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| --- | --- | --- | --- | --- |
| **Table S11. List of canonical pathways associated with the identified gene co-expression modules in B cells of healthy control** | | | | |
| Ingenuity Canonical Pathways | -log(p-value) | Ratio | module | Molecules |
| Chronic Myeloid Leukemia Signaling | 2.45 | 0.0268 | yellow | RBL2,TFDP1,IRS2 |
| p53 Signaling | 2.44 | 0.0265 | yellow | MDM4,RRM2B,IRS2 |
| Glioma Signaling | 2.36 | 0.0248 | yellow | RBL2,TFDP1,IRS2 |
| Aryl Hydrocarbon Receptor Signaling | 2.23 | 0.0222 | yellow | NR2F1,RBL2,TFDP1 |
| Chondroitin Sulfate Biosynthesis | 2.05 | 0.0385 | yellow | SULT1A1,XYLT1 |
| Dermatan Sulfate Biosynthesis | 2.02 | 0.037 | yellow | SULT1A1,XYLT1 |
| Heparan Sulfate Biosynthesis | 1.87 | 0.0308 | yellow | SULT1A1,XYLT1 |
| Cell Cycle: G1/S Checkpoint Regulation | 1.85 | 0.0303 | yellow | RBL2,TFDP1 |
| Caveolar-mediated Endocytosis Signaling | 1.8 | 0.0282 | yellow | CD55,FLOT1 |
| Glycoaminoglycan-protein Linkage Region Biosynthesis | 1.72 | 0.143 | yellow | XYLT1 |
| Non-Small Cell Lung Cancer Signaling | 1.65 | 0.0235 | yellow | TFDP1,IRS2 |
| Actin Cytoskeleton Signaling | 1.64 | 0.0134 | yellow | DIAPH1,ACTR3,IRS2 |
| Small Cell Lung Cancer Signaling | 1.63 | 0.023 | yellow | TFDP1,IRS2 |
| Signaling by Rho Family GTPases | 1.52 | 0.012 | yellow | ACTR3,IRS2,ARHGEF18 |
| Prostate Cancer Signaling | 1.51 | 0.0198 | yellow | TFDP1,IRS2 |
| Leukotriene Biosynthesis | 1.46 | 0.0769 | yellow | ALOX5 |
| Chondroitin Sulfate Degradation (Metazoa) | 1.43 | 0.0714 | yellow | HEXB |
| Dermatan Sulfate Degradation (Metazoa) | 1.4 | 0.0667 | yellow | HEXB |
| Virus Entry via Endocytic Pathways | 1.39 | 0.0169 | yellow | CD55,IRS2 |
| Cdc42 Signaling | 1.37 | 0.0165 | yellow | DIAPH1,ACTR3 |
| Pancreatic Adenocarcinoma Signaling | 1.36 | 0.0164 | yellow | TFDP1,IRS2 |
| Rac Signaling | 1.35 | 0.0163 | yellow | ACTR3,IRS2 |
| CD28 Signaling in T Helper Cells | 1.35 | 0.0161 | yellow | ACTR3,IRS2 |
| fMLP Signaling in Neutrophils | 1.32 | 0.0156 | yellow | ACTR3,IRS2 |
| Pyrimidine Deoxyribonucleotides De Novo Biosynthesis I | 1.22 | 0.0435 | yellow | RRM2B |
| Ovarian Cancer Signaling | 1.21 | 0.0134 | yellow | TFDP1,IRS2 |
| Estrogen-mediated S-phase Entry | 1.16 | 0.0385 | yellow | TFDP1 |
| Regulation of eIF4 and p70S6K Signaling | 1.16 | 0.0127 | yellow | IRS2,PAIP2 |
| Dopamine Degradation | 1.13 | 0.0357 | yellow | SULT1A1 |
| Thyroid Hormone Metabolism II (via Conjugation and/or Degradation) | 1.12 | 0.0345 | yellow | SULT1A1 |
| RhoGDI Signaling | 1.09 | 0.0115 | yellow | ACTR3,ARHGEF18 |
| Role of JAK2 in Hormone-like Cytokine Signaling | 1.08 | 0.0312 | yellow | IRS2 |
| Molecular Mechanisms of Cancer | 1.05 | 0.00775 | yellow | TFDP1,IRS2,ARHGEF18 |
| Complement System | 1.03 | 0.0278 | yellow | CD55 |
| tRNA Charging | 1.01 | 0.0263 | yellow | EPRS |
| NRF2-mediated Oxidative Stress Response | 0.996 | 0.0102 | yellow | IRS2,FKBP5 |
| Systemic Lupus Erythematosus Signaling | 0.996 | 0.0101 | yellow | IRS2,SNRPA1 |
| Dermatan Sulfate Biosynthesis (Late Stages) | 0.975 | 0.0244 | yellow | SULT1A1 |
| Clathrin-mediated Endocytosis Signaling | 0.963 | 0.00966 | yellow | ACTR3,IRS2 |
| Breast Cancer Regulation by Stathmin1 | 0.955 | 0.00957 | yellow | IRS2,ARHGEF18 |
| Chondroitin Sulfate Biosynthesis (Late Stages) | 0.947 | 0.0227 | yellow | SULT1A1 |
| Role of p14/p19ARF in Tumor Suppression | 0.947 | 0.0227 | yellow | IRS2 |
| Integrin Signaling | 0.939 | 0.00939 | yellow | ACTR3,IRS2 |
| Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency | 0.936 | 0.0222 | yellow | NR2F1 |
| IL-9 Signaling | 0.917 | 0.0213 | yellow | IRS2 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 0.903 | 0.0204 | yellow | MDM4 |
| Melatonin Degradation I | 0.893 | 0.02 | yellow | SULT1A1 |
| Docosahexaenoic Acid (DHA) Signaling | 0.863 | 0.0185 | yellow | IRS2 |
| Serotonin Degradation | 0.854 | 0.0182 | yellow | SULT1A1 |
| Superpathway of Melatonin Degradation | 0.854 | 0.0182 | yellow | SULT1A1 |
| Heparan Sulfate Biosynthesis (Late Stages) | 0.833 | 0.0172 | yellow | SULT1A1 |
| Apelin Pancreas Signaling Pathway | 0.833 | 0.0172 | yellow | IRS2 |
| Actin Nucleation by ARP-WASP Complex | 0.807 | 0.0161 | yellow | ACTR3 |
| Ephrin A Signaling | 0.807 | 0.0161 | yellow | IRS2 |
| Melanoma Signaling | 0.801 | 0.0159 | yellow | IRS2 |
| Eicosanoid Signaling | 0.801 | 0.0159 | yellow | ALOX5 |
| Protein Ubiquitination Pathway | 0.796 | 0.00763 | yellow | PSMA7,UBE2E2 |
| Remodeling of Epithelial Adherens Junctions | 0.793 | 0.0156 | yellow | ACTR3 |
| CNTF Signaling | 0.777 | 0.0149 | yellow | IRS2 |
| UVB-Induced MAPK Signaling | 0.777 | 0.0149 | yellow | IRS2 |
| Xenobiotic Metabolism Signaling | 0.767 | 0.0073 | yellow | SULT1A1,IRS2 |
