1.79 | 0.158 | turquoise | MAPK1,MYL6,PTPN14,NFATC3,SMAD3,PTK2,TGFBR2,CAMK2D,PDE7B,GDE1,PLCB1,DUSP7,EYA2,SMPDL3A,KDELR1,PTPRE,YWHAE,HIST1H3C,CREBBP,CREB3,PTPN18,ITPR1,PLCL2,CREB5,TTN,EPM2A,AKAP13,PTPRB,PRKCD,ANAPC5,DUSP4,KDELR2,SIRPA,RAP1B,FLNB,CAMK4,PDE7A,DUSP6,PDE4A,PTPN12,BRAF,FLNA,TGFB2,PRKCE,PDE4D,GNG5,MYL12A,PXN,PTPRK,GNAS,CHP1,GNAQ,NFATC4,CALM1 (includes others),GNAI3,PPP1R3D,PRKCI,CDC14B,PTGS2,PRKCB |
| Antigen Presentation Pathway | 1.79 | 0.265 | turquoise | HLA-DOA,HLA-DMA,HLA-DMB,HLA-B,CIITA,CANX,HLA-DOB,CD74,PSMB6 |
| Glioblastoma Multiforme Signaling | 1.77 | 0.179 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,CDK4,PIK3R5,FZD1,RHOH,WNT7B,PIK3C3,RHOU,PLCB1,IRS2,RHOF,FRS2,E2F2,MDM2,PLCL2,ITPR1,RRAS2,FOXO1,WNT10A,GAB1,PRKCD,E2F7,PIK3R6,PDGFD,FNBP1 |
| Apoptosis Signaling | 1.77 | 0.2 | turquoise | RAP2B,RAP1B,CAPN5,RAP2A,MAP3K14,MAPK1,MAP3K5,FAS,BAK1,CAPNS1,RRAS2,PRKCE,BID,CAPN2,TNFRSF1B,BIRC3,TNF,MCL1,CAPN3 |
| ErbB2-ErbB3 Signaling | 1.76 | 0.211 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,RRAS2,FOXO1,GAB1,PIK3C3,ETV4,PIK3R6,IRS2,STAT5B,FRS2 |
| nNOS Signaling in Neurons | 1.74 | 0.239 | turquoise | CAPN5,CALM1 (includes others),CAMK4,PRKCI,CAPNS1,PRKCD,CHP1,PRKCE,CAPN2,CAPN3,PRKCB |
| Pyridoxal 5'-phosphate Salvage Pathway | 1.74 | 0.219 | turquoise | BRAF,PDXK,MAP3K9,DAPK1,CDK5,MAPK1,PRKCD,CDK4,CSNK1A1,PRKCE,LIMK2,ADPGK,LIMK1,IRAK1 |
| Cancer Drug Resistance By Drug Efflux | 1.74 | 0.239 | turquoise | BRAF,RAP1B,RAP2B,ABCB1,RAP2A,PIK3CA,RRAS2,MAPK1,FOXO1,MDM2,PTGS2 |
| Pancreatic Adenocarcinoma Signaling | 1.73 | 0.189 | turquoise | PIK3CA,PLD3,TFDP1,PA2G4,MAPK1,SMAD3,PIK3R5,CDK4,HBEGF,MDM2,BIRC5,VEGFA,TGFBR2,HMOX1,GAB1,PIK3C3,E2F7,PIK3R6,TGFB2,IRS2,PTGS2,FRS2,E2F2 |
| Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes | 1.73 | 0.205 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,MAPK1,NFATC3,SMAD3,CHP1,SOS2,NFATC4,TGFBR2,CALM1 (includes others),RRAS2,CD80,VAV3,LAT,TGFB2 |
| VDR/RXR Activation | 1.71 | 0.208 | turquoise | CCNC,CCL5,CEBPB,NCOA3,PRKCI,FOXO1,GADD45A,RUNX2,PRKCD,TGFB2,CEBPA,CD14,PRKCE,VDR,RXRA,PRKCB |
| Telomerase Signaling | 1.71 | 0.19 | turquoise | RAP2B,RAP1B,RAP2A,HDAC9,PIK3CA,MAPK1,SOS2,PIK3R5,PTGES3,TERF2,HSP90B1,RRAS2,GAB1,HSP90AB1,ETS2,PIK3C3,PIK3R6,IRS2,TINF2,FRS2,ELK3,IL2RB |
| IL-6 Signaling | 1.71 | 0.184 | turquoise | RAP1B,RAP2B,CXCL8,MAP3K14,RAP2A,ABCB1,PIK3CA,MAPK1,IL6R,SOS2,PIK3R5,CEBPB,VEGFA,RRAS2,GAB1,IL1RN,PIK3C3,PIK3R6,IL1B,CD14,IRS2,TNFRSF1B,TNF,FRS2,MCL1 |
| Regulation of Actin-based Motility by Rho | 1.68 | 0.202 | turquoise | ITGB1,MPRIP,CFL1,MYL6,ARPC1B,ARPC5L,PIP4K2B,PIP5K1B,RHOH,LIMK1,ACTR3,ARPC2,RHOU,RHOF,ARPC4,FNBP1,MYL12A |
| IL-9 Signaling | 1.67 | 0.234 | turquoise | PIK3CA,GAB1,IL9R,PIK3C3,PIK3R6,PIK3R5,SOCS2,IRS2,STAT5B,TNF,FRS2 |
| HIF1α Signaling | 1.66 | 0.185 | turquoise | RAP2B,RAP1B,SLC2A5,RAP2A,PIK3CA,MAPK1,CREBBP,PIK3R5,MDM2,ELOB,ELOC,LDHB,ARNT,VEGFA,RRAS2,GAB1,RBX1,PIK3C3,PIK3R6,IRS2,MMP11,LDHA,FRS2 |
| Signaling by Rho Family GTPases | 1.65 | 0.165 | turquoise | PIK3CA,ARPC1B,MYL6,MAPK1,ARHGEF7,PIK3R5,PIP4K2B,LIMK2,PIP5K1B,RHOH,CLIP1,LIMK1,PTK2,ACTR3,PIK3C3,RHOU,IRS2,RHOF,GNG5,FRS2,MYL12A,ITGB1,MAP3K9,GNAS,CFL1,ARPC5L,GNAQ,RDX,VIM,CDC42EP3,GNAI3,PRKCI,GAB1,CYFIP1,ARPC2,PIK3R6,ARHGEF18,ACTG1,ARHGEF10,ARPC4,FNBP1 |
| IL-2 Signaling | 1.65 | 0.208 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,SOS2,PIK3R6,PIK3R5,IRS2,STAT5B,FRS2,IL2RB |
| ErbB Signaling | 1.62 | 0.19 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,HBEGF,NCK2,PRKCI,RRAS2,GAB1,FOXO1,PRKCD,PIK3C3,PIK3R6,PRKCE,IRS2,FRS2,PRKCB |
| Growth Hormone Signaling | 1.59 | 0.198 | turquoise | PIK3CA,MAPK1,PIK3R5,RPS6KA6,PRKCI,GAB1,PIK3C3,PRKCD,CEBPA,PIK3R6,SOCS2,PRKCE,IRS2,RPS6KA4,STAT5B,FRS2,PRKCB |
| Lipid Antigen Presentation by CD1 | 1.58 | 0.3 | turquoise | CD1A,TRGV9,FCER1G,CANX,PSAP,AP2S1 |
| Inflammasome pathway | 1.58 | 0.3 | turquoise | TLR4,NLRP3,NLRP1,AIM2,PYCARD,IL1B |
| RhoGDI Signaling | 1.58 | 0.172 | turquoise | ARPC1B,MYL6,ARHGEF7,PIP4K2B,LIMK2,PIP5K1B,RHOH,LIMK1,ACTR3,RHOU,GNG5,RHOF,MYL12A,ITGB1,ARHGAP6,GNAS,CFL1,ARPC5L,CREBBP,GNAQ,RDX,GNAI3,ARPC2,ARHGEF18,ARHGEF10,ESR1,ESR2,ACTG1,FNBP1,ARPC4 |
| CNTF Signaling | 1.58 | 0.209 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,MAPK1,PIK3R5,RPS6KA6,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,RPS6KA4,FRS2 |
| IGF-1 Signaling | 1.56 | 0.186 | turquoise | RAP2B,RAP1B,RAP2A,IGFBP4,PIK3CA,PXN,MAPK1,YWHAE,SOS2,PIK3R5,IGFBP7,PTK2,RRAS2,PRKCI,GAB1,FOXO1,PIK3C3,PIK3R6,SOCS2,IRS2,FRS2 |
| p38 MAPK Signaling | 1.56 | 0.186 | turquoise | MAPKAPK3,HIST1H3C,CREBBP,CREB3,MAP3K5,CREB5,FAS,IRAK1,TGFBR2,TRADD,PLA2G6,RPS6KA6,IL1RN,TGFB2,IL1B,MEF2C,RPS6KA4,EEF2K,TNFRSF1B,TNF,IRAK2 |
| Ephrin Receptor Signaling | 1.55 | 0.171 | turquoise | RAP2B,RAP1B,RAP2A,ARPC1B,MAPK1,SOS2,EPHA4,LIMK2,LIMK1,PTK2,VEGFA,NCK2,ACTR3,GNG5,ITGB1,MAP3K14,PXN,GNAS,CFL1,ARPC5L,CXCR4,CREB3,CREBBP,GNAQ,CREB5,GNAI3,RRAS2,ARPC2,PDGFD,ARPC4 |
| Salvage Pathways of Pyrimidine Ribonucleotides | 1.53 | 0.191 | turquoise | MAP3K9,APOBEC3B,DAPK1,MAPK1,UPP1,CDK4,CSNK1A1,LIMK2,APOBEC3G,APOBEC3A,LIMK1,IRAK1,BRAF,CDK5,PRKCD,PRKCE,AK9,ADPGK |
| Estrogen-mediated S-phase Entry | 1.52 | 0.269 | turquoise | CCNA2,TFDP1,E2F7,CDK4,ESR2,ESR1,E2F2 |
| Th17 Activation Pathway | 1.5 | 0.2 | turquoise | IRF4,NFATC3,IL21R,TRGV9,IL6R,NFATC4,IRAK1,STAT4,HSP90B1,HSP90AB1,RORA,FCER1G,IL1B,AHR,IRAK2 |
| Glutathione Redox Reactions I | 1.48 | 0.286 | turquoise | GSTM1,MGST1,GSTM2,MGST2,GPX1,GSTK1 |
| iNOS Signaling | 1.48 | 0.227 | turquoise | TLR4,CALM1 (includes others),LY96,CAMK4,MAPK1,CREBBP,CD14,HMGA1,IRAK1,IRAK2 |
| Dolichyl-diphosphooligosaccharide Biosynthesis | 1.47 | 0.364 | turquoise | ALG13,ALG14,ALG3,ALG1 |
| Granzyme B Signaling | 1.46 | 0.312 | turquoise | PRF1,NUMA1,GZMB,BID,LMNB1 |
| Role of NFAT in Cardiac Hypertrophy | 1.45 | 0.163 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,CAMK1D,MAPK1,SOS2,CSNK1A1,PIK3R5,TGFBR2,CAMK2D,PIK3C3,TGFB2,PLCB1,PRKCE,IRS2,GNG5,FRS2,HDAC9,GNAS,CHP1,GNAQ,ITPR1,NFATC4,PLCL2,CALM1 (includes others),GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,MEF2C,SLC8A1,PRKCB |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 1.45 | 0.181 | turquoise | KCNN3,PIK3CA,KCNN4,CAMK4,MAPK1,CAMK1D,GRIA1,PIK3R5,PLCL2,ITPR1,PRKCI,CAMK2D,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,PLCB1,IRS2,FRS2,PRKCB |
| Synaptic Long Term Potentiation | 1.44 | 0.179 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,MAPK1,GRIA1,CREBBP,CREB3,CHP1,GNAQ,PLCL2,ITPR1,CREB5,CALM1 (includes others),PPP1R3D,RRAS2,CAMK2D,PRKCI,PRKCD,PRKCE,PLCB1,PRKCB |
| NGF Signaling | 1.44 | 0.179 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K9,MAP3K14,PIK3CA,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,MAP3K5,CREB5,RPS6KA6,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,IRS2,RPS6KA4,FRS2 |
| Glucocorticoid Receptor Signaling | 1.44 | 0.154 | turquoise | RAP2B,MAPK1,NFATC3,SMAD3,SOS2,TAF10,CD163,HSPA5,TGFBR2,SMARCB1,IRS2,FRS2,POLR2L,MAP3K14,CXCL8,HSPA9,CREBBP,NCOA3,SMARCD3,HSPA8,GAB1,SMARCA2,IL1RN,PIK3R6,ESR1,TNF,PHF10,RAP1B,RAP2A,PIK3CA,KRT76,PIK3R5,CCL5,CCL3,NR3C1,PTGES3,HSP90B1,HSP90AB1,PIK3C3,ANXA1,TGFB2,CEBPA,STAT5B,FKBP5,SRA1,CHP1,CEBPB,NFATC4,RRAS2,IL1B,PTGS2,NRIP1 |
| Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells | 1.44 | 0.259 | turquoise | PRF1,GZMB,TRGV9,HLA-B,FCER1G,BID,FAS |
| Melatonin Signaling | 1.43 | 0.2 | turquoise | CAMK4,MAPK1,GNAQ,PLCL2,BRAF,CALM1 (includes others),GNAI3,PRKCI,CAMK2D,RORA,PRKCD,PLCB1,PRKCE,PRKCB |
| Nitric Oxide Signaling in the Cardiovascular System | 1.42 | 0.182 | turquoise | PIK3CA,CAMK4,MAPK1,FLT1,PIK3R5,ITPR1,VEGFA,CALM1 (includes others),HSP90B1,PRKCI,HSP90AB1,GAB1,PRKCD,PIK3C3,PIK3R6,CAV1,PRKCE,IRS2,FRS2,PRKCB |
| α-Adrenergic Signaling | 1.42 | 0.189 | turquoise | RAP2B,RAP1B,RAP2A,GNAS,CAMK4,MAPK1,GNAQ,ITPR1,GNAI3,CALM1 (includes others),PRKCI,RRAS2,PRKCD,PRKCE,SLC8A1,GNG5,PRKCB |
| ERK/MAPK Signaling | 1.41 | 0.164 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,DUSP6,SOS2,PIK3R5,PTK2,BRAF,ETS2,PIK3C3,PRKCE,IRS2,FRS2,ITGB1,PXN,HIST1H3C,CREBBP,CREB3,CREB5,PLA2G6,PPP1R3D,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,DUSP4,RPS6KA4,ESR1,ELK3,PRKCB |
| Myc Mediated Apoptosis Signaling | 1.41 | 0.195 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,RRAS2,GAB1,YWHAE,PIK3C3,SOS2,PIK3R6,PIK3R5,BID,IRS2,FRS2,FAS |
| Ascorbate Recycling (Cytosolic) | 1.4 | 0.667 | turquoise | GLRX,GSTO1 |
| Tyrosine Biosynthesis IV | 1.4 | 0.667 | turquoise | PCBD2,PCBD1 |
| Axonal Guidance Signaling | 1.39 | 0.147 | turquoise | RAP2B,DPYSL2,TUBA1B,MAPK1,MYL6,NFATC3,SOS2,LIMK2,TUBB,LIMK1,VEGFA,NCK2,PTK2,WNT7B,PLCB1,TUBA1C,PLXNB2,IRS2,ABLIM2,FRS2,TUBB3,CFL1,BMP8B,PLCL2,GAB1,PRKCD,ARPC2,RTN4,PIK3R6,PDGFD,RAP1B,RAP2A,PIK3CA,ARPC1B,ARHGEF7,PIK3R5,EPHA4,FZD1,ABLIM1,ACTR3,CDK5,SRGAP1,PIK3C3,PRKCE,PSMD14,MMP11,SEMA4A,GNG5,MYL12A,ITGB1,PXN,PLXNC1,GNAS,CXCR4,TUBB4B,ARPC5L,TUBG1,CHP1,GNAQ,TUBA4A,NFATC4,PLXND1,GNAI3,SEMA3A,PRKCI,RRAS2,WNT10A,BMP6,ARPC4,PRKCB |
| GDNF Family Ligand-Receptor Interactions | 1.39 | 0.19 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,ITPR1,DOK3,RRAS2,PDLIM7,GAB1,PIK3C3,PIK3R6,IRS2,FRS2 |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 1.39 | 0.164 | turquoise | RAP1B,PIK3CA,MAPK1,APOA2,PIK3R5,MAP3K5,RHOH,LYZ,PIK3C3,RHOU,PRKCE,SERPINA1,S100A8,IRS2,RHOF,TNFRSF1B,FRS2,MAP3K14,MAP3K9,CREBBP,TLR2,TLR4,PPP1R3D,PRKCI,GAB1,PRKCD,PIK3R6,IRF8,TNF,FNBP1,SIRPA,PRKCB |
| RhoA Signaling | 1.38 | 0.178 | turquoise | ARHGAP6,MPRIP,CFL1,MYL6,ARPC1B,ANLN,ARPC5L,RDX,CDC42EP3,PIP4K2B,RAPGEF6,LIMK2,PIP5K1B,TTN,LIMK1,PTK2,ACTR3,ARPC2,ACTG1,ARPC4,MYL12A |
| Phosphatidylcholine Biosynthesis I | 1.38 | 0.429 | turquoise | CEPT1,CHPT1,PCYT1A |
| Tryptophan Degradation to 2-amino-3-carboxymuconate Semialdehyde | 1.38 | 0.429 | turquoise | AFMID,KMO,KYNU |
| PPARα/RXRα Activation | 1.38 | 0.167 | turquoise | RAP1B,RAP2B,RAP2A,MAPK1,APOA2,CD36,TGFBR3,SMAD3,SOS2,NR2F1,TGFBR2,HSP90B1,HSP90AB1,TGFB2,PLCB1,STAT5B,GOT2,MAP3K14,GNAS,CREBBP,ACVR1,GNAQ,PLCL2,NCOA3,RRAS2,IL1B,MEF2C,RXRA,PRKCB |
| GNRH Signaling | 1.37 | 0.168 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,MAPK1,SOS2,MAP3K5,PTK2,CAMK2D,PLCB1,PRKCE,GNG5,MAP3K14,MAP3K9,PXN,GNAS,CREB3,CREBBP,GNAQ,HBEGF,ITPR1,CREB5,CALM1 (includes others),GNAI3,RRAS2,PRKCI,PRKCD,PRKCB |
| P2Y Purigenic Receptor Signaling Pathway | 1.37 | 0.173 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,CREBBP,CREB3,GNAQ,PIK3R5,PLCL2,CREB5,GNAI3,RRAS2,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,PLCB1,IRS2,GNG5,FRS2,PRKCB |
| IL-12 Signaling and Production in Macrophages | 1.37 | 0.171 | turquoise | PIK3CA,MAPK1,APOA2,PIK3R5,CEBPB,STAT4,TLR2,TLR4,LYZ,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,TGFB2,PRKCE,SERPINA1,S100A8,IRS2,IRF8,REL,RXRA,TNF,FRS2,PRKCB |
| Melanocyte Development and Pigmentation Signaling | 1.36 | 0.181 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,GNAS,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,CREB5,RPS6KA6,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,RPS6KA4,FRS2 |
| Cell Cycle: G1/S Checkpoint Regulation | 1.32 | 0.197 | turquoise | HDAC9,RBL2,CCND2,FOXO1,TFDP1,PA2G4,SMAD3,E2F7,TGFB2,CDK4,CDKN2C,MDM2,E2F2 |
| G-Protein Coupled Receptor Signaling | 1.31 | 0.155 | turquoise | RAP2B,RAP1B,RAP2A,HCAR3,PIK3CA,CAMK4,PDE7A,MAPK1,DUSP6,SOS2,PDE4A,PIK3R5,BRAF,CAMK2D,PDE7B,GDE1,PIK3C3,RGS10,PLCB1,PRKCE,IRS2,PDE4D,FRS2,SMPDL3A,HRH2,GNAS,CNR1,CREB3,CREBBP,GNAQ,GABBR1,CREB5,FPR1,GNAI3,P2RY13,RRAS2,P2RY14,GAB1,RASGRP1,PIK3R6,CALCR,DUSP4,PRKCB |