| Lymphotoxin β Receptor Signaling | 0.764 | 0.0145 | yellow | IRS2 |
| Role of IL-17A in Arthritis | 0.759 | 0.0143 | yellow | IRS2 |
| EGF Signaling | 0.759 | 0.0143 | yellow | IRS2 |
| Thrombopoietin Signaling | 0.747 | 0.0139 | yellow | IRS2 |
| Endometrial Cancer Signaling | 0.747 | 0.0139 | yellow | IRS2 |
| IL-2 Signaling | 0.747 | 0.0139 | yellow | IRS2 |
| Hypoxia Signaling in the Cardiovascular System | 0.747 | 0.0139 | yellow | UBE2E2 |
| SPINK1 General Cancer Pathway | 0.747 | 0.0139 | yellow | IRS2 |
| MSP-RON Signaling Pathway | 0.738 | 0.0135 | yellow | IRS2 |
| Role of JAK1 and JAK3 in γc Cytokine Signaling | 0.726 | 0.0132 | yellow | IRS2 |
| ErbB2-ErbB3 Signaling | 0.726 | 0.0132 | yellow | IRS2 |
| Myc Mediated Apoptosis Signaling | 0.721 | 0.013 | yellow | IRS2 |
| Role of PI3K/AKT Signaling in the Pathogenesis of Influenza | 0.721 | 0.013 | yellow | IRS2 |
| Glioma Invasiveness Signaling | 0.717 | 0.0128 | yellow | IRS2 |
| ErbB4 Signaling | 0.717 | 0.0128 | yellow | IRS2 |
| Role of BRCA1 in DNA Damage Response | 0.706 | 0.0125 | yellow | RBL2 |
| CD40 Signaling | 0.706 | 0.0125 | yellow | IRS2 |
| Cyclins and Cell Cycle Regulation | 0.706 | 0.0125 | yellow | TFDP1 |
| IL-17A Signaling in Airway Cells | 0.706 | 0.0125 | yellow | IRS2 |
| GM-CSF Signaling | 0.706 | 0.0125 | yellow | IRS2 |
| Regulation of Actin-based Motility by Rho | 0.688 | 0.0119 | yellow | ACTR3 |
| IL-15 Signaling | 0.688 | 0.0119 | yellow | IRS2 |
| Antiproliferative Role of Somatostatin Receptor 2 | 0.688 | 0.0119 | yellow | IRS2 |
| Estrogen-Dependent Breast Cancer Signaling | 0.688 | 0.0119 | yellow | IRS2 |
| GDNF Family Ligand-Receptor Interactions | 0.688 | 0.0119 | yellow | IRS2 |
| Neurotrophin/TRK Signaling | 0.688 | 0.0119 | yellow | IRS2 |
| Angiopoietin Signaling | 0.684 | 0.0118 | yellow | IRS2 |
| Growth Hormone Signaling | 0.678 | 0.0116 | yellow | IRS2 |
| FcγRIIB Signaling in B Lymphocytes | 0.674 | 0.0115 | yellow | IRS2 |
| Renal Cell Carcinoma Signaling | 0.674 | 0.0115 | yellow | IRS2 |
| Leptin Signaling in Obesity | 0.674 | 0.0115 | yellow | IRS2 |
| Erythropoietin Signaling | 0.67 | 0.0114 | yellow | IRS2 |
| FLT3 Signaling in Hematopoietic Progenitor Cells | 0.67 | 0.0114 | yellow | IRS2 |
| IL-7 Signaling Pathway | 0.67 | 0.0114 | yellow | IRS2 |
| Macropinocytosis Signaling | 0.666 | 0.0112 | yellow | IRS2 |
| IL-3 Signaling | 0.662 | 0.0111 | yellow | IRS2 |
| Prolactin Signaling | 0.658 | 0.011 | yellow | IRS2 |
| JAK/Stat Signaling | 0.658 | 0.011 | yellow | IRS2 |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 0.652 | 0.0109 | yellow | ACTR3 |
| FGF Signaling | 0.652 | 0.0109 | yellow | IRS2 |
| IL-4 Signaling | 0.652 | 0.0109 | yellow | IRS2 |
| IL-17 Signaling | 0.648 | 0.0108 | yellow | IRS2 |
| Bladder Cancer Signaling | 0.648 | 0.0108 | yellow | TFDP1 |
| Reelin Signaling in Neurons | 0.644 | 0.0106 | yellow | IRS2 |
| VEGF Family Ligand-Receptor Interactions | 0.644 | 0.0106 | yellow | IRS2 |
| LPS-stimulated MAPK Signaling | 0.64 | 0.0105 | yellow | IRS2 |
| NF-κB Activation by Viruses | 0.64 | 0.0105 | yellow | IRS2 |
| PEDF Signaling | 0.64 | 0.0105 | yellow | IRS2 |
| CTLA4 Signaling in Cytotoxic T Lymphocytes | 0.636 | 0.0104 | yellow | IRS2 |
| ATM Signaling | 0.636 | 0.0104 | yellow | MDM4 |
| HER-2 Signaling in Breast Cancer | 0.636 | 0.0104 | yellow | IRS2 |
| Acute Myeloid Leukemia Signaling | 0.633 | 0.0103 | yellow | IRS2 |
| Glucocorticoid Receptor Signaling | 0.629 | 0.00592 | yellow | IRS2,FKBP5 |
| PPAR Signaling | 0.629 | 0.0102 | yellow | NR2F1 |
| PDGF Signaling | 0.629 | 0.0102 | yellow | IRS2 |
| Ceramide Signaling | 0.622 | 0.01 | yellow | IRS2 |
| TR/RXR Activation | 0.622 | 0.01 | yellow | IRS2 |
| RANK Signaling in Osteoclasts | 0.613 | 0.0098 | yellow | IRS2 |
| Melanocyte Development and Pigmentation Signaling | 0.602 | 0.00952 | yellow | IRS2 |
| ErbB Signaling | 0.602 | 0.00952 | yellow | IRS2 |
| FAK Signaling | 0.599 | 0.00943 | yellow | IRS2 |
| SAPK/JNK Signaling | 0.595 | 0.00935 | yellow | IRS2 |
| PAK Signaling | 0.592 | 0.00926 | yellow | IRS2 |
| VEGF Signaling | 0.592 | 0.00926 | yellow | IRS2 |
| Nitric Oxide Signaling in the Cardiovascular System | 0.585 | 0.00909 | yellow | IRS2 |
| Mouse Embryonic Stem Cell Pluripotency | 0.582 | 0.00901 | yellow | IRS2 |
| UVA-Induced MAPK Signaling | 0.582 | 0.00901 | yellow | IRS2 |
| Amyotrophic Lateral Sclerosis Signaling | 0.578 | 0.00893 | yellow | IRS2 |
| IGF-1 Signaling | 0.575 | 0.00885 | yellow | IRS2 |
| T Cell Receptor Signaling | 0.572 | 0.00877 | yellow | IRS2 |
| Apelin Cardiomyocyte Signaling Pathway | 0.572 | 0.00877 | yellow | IRS2 |
| iCOS-iCOSL Signaling in T Helper Cells | 0.569 | 0.0087 | yellow | IRS2 |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 0.565 | 0.00862 | yellow | IRS2 |
| Telomerase Signaling | 0.565 | 0.00862 | yellow | IRS2 |
| RhoA Signaling | 0.559 | 0.00847 | yellow | ACTR3 |
| Paxillin Signaling | 0.559 | 0.00847 | yellow | IRS2 |
| HGF Signaling | 0.553 | 0.00833 | yellow | IRS2 |
| Phagosome Formation | 0.55 | 0.00826 | yellow | IRS2 |
| Atherosclerosis Signaling | 0.547 | 0.0082 | yellow | ALOX5 |
| Th1 Pathway | 0.547 | 0.0082 | yellow | IRS2 |
| Sphingosine-1-phosphate Signaling | 0.544 | 0.00813 | yellow | IRS2 |
| NGF Signaling | 0.544 | 0.00813 | yellow | IRS2 |
| HIF1α Signaling | 0.541 | 0.00806 | yellow | IRS2 |
| Apelin Endothelial Signaling Pathway | 0.541 | 0.00806 | yellow | IRS2 |
| Natural Killer Cell Signaling | 0.538 | 0.008 | yellow | IRS2 |
| Fc Epsilon RI Signaling | 0.538 | 0.008 | yellow | IRS2 |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 0.532 | 0.00787 | yellow | IRS2 |
| Role of Tissue Factor in Cancer | 0.529 | 0.00781 | yellow | IRS2 |
| Endocannabinoid Developing Neuron Pathway | 0.529 | 0.00781 | yellow | IRS2 |
| Renin-Angiotensin Signaling | 0.526 | 0.00775 | yellow | IRS2 |
| CCR3 Signaling in Eosinophils | 0.52 | 0.00763 | yellow | IRS2 |
| PI3K Signaling in B Lymphocytes | 0.52 | 0.00763 | yellow | IRS2 |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 0.519 | 0.00758 | yellow | IRS2 |
| GP6 Signaling Pathway | 0.519 | 0.00758 | yellow | IRS2 |
| Estrogen Receptor Signaling | 0.516 | 0.00752 | yellow | MED30 |
| 14-3-3-mediated Signaling | 0.507 | 0.00735 | yellow | IRS2 |
| IL-6 Signaling | 0.507 | 0.00735 | yellow | IRS2 |
| HMGB1 Signaling | 0.499 | 0.00719 | yellow | IRS2 |
| p70S6K Signaling | 0.499 | 0.00719 | yellow | IRS2 |
| P2Y Purigenic Receptor Signaling Pathway | 0.499 | 0.00719 | yellow | IRS2 |
| Th2 Pathway | 0.499 | 0.00719 | yellow | IRS2 |
| Human Embryonic Stem Cell Pluripotency | 0.495 | 0.00709 | yellow | IRS2 |
| Gα12/13 Signaling | 0.495 | 0.00709 | yellow | IRS2 |
| Insulin Receptor Signaling | 0.489 | 0.00699 | yellow | IRS2 |
| Epithelial Adherens Junction Signaling | 0.487 | 0.00694 | yellow | ACTR3 |
| IL-12 Signaling and Production in Macrophages | 0.481 | 0.00685 | yellow | IRS2 |
| Hereditary Breast Cancer Signaling | 0.478 | 0.00676 | yellow | IRS2 |
| Type II Diabetes Mellitus Signaling | 0.47 | 0.00662 | yellow | IRS2 |
| Endocannabinoid Cancer Inhibition Pathway | 0.458 | 0.00641 | yellow | IRS2 |
| PKCθ Signaling in T Lymphocytes | 0.456 | 0.00637 | yellow | IRS2 |
| Relaxin Signaling | 0.45 | 0.00625 | yellow | IRS2 |
| Gαq Signaling | 0.45 | 0.00625 | yellow | IRS2 |
| Tec Kinase Signaling | 0.439 | 0.00606 | yellow | IRS2 |
| eNOS Signaling | 0.437 | 0.00602 | yellow | IRS2 |
| Glioblastoma Multiforme Signaling | 0.433 | 0.00595 | yellow | IRS2 |
| Aldosterone Signaling in Epithelial Cells | 0.431 | 0.00592 | yellow | IRS2 |
| Axonal Guidance Signaling | 0.428 | 0.00421 | yellow | ACTR3,IRS2 |
| T Cell Exhaustion Signaling Pathway | 0.428 | 0.00588 | yellow | IRS2 |
| CXCR4 Signaling | 0.427 | 0.00585 | yellow | IRS2 |
| Th1 and Th2 Activation Pathway | 0.427 | 0.00585 | yellow | IRS2 |
| PPARα/RXRα Activation | 0.42 | 0.00575 | yellow | NR2F1 |
| Germ Cell-Sertoli Cell Junction Signaling | 0.42 | 0.00575 | yellow | IRS2 |
| Ephrin Receptor Signaling | 0.419 | 0.00571 | yellow | ACTR3 |
| Dendritic Cell Maturation | 0.413 | 0.00562 | yellow | IRS2 |
| NF-κB Signaling | 0.409 | 0.00556 | yellow | IRS2 |
| Role of NFAT in Regulation of the Immune Response | 0.408 | 0.00552 | yellow | IRS2 |
| RAR Activation | 0.397 | 0.00535 | yellow | NR2F1 |
| B Cell Receptor Signaling | 0.397 | 0.00535 | yellow | IRS2 |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 0.391 | 0.00526 | yellow | IRS2 |
| Endothelin-1 Signaling | 0.387 | 0.00521 | yellow | IRS2 |
| ILK Signaling | 0.386 | 0.00518 | yellow | IRS2 |
| 3-phosphoinositide Biosynthesis | 0.384 | 0.00515 | yellow | IRS2 |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 0.383 | 0.00513 | yellow | IRS2 |
| Gap Junction Signaling | 0.375 | 0.005 | yellow | IRS2 |
| mTOR Signaling | 0.373 | 0.00498 | yellow | IRS2 |
| ERK/MAPK Signaling | 0.373 | 0.00498 | yellow | IRS2 |
| Adrenomedullin signaling pathway | 0.371 | 0.00495 | yellow | IRS2 |
| IL-8 Signaling | 0.37 | 0.00493 | yellow | IRS2 |
| Leukocyte Extravasation Signaling | 0.365 | 0.00485 | yellow | IRS2 |
| LPS/IL-1 Mediated Inhibition of RXR Function | 0.365 | 0.00485 | yellow | SULT1A1 |
| Thrombin Signaling | 0.362 | 0.00481 | yellow | IRS2 |
| EIF2 Signaling | 0.351 | 0.00465 | yellow | IRS2 |
| CREB Signaling in Neurons | 0.348 | 0.00461 | yellow | IRS2 |
| AMPK Signaling | 0.347 | 0.00459 | yellow | IRS2 |
| Role of NFAT in Cardiac Hypertrophy | 0.342 | 0.00452 | yellow | IRS2 |
| Phospholipase C Signaling | 0.335 | 0.00442 | yellow | ARHGEF18 |