| Phagosome Maturation | 1.31 | 0.172 | turquoise | TUBA1B,TUBB3,ATP6V1D,VPS41,PRDX5,TUBB4B,PRDX1,HLA-B,TUBG1,TUBA4A,CANX,TUBB,ATP6V1A,VTI1B,DYNLRB1,ATP6V0A1,CTSA,DYNLL1,PIK3C3,TUBA1C,CTSC,NAPA,ATP6V0E1 |
| Pyrimidine Deoxyribonucleotides De Novo Biosynthesis I | 1.3 | 0.261 | turquoise | TYMS,DUT,RRM2B,RRM2,AK9,APOBEC3G |
| Glutathione-mediated Detoxification | 1.3 | 0.261 | turquoise | GSTM1,MGST1,GSTM2,MGST2,GSTO1,GSTK1 |
| IL-17 Signaling | 1.3 | 0.183 | turquoise | RAP2B,RAP1B,RAP2A,CXCL8,MAP3K14,PIK3CA,MAPK1,PIK3R5,CEBPB,RRAS2,GAB1,TIMP1,PIK3C3,PIK3R6,IRS2,PTGS2,FRS2 |
| TGF-β Signaling | 1.3 | 0.183 | turquoise | RAP2B,RAP1B,RAP2A,RUNX3,MAPK1,SMAD3,CREBBP,SOS2,ACVR1,TGIF1,TGFBR2,RRAS2,BMPR1A,RUNX2,TGFB2,VDR,PMEPA1 |
| Agrin Interactions at Neuromuscular Junction | 1.3 | 0.192 | turquoise | ITGB1,RAP1B,RAP2B,RAP2A,GABPB1,PXN,MAPK1,ARHGEF7,ITGAL,LAMC1,PTK2,RRAS2,UTRN,ACTG1 |
| Apelin Cardiomyocyte Signaling Pathway | 1.28 | 0.175 | turquoise | PIK3CA,MAPK1,MYL6,PIK3R5,PLCL2,ITPR1,ARNT,GNAI3,PRKCI,GAB1,PIK3C3,PRKCD,PIK3R6,PRKCE,PLCB1,IRS2,SLC8A1,FRS2,MYL12A,PRKCB |
| Endothelin-1 Signaling | 1.28 | 0.161 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,PIK3R5,BRAF,PLBD1,HMOX1,PIK3C3,PLCB1,PRKCE,IRS2,FRS2,PLA2G16,GNAS,PLD3,GNAQ,PLCL2,ITPR1,PLA2G6,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,RARRES3,PTGS2,PAFAH1B3,PRKCB |
| Docosahexaenoic Acid (DHA) Signaling | 1.27 | 0.204 | turquoise | PIK3CA,GAB1,FOXO1,PIK3C3,PIK3R6,PIK3R5,BIK,IL1B,BID,IRS2,FRS2 |
| ERK5 Signaling | 1.27 | 0.194 | turquoise | RAP1B,RAP2B,RAP2A,YWHAE,CREB3,CREBBP,GNAQ,CREB5,RPS6KA6,RRAS2,GAB1,MEF2C,RPS6KA4 |
| UVB-Induced MAPK Signaling | 1.27 | 0.194 | turquoise | PIK3CA,PRKCI,GAB1,MAPK1,PRKCD,PIK3C3,HIST1H3C,PIK3R6,PIK3R5,PRKCE,IRS2,FRS2,PRKCB |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 1.26 | 0.157 | turquoise | PIK3CA,CAMK4,MAPK1,NFATC3,CSNK1A1,PIK3R5,FZD1,MAP3K5,ACP5,TRADD,BMPR1A,RUNX2,WNT7B,PIK3C3,IRS2,TRAF5,TNFRSF1B,FRS2,BIRC3,ITGB1,MAP3K14,BMP8B,CHP1,NFATC4,CSF1R,IL7,CALM1 (includes others),WNT10A,GAB1,FOXO1,IL1RN,PIK3R6,CALCR,IL1B,BMP6,TNF |
| Role of MAPK Signaling in the Pathogenesis of Influenza | 1.25 | 0.189 | turquoise | PLBD1,RAP2B,RAP1B,PLA2G16,PLA2G6,RAP2A,RRAS2,MAPK1,RARRES3,PTGS2,CCL5,MAP3K5,TNF,PAFAH1B3 |
| UVC-Induced MAPK Signaling | 1.25 | 0.208 | turquoise | BRAF,RAP1B,RAP2B,RAP2A,RRAS2,PRKCI,MAPK1,PRKCD,PRKCE,PRKCB |
| Renin-Angiotensin Signaling | 1.25 | 0.171 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,GNAQ,PIK3R5,ITPR1,CCL5,PTK2,RRAS2,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,IRS2,TNF,FRS2,PRKCB |
| Cardiac Hypertrophy Signaling | 1.24 | 0.156 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MYL6,MAPK1,PIK3R5,MAP3K5,RHOH,TGFBR2,PIK3C3,RHOU,TGFB2,PLCB1,IRS2,RHOF,GNG5,FRS2,MYL12A,MAP3K9,MAP3K14,GNAS,MAPKAPK3,CHP1,IL6R,CREBBP,GNAQ,NFATC4,PLCL2,CALM1 (includes others),GNAI3,RRAS2,GAB1,PIK3R6,MEF2C,FNBP1 |
| CCR5 Signaling in Macrophages | 1.23 | 0.182 | turquoise | CAMK4,GNAS,MAPK1,CD4,TRGV9,CCL5,CCL3,FAS,CALM1 (includes others),GNAI3,PRKCI,PRKCD,FCER1G,PRKCE,GNG5,PRKCB |
| Tumoricidal Function of Hepatic Natural Killer Cells | 1.22 | 0.25 | turquoise | PRF1,GZMB,SRGN,BID,ITGAL,FAS |
| Complement System | 1.22 | 0.222 | turquoise | CFD,CD55,CD59,CR1,C5AR1,ITGAM,ITGAX,CR2 |
| Leukotriene Biosynthesis | 1.21 | 0.308 | turquoise | MGST2,GGT1,ALOX5,DPEP2 |
| Ephrin A Signaling | 1.2 | 0.194 | turquoise | PTK2,PIK3CA,CFL1,GAB1,PIK3C3,VAV3,PIK3R6,PIK3R5,IRS2,EPHA4,FRS2,LIMK1 |
| CTLA4 Signaling in Cytotoxic T Lymphocytes | 1.19 | 0.177 | turquoise | PIK3CA,TRGV9,AP1S2,HLA-B,PIK3R5,CD8A,AP2S1,CD80,GAB1,PIK3C3,LAT,PIK3R6,FCER1G,CD86,IRS2,FRS2,LCP2 |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation | 1.17 | 0.159 | turquoise | IGFBP4,MYL6,COL4A3,SMAD3,CXCR3,CCL5,MYH11,FAS,VEGFA,TGFBR2,TIMP1,TGFB2,TNFRSF1B,COL18A1,TIMP2,COL19A1,CXCL8,IL4R,COL9A1,FLT1,IL6R,IFNAR2,TLR4,LY96,CD14,IL1B,COL4A4,PDGFD,TNF |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 1.16 | 0.167 | turquoise | CXCL8,PIK3CA,C5AR1,NLRP3,MAPK1,PIK3R5,CCL5,TLR2,TLR4,CLEC7A,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,TGFB2,PRKCE,IL1B,IRS2,TNF,FRS2,PRKCB |
| Arsenate Detoxification I (Glutaredoxin) | 1.13 | 0.5 | turquoise | GLRX2,GSTO1 |
| Heme Biosynthesis from Uroporphyrinogen-III I | 1.13 | 0.5 | turquoise | PPOX,FECH |
| Spermine and Spermidine Degradation I | 1.13 | 0.5 | turquoise | SMOX,SAT1 |
| Phenylalanine Degradation I (Aerobic) | 1.13 | 0.5 | turquoise | PCBD2,PCBD1 |
| Neuregulin Signaling | 1.12 | 0.176 | turquoise | ITGB1,RAP1B,RAP2B,RAP2A,MAPK1,SOS2,HBEGF,HSP90B1,PRKCI,RRAS2,HSP90AB1,CDK5,PRKCD,PRKCE,STAT5B,PRKCB |
| Amyotrophic Lateral Sclerosis Signaling | 1.12 | 0.17 | turquoise | CAPN5,PIK3CA,GRIA1,GPX1,PIK3R5,SOD1,VEGFA,CAPNS1,GAB1,PIK3C3,PIK3R6,GLUL,BID,IRS2,CAPN2,BIRC3,FRS2,SSR4,CAPN3 |
| PDGF Signaling | 1.12 | 0.173 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,OCRL,RRAS2,GAB1,PIK3C3,PIK3R6,CAV1,IRS2,PDGFD,FRS2,PRKCB |
| Angiopoietin Signaling | 1.09 | 0.176 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,PIK3R5,BIRC5,PTK2,RRAS2,FOXO1,GAB1,PIK3C3,PIK3R6,IRS2,STAT5B,FRS2 |
| Antiproliferative Role of TOB in T Cell Signaling | 1.08 | 0.231 | turquoise | TGFBR2,CCNA2,MAPK1,PABPC4,SMAD3,TGFB2 |
| Prostanoid Biosynthesis | 1.08 | 0.333 | turquoise | PTGS2,TBXAS1,PTGES3 |
| Heme Biosynthesis II | 1.08 | 0.333 | turquoise | PPOX,FECH,ALAS1 |
| Endometrial Cancer Signaling | 1.06 | 0.181 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,SOS2,PIK3R6,PIK3R5,IRS2,FRS2 |
| TR/RXR Activation | 1.06 | 0.17 | turquoise | PIK3CA,CAMK4,PIK3R5,MDM2,NCOA3,ENO1,KLF9,SLC16A3,LDLR,GAB1,PIK3C3,PIK3R6,IRS2,STRBP,RXRA,THRB,FRS2 |
| RAR Activation | 1.05 | 0.155 | turquoise | PIK3CA,MAPK1,RDH10,SMAD3,MAP3K5,RARG,VEGFA,NR2F1,ALDH1A1,SMARCB1,TGFB2,PRKCE,STAT5B,ZBTB16,CITED2,SRA1,SDR16C5,CREBBP,SMARCD3,CSF2RB,RBP7,PRKCI,SMARCA2,PRKCD,NRIP1,REL,RXRA,PHF10,PRKCB |
| Adrenomedullin signaling pathway | 1.04 | 0.153 | turquoise | RAP2B,RAP1B,RAP2A,KCNN4,PIK3CA,KCNN3,CAMK4,MAPK1,SOS2,PIK3R5,ARNT,PTK2,BRAF,PIK3C3,PLCB1,IRS2,FRS2,GNAS,GNAQ,PLCL2,CEBPB,ITPR1,TTN,CALM1 (includes others),RRAS2,GAB1,IL1RN,PIK3R6,IL1B,RXRA,TNF |
| Reelin Signaling in Neurons | 1.02 | 0.17 | turquoise | ITGB1,MAP3K9,PIK3CA,CNR1,PIK3R5,ITGAL,GAB1,CDK5,PIK3C3,LYN,PIK3R6,LRP8,IRS2,ARHGEF10,FRS2,PAFAH1B3 |
| Small Cell Lung Cancer Signaling | 1.02 | 0.172 | turquoise | PIK3CA,TFDP1,PA2G4,CDK4,PIK3R5,PTK2,GAB1,PIK3C3,PIK3R6,BID,IRS2,PTGS2,TRAF5,RXRA,FRS2 |
| Sperm Motility | 1 | 0.164 | turquoise | PLA2G16,GNAS,CAMK4,PDE4A,PLCL2,ITPR1,PLBD1,PTK2,PLA2G6,CALM1 (includes others),PRKCI,PRKCD,PRKCE,PLCB1,RARRES3,PDE4D,LTK,PRKCB,PAFAH1B3 |
| Induction of Apoptosis by HIV1 | 1 | 0.183 | turquoise | MAP3K14,TRADD,SLC25A4,CXCR4,BID,MAP3K5,TNFRSF1B,TNF,BIRC3,FAS,BAK1 |
| MIF Regulation of Innate Immunity | 1 | 0.2 | turquoise | TLR4,PLA2G6,LY96,MIF,MAPK1,CD14,PTGS2,CD74 |
| Oncostatin M Signaling | 1 | 0.2 | turquoise | RAP2B,RAP1B,MT2A,TIMP3,RAP2A,RRAS2,MAPK1,STAT5B |
| Antioxidant Action of Vitamin C | 0.996 | 0.167 | turquoise | SLC2A5,PLA2G16,PLD3,MAPK1,PLCL2,GLRX,GSTO1,PLBD1,HMOX1,PLA2G6,CSF2RB,PLCB1,RARRES3,TXN,STAT5B,TNF,PAFAH1B3 |
| MSP-RON Signaling Pathway | 0.991 | 0.176 | turquoise | PIK3CA,PIK3R5,TLR2,TLR4,CSF2RB,ITGAM,GAB1,PIK3C3,PIK3R6,IRS2,ACTG1,FRS2,TNF |
| Iron homeostasis signaling pathway | 0.987 | 0.16 | turquoise | ATP6V1D,MAPK1,SMAD3,HSPA9,BMP8B,IL6R,SLC25A37,CD163,ATP6V1A,HMOX2,ATP6V0A1,ARNT,HMOX1,HSCB,BMPR1A,FECH,TFRC,BMP6,STAT5B,ATP6V0E1,SLC11A1 |
| OX40 Signaling Pathway | 0.983 | 0.191 | turquoise | HLA-DOA,HLA-DMA,TRGV9,CD4,HLA-DMB,HLA-B,FCER1G,HLA-DOB,TRAF5 |
| HMGB1 Signaling | 0.971 | 0.158 | turquoise | RAP2B,RAP1B,RAP2A,CXCL8,PIK3CA,MAPK1,PIK3R5,RHOH,TLR4,RRAS2,GAB1,PIK3C3,PIK3R6,TGFB2,RHOU,IL1B,IRS2,TNFRSF1B,RHOF,TNF,FRS2,FNBP1 |
| Pentose Phosphate Pathway | 0.963 | 0.3 | turquoise | PGD,TKT,TALDO1 |
| Mechanisms of Viral Exit from Host Cells | 0.951 | 0.195 | turquoise | PRKCI,CHMP2A,PRKCD,PRKCE,SH3GLB1,LMNB1,ACTG1,PRKCB |
| Role of IL-17F in Allergic Inflammatory Airway Diseases | 0.951 | 0.195 | turquoise | CXCL8,RPS6KA6,MAPK1,CREBBP,CREB3,IL1B,RPS6KA4,CREB5 |
| Pyruvate Fermentation to Lactate | 0.947 | 0.4 | turquoise | LDHA,LDHB |
| Tetrahydrofolate Salvage from 5,10-methenyltetrahydrofolate | 0.947 | 0.4 | turquoise | MTHFD2,MTHFD1 |
| Serine Biosynthesis | 0.947 | 0.4 | turquoise | PSAT1,PHGDH |
| Estrogen Receptor Signaling | 0.939 | 0.158 | turquoise | RAP2B,RAP1B,RAP2A,SRA1,MAPK1,CCNC,HIST1H3C,CREBBP,SOS2,MED30,TAF10,NR3C1,NCOA3,DDX5,RRAS2,THRAP3,RUNX2,NRIP1,ESR2,ESR1,POLR2L |
| Hereditary Breast Cancer Signaling | 0.928 | 0.155 | turquoise | RAP2B,RAP1B,RAP2A,HDAC9,PIK3CA,WEE1,CREBBP,TUBG1,PIK3R5,CDK4,SMARCD3,CHEK1,RRAS2,GAB1,GADD45A,SMARCA2,PIK3C3,SMARCB1,PIK3R6,IRS2,FRS2,POLR2L,PHF10 |
| IL-10 Signaling | 0.921 | 0.174 | turquoise | CCR1,MAP3K14,HMOX1,IL4R,MAPK1,IL1RN,FCGR2A,BLVRA,IL1B,CD14,FCGR2B,TNF |
| Methylthiopropionate Biosynthesis | 0.921 | 1 | turquoise | ADI1 |
| Glutamine Biosynthesis I | 0.921 | 1 | turquoise | GLUL |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 0.907 | 0.157 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,BMP8B,SOS2,PIK3R5,FZD1,RRAS2,GAB1,WNT10A,BMPR1A,WNT7B,PIK3C3,PIK3R6,IRS2,BMP6,FRS2,TCL1A |
| Ovarian Cancer Signaling | 0.907 | 0.154 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,TFDP1,PA2G4,MAPK1,FGF9,PIK3R5,CDK4,FZD1,VEGFA,BRAF,RRAS2,ARRB1,WNT10A,GAB1,WNT7B,PIK3C3,PIK3R6,IRS2,PTGS2,FRS2 |
| PI3K/AKT Signaling | 0.907 | 0.157 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3CA,MAPK1,YWHAE,SOS2,MDM2,MAP3K5,OCRL,HSP90B1,RRAS2,GAB1,HSP90AB1,FOXO1,LIMS1,PTGS2,MCL1,THEM4 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 0.896 | 0.184 | turquoise | MDM4,GADD45A,YWHAE,WEE1,TOP2A,MDM2,AURKA,HIPK2,CHEK1 |
| Antiproliferative Role of Somatostatin Receptor 2 | 0.893 | 0.167 | turquoise | BRAF,RAP1B,RAP2B,RAP2A,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,PIK3R6,PIK3R5,IRS2,GNG5,FRS2 |
| CREB Signaling in Neurons | 0.893 | 0.147 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MAPK1,GRIA1,SOS2,PIK3R5,CAMK2D,PIK3C3,PRKCE,PLCB1,IRS2,GNG5,FRS2,POLR2L,GNAS,CREB3,CREBBP,GNAQ,PLCL2,ITPR1,CREB5,GNAI3,CALM1 (includes others),RRAS2,PRKCI,GAB1,PRKCD,PIK3R6,PRKCB |
| Endocannabinoid Developing Neuron Pathway | 0.879 | 0.156 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,CNR1,CREBBP,CREB3,PIK3R5,CREB5,BRAF,GNAI3,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,MGLL,GNG5,FRS2 |
| FGF Signaling | 0.87 | 0.163 | turquoise | PIK3CA,MAPK1,FGF9,SOS2,CREB3,CREBBP,PIK3R5,ITPR1,MAP3K5,CREB5,GAB1,PIK3C3,PIK3R6,IRS2,FRS2 |
| Colorectal Cancer Metastasis Signaling | 0.863 | 0.145 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SMAD3,SOS2,PIK3R5,FZD1,RHOH,TGFBR2,BRAF,VEGFA,ARRB1,WNT7B,PIK3C3,RHOU,TGFB2,MMP11,IRS2,RHOF,GNG5,FRS2,GNAS,GRK3,IL6R,BIRC5,TLR2,TLR4,RRAS2,WNT10A,GAB1,PIK3R6,PTGS2,TNF,FNBP1 |
| Type II Diabetes Mellitus Signaling | 0.86 | 0.152 | turquoise | MAP3K14,PIK3CA,MAPK1,CD36,PKM,PIK3R5,CEBPB,MAP3K5,TRADD,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,SOCS2,IRS2,SLC27A3,TNFRSF1B,TNF,FRS2,ACSL1,PRKCB |
| Phospholipases | 0.854 | 0.175 | turquoise | PLA2G16,PLBD1,PLA2G6,HMOX1,PLD3,PLCB1,RARRES3,PLCL2,PLA1A,PAFAH1B3 |
| Amyloid Processing | 0.854 | 0.18 | turquoise | CAPN5,CAPNS1,MAPK1,CDK5,CSNK1A1,PRKCE,CAPN2,BACE2,CAPN3 |
| Atherosclerosis Signaling | 0.848 | 0.156 | turquoise | PLA2G16,CXCL8,CXCR4,APOA2,CD36,SELPLG,PLBD1,PLA2G6,LYZ,IL1RN,RARRES3,IL1B,S100A8,SERPINA1,PDGFD,COL18A1,ALOX5,TNF,PAFAH1B3 |
| Corticotropin Releasing Hormone Signaling | 0.842 | 0.153 | turquoise | RAP1B,GNAS,CAMK4,MAPK1,CNR1,CREBBP,CREB3,GNAQ,CRH,ITPR1,CREB5,VEGFA,BRAF,CALM1 (includes others),GNAI3,PRKCI,PRKCD,PRKCE,MEF2C,PTGS2,PRKCB |
| Bladder Cancer Signaling | 0.842 | 0.161 | turquoise | RAP1B,RAP2B,RAP2A,CXCL8,DAPK1,TFDP1,MAPK1,PA2G4,FGF9,CDK4,MDM2,VEGFA,RRAS2,MMP11,RASSF1 |
| Ephrin B Signaling | 0.824 | 0.167 | turquoise | NCK2,PTK2,GNAI3,PXN,GNAS,CFL1,MAPK1,CXCR4,VAV3,GNAQ,GNG5,LIMK1 |
| Role of p14/p19ARF in Tumor Suppression | 0.818 | 0.182 | turquoise | PIK3CA,GAB1,PIK3C3,PIK3R6,PIK3R5,IRS2,MDM2,FRS2 |
| LPS/IL-1 Mediated Inhibition of RXR Function | 0.815 | 0.146 | turquoise | ABCG1,ALAS1,FMO5,ABCB9,IRAK1,GSTM2,ALDH1A1,PPARGC1B,FABP5,HS3ST1,TNFRSF1B,GSTK1,ABCB1,GSTM1,MGST1,GSTO1,TLR4,LY96,MGST2,IL1RN,SMOX,SULT1A1,IL1B,CD14,SLC27A3,RXRA,TNF,ABCC4,NDST1,ACSL1 |
| TCA Cycle II (Eukaryotic) | 0.815 | 0.208 | turquoise | SDHA,SDHB,IDH3G,SUCLG1,MDH2 |
| Tryptophan Degradation III (Eukaryotic) | 0.815 | 0.208 | turquoise | HSD17B10,AFMID,KMO,KYNU,HSD17B8 |
| Arginine Biosynthesis IV | 0.807 | 0.333 | turquoise | GLUD1,ASL |
| Urea Cycle | 0.807 | 0.333 | turquoise | ASL,ARG1 |
| Pentose Phosphate Pathway (Non-oxidative Branch) | 0.807 | 0.333 | turquoise | TKT,TALDO1 |
| Adenine and Adenosine Salvage III | 0.807 | 0.333 | turquoise | ADA2,ADA |
| Purine Ribonucleosides Degradation to Ribose-1-phosphate | 0.807 | 0.333 | turquoise | ADA2,ADA |
| GDP-mannose Biosynthesis | 0.807 | 0.333 | turquoise | GPI,PMM1 |
| RANK Signaling in Osteoclasts | 0.796 | 0.157 | turquoise | MAP3K14,MAP3K9,PIK3CA,CAMK4,MAPK1,CHP1,PIK3R5,MAP3K5,CALM1 (includes others),GAB1,PIK3C3,PIK3R6,IRS2,TRAF5,BIRC3,FRS2 |
| Differential Regulation of Cytokine Production in Macrophages and T Helper Cells by IL-17A and IL-17F | 0.79 | 0.222 | turquoise | IL1B,CCL5,CCL3,TNF |
| Purine Nucleotides Degradation II (Aerobic) | 0.79 | 0.222 | turquoise | ADA2,NT5E,IMPDH1,ADA |
| PEDF Signaling | 0.788 | 0.158 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,PIK3R6,PIK3R5,IRS2,CFLAR,TCF7,FRS2,FAS |
| Thyroid Cancer Signaling | 0.78 | 0.178 | turquoise | RAP2B,RAP1B,BRAF,RAP2A,CXCL8,RRAS2,MAPK1,RXRA |
| FAT10 Cancer Signaling Pathway | 0.78 | 0.178 | turquoise | TGFBR2,CXCR4,SMAD3,TGFBR3,TGFB2,ACVR1,TNFRSF1B,TNF |
| Mouse Embryonic Stem Cell Pluripotency | 0.757 | 0.153 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,ID2,MAPK1,CREBBP,SOS2,PIK3R5,FZD1,RRAS2,GAB1,BMPR1A,PIK3C3,PIK3R6,IRS2,FRS2 |
| Factors Promoting Cardiogenesis in Vertebrates | 0.752 | 0.157 | turquoise | TGFBR2,PRKCI,BMPR1A,PRKCD,TGFBR3,BMP8B,CDC6,TGFB2,ACVR1,PRKCE,MEF2C,FZD1,BMP6,PRKCB |
| April Mediated Signaling | 0.742 | 0.179 | turquoise | MAP3K14,MAPK1,NFATC3,TNFRSF13B,NFATC4,TRAF5,TNFRSF17 |
| Adipogenesis pathway | 0.712 | 0.148 | turquoise | HDAC9,ARNTL,DGKD,TXNIP,SMAD3,XBP1,CEBPD,FBXW7,CEBPB,FZD1,NFATC4,CDK5,FOXO1,BMPR1A,EZH2,CEBPA,TCF7,STAT5B,TNF |
| Sertoli Cell-Sertoli Cell Junction Signaling | 0.706 | 0.144 | turquoise | RAP1B,RAP2B,ITGB1,TUBA1B,MAP3K9,MAP3K14,RAP2A,TUBB3,MAPK1,TUBB4B,TGFBR3,TUBG1,TUBA4A,AFDN,YBX3,MAP3K5,TUBB,RRAS2,KEAP1,TUBA1C,VCL,ACTN4,ACTG1,TNF,ACTN1 |
| Circadian Rhythm Signaling | 0.703 | 0.182 | turquoise | ARNTL,NR1D1,BHLHE41,CREBBP,CREB3,CREB5 |
| Role of IL-17A in Psoriasis | 0.701 | 0.231 | turquoise | CXCL8,S100A9,S100A8 |
| NAD biosynthesis II (from tryptophan) | 0.701 | 0.231 | turquoise | AFMID,KMO,KYNU |
| Lymphotoxin β Receptor Signaling | 0.695 | 0.159 | turquoise | MAP3K14,PIK3CA,MAPK1,GAB1,PIK3C3,CREBBP,PIK3R6,PIK3R5,IRS2,TRAF5,FRS2 |
| Sphingosine and Sphingosine-1-phosphate Metabolism | 0.695 | 0.286 | turquoise | SGPP2,SGPP1 |
| Superpathway of Serine and Glycine Biosynthesis I | 0.695 | 0.286 | turquoise | PSAT1,PHGDH |
| Aspartate Degradation II | 0.695 | 0.286 | turquoise | GOT2,MDH2 |
| PXR/RXR Activation | 0.686 | 0.161 | turquoise | ABCB1,GSTM1,ALDH1A1,GSTM2,FOXO1,ALAS1,RXRA,TNF,NR3C1,ABCB9 |
| Role of IL-17A in Arthritis | 0.668 | 0.157 | turquoise | CXCL8,PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R6,PIK3R5,IRS2,CCL5,PTGS2,FRS2 |
| B Cell Activating Factor Signaling | 0.664 | 0.171 | turquoise | MAP3K14,MAPK1,NFATC3,TNFRSF13B,NFATC4,TRAF5,TNFRSF17 |
| Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza | 0.664 | 0.171 | turquoise | CCR1,CXCL8,IL1RN,IL1B,CCL5,CCL3,TNF |
| Sphingosine-1-phosphate Signaling | 0.658 | 0.146 | turquoise | PIK3CA,MAPK1,GNAQ,PIK3R5,PLCL2,RHOH,PTK2,GNAI3,GAB1,PIK3C3,RHOU,PIK3R6,PLCB1,IRS2,PDGFD,RHOF,FRS2,FNBP1 |
| Eicosanoid Signaling | 0.658 | 0.159 | turquoise | PLA2G16,PLBD1,PLA2G6,RARRES3,PTGS2,GGT1,ALOX5,TBXAS1,DPEP2,PAFAH1B3 |
| Glutamate Receptor Signaling | 0.648 | 0.161 | turquoise | CALM1 (includes others),HOMER2,SLC1A4,CAMK4,GRIA1,GLUL,SLC38A1,HOMER3,GNG5 |
| UDP-D-xylose and UDP-D-glucuronate Biosynthesis | 0.646 | 0.5 | turquoise | UXS1 |
| Dolichol and Dolichyl Phosphate Biosynthesis | 0.646 | 0.5 | turquoise | DHDDS |
| β-alanine Degradation I | 0.646 | 0.5 | turquoise | ABAT |
| Spermine Biosynthesis | 0.646 | 0.5 | turquoise | SMS |
| Spermidine Biosynthesis I | 0.646 | 0.5 | turquoise | SRM |
| Sulfate Activation for Sulfonation | 0.646 | 0.5 | turquoise | PAPSS1 |
| Glycine Degradation (Creatine Biosynthesis) | 0.646 | 0.5 | turquoise | GATM |
| Glutamate Biosynthesis II | 0.646 | 0.5 | turquoise | GLUD1 |
| Glutamate Degradation X | 0.646 | 0.5 | turquoise | GLUD1 |
| Phenylalanine Degradation IV (Mammalian, via Side Chain) | 0.635 | 0.214 | turquoise | SMOX,SLC27A3,GOT2 |
| Colanic Acid Building Blocks Biosynthesis | 0.635 | 0.214 | turquoise | GPI,PMM1,GALK2 |
| tRNA Splicing | 0.629 | 0.167 | turquoise | SMPDL3A,PDE7B,PDE7A,GDE1,TSEN54,PDE4A,PDE4D |
| Polyamine Regulation in Colon Cancer | 0.62 | 0.19 | turquoise | PSME2,SAT1,OAZ1,PSME4 |
| FcγRIIB Signaling in B Lymphocytes | 0.616 | 0.149 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,RRAS2,GAB1,PIK3C3,PIK3R6,LYN,PIK3R5,IRS2,FCGR2B,FRS2 |
| Human Embryonic Stem Cell Pluripotency | 0.607 | 0.142 | turquoise | PIK3CA,GNAS,SMAD3,BMP8B,ACVR1,PIK3R5,FZD1,TGFBR2,FOXO1,GAB1,WNT10A,BMPR1A,WNT7B,PIK3C3,PIK3R6,TGFB2,IRS2,PDGFD,BMP6,FRS2 |
| Airway Pathology in Chronic Obstructive Pulmonary Disease | 0.606 | 0.25 | turquoise | CXCL8,TNF |
| Sucrose Degradation V (Mammalian) | 0.606 | 0.25 | turquoise | TPI1,ALDOA |
| Histidine Degradation III | 0.606 | 0.25 | turquoise | MTHFD2,MTHFD1 |
| CD40 Signaling | 0.602 | 0.15 | turquoise | MAP3K14,PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R6,PIK3R5,IRS2,PTGS2,TRAF5,FRS2,FCER2 |
| BMP signaling pathway | 0.602 | 0.15 | turquoise | RAP1B,RAP2B,RAP2A,MAGED1,RRAS2,CAMK4,MAPK1,BMPR1A,RUNX2,BMP8B,CREBBP,BMP6 |
| Triacylglycerol Biosynthesis | 0.595 | 0.163 | turquoise | PLPP5,ABHD5,LPCAT2,LPCAT4,MBOAT1,GPAT3,AGPAT3 |
| Acute Phase Response Signaling | 0.592 | 0.139 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K14,PIK3CA,MAPK1,APOA2,IL6R,SOS2,CEBPB,MAP3K5,NR3C1,HMOX2,IRAK1,TRADD,HMOX1,RRAS2,RBP7,IL1RN,IL1B,SOCS2,SERPINA1,TNFRSF1B,TNF |
| UVA-Induced MAPK Signaling | 0.592 | 0.144 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,PIK3R5,PLCL2,RPS6KA6,RRAS2,GAB1,PIK3C3,PIK3R6,PLCB1,IRS2,RPS6KA4,FRS2 |
| G Beta Gamma Signaling | 0.585 | 0.143 | turquoise | RAP2B,RAP1B,RAP2A,GNAS,MAPK1,SOS2,GNAQ,HBEGF,GNAI3,PRKCI,RRAS2,PRKCD,CAV1,PRKCE,GNG5,DNM2,PRKCB |
| Sumoylation Pathway | 0.585 | 0.146 | turquoise | RANBP2,CREBBP,MDM2,MAP3K5,RHOH,NR3C1,FAS,STUB1,RHOU,MYB,CEBPA,CBX4,RHOF,FNBP1 |
| Hepatic Cholestasis | 0.582 | 0.139 | turquoise | CXCL8,MAP3K14,ABCB1,SLC22A7,IRAK1,TLR4,LY96,PRKCI,SLCO3A1,ABCB4,IL1RN,PRKCD,TGFB2,PRKCE,IL1B,CD14,TNFRSF1B,RXRA,TNF,ESR1,PRKCB,IRAK2 |
| TNFR2 Signaling | 0.577 | 0.172 | turquoise | MAP3K14,TBK1,TNFRSF1B,TNF,BIRC3 |
| Telomere Extension by Telomerase | 0.575 | 0.2 | turquoise | TERF2,XRCC6,TINF2 |
| Adenosine Nucleotides Degradation II | 0.575 | 0.2 | turquoise | ADA2,NT5E,ADA |
| Vitamin-C Transport | 0.575 | 0.2 | turquoise | TXN,GLRX,GSTO1 |
| LXR/RXR Activation | 0.567 | 0.142 | turquoise | APOA2,CD36,ABCG1,TLR4,LY96,LYZ,LDLR,IL1RN,CD14,IL1B,SERPINA1,S100A8,PTGS2,TNFRSF1B,RXRA,TNF,CYP51A1 |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 0.565 | 0.138 | turquoise | GNAS,CAMK4,CSNK1G3,CREBBP,CREB3,CHP1,GNAQ,CSNK1A1,PAWR,PLCL2,ITPR1,CREB5,CALM1 (includes others),GNAI3,PPP1R3D,PRKCI,CDK5,PRKCD,PRKCE,PLCB1,CAMKK2,PRKCB |
| Toll-like Receptor Signaling | 0.565 | 0.149 | turquoise | TLR2,TLR4,MAP3K14,LY96,MAPK1,IL1RN,IL1B,CD14,TNF,IRAK1,IRAK2 |
| Osteoarthritis Pathway | 0.541 | 0.135 | turquoise | SIK3,SMAD3,FZD1,OCRL,TGFBR2,VEGFA,BMPR1A,RUNX2,ANXA5,NAMPT,S100A8,TNFRSF1B,ITGB1,TIMP3,CXCL8,CREB3,CREBBP,ANXA2,CEBPB,CREB5,TLR2,TLR4,S100A9,IL1B,MEF2C,PTGS2,TNF |
| Fatty Acid β-oxidation I | 0.539 | 0.167 | turquoise | HSD17B10,SLC27A3,ACAA2,ACSL1,HSD17B8 |
| Granulocyte Adhesion and Diapedesis | 0.535 | 0.137 | turquoise | ITGB1,CSF3R,CXCL8,CD99,HRH2,C5AR1,CXCR4,CKLF,RDX,CCL5,CCL3,ITGAL,FPR1,SELPLG,GNAI3,ITGAM,IL1RN,IL1B,MMP11,TNFRSF1B,CXCL2,TNF |
| Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F | 0.529 | 0.174 | turquoise | IL1B,CCL5,CCL3,TNF |
| Folate Transformations I | 0.529 | 0.222 | turquoise | MTHFD2,MTHFD1 |
| tRNA Charging | 0.519 | 0.158 | turquoise | WARS,CARS,TARS,VARS,SARS,EPRS |
| Death Receptor Signaling | 0.509 | 0.141 | turquoise | MAP3K14,TRADD,TNFRSF25,BID,TBK1,MAP3K5,CFLAR,TNFRSF1B,BIRC3,ACTG1,TNF,FAS,LIMK1 |
| Ceramide Signaling | 0.504 | 0.14 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CNKSR1,PIK3R5,RRAS2,GAB1,PIK3C3,PIK3R6,IRS2,TNFRSF1B,TNF,FRS2 |
| L-carnitine Biosynthesis | 0.496 | 0.333 | turquoise | TMLHE |
| NADH Repair | 0.496 | 0.333 | turquoise | GAPDH |
| Coenzyme A Biosynthesis | 0.496 | 0.333 | turquoise | PPCDC |
| S-methyl-5-thio-α-D-ribose 1-phosphate Degradation | 0.496 | 0.333 | turquoise | ADI1 |
| Glutathione Biosynthesis | 0.496 | 0.333 | turquoise | GCLC |
| L-cysteine Degradation III | 0.496 | 0.333 | turquoise | GOT2 |
| 4-hydroxyproline Degradation I | 0.496 | 0.333 | turquoise | GOT2 |
| Thiosulfate Disproportionation III (Rhodanese) | 0.496 | 0.333 | turquoise | TST |
| Glutamate Degradation II | 0.496 | 0.333 | turquoise | GOT2 |
| 4-aminobutyrate Degradation I | 0.496 | 0.333 | turquoise | ABAT |
| Aspartate Biosynthesis | 0.496 | 0.333 | turquoise | GOT2 |
| cAMP-mediated signaling | 0.487 | 0.132 | turquoise | HCAR3,CAMK4,MAPK1,CAMK1D,PDE7A,DUSP6,PDE4A,BRAF,CAMK2D,PDE7B,GDE1,RGS10,PDE4D,SMPDL3A,HRH2,GNAS,CNR1,CREB3,CREBBP,GABBR1,CREB5,FPR1,P2RY13,GNAI3,AKAP13,CALM1 (includes others),P2RY14,DUSP4,PKIG |
| EGF Signaling | 0.481 | 0.143 | turquoise | PIK3CA,MAPK1,GAB1,PIK3C3,SOS2,PIK3R6,PIK3R5,IRS2,ITPR1,FRS2 |
| Gα12/13 Signaling | 0.478 | 0.135 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,PXN,MAPK1,MYL6,PIK3R5,MAP3K5,PTK2,RRAS2,GAB1,PIK3C3,VAV3,PIK3R6,IRS2,MEF2C,FRS2,MYL12A |
| Granzyme A Signaling | 0.475 | 0.176 | turquoise | GZMA,PRF1,CREBBP |
| Calcium Transport I | 0.466 | 0.2 | turquoise | ANXA5,ATP2B4 |
| Opioid Signaling Pathway | 0.453 | 0.13 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,CAMK1D,MAPK1,SOS2,BRAF,ARRB1,CAMK2D,RGS10,PRKCE,PLCB1,GNG5,SIGMAR1,GNAS,GRK3,CREB3,CREBBP,ITPR1,CREB5,AP2S1,CALM1 (includes others),GNAI3,RPS6KA6,RRAS2,PRKCI,PRKCD,LYN,RPS6KA4,PRKCB |
| IL-17A Signaling in Gastric Cells | 0.452 | 0.16 | turquoise | CXCL8,MAPK1,CCL5,TNF |
| Gαi Signaling | 0.45 | 0.134 | turquoise | RAP2B,RAP1B,RAP2A,GNAS,MAPK1,CNR1,SOS2,GABBR1,FPR1,GNAI3,P2RY13,P2RY14,RRAS2,RGS10,CAV1,GNG5 |