| Superpathway of Inositol Phosphate Compounds | 0.333 | 0.00439 | yellow | IRS2 |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 0.331 | 0.00437 | yellow | IRS2 |
| Cardiac Hypertrophy Signaling | 0.32 | 0.00422 | yellow | IRS2 |
| Huntington's Disease Signaling | 0.307 | 0.00405 | yellow | IRS2 |
| Colorectal Cancer Metastasis Signaling | 0.305 | 0.00402 | yellow | IRS2 |
| G-Protein Coupled Receptor Signaling | 0.272 | 0.0036 | yellow | IRS2 |
| Neuroinflammation Signaling Pathway | 0.252 | 0.00336 | yellow | IRS2 |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 0.243 | 0.00325 | yellow | IRS2 |
| Oxidative Phosphorylation | 14.6 | 0.429 | turquoise | COX7B,SDHB,NDUFA9,ATP5PD,NDUFA7,ATP5F1D,UQCRH,COX6C,COX5B,COX8A,ATP5MG,NDUFB8,NDUFA1,NDUFA2,NDUFB3,ATP5F1E,NDUFB10,NDUFS6,NDUFAB1,ATP5ME,ATP5MC3,NDUFS4,ATP5PF,ATP5MC2,COX17,COX6B1,NDUFB4,ATP5F1A,NDUFA13,UQCRB,NDUFS5,ATP5F1C,NDUFB11,ATP5F1B,NDUFA11,NDUFA6,NDUFB7,COX5A,COX7A2,UQCRC1,UQCRQ,NDUFB2 |
| Mitochondrial Dysfunction | 11 | 0.314 | turquoise | FURIN,NDUFA9,ATP5F1D,COX8A,ATP5MG,NDUFB8,NDUFA1,NDUFB3,NDUFB10,NDUFS6,ATP5MC3,ATP5PF,ATP5MC2,ATP5F1A,NDUFS5,ATP5F1C,PRDX3,NDUFB11,ATP5F1B,NDUFA6,TXN2,NDUFB7,VDAC1,NDUFB2,HSD17B10,COX7B,SDHB,ATP5PD,NDUFA7,UQCRH,PRDX5,COX6C,COX5B,ATP5F1E,NDUFA2,NDUFAB1,ATP5ME,NDUFS4,NDUFB4,COX17,COX6B1,GLRX2,VDAC3,NDUFA13,UQCRB,NDUFA11,COX5A,COX7A2,UQCRC1,UQCRQ |
| B Cell Development | 8.51 | 0.593 | turquoise | CD19,HLA-DOA,SPN,CD79B,IGH,HLA-B,IL7,IL7R,CD80,HLA-DMA,IGLC1,HLA-DMB,IGHM,HLA-DOB,CD86,IGHD |
| Sirtuin Signaling Pathway | 5.68 | 0.212 | 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,H3F3A/H3F3B,ATP5F1B,XRCC6,NDUFA6,NDUFB7,IDH2,VDAC1,TNF,NDUFB2,GABPB1,SDHB,NDUFA7,DUSP6,ATP5F1E,NDUFA2,SP1,GADD45A,PGAM1,ATG4A,NAMPT,GOT2,NDUFAB1,NDUFS4,ARNTL,NDUFB4,SLC25A4,TUBA4A,GLUD1,SOD1,VDAC3,NDUFA13,FOXO1,NDUFA11,LDHA |
| Phagosome Formation | 5.41 | 0.264 | turquoise | FCAR,PIK3CA,PIK3R5,RHOH,IGHG3,PIK3C3,RHOU,PLCB1,PRKCE,RHOF,FRS2,FCGR3A/FCGR3B,FCGR1B,CR2,FCER2,ITGB1,PIK3C2B,C5AR1,FCGR2A,TLR2,MARCKS,TLR4,CLEC7A,CR1,PRKCI,ITGAM,GAB1,PRKCD,FCER1G,PIK3R6,FNBP1,ITGAX |
| Role of NFAT in Regulation of the Immune Response | 5.27 | 0.232 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,HLA-DOA,CAMK4,MAPK1,NFATC3,CD4,SOS2,HLA-B,PIK3R5,CSNK1A1,HLA-DMA,PIK3C3,HLA-DMB,PLCB1,GNG5,FRS2,FCGR3A/FCGR3B,FCGR1B,PIK3C2B,GNAS,CD79B,FCGR2A,CSNK1G3,TRGV9,GNAQ,ITPR1,CALM1 (includes others),GNAI3,RRAS2,GAB1,CD80,LAT,PIK3R6,FCER1G,LYN,CD86,HLA-DOB,MEF2C,LCP2 |
| T Cell Exhaustion Signaling Pathway | 5.21 | 0.235 | 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,FRS2,BTLA,PIK3C2B,IRF4,TRGV9,IL6R,MGAT5,ACVR1,IFNAR2,STAT4,RRAS2,GAB1,CD80,FOXO1,PIK3R6,FCER1G,CD86,HLA-DOB,TCF7,FOXP1 |
| Integrin Signaling | 5.18 | 0.221 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MPRIP,ARPC1B,MAPK1,ARF1,ARHGEF7,SOS2,PIK3R5,RHOH,ITGB7,PTEN,NCK2,BRAF,PTK2,ARF4,PIK3C3,RHOU,CAV1,ITGAV,VCL,RHOF,FRS2,ACTN1,MYL12A,ITGB1,CAPN5,PIK3C2B,PXN,ARPC5L,ITGAL,ITGAM,CAPNS1,RRAS2,GAB1,LIMS1,ARPC2,PIK3R6,ZYX,CAPN2,ACTN4,ARPC4,FNBP1,CAPN3,ITGAX |
| Graft-versus-Host Disease Signaling | 4.91 | 0.385 | turquoise | HLA-DOA,GZMB,TRGV9,HLA-B,FAS,PRF1,CD80,IL1RN,HLA-DMA,HLA-DMB,FCER1G,HLA-DOB,IL1B,CD86,TNF |
| Communication between Innate and Adaptive Immune Cells | 4.89 | 0.295 | turquoise | CXCL8,CD79B,IGHE,CD4,TRGV9,HLA-B,CCL5,CD8A,CCL3,TNFRSF17,TLR2,TLR4,IGHG3,CD80,IL1RN,FCER1G,IL1B,IGHM,CD86,TNFRSF13B,IGHA1,TNF,IGHD |
| Autoimmune Thyroid Disease Signaling | 4.85 | 0.4 | turquoise | HLA-DOA,GZMB,TRGV9,HLA-B,FAS,PRF1,IGHG3,CD80,HLA-DMA,HLA-DMB,FCER1G,TSHR,HLA-DOB,CD86 |
| T Helper Cell Differentiation | 4.74 | 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 |
| Unfolded protein response | 4.63 | 0.327 | turquoise | P4HB,ERN1,HSPA9,XBP1,CEBPD,CANX,DNAJC3,CEBPB,HSPA5,MBTPS2,HSPA8,SEL1L,HSP90B1,PDIA6,EDEM1,VCP,ERO1B,CEBPA |
| Primary Immunodeficiency Signaling | 4.6 | 0.366 | turquoise | IL7R,CD19,IGHG3,DCLRE1C,CD4,IGH,IGLC1,IGLL1/IGLL5,ADA,CIITA,IGHM,TNFRSF13B,IGHA1,CD8A,IGHD |
| IL-4 Signaling | 4.58 | 0.272 | turquoise | RAP2B,RAP1B,PIK3C2B,RAP2A,IL4R,PIK3CA,HLA-DOA,IRF4,IL13RA1,NFATC3,IGH,HLA-B,SOS2,PIK3R5,HMGA1,NR3C1,RRAS2,GAB1,HLA-DMA,PIK3C3,HLA-DMB,PIK3R6,HLA-DOB,FRS2,FCER2 |
| Germ Cell-Sertoli Cell Junction Signaling | 4.57 | 0.224 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,MAPK1,PIK3R5,AFDN,TUBB,RHOH,LIMK1,TGFBR2,PTK2,KEAP1,PIK3C3,RHOU,TUBA1C,VCL,RHOF,FRS2,ACTN1,ITGB1,MAP3K14,MAP3K9,PIK3C2B,TUBB3,PXN,CFL1,TUBB4B,TUBG1,TUBA4A,RRAS2,GAB1,PIK3R6,ZYX,ACTN4,TNF,FNBP1,CTNND1 |
| iCOS-iCOSL Signaling in T Helper Cells | 4.54 | 0.252 | turquoise | HLA-DOA,PIK3CA,CAMK4,NFATC3,CD4,HLA-B,PIK3R5,PTEN,CAMK2D,HLA-DMA,PIK3C3,HLA-DMB,FRS2,ICOSLG/LOC102723996,IL2RB,PIK3C2B,TRGV9,ITPR1,CALM1 (includes others),GAB1,CD80,LAT,PIK3R6,FCER1G,CD86,HLA-DOB,PLEKHA1,PLEKHA2,LCP2 |