| Role of BRCA1 in DNA Damage Response | 0.438 | 0.138 | turquoise | RBL2,ABRAXAS1,GADD45A,SMARCA2,E2F7,SMARCB1,BRIP1,E2F2,SMARCD3,PHF10,CHEK1 |
| Cyclins and Cell Cycle Regulation | 0.438 | 0.138 | turquoise | CCNA2,HDAC9,CCND2,PA2G4,TFDP1,WEE1,E2F7,CDK4,TGFB2,CDKN2C,E2F2 |
| Relaxin Signaling | 0.435 | 0.131 | turquoise | SMPDL3A,RAP1B,PIK3CA,GNAS,MAPK1,PDE7A,GNAQ,PIK3R5,PDE4A,BRAF,VEGFA,GNAI3,GAB1,PDE7B,GDE1,PIK3C3,PIK3R6,IRS2,PDE4D,GNG5,FRS2 |
| ATM Signaling | 0.435 | 0.135 | turquoise | CREB3,CREBBP,MDM2,CBX5,CREB5,SMC1A,CHEK1,MDM4,RNF168,GADD45A,RAD17,BID,TLK1 |
| 1D-myo-inositol Hexakisphosphate Biosynthesis II (Mammalian) | 0.432 | 0.167 | turquoise | ITPKB,INPP5A,OCRL |
| D-myo-inositol (1,3,4)-trisphosphate Biosynthesis | 0.432 | 0.167 | turquoise | ITPKB,INPP5A,OCRL |
| Stearate Biosynthesis I (Animals) | 0.432 | 0.146 | turquoise | SRD5A3,LPCAT4,SLC27A3,TBXAS1,ACSL1,THEM4 |
| Fatty Acid α-oxidation | 0.432 | 0.167 | turquoise | TMLHE,ALDH1A1,PTGS2 |
| Synaptic Long Term Depression | 0.424 | 0.13 | turquoise | RAP2B,RAP1B,PLA2G16,RAP2A,GNAS,MAPK1,GRIA1,GNAQ,CRH,PLCL2,ITPR1,PLBD1,PLA2G6,GNAI3,RRAS2,PRKCI,PRKCD,LYN,PRKCE,PLCB1,RARRES3,PRKCB,PAFAH1B3 |
| AMPK Signaling | 0.417 | 0.128 | turquoise | PFKFB3,CAB39,PIK3CA,GNAS,MAPK1,CREBBP,CREB3,AK3,PIK3R5,RAB8A,RAB39A,CREB5,PPM1G,SMARCD3,CCNA2,FOXO1,GAB1,SMARCA2,PIK3C3,SMARCB1,PIK3R6,RAB11A,IRS2,AK9,EEF2K,FRS2,CAMKK2,PHF10 |
| UDP-N-acetyl-D-galactosamine Biosynthesis II | 0.411 | 0.182 | turquoise | GPI,UAP1 |
| TWEAK Signaling | 0.41 | 0.147 | turquoise | TRADD,MAP3K14,TNFRSF25,BID,BIRC3 |
| Apelin Pancreas Signaling Pathway | 0.402 | 0.138 | turquoise | PIK3CA,GAB1,ERN1,PIK3C3,PIK3R5,PIK3R6,IRS2,FRS2 |
| Airway Inflammation in Asthma | 0.397 | 0.25 | turquoise | TNF |
| Uracil Degradation II (Reductive) | 0.397 | 0.25 | turquoise | DPYSL2 |
| Retinoate Biosynthesis II | 0.397 | 0.25 | turquoise | RBP7 |
| Pentose Phosphate Pathway (Oxidative Branch) | 0.397 | 0.25 | turquoise | PGD |
| Eumelanin Biosynthesis | 0.397 | 0.25 | turquoise | MIF |
| Glutathione Redox Reactions II | 0.397 | 0.25 | turquoise | GLRX |
| Thymine Degradation | 0.397 | 0.25 | turquoise | DPYSL2 |
| Melatonin Degradation II | 0.397 | 0.25 | turquoise | SMOX |
| Arginine Degradation I (Arginase Pathway) | 0.397 | 0.25 | turquoise | ARG1 |
| Trans, trans-farnesyl Diphosphate Biosynthesis | 0.397 | 0.25 | turquoise | IDI1 |
| NAD Biosynthesis III | 0.397 | 0.25 | turquoise | NAMPT |
| L-cysteine Degradation I | 0.397 | 0.25 | turquoise | GOT2 |
| Molybdenum Cofactor Biosynthesis | 0.397 | 0.25 | turquoise | GPHN |
| Acetate Conversion to Acetyl-CoA | 0.397 | 0.25 | turquoise | ACSL1 |
| GADD45 Signaling | 0.394 | 0.158 | turquoise | CCND2,GADD45A,CDK4 |
| Putrescine Degradation III | 0.394 | 0.158 | turquoise | ALDH1A1,SMOX,SAT1 |
| PTEN Signaling | 0.39 | 0.13 | turquoise | RAP2B,ITGB1,RAP1B,RAP2A,PIK3CA,MAPK1,FLT1,TGFBR3,SOS2,PIK3R5,OCRL,TGFBR2,PTK2,RRAS2,FOXO1,BMPR1A |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 0.368 | 0.126 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,ID2,MAPK1,FGF9,SMAD3,SOS2,PIK3R5,FZD1,TGFBR2,BRAF,NOTCH4,RRAS2,WNT10A,GAB1,WNT7B,PIK3C3,PIK3R6,TGFB2,IRS2,PDGFD,FRS2 |
| Cleavage and Polyadenylation of Pre-mRNA | 0.365 | 0.167 | turquoise | PAPOLA,PABPN1 |
| Glycogen Degradation II | 0.365 | 0.167 | turquoise | PGM1,TYMP |
| Mevalonate Pathway I | 0.365 | 0.167 | turquoise | PMVK,IDI1 |
| Pregnenolone Biosynthesis | 0.365 | 0.167 | turquoise | MICAL2,MICAL3 |
| CD27 Signaling in Lymphocytes | 0.361 | 0.135 | turquoise | MAP3K9,MAP3K14,CD70,BID,MAP3K5,TRAF5,CD27 |
| Cellular Effects of Sildenafil (Viagra) | 0.35 | 0.127 | turquoise | CALM1 (includes others),KCNN3,KCNN4,GNAS,MPRIP,CAMK4,MYL6,PABPC4,PDE4A,PLCB1,PDE4D,MYH11,ITPR1,PLCL2,ACTG1,MYL12A |
| Role of PI3K/AKT Signaling in the Pathogenesis of Influenza | 0.349 | 0.13 | turquoise | GNAI3,PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R6,PIK3R5,IRS2,CCL5,FRS2 |
| Wnt/Ca+ pathway | 0.344 | 0.131 | turquoise | NFATC3,CREB3,CREBBP,PLCB1,FZD1,NFATC4,PLCL2,CREB5 |
| autophagy | 0.341 | 0.132 | turquoise | ATG13,CTSA,VPS41,PIK3C3,WIPI1,ATG4A,CTSC |
| Tetrapyrrole Biosynthesis II | 0.325 | 0.2 | turquoise | ALAS1 |
| CMP-N-acetylneuraminate Biosynthesis I (Eukaryotes) | 0.325 | 0.2 | turquoise | NANS |
| Citrulline-Nitric Oxide Cycle | 0.325 | 0.2 | turquoise | ASL |
| Rapoport-Luebering Glycolytic Shunt | 0.325 | 0.2 | turquoise | PGAM1 |
| Galactose Degradation I (Leloir Pathway) | 0.325 | 0.2 | turquoise | GALK2 |
| Lactose Degradation III | 0.325 | 0.2 | turquoise | PSAP |
| dTMP De Novo Biosynthesis | 0.325 | 0.2 | turquoise | TYMS |
| Glutamate Degradation III (via 4-aminobutyrate) | 0.325 | 0.2 | turquoise | ABAT |
| Folate Polyglutamylation | 0.325 | 0.2 | turquoise | MTHFD1 |
| Fatty Acid Activation | 0.323 | 0.154 | turquoise | SLC27A3,ACSL1 |
| Urate Biosynthesis/Inosine 5'-phosphate Degradation | 0.323 | 0.154 | turquoise | NT5E,IMPDH1 |
| γ-glutamyl Cycle | 0.323 | 0.154 | turquoise | GCLC,GGT1 |
| Leptin Signaling in Obesity | 0.321 | 0.126 | turquoise | PIK3CA,MAPK1,GAB1,FOXO1,PIK3C3,PIK3R6,PIK3R5,PLCB1,IRS2,PLCL2,FRS2 |
| Calcium Signaling | 0.316 | 0.123 | turquoise | RAP2B,RAP1B,RAP2A,HDAC9,CAMK4,TP63,MAPK1,MYL6,CAMK1D,NFATC3,GRIA1,CHP1,CREB3,CREBBP,NFATC4,MYH11,ITPR1,CREB5,CALM1 (includes others),CAMK2D,MEF2C,SLC8A1,ATP2B4,CAMKK2 |
| Agranulocyte Adhesion and Diapedesis | 0.307 | 0.123 | turquoise | ITGB1,CXCL8,CD99,C5AR1,MYL6,CXCR4,CKLF,RDX,MYH11,CCL5,CCL3,ITGB7,SELPLG,GNAI3,IL1RN,IL1B,PODXL,MMP11,CXCL2,ACTG1,TNF |
| G Protein Signaling Mediated by Tubby | 0.306 | 0.133 | turquoise | GNAS,GNAQ,PLCB1,GNG5 |
| Endocannabinoid Cancer Inhibition Pathway | 0.291 | 0.122 | turquoise | PIK3CA,MAPK1,CNR1,CREBBP,CREB3,GNAQ,PIK3R5,VIM,CREB5,PTK2,VEGFA,GNAI3,CCND2,GAB1,PIK3C3,PIK3R6,IRS2,FRS2,CAMKK2 |
| DNA Double-Strand Break Repair by Non-Homologous End Joining | 0.288 | 0.143 | turquoise | DCLRE1C,XRCC6 |
| Chondroitin Sulfate Degradation (Metazoa) | 0.288 | 0.143 | turquoise | CEMIP2,HEXB |
| Isoleucine Degradation I | 0.288 | 0.143 | turquoise | HSD17B10,BCAT1 |
| Glycogen Degradation III | 0.288 | 0.143 | turquoise | PGM1,TYMP |
| Cell Cycle Control of Chromosomal Replication | 0.287 | 0.125 | turquoise | MCM6,CDK5,CDT1,CDC6,TOP2A,CDK4,MCM4 |
| Retinoate Biosynthesis I | 0.283 | 0.129 | turquoise | RBP7,ALDH1A1,RDH10,SDR16C5 |
| Superpathway of D-myo-inositol (1,4,5)-trisphosphate Metabolism | 0.272 | 0.13 | turquoise | ITPKB,INPP5A,OCRL |
| Chondroitin and Dermatan Biosynthesis | 0.271 | 0.167 | turquoise | CHPF |
| Arginine Degradation VI (Arginase 2 Pathway) | 0.271 | 0.167 | turquoise | ARG1 |
| Glycine Cleavage Complex | 0.271 | 0.167 | turquoise | GLDC |
| Selenocysteine Biosynthesis II (Archaea and Eukaryotes) | 0.271 | 0.167 | turquoise | SARS |
| UDP-N-acetyl-D-glucosamine Biosynthesis II | 0.271 | 0.167 | turquoise | UAP1 |
| Zymosterol Biosynthesis | 0.271 | 0.167 | turquoise | CYP51A1 |
| Glycogen Biosynthesis II (from UDP-D-Glucose) | 0.271 | 0.167 | turquoise | GYG1 |
| GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells | 0.266 | 0.12 | turquoise | GNAI3,GNAS,PRKCI,GPBAR1,PRKCD,GNAQ,PRKCE,PLCB1,ITPR1,PLCL2,GNG5,FFAR1,PRKCB |
| Inhibition of Angiogenesis by TSP1 | 0.262 | 0.125 | turquoise | TGFBR2,VEGFA,MAPK1,CD36 |
| Role of JAK2 in Hormone-like Cytokine Signaling | 0.262 | 0.125 | turquoise | SOCS2,IRS2,STAT5B,SIRPA |
| Superpathway of Citrulline Metabolism | 0.257 | 0.133 | turquoise | ASL,ARG1 |
| Dermatan Sulfate Degradation (Metazoa) | 0.257 | 0.133 | turquoise | CEMIP2,HEXB |
| Histidine Degradation VI | 0.257 | 0.133 | turquoise | MICAL2,MICAL3 |
| Parkinson's Signaling | 0.257 | 0.133 | turquoise | UCHL1,MAPK1 |
| Triacylglycerol Degradation | 0.254 | 0.122 | turquoise | PNPLA7,ABHD2,MGLL,NDST1,PLA1A |
| RAN Signaling | 0.23 | 0.125 | turquoise | RANBP2,KPNA2 |
| Glutaryl-CoA Degradation | 0.23 | 0.125 | turquoise | HSD17B10,HSD17B8 |
| Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate) | 0.23 | 0.125 | turquoise | PMVK,IDI1 |
| Thioredoxin Pathway | 0.228 | 0.143 | turquoise | TXN |
| Glycoaminoglycan-protein Linkage Region Biosynthesis | 0.228 | 0.143 | turquoise | XYLT1 |
| Phosphatidylethanolamine Biosynthesis II | 0.193 | 0.125 | turquoise | CEPT1 |
| Superoxide Radicals Degradation | 0.193 | 0.125 | turquoise | SOD1 |
| Coagulation System | 0 | 0.0857 | turquoise | SERPINA5,PLAUR,SERPINA1 |
| FXR/RXR Activation | 0 | 0.0887 | turquoise | ABCB4,FOXO1,IL1RN,APOA2,CREBBP,IL1B,SERPINA1,SLC22A7,SLC51B,RXRA,TNF |
| Tight Junction Signaling | 0 | 0.097 | turquoise | TIAM1,MYL6,CDK4,AFDN,YBX3,MYH11,VTI1B,TGFBR2,PRKCI,TGFB2,CEBPA,VCL,TNFRSF1B,ACTG1,NAPA,TNF |
| Activation of IRF by Cytosolic Pattern Recognition Receptors | 0 | 0.082 | turquoise | PPIB,CREBBP,SIKE1,TBK1,TNF |
| Role of RIG1-like Receptors in Antiviral Innate Immunity | 0 | 0.0476 | turquoise | CREBBP,TBK1 |
| Role of PKR in Interferon Induction and Antiviral Response | 0 | 0.0732 | turquoise | BID,TRAF5,TNF |
| IL-22 Signaling | 0 | 0.0833 | turquoise | MAPK1,STAT5B |
| 4-1BB Signaling in T Lymphocytes | 0 | 0.0938 | turquoise | MAP3K14,MAPK1,MAP3K5 |
| IL-15 Production | 0 | 0.107 | turquoise | PTK2,PRKCI,LTK |
| Role of Cytokines in Mediating Communication between Immune Cells | 0 | 0.0962 | turquoise | CXCL8,IL1RN,IL32,IL1B,TNF |
| Cardiomyocyte Differentiation via BMP Receptors | 0 | 0.105 | turquoise | BMPR1A,MEF2C |
| CDK5 Signaling | 0 | 0.0962 | turquoise | ITGB1,LAMC1,RAP1B,RAP2B,RAP2A,PPP1R3D,GNAS,RRAS2,MAPK1,CDK5 |
| Cell Cycle Regulation by BTG Family Proteins | 0 | 0.108 | turquoise | E2F7,BTG1,CDK4,E2F2 |
| Mitotic Roles of Polo-Like Kinase | 0 | 0.111 | turquoise | HSP90B1,HSP90AB1,PTTG1,WEE1,ANAPC5,KIF11,SMC1A |
| Maturity Onset Diabetes of Young (MODY) Signaling | 0 | 0.05 | turquoise | GAPDH |
| Role of CHK Proteins in Cell Cycle Checkpoint Control | 0 | 0.0877 | turquoise | RAD17,E2F7,TLK1,E2F2,CHEK1 |
| DNA Methylation and Transcriptional Repression Signaling | 0 | 0.1 | turquoise | CHD3,ARID4B,MBD2 |
| Androgen Signaling | 0 | 0.104 | turquoise | GNAI3,CALM1 (includes others),PRKCI,GNAS,CAMK4,MAPK1,PRKCD,SMAD3,CREBBP,GNAQ,PRKCE,GNG5,POLR2L,PRKCB |
| Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency | 0 | 0.111 | turquoise | NR2F1,ETS2,PHC1,JARID2,SH3GLB1 |
| Basal Cell Carcinoma Signaling | 0 | 0.0735 | turquoise | WNT10A,WNT7B,BMP8B,FZD1,BMP6 |
| Retinoic acid Mediated Apoptosis Signaling | 0 | 0.0847 | turquoise | BID,TNFRSF10C,CFLAR,RXRA,RARG |
| IL-1 Signaling | 0 | 0.0879 | turquoise | MAP3K14,GNAI3,GNAS,MAPK1,GNAQ,GNG5,IRAK1,IRAK2 |
| Neuroprotective Role of THOP1 in Alzheimer's Disease | 0 | 0.0777 | turquoise | GZMA,CFD,GZMK,NFYA,YWHAE,GZMB,HLA-B,IDE |
| Role of Wnt/GSK-3β Signaling in the Pathogenesis of Influenza | 0 | 0.0833 | turquoise | WNT10A,WNT7B,CSNK1G3,CSNK1A1,FZD1,NCOA3 |
| TNFR1 Signaling | 0 | 0.104 | turquoise | TRADD,MAP3K14,BID,TNF,BIRC3 |
| Intrinsic Prothrombin Activation Pathway | 0 | 0.0244 | turquoise | COL18A1 |
| Assembly of RNA Polymerase II Complex | 0 | 0.04 | turquoise | TAF10,POLR2L |
| IL-17A Signaling in Airway Cells | 0 | 0.1 | turquoise | PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R5,PIK3R6,IRS2,FRS2 |
| IL-17A Signaling in Fibroblasts | 0 | 0.0857 | turquoise | MAPK1,CEBPD,CEBPB |
| Role of JAK1, JAK2 and TYK2 in Interferon Signaling | 0 | 0.0417 | turquoise | IFNAR2 |
| Role of JAK family kinases in IL-6-type Cytokine Signaling | 0 | 0.12 | turquoise | MAPK1,IL6R,STAT5B |