| Glioma Signaling | 4.52 | 0.248 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,CAMK1D,PA2G4,MAPK1,IDH3G,SOS2,CDK4,PIK3R5,PTEN,CAMK2D,PIK3C3,PRKCE,FRS2,E2F2,PIK3C2B,TFDP1,MDM2,CALM1 (includes others),PRKCI,RRAS2,GAB1,PRKCD,E2F7,PIK3R6,IDH2,PDGFD |
| Phospholipase C Signaling | 4.48 | 0.208 | turquoise | PEBP1,RAP2B,RAP1B,RAP2A,MPRIP,CAMK4,MYL6,MAPK1,NFATC3,ARHGEF7,SOS2,RHOH,HMOX1,IGHG3,AHNAK,RHOU,PLCB1,PRKCE,RHOF,GNG5,MYL12A,ITGB1,HDAC9,PLD3,GNAS,CD79B,FCGR2A,TRGV9,CREB3,CREBBP,GNAQ,ITPR1,CREB5,PLD4,CALM1 (includes others),PLA2G6,MARCKS,PRKCI,RRAS2,PRKCD,LAT,FCER1G,LYN,MEF2C,ARHGEF10,LCP2,FNBP1 |
| Role of Tissue Factor in Cancer | 4.44 | 0.242 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,PIK3R5,LIMK1,PTEN,VEGFA,ARRB1,PIK3C3,ITGAV,PLCB1,STAT5B,FRS2,ITGB1,CXCL8,PIK3C2B,P4HB,CFL1,GNAQ,HBEGF,PLAUR,RPS6KA6,RRAS2,GAB1,PDIA6,PIK3R6,LYN,IL1B,RPS6KA4 |
| Glioma Invasiveness Signaling | 4.37 | 0.282 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,HMMR,PIK3R5,PLAUR,RHOH,PTK2,RRAS2,GAB1,TIMP1,PIK3C3,PIK3R6,ITGAV,RHOU,RHOF,FRS2,FNBP1,TIMP2 |
| Allograft Rejection Signaling | 4.37 | 0.368 | turquoise | HLA-DOA,GZMB,TRGV9,HLA-B,FAS,PRF1,IGHG3,CD80,HLA-DMA,HLA-DMB,FCER1G,HLA-DOB,CD86,TNF |
| Dendritic Cell Maturation | 4.34 | 0.219 | turquoise | PIK3CA,HLA-DOA,MAPK1,IL32,HLA-B,PIK3R5,IGHG3,HLA-DMA,CD1A,PIK3C3,HLA-DMB,PLCB1,COL18A1,TNFRSF1B,FRS2,FCGR3A/FCGR3B,FCGR1B,PIK3C2B,MAP3K14,FCGR2A,TYROBP,TRGV9,CREBBP,CREB3,CD58,CREB5,TLR2,STAT4,TLR4,GAB1,CD80,IL1RN,PIK3R6,FCER1G,CD86,IL1B,HLA-DOB,IRF8,TNF |
| Prolactin Signaling | 4.2 | 0.264 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,CREBBP,SOS2,PIK3R5,CEBPB,NR3C1,RRAS2,PRKCI,GAB1,SP1,PRKCD,PIK3C3,PIK3R6,PRKCE,SOCS2,TCF7,STAT5B,SOCS5,FRS2 |
| Remodeling of Epithelial Adherens Junctions | 4.19 | 0.297 | turquoise | TUBA1B,TUBB3,ARPC1B,TUBB4B,ARPC5L,TUBG1,TUBA4A,TUBB,CLIP1,MAPRE2,ARPC2,ZYX,TUBA1C,VCL,ACTN4,ACTN1,DNM2,ARPC4,CTNND1 |
| Th1 and Th2 Activation Pathway | 4.03 | 0.216 | turquoise | PIK3CA,HLA-DOA,NFATC3,KLRD1,CD4,TGFBR3,HAVCR2,HLA-B,PIK3R5,CXCR3,CD8A,TBX21,TGFBR2,NFIL3,HLA-DMA,PIK3C3,HLA-DMB,STAT5B,FRS2,ICOSLG/LOC102723996,IL2RB,CCR1,RUNX3,PIK3C2B,IL4R,CXCR4,BHLHE41,IL6R,ACVR1,STAT4,GAB1,CD80,GFI1,PIK3R6,CD86,HLA-DOB,GATA3 |
| Paxillin Signaling | 3.9 | 0.237 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,ARF1,ARHGEF7,SOS2,PIK3R5,PTPN12,ITGB7,NCK2,PTK2,PIK3C3,ITGAV,VCL,FRS2,ACTN1,ITGB1,PIK3C2B,PXN,ITGAL,ITGAM,RRAS2,GAB1,PIK3R6,ACTN4,ITGAX |
| B Cell Receptor Signaling | 3.85 | 0.209 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MAPK1,NFATC3,SOS2,PIK3R5,PTEN,PAX5,PTK2,IGHG3,CAMK2D,PIK3C3,CD22,IGHM,FRS2,IGHD,MAP3K9,PIK3C2B,MAP3K14,CD19,CFL1,CD79B,FCGR2A,IGHE,CREB3,CREBBP,CREB5,CALM1 (includes others),RRAS2,GAB1,FOXO1,VAV3,PIK3R6,LYN,MEF2C,IGHA1 |
| IL-8 Signaling | 3.7 | 0.202 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,PIK3R5,RHOH,LIMK1,IRAK1,VEGFA,PTK2,BRAF,HMOX1,PIK3C3,RHOU,ITGAV,PRKCE,RHOF,GNG5,FRS2,LASP1,CR2,CXCL8,PIK3C2B,PLD3,GNAS,FLT1,HBEGF,CSTB,PLD4,GNAI3,ITGAM,PRKCI,CCND2,RRAS2,GAB1,PRKCD,PIK3R6,PTGS2,FNBP1,ITGAX |
| fMLP Signaling in Neutrophils | 3.65 | 0.227 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,ARPC1B,MAPK1,NFATC3,PIK3R5,PIK3C3,PLCB1,PRKCE,GNG5,FRS2,PIK3C2B,GNAS,ARPC5L,ITPR1,FPR1,CALM1 (includes others),GNAI3,NCF1,PRKCI,RRAS2,GAB1,ARPC2,PRKCD,PIK3R6,ARPC4 |
| Role of JAK1 and JAK3 in γc Cytokine Signaling | 3.58 | 0.263 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,IL4R,PIK3CA,IL15RA,MAPK1,IL9R,IL21R,PIK3R5,IL7,IL7R,RRAS2,GAB1,PIK3C3,PIK3R6,STAT5B,FRS2,IL2RB |
| Regulation of Cellular Mechanics by Calpain Protease | 3.54 | 0.283 | turquoise | RAP2B,RAP1B,ITGB1,CAPN5,RAP2A,PXN,MAPK1,CDK4,PTK2,CCNA2,CAPNS1,RRAS2,CAPN2,VCL,ACTN4,ACTN1,CAPN3 |
| Virus Entry via Endocytic Pathways | 3.51 | 0.229 | turquoise | RAP2B,RAP1B,RAP2A,FLNB,PIK3CA,HLA-B,PIK3R5,AP1B1,ITGB7,FLNA,PIK3C3,CAV1,PRKCE,FRS2,DNM2,ITGB1,PIK3C2B,AP1S2,ITGAL,AP2S1,PRKCI,RRAS2,GAB1,AP3B1,PRKCD,PIK3R6,TFRC |
| Calcium-induced T Lymphocyte Apoptosis | 3.51 | 0.291 | turquoise | HLA-DOA,CAMK4,TRGV9,CD4,HLA-B,ATP2A3,ITPR1,CALM1 (includes others),PRKCI,HLA-DMA,PRKCD,HLA-DMB,FCER1G,HLA-DOB,PRKCE,CAPN2 |
| Hematopoiesis from Pluripotent Stem Cells | 3.49 | 0.343 | turquoise | CXCL8,IGHG3,TRGV9,IGH,CD4,IGLC1,FCER1G,IGHM,IGHA1,CD8A,IL7,IGHD |
| Natural Killer Cell Signaling | 3.46 | 0.224 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,KLRD1,SOS2,PIK3R5,CD300A,SH2D1A,PIK3C3,PRKCE,HCST,FRS2,FCGR3A/FCGR3B,PIK3C2B,TYROBP,FCGR2A,SH3BP2,PRKCI,RRAS2,GAB1,VAV3,PRKCD,LAT,FCER1G,PIK3R6,LCP2 |
| Th2 Pathway | 3.37 | 0.216 | turquoise | HLA-DOA,PIK3CA,TGFBR3,CD4,HLA-B,PIK3R5,TBX21,TGFBR2,HLA-DMA,PIK3C3,HLA-DMB,STAT5B,FRS2,ICOSLG/LOC102723996,IL2RB,CCR1,RUNX3,PIK3C2B,IL4R,CXCR4,BHLHE41,ACVR1,STAT4,CD80,GAB1,GFI1,PIK3R6,HLA-DOB,CD86,GATA3 |