| Hematopoiesis from Multipotent Stem Cells | 0 | 0.0833 | turquoise | IL7 |
| Transcriptional Regulatory Network in Embryonic Stem Cells | 0 | 0.02 | turquoise | SKIL |
| nNOS Signaling in Skeletal Muscle Cells | 0 | 0.075 | turquoise | CALM1 (includes others),CAMK4,CAPN3 |
| Netrin Signaling | 0 | 0.108 | turquoise | NCK2,NFATC3,CHP1,ABLIM2,NFATC4,ABLIM1,ENAH |
| Heparan Sulfate Biosynthesis | 0 | 0.108 | turquoise | PNPLA7,SULT1A1,XYLT1,EXT1,HS3ST1,NDST1,PLA1A |
| Bupropion Degradation | 0 | 0.0833 | turquoise | CYP51A1,CYP1B1 |
| Glucose and Glucose-1-phosphate Degradation | 0 | 0.1 | turquoise | PGM1 |
| Thyroid Hormone Metabolism II (via Conjugation and/or Degradation) | 0 | 0.0345 | turquoise | SULT1A1 |
| Nicotine Degradation III | 0 | 0.0465 | turquoise | CYP51A1,CYP1B1 |
| Dopamine Degradation | 0 | 0.107 | turquoise | ALDH1A1,SMOX,SULT1A1 |
| Heparan Sulfate Biosynthesis (Late Stages) | 0 | 0.103 | turquoise | PNPLA7,SULT1A1,EXT1,HS3ST1,NDST1,PLA1A |
| Pyrimidine Ribonucleotides De Novo Biosynthesis | 0 | 0.0465 | turquoise | SLC25A42,AK9 |
| Androgen Biosynthesis | 0 | 0.0833 | turquoise | SRD5A3 |
| Ubiquinol-10 Biosynthesis (Eukaryotic) | 0 | 0.118 | turquoise | MICAL2,MICAL3 |
| Acyl-CoA Hydrolysis | 0 | 0.1 | turquoise | THEM4 |
| The Visual Cycle | 0 | 0.105 | turquoise | RBP7,RDH10 |
| D-myo-inositol-5-phosphate Metabolism | 0 | 0.0779 | turquoise | ATP1A1,SGPP2,PPFIBP2,PLCB1,PIP4K2B,SGPP1,PAWR,ACP5,PPM1K,OCRL,PTPN12,SIRPA |
| Melatonin Degradation I | 0 | 0.06 | turquoise | SULT1A1,CYP51A1,CYP1B1 |
| γ-linolenate Biosynthesis II (Animals) | 0 | 0.118 | turquoise | SLC27A3,ACSL1 |
| NAD Salvage Pathway II | 0 | 0.0952 | turquoise | NT5E,ACP5 |
| D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis | 0 | 0.111 | turquoise | PLCB1,PIP4K2B,PIP5K1B |
| Estrogen Biosynthesis | 0 | 0.108 | turquoise | HSD17B10,CYP51A1,CYP1B1,HSD17B8 |
| Tryptophan Degradation X (Mammalian, via Tryptamine) | 0 | 0.1 | turquoise | ALDH1A1,SMOX |
| Chondroitin Sulfate Biosynthesis | 0 | 0.0962 | turquoise | SULT1A1,XYLT1,CHPF,HS3ST1,NDST1 |
| Dermatan Sulfate Biosynthesis | 0 | 0.0926 | turquoise | SULT1A1,XYLT1,CHPF,HS3ST1,NDST1 |
| Cholesterol Biosynthesis I | 0 | 0.0769 | turquoise | CYP51A1 |
| NAD Phosphorylation and Dephosphorylation | 0 | 0.1 | turquoise | ACP5 |
| Dermatan Sulfate Biosynthesis (Late Stages) | 0 | 0.0732 | turquoise | SULT1A1,HS3ST1,NDST1 |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0 | 0.0735 | turquoise | ATP1A1,SGPP2,PPFIBP2,SGPP1,PAWR,ACP5,PPM1K,OCRL,PTPN12,SIRPA |
| Nicotine Degradation II | 0 | 0.0612 | turquoise | FMO5,CYP51A1,CYP1B1 |
| Citrulline Biosynthesis | 0 | 0.111 | turquoise | ARG1 |
| Superpathway of Inositol Phosphate Compounds | 0 | 0.11 | turquoise | CD19,PIK3CA,PPFIBP2,PIK3R5,PIP4K2B,PAWR,PIP5K1B,ACP5,PPM1K,INPP5A,PTPN12,OCRL,ATP1A1,GAB1,ITPKB,CD80,PIK3C3,SGPP2,PIK3R6,CD86,PLCB1,SGPP1,IRS2,FRS2,SIRPA |
| Valine Degradation I | 0 | 0.111 | turquoise | BCAT1,ABAT |
| Mitochondrial L-carnitine Shuttle Pathway | 0 | 0.118 | turquoise | SLC27A3,ACSL1 |
| Serotonin Degradation | 0 | 0.0545 | turquoise | ALDH1A1,SMOX,SULT1A1 |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0 | 0.0735 | turquoise | ATP1A1,SGPP2,PPFIBP2,SGPP1,PAWR,ACP5,PPM1K,OCRL,PTPN12,SIRPA |
| Leucine Degradation I | 0 | 0.111 | turquoise | BCAT1 |
| 3-phosphoinositide Degradation | 0 | 0.0867 | turquoise | INPP4A,ATP1A1,SGPP2,PPFIBP2,MTM1,MTMR1,SGPP1,PAWR,ACP5,PPM1K,PTPN12,OCRL,SIRPA |
| D-myo-inositol (1,4,5)-trisphosphate Degradation | 0 | 0.118 | turquoise | INPP5A,OCRL |
| 3-phosphoinositide Biosynthesis | 0 | 0.113 | turquoise | CD19,PIK3CA,PPFIBP2,PIK3R5,PIP4K2B,PAWR,PIP5K1B,ACP5,PPM1K,PTPN12,OCRL,ATP1A1,GAB1,CD80,PIK3C3,SGPP2,PIK3R6,CD86,SGPP1,IRS2,FRS2,SIRPA |
| Retinol Biosynthesis | 0 | 0.0526 | turquoise | RBP7,RDH10 |
| Pyrimidine Ribonucleotides Interconversion | 0 | 0.0488 | turquoise | SLC25A42,AK9 |
| Purine Nucleotides De Novo Biosynthesis II | 0 | 0.0909 | turquoise | IMPDH1 |
| Cholesterol Biosynthesis II (via 24,25-dihydrolanosterol) | 0 | 0.0769 | turquoise | CYP51A1 |
| Histamine Degradation | 0 | 0.0667 | turquoise | ALDH1A1 |
| Chondroitin Sulfate Biosynthesis (Late Stages) | 0 | 0.0909 | turquoise | SULT1A1,CHPF,HS3ST1,NDST1 |
| Guanosine Nucleotides Degradation III | 0 | 0.0833 | turquoise | NT5E |
| Cholesterol Biosynthesis III (via Desmosterol) | 0 | 0.0769 | turquoise | CYP51A1 |
| Superpathway of Melatonin Degradation | 0 | 0.0727 | turquoise | SMOX,SULT1A1,CYP1B1,CYP51A1 |
| Noradrenaline and Adrenaline Degradation | 0 | 0.0625 | turquoise | ALDH1A1,SMOX |
| Acetone Degradation I (to Methylglyoxal) | 0 | 0.069 | turquoise | CYP51A1,CYP1B1 |
| GDP-glucose Biosynthesis | 0 | 0.111 | turquoise | PGM1 |
| Oxidative Ethanol Degradation III | 0 | 0.118 | turquoise | ALDH1A1,ACSL1 |
| Ethanol Degradation IV | 0 | 0.0952 | turquoise | ALDH1A1,ACSL1 |
| Ethanol Degradation II | 0 | 0.069 | turquoise | ALDH1A1,ACSL1 |
| Superpathway of Methionine Degradation | 0 | 0.0294 | turquoise | GOT2 |
| Superpathway of Cholesterol Biosynthesis | 0 | 0.111 | turquoise | PMVK,IDI1,CYP51A1 |
| DNA damage-induced 14-3-3σ Signaling | 0 | 0.0526 | turquoise | RAD17 |
| Gαs Signaling | 0 | 0.0962 | turquoise | BRAF,HCAR3,HRH2,GNAS,MAPK1,CNR1,CREB3,CREBBP,GNG5,CREB5 |
| Inhibition of Matrix Metalloproteases | 0 | 0.105 | turquoise | TIMP3,TIMP1,MMP11,TIMP2 |
| HIPPO signaling | 0 | 0.0833 | turquoise | PPP1R3D,SAV1,YWHAE,RASSF6,SMAD3,TEAD2,RASSF1 |
| PCP pathway | 0 | 0.103 | turquoise | WNT10A,VANGL1,WNT7B,DAAM1,FZD1,PRICKLE1 |
| Nucleotide Excision Repair Pathway | 0 | 0.0286 | turquoise | POLR2L |
| Cardiac β-adrenergic Signaling | 0 | 0.0935 | turquoise | SMPDL3A,AKAP13,PPP1R3D,GNAS,PDE7B,PDE7A,GDE1,GRK3,PDE4A,PDE4D,GNG5,SLC8A1,PKIG |
| Interferon Signaling | 0 | 0.0556 | turquoise | IFNAR2,BAK1 |
| GABA Receptor Signaling | 0 | 0.0753 | turquoise | KCNN4,KCNN3,GNAS,ABAT,GABBR1,GPHN,AP2S1 |
| Wnt/β-catenin Signaling | 0 | 0.0838 | turquoise | TGFBR3,CSNK1G3,CREBBP,ACVR1,CSNK1A1,GNAQ,MDM2,FZD1,RARG,TGFBR2,WNT10A,WNT7B,TLE3,TGFB2 |
| Serotonin Receptor Signaling | 0 | 0.05 | turquoise | SMOX,PCBD1 |
| Insulin Receptor Signaling | 0 | 0.119 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,PIK3R5,OCRL,PPP1R3D,PRKCI,RRAS2,GAB1,FOXO1,PIK3C3,PIK3R6,IRS2,FRS2 |
| Dopamine Receptor Signaling | 0 | 0.0395 | turquoise | PPP1R3D,SMOX,PCBD1 |
| Notch Signaling | 0 | 0.108 | turquoise | NOTCH4,FURIN,DTX1,DTX4 |
| GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell | 0 | 0.0833 | turquoise | GNAI3,GNAS,GNAQ,PLCB1,ITPR1,PLCL2 |
| Gustation Pathway | 0 | 0.0775 | turquoise | SMPDL3A,P2RY13,P2RY14,PDE7A,PDE7B,GDE1,PDE4A,P2RY8,PDE4D,ITPR1,GNG5 |
| SPINK1 Pancreatic Cancer Pathway | 0 | 0.0727 | turquoise | TGFBR2,CTSA,SMAD3,CELA3B |
| NER Pathway | 0 | 0.0714 | turquoise | UBE2N,RBX1,COPS6,TOP2A,COPS8,POLD4,POLR2L |
| Apelin Liver Signaling Pathway | 0 | 0.115 | turquoise | COL18A1,TNF,FAS |
| Apelin Cardiac Fibroblast Signaling Pathway | 0 | 0.0455 | turquoise | TGFB2 |
| Apelin Adipocyte Signaling Pathway | 0 | 0.118 | turquoise | GSTM1,GNAI3,MGST1,GSTM2,MAPK1,MGST2,GPX1,SOD1,GSTK1 |
| Apelin Muscle Signaling Pathway | 0 | 0.0556 | turquoise | GNAS |
| Cleavage and Polyadenylation of Pre-mRNA | 1.53 | 0.0833 | grey | PAPOLA |
| Tight Junction Signaling | 1.19 | 0.0121 | grey | JAM3,PATJ |
| nNOS Signaling in Skeletal Muscle Cells | 1.02 | 0.025 | grey | SNTB1 |
| Triacylglycerol Degradation | 1.01 | 0.0244 | grey | ABHD6 |
| Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency | 0.971 | 0.0222 | grey | PHC3 |
| nNOS Signaling in Neurons | 0.963 | 0.0217 | grey | CAPN7 |
| Amyloid Processing | 0.928 | 0.02 | grey | CAPN7 |
| Regulation of Cellular Mechanics by Calpain Protease | 0.854 | 0.0167 | grey | CAPN7 |
| HIPPO signaling | 0.721 | 0.0119 | grey | PATJ |
| Apoptosis Signaling | 0.674 | 0.0105 | grey | CAPN7 |
| FAK Signaling | 0.631 | 0.00943 | grey | CAPN7 |
| Amyotrophic Lateral Sclerosis Signaling | 0.611 | 0.00893 | grey | CAPN7 |
| Adipogenesis pathway | 0.561 | 0.00781 | grey | TXNIP |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0.539 | 0.00735 | grey | MTMR7 |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0.539 | 0.00735 | grey | MTMR7 |
| Cardiac β-adrenergic Signaling | 0.53 | 0.00719 | grey | AKAP13 |
| 3-phosphoinositide Degradation | 0.503 | 0.00667 | grey | MTMR7 |
| D-myo-inositol-5-phosphate Metabolism | 0.493 | 0.00649 | grey | MTMR7 |
| Regulation of eIF4 and p70S6K Signaling | 0.484 | 0.00633 | grey | RPS3A |
| Granulocyte Adhesion and Diapedesis | 0.478 | 0.00621 | grey | JAM3 |
| Agranulocyte Adhesion and Diapedesis | 0.457 | 0.00585 | grey | JAM3 |
| Sertoli Cell-Sertoli Cell Junction Signaling | 0.451 | 0.00575 | grey | JAM3 |
| 3-phosphoinositide Biosynthesis | 0.413 | 0.00515 | grey | MTMR7 |
| mTOR Signaling | 0.401 | 0.00498 | grey | RPS3A |
| Leukocyte Extravasation Signaling | 0.394 | 0.00485 | grey | JAM3 |
| Integrin Signaling | 0.382 | 0.00469 | grey | CAPN7 |
| EIF2 Signaling | 0.379 | 0.00465 | grey | RPS3A |
| cAMP-mediated signaling | 0.372 | 0.00455 | grey | AKAP13 |
| Superpathway of Inositol Phosphate Compounds | 0.36 | 0.00439 | grey | MTMR7 |
| Huntington's Disease Signaling | 0.334 | 0.00405 | grey | CAPN7 |
| Protein Kinase A Signaling | 0.21 | 0.00263 | grey | AKAP13 |
| Wnt/β-catenin Signaling | 1.96 | 0.024 | brown | SOX4,TLE3,CD44,TLE1 |
| Amyloid Processing | 1.56 | 0.04 | brown | PRKACB,BACE2 |
| Epithelial Adherens Junction Signaling | 1.41 | 0.0208 | brown | WASF1,JUP,PTEN |
| Actin Nucleation by ARP-WASP Complex | 1.39 | 0.0323 | brown | RHOB,WASF1 |
| Ovarian Cancer Signaling | 1.38 | 0.0201 | brown | PRKACB,CD44,PTEN |
| D-myo-inositol-5-phosphate Metabolism | 1.34 | 0.0195 | brown | PLD4,PTPRJ,PTEN |
| Calcium Transport I | 1.3 | 0.1 | brown | ATP2A3 |
| Tec Kinase Signaling | 1.27 | 0.0182 | brown | TNFRSF21,RHOB,TNFRSF10B |
| Guanosine Nucleotides Degradation III | 1.22 | 0.0833 | brown | NT5E |
| RhoGDI Signaling | 1.21 | 0.0172 | brown | RHOB,CD44,WASF1 |
| Sertoli Cell-Sertoli Cell Junction Signaling | 1.21 | 0.0172 | brown | PRKACB,JUP,PTEN |
| Glioma Invasiveness Signaling | 1.21 | 0.0256 | brown | RHOB,CD44 |
| BMP signaling pathway | 1.19 | 0.025 | brown | PRKACB,BMP3 |
| Choline Biosynthesis III | 1.19 | 0.0769 | brown | PLD4 |
| Leukotriene Biosynthesis | 1.19 | 0.0769 | brown | ALOX5 |
| Urate Biosynthesis/Inosine 5'-phosphate Degradation | 1.19 | 0.0769 | brown | NT5E |
| DNA Double-Strand Break Repair by Non-Homologous End Joining | 1.15 | 0.0714 | brown | LIG4 |
| Regulation of Actin-based Motility by Rho | 1.15 | 0.0238 | brown | RHOB,WASF1 |
| Adenosine Nucleotides Degradation II | 1.13 | 0.0667 | brown | NT5E |
| ILK Signaling | 1.11 | 0.0155 | brown | LIMS2,RHOB,PTEN |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 1.09 | 0.0217 | brown | PLD4,PTEN |
| Death Receptor Signaling | 1.09 | 0.0217 | brown | TNFRSF21,TNFRSF10B |
| Purine Nucleotides Degradation II (Aerobic) | 1.05 | 0.0556 | brown | NT5E |
| D-myo-inositol (1,3,4)-trisphosphate Biosynthesis | 1.05 | 0.0556 | brown | PTEN |
| Integrin Signaling | 1.01 | 0.0141 | brown | RHOB,ASAP1,PTEN |
| Neuroprotective Role of THOP1 in Alzheimer's Disease | 1 | 0.0194 | brown | MME,PRKACB |
| NAD Salvage Pathway II | 0.987 | 0.0476 | brown | NT5E |
| Endoplasmic Reticulum Stress Pathway | 0.987 | 0.0476 | brown | XBP1 |
| FAK Signaling | 0.983 | 0.0189 | brown | ASAP1,PTEN |