| Th1 Pathway | 3.27 | 0.221 | turquoise | HLA-DOA,PIK3CA,KLRD1,NFATC3,HAVCR2,CD4,HLA-B,PIK3R5,CXCR3,CD8A,TBX21,NFIL3,HLA-DMA,PIK3C3,HLA-DMB,FRS2,ICOSLG/LOC102723996,RUNX3,PIK3C2B,IL6R,STAT4,GAB1,CD80,PIK3R6,HLA-DOB,CD86,GATA3 |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 3.25 | 0.239 | turquoise | PXN,PLD3,MAPK1,ARPC1B,FCGR2A,ARPC5L,FYB1,PTEN,NCK2,PLD4,HMOX1,PLA2G6,NCF1,PRKCI,ARPC2,PRKCD,VAV3,LYN,PRKCE,LCP2,ARPC4,FCGR3A/FCGR3B |
| Rac Signaling | 3.21 | 0.22 | turquoise | ITGB1,RAP1B,RAP2B,PIK3C2B,RAP2A,TIAM1,PIK3CA,CFL1,MAPK1,ARPC1B,ARPC5L,PIK3R5,PIP4K2B,PIP5K1B,LIMK1,PTK2,RRAS2,PRKCI,CYFIP2,GAB1,CYFIP1,ARPC2,PIK3C3,PIK3R6,SH3RF1,FRS2,ARPC4 |
| mTOR Signaling | 3.19 | 0.194 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,RPS3A,MAPK1,RPS27,PIK3R5,EIF4G1,RHOH,RPS11,VEGFA,HMOX1,PIK3C3,RHOU,EIF3A,PRKCE,RHOF,RPS17,FRS2,PIK3C2B,PLD3,RPS8,EIF4G3,EIF3E,EIF3M,ATG13,PLD4,RPS6KA6,PRKCI,RRAS2,GAB1,EIF4A3,PRKCD,RPS27L,PIK3R6,PRR5,RPS6KA4,FNBP1 |
| CD28 Signaling in T Helper Cells | 3.15 | 0.218 | turquoise | HLA-DOA,PIK3CA,CAMK4,ARPC1B,NFATC3,CD4,HLA-B,PIK3R5,HLA-DMA,PIK3C3,HLA-DMB,FRS2,PIK3C2B,ARPC5L,TRGV9,ITPR1,CALM1 (includes others),GAB1,CD80,ARPC2,LAT,PIK3R6,FCER1G,HLA-DOB,CD86,ARPC4,LCP2 |
| FAK Signaling | 3.12 | 0.226 | turquoise | RAP2B,RAP1B,ITGB1,CAPN5,RAP2A,PIK3C2B,PIK3CA,PXN,MAPK1,ARHGEF7,HMMR,SOS2,PIK3R5,PTEN,PTK2,RRAS2,CAPNS1,GAB1,PIK3C3,PIK3R6,CAPN2,VCL,FRS2,CAPN3 |
| IL-7 Signaling Pathway | 3.11 | 0.239 | turquoise | PIK3C2B,PIK3CA,MAPK1,IGH,SOS2,PIK3R5,IL7,BAK1,IL7R,PTK2,PAX5,GAB1,FOXO1,PIK3C3,PIK3R6,LYN,IGHM,CXCR5,STAT5B,FRS2,MCL1 |
| NF-κB Activation by Viruses | 3.04 | 0.232 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3C2B,MAP3K14,PIK3CA,MAPK1,CD4,PIK3R5,ITGAL,RRAS2,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,ITGAV,PRKCE,CXCR5,FRS2,CR2 |
| Systemic Lupus Erythematosus Signaling | 3.03 | 0.192 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MAPK1,NFATC3,SOS2,TXNL4A,HLA-B,PIK3R5,SNRPN,IGHG3,PRPF4B,PIK3C3,CD22,IGHM,FRS2,FCGR3A/FCGR3B,FCGR1B,PIK3C2B,CD79B,FCGR2A,IGH,TRGV9,IL6R,RRAS2,GAB1,CD80,IL1RN,CD72,LAT,PIK3R6,FCER1G,LYN,CD86,IL1B,TNF |
| SPINK1 General Cancer Pathway | 3 | 0.25 | turquoise | RAP2B,RAP1B,GZMA,MT2A,RAP2A,MT1G,PIK3C2B,PIK3CA,MAPK1,MT1X,IL6R,PIK3R5,MT1E,RRAS2,GAB1,PIK3C3,PIK3R6,FRS2 |
| PAK Signaling | 3 | 0.222 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3C2B,PIK3CA,PXN,MAPK1,CFL1,MYL6,ARHGEF7,SOS2,PIK3R5,LIMK1,PTK2,NCK2,RRAS2,GAB1,PIK3C3,PIK3R6,PDGFD,TNF,FRS2,MYL12A |
| VEGF Signaling | 3 | 0.222 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,PXN,MAPK1,FLT1,YWHAE,SOS2,PIK3R5,ARNT,VEGFA,PTK2,RRAS2,EIF1,GAB1,FOXO1,PIK3C3,PIK3R6,VCL,ACTN4,FRS2,ACTN1 |
| Altered T Cell and B Cell Signaling in Rheumatoid Arthritis | 2.99 | 0.244 | turquoise | MAP3K14,HLA-DOA,CD79B,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 | 2.98 | 0.238 | turquoise | RAP2B,RAP1B,HSD17B10,RAP2A,PIK3C2B,PIK3CA,MAPK1,CREBBP,CREB3,PIK3R5,CREB5,HSD17B8,RRAS2,GAB1,SP1,PIK3C3,PIK3R6,STAT5B,FRS2,ESR1 |
| Aryl Hydrocarbon Receptor Signaling | 2.9 | 0.207 | turquoise | MAPK1,CDK4,RARG,FAS,ARNT,CHEK1,CCNA2,HSP90B1,NCOA7,GSTM2,ALDH1A1,SP1,AHR,GSTK1,GSTM1,MGST1,TFDP1,MDM2,NCOA3,GSTO1,CYP1B1,CCND2,MGST2,IL1B,NRIP1,RXRA,ESR1,TNF |
| EIF2 Signaling | 2.89 | 0.186 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,RPS3A,MAPK1,RPS27,ATF5,SOS2,PIK3R5,EIF4G1,HSPA5,RPL7,RPS11,VEGFA,EIF1,PIK3C3,EIF3A,RPS17,FRS2,EIF2AK1,PIK3C2B,RPS8,AGO2,RPL7L1,EIF4G3,RPL23,EIF3E,RPL28,EIF3M,RPL15,WARS,RRAS2,GAB1,EIF4A3,RPL26L1,RPS27L,PIK3R6,RPL10,RPLP0 |
| Chemokine Signaling | 2.85 | 0.243 | turquoise | RAP2B,RAP1B,RAP2A,MPRIP,CAMK4,MAPK1,CFL1,CAMK1D,CXCR4,GNAQ,CCL5,LIMK1,PTK2,CALM1 (includes others),GNAI3,RRAS2,CAMK2D,PLCB1 |
| 14-3-3-mediated Signaling | 2.85 | 0.206 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,YWHAH,MAPK1,PIK3R5,TUBB,PIK3C3,PLCB1,PRKCE,TUBA1C,FRS2,PIK3C2B,TUBB3,YWHAE,TUBB4B,TUBG1,TUBA4A,VIM,PRKCI,RRAS2,FOXO1,GAB1,PRKCD,PIK3R6,TNF |
| Cholecystokinin/Gastrin-mediated Signaling | 2.81 | 0.219 | turquoise | RAP2B,RAP1B,RAP2A,PXN,MAPK1,SOS2,GNAQ,ITPR1,RHOH,PTK2,PRKCI,RRAS2,IL1RN,PRKCD,RHOU,PRKCE,PLCB1,IL1B,MEF2C,PTGS2,RHOF,TNF,FNBP1 |
| Melanoma Signaling | 2.8 | 0.254 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,CDK4,PIK3R5,MDM2,PTEN,BRAF,RRAS2,GAB1,PIK3C3,PIK3R6,FRS2 |
| NRF2-mediated Oxidative Stress Response | 2.79 | 0.188 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,USP14,MAPK1,PRDX1,PPIB,PIK3R5,GCLC,DNAJC3,HMOX1,GSTM2,KEAP1,PIK3C3,VCP,PRKCE,TXN,FRS2,GSTK1,PIK3C2B,GSTM1,MGST1,CREBBP,DNAJC1,SOD1,GSTO1,PRKCI,RRAS2,MGST2,GAB1,PRKCD,DNAJB11,RBX1,PIK3R6,ABCC4,DNAJC7 |