| Nitric Oxide Signaling in the Cardiovascular System | 0.955 | 0.0182 | brown | PRKACB,ATP2A3 |
| Phospholipase C Signaling | 0.951 | 0.0133 | brown | PLD4,RHOB,IGHG1 |
| Superpathway of D-myo-inositol (1,4,5)-trisphosphate Metabolism | 0.951 | 0.0435 | brown | PTEN |
| Superpathway of Inositol Phosphate Compounds | 0.943 | 0.0132 | brown | PLD4,PTPRJ,PTEN |
| p53 Signaling | 0.936 | 0.0177 | brown | TNFRSF10B,PTEN |
| RhoA Signaling | 0.907 | 0.0169 | brown | CDC42EP3,WASF1 |
| Gαi Signaling | 0.9 | 0.0168 | brown | PRKACB,RGS10 |
| Phagosome Formation | 0.886 | 0.0165 | brown | RHOB,IGHG1 |
| D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis | 0.883 | 0.037 | brown | PLD4 |
| Rac Signaling | 0.876 | 0.0163 | brown | CD44,WASF1 |
| Protein Kinase A Signaling | 0.873 | 0.0105 | brown | PRKACB,PTPRJ,CDC14B,PTEN |
| Signaling by Rho Family GTPases | 0.86 | 0.012 | brown | RHOB,CDC42EP3,WASF1 |
| Sonic Hedgehog Signaling | 0.854 | 0.0345 | brown | PRKACB |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0.807 | 0.0147 | brown | PTPRJ,PTEN |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0.807 | 0.0147 | brown | PTPRJ,PTEN |
| Cardiac β-adrenergic Signaling | 0.79 | 0.0144 | brown | PRKACB,ATP2A3 |
| Autoimmune Thyroid Disease Signaling | 0.78 | 0.0286 | brown | IGHG1 |
| Hematopoiesis from Pluripotent Stem Cells | 0.78 | 0.0286 | brown | IGHG1 |
| Gustation Pathway | 0.777 | 0.0141 | brown | PRKACB,P2RX1 |
| Insulin Receptor Signaling | 0.772 | 0.014 | brown | PRKACB,PTEN |
| Allograft Rejection Signaling | 0.747 | 0.0263 | brown | IGHG1 |
| 3-phosphoinositide Degradation | 0.74 | 0.0133 | brown | PTPRJ,PTEN |
| Primary Immunodeficiency Signaling | 0.717 | 0.0244 | brown | IGHG1 |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 0.701 | 0.0126 | brown | PRKACB,ATP2A3 |
| Gαq Signaling | 0.699 | 0.0125 | brown | PLD4,RHOB |
| FAT10 Cancer Signaling Pathway | 0.682 | 0.0222 | brown | ACKR3 |
| Tight Junction Signaling | 0.678 | 0.0121 | brown | PRKACB,PTEN |
| Cancer Drug Resistance By Drug Efflux | 0.674 | 0.0217 | brown | PTEN |
| Glioblastoma Multiforme Signaling | 0.668 | 0.0119 | brown | RHOB,PTEN |
| Nicotine Degradation II | 0.65 | 0.0204 | brown | FMO1 |
| Germ Cell-Sertoli Cell Junction Signaling | 0.644 | 0.0115 | brown | RHOB,JUP |
| Phototransduction Pathway | 0.642 | 0.02 | brown | PRKACB |
| Axonal Guidance Signaling | 0.636 | 0.00842 | brown | MME,PRKACB,BMP3,ADAM23 |
| Semaphorin Signaling in Neurons | 0.627 | 0.0192 | brown | RHOB |
| autophagy | 0.62 | 0.0189 | brown | CTSH |
| Calcium-induced T Lymphocyte Apoptosis | 0.606 | 0.0182 | brown | ATP2A3 |
| Unfolded protein response | 0.606 | 0.0182 | brown | XBP1 |
| SPINK1 Pancreatic Cancer Pathway | 0.606 | 0.0182 | brown | CPM |
| RAR Activation | 0.599 | 0.0107 | brown | PRKACB,PTEN |
| B Cell Receptor Signaling | 0.599 | 0.0107 | brown | IGHG1,PTEN |
| Phospholipases | 0.592 | 0.0175 | brown | PLD4 |
| Apelin Pancreas Signaling Pathway | 0.585 | 0.0172 | brown | PRKACB |
| Retinoic acid Mediated Apoptosis Signaling | 0.578 | 0.0169 | brown | TNFRSF10B |
| 3-phosphoinositide Biosynthesis | 0.577 | 0.0103 | brown | PTPRJ,PTEN |
| Calcium Signaling | 0.573 | 0.0103 | brown | PRKACB,ATP2A3 |
| PXR/RXR Activation | 0.561 | 0.0161 | brown | PRKACB |
| Melanoma Signaling | 0.554 | 0.0159 | brown | PTEN |
| mTOR Signaling | 0.554 | 0.00995 | brown | PLD4,RHOB |
| Eicosanoid Signaling | 0.554 | 0.0159 | brown | ALOX5 |
| IL-8 Signaling | 0.55 | 0.00985 | brown | PLD4,RHOB |
| Netrin Signaling | 0.544 | 0.0154 | brown | PRKACB |
| Basal Cell Carcinoma Signaling | 0.527 | 0.0147 | brown | BMP3 |
| Melatonin Signaling | 0.516 | 0.0143 | brown | PRKACB |
| AMPK Signaling | 0.507 | 0.00917 | brown | PRKACB,TBC1D1 |
| Endometrial Cancer Signaling | 0.506 | 0.0139 | brown | PTEN |
| Hypoxia Signaling in the Cardiovascular System | 0.506 | 0.0139 | brown | PTEN |
| GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell | 0.506 | 0.0139 | brown | PRKACB |
| cAMP-mediated signaling | 0.502 | 0.00909 | brown | PRKACB,RGS10 |
| Toll-like Receptor Signaling | 0.496 | 0.0135 | brown | TICAM2 |
| Molecular Mechanisms of Cancer | 0.491 | 0.00775 | brown | PRKACB,RHOB,BMP3 |
| ErbB2-ErbB3 Signaling | 0.487 | 0.0132 | brown | PTEN |
| Dopamine Receptor Signaling | 0.487 | 0.0132 | brown | PRKACB |
| Apelin Adipocyte Signaling Pathway | 0.487 | 0.0132 | brown | PRKACB |
| Communication between Innate and Adaptive Immune Cells | 0.478 | 0.0128 | brown | IGHG1 |
| IL-17A Signaling in Airway Cells | 0.469 | 0.0125 | brown | PTEN |
| Cardiac Hypertrophy Signaling | 0.46 | 0.00844 | brown | PRKACB,RHOB |
| Opioid Signaling Pathway | 0.455 | 0.00837 | brown | PRKACB,RGS10 |
| HIPPO signaling | 0.451 | 0.0119 | brown | CD44 |
| Small Cell Lung Cancer Signaling | 0.439 | 0.0115 | brown | PTEN |
| Leptin Signaling in Obesity | 0.439 | 0.0115 | brown | PRKACB |
| IL-7 Signaling Pathway | 0.435 | 0.0114 | brown | IGHG1 |
| Colorectal Cancer Metastasis Signaling | 0.433 | 0.00803 | brown | PRKACB,RHOB |
| Factors Promoting Cardiogenesis in Vertebrates | 0.432 | 0.0112 | brown | BMP3 |
| Macropinocytosis Signaling | 0.432 | 0.0112 | brown | RAB34 |
| α-Adrenergic Signaling | 0.428 | 0.0111 | brown | PRKACB |
| Neuregulin Signaling | 0.424 | 0.011 | brown | PTEN |
| IL-1 Signaling | 0.424 | 0.011 | brown | PRKACB |
| Sumoylation Pathway | 0.406 | 0.0104 | brown | RHOB |
| Acute Myeloid Leukemia Signaling | 0.402 | 0.0103 | brown | JUP |
| NER Pathway | 0.399 | 0.0102 | brown | LIG4 |
| Prostate Cancer Signaling | 0.389 | 0.0099 | brown | PTEN |
| Antioxidant Action of Vitamin C | 0.386 | 0.0098 | brown | PLD4 |
| CDK5 Signaling | 0.38 | 0.00962 | brown | PRKACB |
| Gαs Signaling | 0.38 | 0.00962 | brown | PRKACB |
| Cholecystokinin/Gastrin-mediated Signaling | 0.377 | 0.00952 | brown | RHOB |
| Melanocyte Development and Pigmentation Signaling | 0.377 | 0.00952 | brown | PRKACB |
| G-Protein Coupled Receptor Signaling | 0.375 | 0.00719 | brown | PRKACB,RGS10 |
| GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells | 0.368 | 0.00926 | brown | PRKACB |
| IGF-1 Signaling | 0.353 | 0.00885 | brown | PRKACB |
| Apelin Cardiomyocyte Signaling Pathway | 0.35 | 0.00877 | brown | ATP2A3 |
| iCOS-iCOSL Signaling in T Helper Cells | 0.347 | 0.0087 | brown | PTEN |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 0.344 | 0.00862 | brown | PRKACB |
| Sperm Motility | 0.344 | 0.00862 | brown | PRKACB |
| Neuroinflammation Signaling Pathway | 0.34 | 0.00671 | brown | TICAM2,BACE2 |
| G Beta Gamma Signaling | 0.336 | 0.0084 | brown | PRKACB |
| Glioma Signaling | 0.331 | 0.00826 | brown | PTEN |
| Pancreatic Adenocarcinoma Signaling | 0.328 | 0.0082 | brown | PLD4 |
| Atherosclerosis Signaling | 0.328 | 0.0082 | brown | ALOX5 |
| Synaptic Long Term Potentiation | 0.326 | 0.00813 | brown | PRKACB |
| Sphingosine-1-phosphate Signaling | 0.326 | 0.00813 | brown | RHOB |
| PTEN Signaling | 0.326 | 0.00813 | brown | PTEN |
| Cellular Effects of Sildenafil (Viagra) | 0.318 | 0.00794 | brown | PRKACB |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 0.316 | 0.00787 | brown | BMP3 |
| PI3K/AKT Signaling | 0.316 | 0.00787 | brown | PTEN |
| Role of Tissue Factor in Cancer | 0.313 | 0.00781 | brown | PTEN |
| Adipogenesis pathway | 0.313 | 0.00781 | brown | XBP1 |
| Endocannabinoid Developing Neuron Pathway | 0.313 | 0.00781 | brown | PRKACB |
| Renin-Angiotensin Signaling | 0.311 | 0.00775 | brown | PRKACB |
| PI3K Signaling in B Lymphocytes | 0.306 | 0.00763 | brown | PTEN |
| Iron homeostasis signaling pathway | 0.306 | 0.00763 | brown | BMP3 |
| Phagosome Maturation | 0.299 | 0.00746 | brown | CTSH |
| Androgen Signaling | 0.298 | 0.00741 | brown | PRKACB |
| Corticotropin Releasing Hormone Signaling | 0.292 | 0.0073 | brown | PRKACB |
| HMGB1 Signaling | 0.288 | 0.00719 | brown | RHOB |
| P2Y Purigenic Receptor Signaling Pathway | 0.288 | 0.00719 | brown | PRKACB |
| Human Embryonic Stem Cell Pluripotency | 0.284 | 0.00709 | brown | BMP3 |
| Hereditary Breast Cancer Signaling | 0.27 | 0.00676 | brown | PTEN |
| Endocannabinoid Cancer Inhibition Pathway | 0.255 | 0.00641 | brown | PRKACB |
| Hepatic Cholestasis | 0.251 | 0.00633 | brown | PRKACB |
| Mitochondrial Dysfunction | 0.249 | 0.00629 | brown | BACE2 |
| Relaxin Signaling | 0.248 | 0.00625 | brown | PRKACB |
| eNOS Signaling | 0.237 | 0.00602 | brown | PRKACB |
| GNRH Signaling | 0.236 | 0.00599 | brown | PRKACB |
| CXCR4 Signaling | 0.23 | 0.00585 | brown | RHOB |
| PPARα/RXRα Activation | 0.225 | 0.00575 | brown | PRKACB |
| Dendritic Cell Maturation | 0.219 | 0.00562 | brown | IGHG1 |
| NF-κB Signaling | 0.216 | 0.00556 | brown | PRKACB |
| Endothelin-1 Signaling | 0.199 | 0.00521 | brown | PLD4 |
| Glucocorticoid Receptor Signaling | 0 | 0.00296 | brown | PRKACB |
| Leukocyte Extravasation Signaling | 0 | 0.00485 | brown | CD44 |
| Actin Cytoskeleton Signaling | 0 | 0.00446 | brown | WASF1 |
| NRF2-mediated Oxidative Stress Response | 0 | 0.00508 | brown | FMO1 |
| LPS/IL-1 Mediated Inhibition of RXR Function | 0 | 0.00485 | brown | FMO1 |
| Clathrin-mediated Endocytosis Signaling | 0 | 0.00483 | brown | CD2AP |
| Thrombin Signaling | 0 | 0.00481 | brown | RHOB |
| CREB Signaling in Neurons | 0 | 0.00461 | brown | PRKACB |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 0 | 0.00513 | brown | RHOB |
| Systemic Lupus Erythematosus Signaling | 0 | 0.00505 | brown | IGHG1 |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 0 | 0.00437 | brown | BMP3 |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 0 | 0.00325 | brown | IGHG1 |
| Role of NFAT in Cardiac Hypertrophy | 0 | 0.00452 | brown | PRKACB |
| Breast Cancer Regulation by Stathmin1 | 0 | 0.00478 | brown | PRKACB |
| Gap Junction Signaling | 0 | 0.005 | brown | PRKACB |
| ERK/MAPK Signaling | 0 | 0.00498 | brown | PRKACB |
| Xenobiotic Metabolism Signaling | 0 | 0.00365 | brown | FMO1 |
| Adrenomedullin signaling pathway | 0 | 0.00495 | brown | PRKACB |
| Prolactin Signaling | 3.53 | 0.0549 | blue | PIK3C2B,PIK3CA,SP1,PIK3R5,SOCS5 |
| IGF-1 Signaling | 3.09 | 0.0442 | blue | PIK3C2B,PIK3CA,YWHAH,PIK3R5,SOCS5 |
| UVB-Induced MAPK Signaling | 3.04 | 0.0597 | blue | PIK3C2B,PIK3CA,H3F3A/H3F3B,PIK3R5 |
| Endometrial Cancer Signaling | 2.93 | 0.0556 | blue | PIK3C2B,PIK3CA,CTNNA1,PIK3R5 |
| Apelin Endothelial Signaling Pathway | 2.91 | 0.0403 | blue | PIK3C2B,PIK3CA,SP1,SMAD3,PIK3R5 |
| fMLP Signaling in Neutrophils | 2.85 | 0.0391 | blue | PIK3C2B,PIK3CA,NCF1,NFATC3,PIK3R5 |
| ErbB2-ErbB3 Signaling | 2.84 | 0.0526 | blue | PIK3C2B,PIK3CA,SP1,PIK3R5 |
| Myc Mediated Apoptosis Signaling | 2.82 | 0.0519 | blue | PIK3C2B,PIK3CA,YWHAH,PIK3R5 |
| GP6 Signaling Pathway | 2.79 | 0.0379 | blue | PIK3C2B,PIK3CA,COL4A3,PIK3R5,RASGRP2 |
| IL-17A Signaling in Airway Cells | 2.76 | 0.05 | blue | PIK3C2B,PIK3CA,TRAF3IP2,PIK3R5 |
| p70S6K Signaling | 2.69 | 0.036 | blue | PIK3C2B,PIK3CA,YWHAH,CD79B,PIK3R5 |
| Antiproliferative Role of Somatostatin Receptor 2 | 2.68 | 0.0476 | blue | PIK3C2B,PIK3CA,GUCY2C,PIK3R5 |
| Estrogen-Dependent Breast Cancer Signaling | 2.68 | 0.0476 | blue | PIK3C2B,PIK3CA,SP1,PIK3R5 |
| Growth Hormone Signaling | 2.64 | 0.0465 | blue | PIK3C2B,PIK3CA,PIK3R5,SOCS5 |
| FcγRIIB Signaling in B Lymphocytes | 2.62 | 0.046 | blue | PIK3C2B,PIK3CA,CD79B,PIK3R5 |
| EIF2 Signaling | 2.58 | 0.0279 | blue | RPL15,PIK3C2B,PIK3CA,PIK3R5,EIF4G3,AGO2 |
| JAK/Stat Signaling | 2.55 | 0.044 | blue | PIK3C2B,PIK3CA,PIK3R5,SOCS5 |