| Xenobiotic Metabolism Signaling | 2.76 | 0.175 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,CAMK1D,MAPK1,PIK3R5,GCLC,FMO5,ARNT,HMOX1,HSP90B1,GSTM2,ALDH1A1,CAMK2D,KEAP1,PIK3C3,PRKCE,HS3ST1,FRS2,AHR,CITED2,GSTK1,ABCB1,GSTM1,MAP3K14,PIK3C2B,MAP3K9,SRA1,MGST1,CREBBP,GSTO1,CYP1B1,PRKCI,RRAS2,MGST2,GAB1,SMOX,PRKCD,RBX1,PIK3R6,IL1B,NRIP1,RXRA,TNF,NDST1,DNAJC7 |
| CXCR4 Signaling | 2.75 | 0.193 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MYL6,MAPK1,CD4,PIK3R5,RHOH,PTK2,PIK3C3,RHOU,PLCB1,PRKCE,RHOF,GNG5,FRS2,MYL12A,PIK3C2B,PXN,GNAS,CXCR4,GNAQ,ITPR1,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,LYN,ELMO1,FNBP1 |
| Tec Kinase Signaling | 2.72 | 0.194 | turquoise | PIK3CA,GTF2I,PIK3R5,RHOH,FAS,PTK2,PIK3C3,RHOU,PRKCE,GNG5,STAT5B,RHOF,FRS2,ITGB1,PIK3C2B,GNAS,IGH,TRGV9,GNAQ,STAT4,GNAI3,TLR4,PRKCI,GAB1,PRKCD,VAV3,TNFRSF25,FCER1G,PIK3R6,LYN,TNF,FNBP1 |
| FLT3 Signaling in Hematopoietic Progenitor Cells | 2.72 | 0.227 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,CREB5,STAT4,RPS6KA6,RRAS2,GAB1,PIK3C3,PIK3R6,RPS6KA4,STAT5B,FRS2 |
| ErbB2-ErbB3 Signaling | 2.71 | 0.237 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,PTEN,RRAS2,GAB1,FOXO1,SP1,ETV4,PIK3C3,PIK3R6,STAT5B,FRS2 |
| Protein Ubiquitination Pathway | 2.69 | 0.176 | turquoise | PSMB3,USP14,PSMB10,UBE2N,USP53,HLA-B,FBXW7,DNAJC3,UBE2W,ELOB,HSPA5,ELOC,UCHL1,HSP90B1,STUB1,HSPE1,PSMD14,PSMA3,PSMC2,PSMA2,BIRC3,UBE2Q2,PSMA6,UBE2Q1,HSPA9,PSME2,DNAJC1,MDM2,PSMA1,PSMB6,PSMD8,HSPA8,USP44,PSMB7,UBE2L3,PSMB2,HSCB,UBE2G1,DNAJB11,RBX1,PSMA5,ANAPC5,HSPB11,SMURF2,DNAJC7,UBE2C |
| Prostate Cancer Signaling | 2.68 | 0.218 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,TFDP1,PA2G4,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,MDM2,CREB5,PTEN,HSP90B1,RRAS2,GAB1,FOXO1,PIK3C3,PIK3R6,FRS2 |
| Glycolysis I | 2.67 | 0.364 | turquoise | PGK1,ENO1,GPI,TPI1,PGAM1,PKM,GAPDH,ALDOA |
| Macropinocytosis Signaling | 2.65 | 0.225 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3C2B,PIK3CA,PIK3R5,CSF1R,ITGB7,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,CD14,ACTN4,PDGFD,FRS2 |
| Nur77 Signaling in T Lymphocytes | 2.64 | 0.271 | turquoise | CALM1 (includes others),HDAC9,HLA-DOA,CAMK4,CD80,HLA-DMA,TRGV9,HLA-DMB,HLA-B,FCER1G,HLA-DOB,CD86,RXRA |
| Type I Diabetes Mellitus Signaling | 2.62 | 0.216 | turquoise | MAP3K14,HLA-DOA,MAPK1,GZMB,TRGV9,HLA-B,FAS,IRAK1,TRADD,PRF1,CD80,HLA-DMA,HLA-DMB,FCER1G,IL1B,HLA-DOB,SOCS2,BID,CD86,TNFRSF1B,SOCS5,TNF |
| Breast Cancer Regulation by Stathmin1 | 2.59 | 0.182 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,CAMK4,CAMK1D,MAPK1,ARHGEF7,SOS2,PIK3R5,TUBB,LIMK1,CAMK2D,PIK3C3,PLCB1,PRKCE,TUBA1C,GNG5,FRS2,E2F2,PIK3C2B,TUBB3,GNAS,TUBB4B,TUBG1,GNAQ,TUBA4A,ITPR1,CALM1 (includes others),GNAI3,PRKCI,RRAS2,GAB1,PRKCD,E2F7,PIK3R6,ARHGEF10 |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 2.58 | 0.169 | turquoise | RAP2B,MAPK1,NFATC3,IL32,CSNK1A1,VEGFA,CAMK2D,PLCB1,TRAF5,FRS2,MAP3K14,PIK3C2B,CXCL8,MIF,CREBBP,IL6R,CREB3,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,GNAQ,CEBPB,TLR4,CALM1 (includes others),RRAS2,PRKCI,WNT10A,IL1B |
| Hypoxia Signaling in the Cardiovascular System | 2.58 | 0.236 | turquoise | P4HB,UBE2Q1,UBE2N,CREBBP,CREB3,MDM2,UBE2W,CREB5,ARNT,PTEN,VEGFA,UBE2L3,HSP90B1,UBE2G1,LDHA,UBE2Q2,UBE2C |
| Acute Myeloid Leukemia Signaling | 2.55 | 0.216 | turquoise | RAP2B,RAP1B,CSF3R,RAP2A,PIK3C2B,PIK3CA,MAPK1,IDH3G,SOS2,PIK3R5,CSF1R,BRAF,CSF2RB,RRAS2,GAB1,PIK3C3,PIK3R6,CEBPA,IDH2,STAT5B,FRS2 |
| Actin Cytoskeleton Signaling | 2.55 | 0.179 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MPRIP,ARPC1B,MYL6,MAPK1,ARHGEF7,SOS2,PIK3R5,PIP5K1B,LIMK1,PTK2,CYFIP2,FLNA,PIK3C3,VCL,SSH2,FRS2,ACTN1,MYL12A,ITGB1,PIK3C2B,PXN,TIAM1,CFL1,ARPC5L,FGF9,RDX,RRAS2,GAB1,CYFIP1,VAV3,ARPC2,PIK3R6,CD14,ACTN4,PDGFD,ARPC4 |
| JAK/Stat Signaling | 2.53 | 0.22 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,PIAS2,MAPK1,SOS2,GNAQ,PIK3R5,CEBPB,STAT4,RRAS2,GAB1,PIK3C3,PIK3R6,SOCS2,STAT5B,SOCS5,FRS2 |
| Non-Small Cell Lung Cancer Signaling | 2.52 | 0.224 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,TFDP1,PA2G4,MAPK1,SOS2,PIK3R5,CDK4,ITPR1,RRAS2,GAB1,PIK3C3,PIK3R6,RXRA,FRS2,RASSF1 |
| PKCθ Signaling in T Lymphocytes | 2.49 | 0.191 | turquoise | RAP2B,RAP1B,RAP2A,HLA-DOA,PIK3CA,MAPK1,NFATC3,CD4,SOS2,HLA-B,PIK3R5,CAMK2D,HLA-DMA,PIK3C3,HLA-DMB,FRS2,MAP3K9,MAP3K14,PIK3C2B,TRGV9,RRAS2,GAB1,CD80,VAV3,LAT,FCER1G,PIK3R6,HLA-DOB,CD86,LCP2 |
| Epithelial Adherens Junction Signaling | 2.47 | 0.194 | turquoise | RAP1B,RAP2B,RAP2A,TUBA1B,MYL6,ARPC1B,TGFBR3,AFDN,TUBB,CLIP1,PTEN,TGFBR2,KEAP1,TUBA1C,VCL,ACTN1,TUBB3,ARPC5L,TUBB4B,TUBG1,ACVR1,TUBA4A,RRAS2,ARPC2,ZYX,ACTN4,ARPC4,CTNND1 |
| CCR3 Signaling in Eosinophils | 2.46 | 0.198 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MPRIP,MAPK1,PIK3R5,LIMK1,PIK3C3,PLCB1,PRKCE,GNG5,FRS2,PIK3C2B,GNAS,CFL1,ITPR1,CALM1 (includes others),PLA2G6,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6 |