| Role of p14/p19ARF in Tumor Suppression | 2.55 | 0.0682 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| AMPK Signaling | 2.55 | 0.0275 | blue | PIK3C2B,PIK3CA,RAB1A,TBC1D1,PIK3R5,PFKFB2 |
| IL-4 Signaling | 2.54 | 0.0435 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| IL-17 Signaling | 2.52 | 0.043 | blue | PIK3C2B,PIK3CA,TRAF3IP2,PIK3R5 |
| Actin Cytoskeleton Signaling | 2.49 | 0.0268 | blue | PIK3C2B,PIK3CA,CYFIP2,MPRIP,ARHGEF7,PIK3R5 |
| CTLA4 Signaling in Cytotoxic T Lymphocytes | 2.47 | 0.0417 | blue | PIK3C2B,PIK3CA,PIK3R5,AP1B1 |
| IL-9 Signaling | 2.47 | 0.0638 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Regulation of eIF4 and p70S6K Signaling | 2.45 | 0.0316 | blue | PIK3C2B,PIK3CA,PIK3R5,EIF4G3,AGO2 |
| T Cell Exhaustion Signaling Pathway | 2.32 | 0.0294 | blue | PIK3C2B,PIK3CA,NFATC3,SMAD3,PIK3R5 |
| FAK Signaling | 2.32 | 0.0377 | blue | PIK3C2B,PIK3CA,ARHGEF7,PIK3R5 |
| Th1 and Th2 Activation Pathway | 2.31 | 0.0292 | blue | PIK3C2B,PIK3CA,NFATC3,BHLHE41,PIK3R5 |
| SAPK/JNK Signaling | 2.3 | 0.0374 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| Docosahexaenoic Acid (DHA) Signaling | 2.3 | 0.0556 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| PAK Signaling | 2.29 | 0.037 | blue | PIK3C2B,PIK3CA,ARHGEF7,PIK3R5 |
| Nitric Oxide Signaling in the Cardiovascular System | 2.26 | 0.0364 | blue | PIK3C2B,PIK3CA,GUCY2C,PIK3R5 |
| Chronic Myeloid Leukemia Signaling | 2.23 | 0.0357 | blue | PIK3C2B,PIK3CA,SMAD3,PIK3R5 |
| p53 Signaling | 2.22 | 0.0354 | blue | PIK3C2B,PIK3CA,GADD45B,PIK3R5 |
| Apelin Pancreas Signaling Pathway | 2.21 | 0.0517 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Role of NFAT in Regulation of the Immune Response | 2.21 | 0.0276 | blue | PIK3C2B,PIK3CA,CD79B,NFATC3,PIK3R5 |
| T Cell Receptor Signaling | 2.2 | 0.0351 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| iCOS-iCOSL Signaling in T Helper Cells | 2.19 | 0.0348 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| Telomerase Signaling | 2.18 | 0.0345 | blue | PIK3C2B,PIK3CA,SP1,PIK3R5 |
| Virus Entry via Endocytic Pathways | 2.15 | 0.0339 | blue | PIK3C2B,PIK3CA,PIK3R5,AP1B1 |
| Paxillin Signaling | 2.15 | 0.0339 | blue | PIK3C2B,PIK3CA,ARHGEF7,PIK3R5 |
| B Cell Receptor Signaling | 2.15 | 0.0267 | blue | PIK3C2B,PIK3CA,CD79B,NFATC3,PIK3R5 |
| Ephrin A Signaling | 2.13 | 0.0484 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Melanoma Signaling | 2.11 | 0.0476 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Pancreatic Adenocarcinoma Signaling | 2.1 | 0.0328 | blue | PIK3C2B,PIK3CA,SMAD3,PIK3R5 |
| Th1 Pathway | 2.1 | 0.0328 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| Rac Signaling | 2.09 | 0.0325 | blue | PIK3C2B,PIK3CA,CYFIP2,PIK3R5 |
| CD28 Signaling in T Helper Cells | 2.08 | 0.0323 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| HIF1α Signaling | 2.08 | 0.0323 | blue | SLC2A5,PIK3C2B,PIK3CA,PIK3R5 |
| Systemic Lupus Erythematosus Signaling | 2.05 | 0.0253 | blue | PIK3C2B,PIK3CA,CD79B,NFATC3,PIK3R5 |
| CNTF Signaling | 2.04 | 0.0448 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Gap Junction Signaling | 2.03 | 0.025 | blue | PIK3C2B,PIK3CA,GUCY2C,SP1,PIK3R5 |
| ERK/MAPK Signaling | 2.02 | 0.0249 | blue | PIK3C2B,PIK3CA,H3F3A/H3F3B,YWHAH,PIK3R5 |
| Lymphotoxin β Receptor Signaling | 2 | 0.0435 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| CCR3 Signaling in Eosinophils | 2 | 0.0305 | blue | PIK3C2B,PIK3CA,MPRIP,PIK3R5 |
| Role of IL-17A in Arthritis | 1.99 | 0.0429 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| EGF Signaling | 1.99 | 0.0429 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Leukocyte Extravasation Signaling | 1.97 | 0.0243 | blue | PIK3C2B,PIK3CA,NCF1,CTNNA1,PIK3R5 |
| Clathrin-mediated Endocytosis Signaling | 1.97 | 0.0242 | blue | PIK3C2B,PIK3CA,PIK3R5,AP1B1,HIP1R |
| Thrombopoietin Signaling | 1.95 | 0.0417 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| IL-2 Signaling | 1.95 | 0.0417 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| SPINK1 General Cancer Pathway | 1.95 | 0.0417 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Protein Kinase A Signaling | 1.95 | 0.0184 | blue | H3F3A/H3F3B,YWHAH,PTPRJ,NFATC3,SMAD3,ADD1,AKAP7 |
| 14-3-3-mediated Signaling | 1.94 | 0.0294 | blue | PIK3C2B,PIK3CA,YWHAH,PIK3R5 |
| MSP-RON Signaling Pathway | 1.92 | 0.0405 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Integrin Signaling | 1.92 | 0.0235 | blue | PIK3C2B,PIK3CA,MPRIP,ARHGEF7,PIK3R5 |
| HMGB1 Signaling | 1.91 | 0.0288 | blue | PIK3C2B,PIK3CA,SP1,PIK3R5 |
| Th2 Pathway | 1.91 | 0.0288 | blue | PIK3C2B,PIK3CA,BHLHE41,PIK3R5 |
| Human Embryonic Stem Cell Pluripotency | 1.89 | 0.0284 | blue | PIK3C2B,PIK3CA,SMAD3,PIK3R5 |
| Gα12/13 Signaling | 1.89 | 0.0284 | blue | PIK3C2B,PIK3CA,TBXA2R,PIK3R5 |
| Role of JAK1 and JAK3 in γc Cytokine Signaling | 1.89 | 0.0395 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Role of PI3K/AKT Signaling in the Pathogenesis of Influenza | 1.88 | 0.039 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Glioma Invasiveness Signaling | 1.86 | 0.0385 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| ErbB4 Signaling | 1.86 | 0.0385 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| CD40 Signaling | 1.83 | 0.0375 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| GM-CSF Signaling | 1.83 | 0.0375 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Hereditary Breast Cancer Signaling | 1.82 | 0.027 | blue | PIK3C2B,PIK3CA,GADD45B,PIK3R5 |
| Type II Diabetes Mellitus Signaling | 1.79 | 0.0265 | blue | PIK3C2B,PIK3CA,PIK3R5,SOCS5 |
| IL-15 Signaling | 1.77 | 0.0357 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| GDNF Family Ligand-Receptor Interactions | 1.77 | 0.0357 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Neurotrophin/TRK Signaling | 1.77 | 0.0357 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Angiopoietin Signaling | 1.76 | 0.0353 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Non-Small Cell Lung Cancer Signaling | 1.76 | 0.0353 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Renal Cell Carcinoma Signaling | 1.73 | 0.0345 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Small Cell Lung Cancer Signaling | 1.73 | 0.0345 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Leptin Signaling in Obesity | 1.73 | 0.0345 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| PKCθ Signaling in T Lymphocytes | 1.73 | 0.0255 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| Erythropoietin Signaling | 1.72 | 0.0341 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| FLT3 Signaling in Hematopoietic Progenitor Cells | 1.72 | 0.0341 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| IL-7 Signaling Pathway | 1.72 | 0.0341 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Macropinocytosis Signaling | 1.71 | 0.0337 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Relaxin Signaling | 1.71 | 0.025 | blue | PIK3C2B,PIK3CA,GUCY2C,PIK3R5 |
| Gαq Signaling | 1.71 | 0.025 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| IL-3 Signaling | 1.69 | 0.0333 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| FGF Signaling | 1.67 | 0.0326 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Glucocorticoid Receptor Signaling | 1.66 | 0.0178 | blue | PIK3C2B,PIK3CA,YWHAH,NFATC3,SMAD3,PIK3R5 |
| Reelin Signaling in Neurons | 1.65 | 0.0319 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| VEGF Family Ligand-Receptor Interactions | 1.65 | 0.0319 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| LPS-stimulated MAPK Signaling | 1.63 | 0.0316 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| NF-κB Activation by Viruses | 1.63 | 0.0316 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| PEDF Signaling | 1.63 | 0.0316 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| HER-2 Signaling in Breast Cancer | 1.62 | 0.0312 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Acute Myeloid Leukemia Signaling | 1.61 | 0.0309 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| PDGF Signaling | 1.6 | 0.0306 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Germ Cell-Sertoli Cell Junction Signaling | 1.59 | 0.023 | blue | PIK3C2B,PIK3CA,CTNNA1,PIK3R5 |
| Ceramide Signaling | 1.58 | 0.03 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| TR/RXR Activation | 1.58 | 0.03 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Prostate Cancer Signaling | 1.57 | 0.0297 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Dendritic Cell Maturation | 1.56 | 0.0225 | blue | PIK3C2B,PIK3CA,PIK3R5,CD58 |
| RANK Signaling in Osteoclasts | 1.55 | 0.0294 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Melanocyte Development and Pigmentation Signaling | 1.52 | 0.0286 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| ErbB Signaling | 1.52 | 0.0286 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| VEGF Signaling | 1.49 | 0.0278 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 1.47 | 0.0211 | blue | PIK3C2B,PIK3CA,SMAD3,PIK3R5 |
| Mouse Embryonic Stem Cell Pluripotency | 1.46 | 0.027 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| UVA-Induced MAPK Signaling | 1.46 | 0.027 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Endothelin-1 Signaling | 1.45 | 0.0208 | blue | PIK3C2B,PIK3CA,GUCY2C,PIK3R5 |
| Amyotrophic Lateral Sclerosis Signaling | 1.45 | 0.0268 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| 3-phosphoinositide Biosynthesis | 1.44 | 0.0206 | blue | PIK3C2B,PIK3CA,PTPRJ,PIK3R5 |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 1.43 | 0.0205 | blue | PIK3C2B,PIK3CA,NCF1,PIK3R5 |
| Apelin Cardiomyocyte Signaling Pathway | 1.43 | 0.0263 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Molecular Mechanisms of Cancer | 1.41 | 0.0155 | blue | PIK3C2B,PIK3CA,ARHGEF7,SMAD3,CTNNA1,PIK3R5 |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 1.41 | 0.0259 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| mTOR Signaling | 1.39 | 0.0199 | blue | PIK3C2B,PIK3CA,PIK3R5,EIF4G3 |
| Adrenomedullin signaling pathway | 1.39 | 0.0198 | blue | PIK3C2B,PIK3CA,GUCY2C,PIK3R5 |
| HGF Signaling | 1.38 | 0.025 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Glioma Signaling | 1.37 | 0.0248 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Phagosome Formation | 1.37 | 0.0248 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Phosphatidylcholine Biosynthesis I | 1.36 | 0.143 | blue | PCYT1A |
| Sphingosine-1-phosphate Signaling | 1.35 | 0.0244 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| NGF Signaling | 1.35 | 0.0244 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| PTEN Signaling | 1.35 | 0.0244 | blue | PIK3CA,YWHAH,PIK3R5 |
| Thrombin Signaling | 1.35 | 0.0192 | blue | PIK3C2B,PIK3CA,MPRIP,PIK3R5 |
| Breast Cancer Regulation by Stathmin1 | 1.34 | 0.0191 | blue | PIK3C2B,PIK3CA,ARHGEF7,PIK3R5 |
| Natural Killer Cell Signaling | 1.33 | 0.024 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Fc Epsilon RI Signaling | 1.33 | 0.024 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 1.32 | 0.0236 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 1.32 | 0.0162 | blue | PIK3C2B,PIK3CA,TRAF3IP2,NFATC3,PIK3R5 |
| Role of Tissue Factor in Cancer | 1.31 | 0.0234 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Endocannabinoid Developing Neuron Pathway | 1.31 | 0.0234 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Renin-Angiotensin Signaling | 1.3 | 0.0233 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| PI3K Signaling in B Lymphocytes | 1.28 | 0.0229 | blue | PIK3CA,CD79B,NFATC3 |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 1.27 | 0.0227 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| IL-6 Signaling | 1.24 | 0.0221 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Phospholipase C Signaling | 1.24 | 0.0177 | blue | MPRIP,CD79B,NFATC3,ARHGEF7 |
| Superpathway of Inositol Phosphate Compounds | 1.23 | 0.0175 | blue | PIK3C2B,PIK3CA,PTPRJ,PIK3R5 |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 1.22 | 0.0175 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| P2Y Purigenic Receptor Signaling Pathway | 1.22 | 0.0216 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Insulin Receptor Signaling | 1.19 | 0.021 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| IL-12 Signaling and Production in Macrophages | 1.17 | 0.0205 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Ovarian Cancer Signaling | 1.15 | 0.0201 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Pregnenolone Biosynthesis | 1.13 | 0.0833 | blue | MICAL3 |
| Huntington's Disease Signaling | 1.13 | 0.0162 | blue | PIK3C2B,PIK3CA,SP1,PIK3R5 |
| Colorectal Cancer Metastasis Signaling | 1.12 | 0.0161 | blue | PIK3C2B,PIK3CA,SMAD3,PIK3R5 |
| Signaling by Rho Family GTPases | 1.12 | 0.0161 | blue | PIK3C2B,PIK3CA,ARHGEF7,PIK3R5 |
| Endocannabinoid Cancer Inhibition Pathway | 1.1 | 0.0192 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Choline Biosynthesis III | 1.1 | 0.0769 | blue | PCYT1A |
| Chondroitin Sulfate Degradation (Metazoa) | 1.06 | 0.0714 | blue | HEXDC |
| Tec Kinase Signaling | 1.05 | 0.0182 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| eNOS Signaling | 1.04 | 0.0181 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Dermatan Sulfate Degradation (Metazoa) | 1.04 | 0.0667 | blue | HEXDC |
| Histidine Degradation VI | 1.04 | 0.0667 | blue | MICAL3 |
| Glioblastoma Multiforme Signaling | 1.03 | 0.0179 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Aldosterone Signaling in Epithelial Cells | 1.02 | 0.0178 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| CXCR4 Signaling | 1.01 | 0.0175 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Sirtuin Signaling Pathway | 1 | 0.0147 | blue | PGK1,GADD45B,H3F3A/H3F3B,SP1 |
| Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes | 1 | 0.0241 | blue | NFATC3,SMAD3 |
| HIPPO signaling | 0.996 | 0.0238 | blue | YWHAH,SMAD3 |
| Ubiquinol-10 Biosynthesis (Eukaryotic) | 0.983 | 0.0588 | blue | MICAL3 |
| G-Protein Coupled Receptor Signaling | 0.983 | 0.0144 | blue | PIK3C2B,PIK3CA,TBXA2R,PIK3R5 |
| NF-κB Signaling | 0.963 | 0.0167 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| GADD45 Signaling | 0.939 | 0.0526 | blue | GADD45B |
| Lipid Antigen Presentation by CD1 | 0.917 | 0.05 | blue | AP1B1 |
| Neuroinflammation Signaling Pathway | 0.903 | 0.0134 | blue | PIK3C2B,PIK3CA,NFATC3,PIK3R5 |
| ILK Signaling | 0.896 | 0.0155 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Glycolysis I | 0.879 | 0.0455 | blue | PGK1 |
| NRF2-mediated Oxidative Stress Response | 0.876 | 0.0152 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Gluconeogenesis I | 0.86 | 0.0435 | blue | PGK1 |
| Osteoarthritis Pathway | 0.86 | 0.015 | blue | SP1,SMAD3,CTNNA1 |
| IL-8 Signaling | 0.848 | 0.0148 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| CDP-diacylglycerol Biosynthesis I | 0.827 | 0.04 | blue | AGPAT5 |
| Antiproliferative Role of TOB in T Cell Signaling | 0.812 | 0.0385 | blue | SMAD3 |
| B Cell Development | 0.796 | 0.037 | blue | CD79B |
| Phosphatidylglycerol Biosynthesis II (Non-plastidic) | 0.796 | 0.037 | blue | AGPAT5 |
| CREB Signaling in Neurons | 0.788 | 0.0138 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Role of NFAT in Cardiac Hypertrophy | 0.77 | 0.0136 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| DNA Methylation and Transcriptional Repression Signaling | 0.754 | 0.0333 | blue | H3F3A/H3F3B |
| Role of JAK2 in Hormone-like Cytokine Signaling | 0.73 | 0.0312 | blue | SOCS5 |
| Axonal Guidance Signaling | 0.721 | 0.0105 | blue | PIK3C2B,PIK3CA,NFATC3,ARHGEF7,PIK3R5 |
| Circadian Rhythm Signaling | 0.717 | 0.0303 | blue | BHLHE41 |
| Cellular Effects of Sildenafil (Viagra) | 0.712 | 0.0159 | blue | MPRIP,GUCY2C |
| Cardiac Hypertrophy Signaling | 0.71 | 0.0127 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| PI3K/AKT Signaling | 0.708 | 0.0157 | blue | PIK3CA,YWHAH |
| IL-17A Signaling in Fibroblasts | 0.695 | 0.0286 | blue | TRAF3IP2 |
| April Mediated Signaling | 0.654 | 0.0256 | blue | NFATC3 |
| B Cell Activating Factor Signaling | 0.635 | 0.0244 | blue | NFATC3 |
| Role of IL-17F in Allergic Inflammatory Airway Diseases | 0.635 | 0.0244 | blue | TRAF3IP2 |
| Triacylglycerol Biosynthesis | 0.616 | 0.0233 | blue | AGPAT5 |
| FAT10 Cancer Signaling Pathway | 0.599 | 0.0222 | blue | SMAD3 |
| Xenobiotic Metabolism Signaling | 0.59 | 0.0109 | blue | PIK3C2B,PIK3CA,PIK3R5 |
| Cancer Drug Resistance By Drug Efflux | 0.59 | 0.0217 | blue | PIK3CA |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 0.567 | 0.0204 | blue | YWHAH |
| Transcriptional Regulatory Network in Embryonic Stem Cells | 0.559 | 0.02 | blue | H3F3A/H3F3B |
| Phototransduction Pathway | 0.559 | 0.02 | blue | GUCY2C |
| SPINK1 Pancreatic Cancer Pathway | 0.524 | 0.0182 | blue | SMAD3 |
| Acute Phase Response Signaling | 0.516 | 0.0116 | blue | PIK3CA,SOCS5 |
| Sertoli Cell-Sertoli Cell Junction Signaling | 0.513 | 0.0115 | blue | SPTBN1,CTNNA1 |
| Wnt/Ca+ pathway | 0.488 | 0.0164 | blue | NFATC3 |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation | 0.487 | 0.011 | blue | COL4A3,SMAD3 |
| Eicosanoid Signaling | 0.476 | 0.0159 | blue | TBXA2R |
| RAR Activation | 0.471 | 0.0107 | blue | PIK3CA,SMAD3 |
| Remodeling of Epithelial Adherens Junctions | 0.471 | 0.0156 | blue | CTNNA1 |
| Netrin Signaling | 0.466 | 0.0154 | blue | NFATC3 |
| Cell Cycle: G1/S Checkpoint Regulation | 0.46 | 0.0152 | blue | SMAD3 |
| ERK5 Signaling | 0.455 | 0.0149 | blue | YWHAH |
| IL-10 Signaling | 0.445 | 0.0145 | blue | SP1 |
| Agrin Interactions at Neuromuscular Junction | 0.425 | 0.0137 | blue | ARHGEF7 |
| Chemokine Signaling | 0.42 | 0.0135 | blue | MPRIP |
| Th17 Activation Pathway | 0.416 | 0.0133 | blue | NFATC3 |
| VDR/RXR Activation | 0.408 | 0.013 | blue | SP1 |
| Communication between Innate and Adaptive Immune Cells | 0.403 | 0.0128 | blue | CD79B |
| Altered T Cell and B Cell Signaling in Rheumatoid Arthritis | 0.403 | 0.0128 | blue | CD79B |
| cAMP-mediated signaling | 0.383 | 0.00909 | blue | TBXA2R,AKAP7 |
| Regulation of Actin-based Motility by Rho | 0.379 | 0.0119 | blue | MPRIP |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 0.349 | 0.0109 | blue | NCF1 |
| GABA Receptor Signaling | 0.346 | 0.0108 | blue | AP1B1 |
| TGF-β Signaling | 0.346 | 0.0108 | blue | SMAD3 |
| ATM Signaling | 0.335 | 0.0104 | blue | GADD45B |
| Sumoylation Pathway | 0.335 | 0.0104 | blue | SP1 |
| NER Pathway | 0.329 | 0.0102 | blue | H3F3A/H3F3B |
| Type I Diabetes Mellitus Signaling | 0.317 | 0.0098 | blue | SOCS5 |
| Antioxidant Action of Vitamin C | 0.317 | 0.0098 | blue | SLC2A5 |
| Gαs Signaling | 0.311 | 0.00962 | blue | ADD1 |
| p38 MAPK Signaling | 0.286 | 0.00885 | blue | H3F3A/H3F3B |
| RhoA Signaling | 0.273 | 0.00847 | blue | MPRIP |
| Gαi Signaling | 0.271 | 0.0084 | blue | TBXA2R |
| Cdc42 Signaling | 0.266 | 0.00826 | blue | MPRIP |
| Adipogenesis pathway | 0.249 | 0.00781 | blue | SMAD3 |
| Iron homeostasis signaling pathway | 0.243 | 0.00763 | blue | SMAD3 |
| STAT3 Pathway | 0.241 | 0.00758 | blue | SOCS5 |
| Estrogen Receptor Signaling | 0.239 | 0.00752 | blue | H3F3A/H3F3B |
| Aryl Hydrocarbon Receptor Signaling | 0.235 | 0.00741 | blue | SP1 |
| Androgen Signaling | 0.235 | 0.00741 | blue | SMAD3 |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0.233 | 0.00735 | blue | PTPRJ |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0.233 | 0.00735 | blue | PTPRJ |
| Corticotropin Releasing Hormone Signaling | 0.231 | 0.0073 | blue | GUCY2C |
| Cardiac β-adrenergic Signaling | 0.227 | 0.00719 | blue | AKAP7 |
| Epithelial Adherens Junction Signaling | 0.218 | 0.00694 | blue | CTNNA1 |
| 3-phosphoinositide Degradation | 0.207 | 0.00667 | blue | PTPRJ |
| D-myo-inositol-5-phosphate Metabolism | 0.2 | 0.00649 | blue | PTPRJ |
| Synaptic Long Term Depression | 0 | 0.00565 | blue | GUCY2C |
| PPARα/RXRα Activation | 0 | 0.00575 | blue | SMAD3 |
| Tight Junction Signaling | 0 | 0.00606 | blue | CTNNA1 |
| RhoGDI Signaling | 0 | 0.00575 | blue | ARHGEF7 |
| Wnt/β-catenin Signaling | 0 | 0.00599 | blue | TLE1 |
| Opioid Signaling Pathway | 0 | 0.00418 | blue | AP1B1 |
| Calcium Signaling | 0 | 0.00513 | blue | NFATC3 |
| Chondroitin Sulfate Biosynthesis | 2.32 | 0.0385 | green | UST,XYLT1 |
| Dermatan Sulfate Biosynthesis | 2.29 | 0.037 | green | UST,XYLT1 |
| Diphthamide Biosynthesis | 2.23 | 0.333 | green | DPH5 |
| Heparan Sulfate Biosynthesis | 2.13 | 0.0308 | green | UST,XYLT1 |
| Trans, trans-farnesyl Diphosphate Biosynthesis | 2.1 | 0.25 | green | IDI1 |
| Glycoaminoglycan-protein Linkage Region Biosynthesis | 1.86 | 0.143 | green | XYLT1 |
| Mevalonate Pathway I | 1.63 | 0.0833 | green | IDI1 |
| RAN Signaling | 1.5 | 0.0625 | green | KPNA1 |
| Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate) | 1.5 | 0.0625 | green | IDI1 |
| Polyamine Regulation in Colon Cancer | 1.39 | 0.0476 | green | PSME4 |
| D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis | 1.28 | 0.037 | green | PIP5K1B |
| Superpathway of Cholesterol Biosynthesis | 1.28 | 0.037 | green | IDI1 |
| 3-phosphoinositide Biosynthesis | 1.25 | 0.0103 | green | PAWR,PIP5K1B |
| EIF2 Signaling | 1.17 | 0.0093 | green | RPL7L1,RPL28 |
| Superpathway of Inositol Phosphate Compounds | 1.12 | 0.00877 | green | PAWR,PIP5K1B |
| Dermatan Sulfate Biosynthesis (Late Stages) | 1.11 | 0.0244 | green | UST |
| Chondroitin Sulfate Biosynthesis (Late Stages) | 1.08 | 0.0227 | green | UST |
| Heparan Sulfate Biosynthesis (Late Stages) | 0.963 | 0.0172 | green | UST |
| Pyridoxal 5'-phosphate Salvage Pathway | 0.921 | 0.0156 | green | PRPF4B |
| Regulation of Actin-based Motility by Rho | 0.812 | 0.0119 | green | PIP5K1B |
| TGF-β Signaling | 0.772 | 0.0108 | green | SMURF2 |
| Salvage Pathways of Pyrimidine Ribonucleotides | 0.767 | 0.0106 | green | PRPF4B |
| RhoA Signaling | 0.678 | 0.00847 | green | PIP5K1B |
| Rac Signaling | 0.662 | 0.00813 | green | PIP5K1B |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0.623 | 0.00735 | green | PAWR |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0.623 | 0.00735 | green | PAWR |
| 3-phosphoinositide Degradation | 0.587 | 0.00667 | green | PAWR |
| D-myo-inositol-5-phosphate Metabolism | 0.577 | 0.00649 | green | PAWR |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 0.565 | 0.00629 | green | PAWR |
| Aldosterone Signaling in Epithelial Cells | 0.542 | 0.00592 | green | PIP5K1B |
| RhoGDI Signaling | 0.532 | 0.00575 | green | PIP5K1B |
| Systemic Lupus Erythematosus Signaling | 0.485 | 0.00505 | green | PRPF4B |
| LPS/IL-1 Mediated Inhibition of RXR Function | 0.471 | 0.00485 | green | UST |
| Actin Cytoskeleton Signaling | 0.442 | 0.00446 | green | PIP5K1B |
| Huntington's Disease Signaling | 0.409 | 0.00405 | green | PSME4 |
| Signaling by Rho Family GTPases | 0.406 | 0.00402 | green | PIP5K1B |
| Protein Ubiquitination Pathway | 0.388 | 0.00382 | green | SMURF2 |
| Xenobiotic Metabolism Signaling | 0.374 | 0.00365 | green | UST |