| Neuroinflammation Signaling Pathway | 2.45 | 0.168 | turquoise | HLA-DOA,MAPK1,TICAM2,NFATC3,TGFBR3,HLA-B,CX3CR1,IDE,TGFBR2,BIRC3,FRS2,CXCL8,PIK3C2B,CD200,CREBBP,IL6R,CREB3,TBK1,CREB5,TLR2,PLA2G6,GAB1,PIK3R6,CD86,CFLAR,TNF,PIK3CA,PYCARD,GRIA1,PIK3R5,FZD1,CCL5,CCL3,FAS,IRAK1,HMOX1,HLA-DMA,PIK3C3,HLA-DMB,NLRP3,TYROBP,ACVR1,GABBR1,BIRC5,CSF1R,TLR4,CD80,HLA-DOB,IL1B,PTGS2 |
| Actin Nucleation by ARP-WASP Complex | 2.44 | 0.242 | turquoise | ITGB1,RAP1B,RAP2B,RAP2A,ARPC1B,ARPC5L,SOS2,RHOH,NCK2,RRAS2,ARPC2,RHOU,RHOF,ARPC4,FNBP1 |
| Chronic Myeloid Leukemia Signaling | 2.43 | 0.205 | turquoise | RAP2B,RAP1B,RAP2A,HDAC9,PIK3C2B,PIK3CA,TFDP1,PA2G4,MAPK1,SMAD3,SOS2,CDK4,PIK3R5,MDM2,TGFBR2,RRAS2,GAB1,PIK3C3,E2F7,PIK3R6,STAT5B,FRS2,E2F2 |
| ILK Signaling | 2.41 | 0.181 | turquoise | FLNB,PIK3CA,MYL6,MAPK1,PIK3R5,RHOH,ITGB7,PTEN,VEGFA,PTK2,NCK2,FLNA,PIK3C3,RHOU,VCL,RHOF,FRS2,ACTN1,DSP,ITGB1,PIK3C2B,PXN,CFL1,CREB3,CREBBP,VIM,CREB5,GAB1,LIMS1,PIK3R6,RPS6KA4,ACTN4,PTGS2,TNF,FNBP1 |
| STAT3 Pathway | 2.41 | 0.197 | turquoise | RAP2B,RAP1B,MAP3K9,RAP2A,IL4R,IL15RA,IL5RA,FLT1,IL13RA1,MAPK1,IL9R,IL21R,TGFBR3,IL6R,NDUFA13,IL7R,VEGFA,TGFBR2,CSF2RB,RRAS2,BMPR1A,IL1B,SOCS2,BMP6,SOCS5,IL2RB |
| Renal Cell Carcinoma Signaling | 2.4 | 0.218 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,CREBBP,SOS2,PIK3R5,ELOB,ELOC,ARNT,VEGFA,RRAS2,GAB1,RBX1,PIK3C3,PIK3R6,FRS2 |
| Cancer Drug Resistance By Drug Efflux | 2.34 | 0.261 | turquoise | BRAF,RAP1B,RAP2B,ABCB1,RAP2A,PIK3CA,RRAS2,MAPK1,FOXO1,MDM2,PTGS2,PTEN |
| TREM1 Signaling | 2.31 | 0.229 | turquoise | ITGB1,CXCL8,TREM1,NLRP3,MAPK1,TYROBP,CIITA,CCL3,IRAK1,TLR2,TLR4,IL1B,CD86,STAT5B,TNF,ITGAX |
| Lipid Antigen Presentation by CD1 | 2.29 | 0.35 | turquoise | CD1A,TRGV9,FCER1G,CANX,PSAP,AP1B1,AP2S1 |
| CDP-diacylglycerol Biosynthesis I | 2.28 | 0.32 | turquoise | AGPAT5,ABHD5,LPCAT2,LPCAT4,MBOAT1,GPAT3,AGPAT3,CDS2 |
| Heme Degradation | 2.26 | 0.75 | turquoise | HMOX1,BLVRA,HMOX2 |
| Huntington's Disease Signaling | 2.25 | 0.17 | turquoise | SDHB,PIK3CA,ATP5F1D,MAPK1,SOS2,PIK3R5,HSPA5,VTI1B,ATP5F1E,CDK5,SP1,PIK3C3,PLCB1,PRKCE,GNG5,FRS2,NAPA,DNM2,POLR2L,CAPN5,ATP5PF,PIK3C2B,HDAC9,ATP5F1A,CREB3,CREBBP,HSPA9,PSME2,GNAQ,ITPR1,CREB5,HSPA8,ATP5F1C,PRKCI,CAPNS1,GAB1,ATP5F1B,PRKCD,PIK3R6,PSME4,CAPN2,CAPN3 |
| IL-15 Signaling | 2.21 | 0.214 | turquoise | RAP2B,RAP1B,RAP2A,CXCL8,PIK3C2B,PIK3CA,IL15RA,MAPK1,PIK3R5,PTK2,RRAS2,GAB1,PIK3C3,PIK3R6,STAT5B,TNF,FRS2,IL2RB |
| Leukocyte Extravasation Signaling | 2.2 | 0.175 | turquoise | RAP1B,CD99,PIK3CA,SPN,MYL6,MAPK1,PIK3R5,AFDN,RHOH,PTK2,TIMP1,PIK3C3,PRKCE,MMP11,VCL,FRS2,ACTN1,TIMP2,ITGB1,PIK3C2B,PXN,ARHGAP6,CXCR4,RDX,ITGAL,SELPLG,GNAI3,NCF1,ITGAM,PRKCI,GAB1,VAV3,PRKCD,PIK3R6,ACTN4,CTNND1 |
| Thrombopoietin Signaling | 2.18 | 0.222 | turquoise | RAP1B,RAP2B,RAP2A,PIK3C2B,PIK3CA,MAPK1,PIK3R5,PRKCI,RRAS2,GAB1,PIK3C3,PRKCD,PIK3R6,PRKCE,STAT5B,FRS2 |
| Apelin Endothelial Signaling Pathway | 2.17 | 0.194 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,GNAS,CAMK4,MAPK1,SMAD3,PIK3R5,ARNT,CALM1 (includes others),GNAI3,RRAS2,PRKCI,GAB1,SP1,PRKCD,PIK3C3,PIK3R6,PRKCE,PLCB1,MEF2C,FRS2 |
| Regulation of eIF4 and p70S6K Signaling | 2.17 | 0.184 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,RPS3A,EIF4EBP2,MAPK1,RPS27,SOS2,PIK3R5,EIF4G1,RPS11,EIF1,PIK3C3,EIF3A,RPS17,FRS2,ITGB1,PIK3C2B,RPS8,EIF4G3,AGO2,EIF3E,EIF3M,RRAS2,GAB1,EIF4A3,RPS27L,PIK3R6 |
| Clathrin-mediated Endocytosis Signaling | 2.16 | 0.174 | turquoise | PIK3CA,ARPC1B,PICALM,APOA2,PIK3R5,SH3GLB1,AP1B1,ITGB7,VEGFA,CD2AP,ARRB1,SNX9,PIK3C3,SERPINA1,S100A8,LDLRAP1,SH3KBP1,FRS2,DNM2,ITGB1,PIK3C2B,ARPC5L,FGF9,AP1S2,MDM2,AP2S1,HSPA8,LDLR,GAB1,AP3B1,ARPC2,PIK3R6,TFRC,PDGFD,ARPC4,HIP1R |
| PPAR Signaling | 2.15 | 0.204 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K14,SRA1,MAPK1,CREBBP,SOS2,HSP90B1,RRAS2,IL1RN,IL1B,PTGS2,NRIP1,PDGFD,TNFRSF1B,RXRA,STAT5B,TNF,CITED2 |
| Fc Epsilon RI Signaling | 2.13 | 0.192 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,IGH,SOS2,PIK3R5,PLA2G6,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,VAV3,LAT,PIK3R6,FCER1G,LYN,PRKCE,TNF,FRS2,LCP2 |
| NF-κB Signaling | 2.12 | 0.178 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,UBE2N,TGFBR3,PIK3R5,IRAK1,TNFRSF17,TGFBR2,BRAF,TRADD,BMPR1A,PIK3C3,TRAF5,TNFRSF1B,FRS2,MAP3K14,PIK3C2B,FLT1,TRGV9,CREBBP,TBK1,TLR2,TLR4,RRAS2,GAB1,IL1RN,FCER1G,PIK3R6,IL1B,TNF |
| GP6 Signaling Pathway | 2.12 | 0.189 | turquoise | RAP1B,PIK3C2B,COL19A1,PIK3CA,CAMK4,COL4A3,PIK3R5,ITPR1,LAMC1,PTK2,CALM1 (includes others),PRKCI,GAB1,PRKCD,PIK3C3,LAT,FCER1G,PIK3R6,LYN,PRKCE,COL4A4,COL18A1,FRS2,LCP2,RASGRP2 |
| p70S6K Signaling | 2.11 | 0.187 | turquoise | RAP1B,RAP2B,RAP2A,PIK3CA,MAPK1,YWHAH,SOS2,PIK3R5,PIK3C3,PLCB1,PRKCE,EEF2K,FRS2,PIK3C2B,IL4R,CD19,YWHAE,CD79B,GNAQ,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,LYN |
| MIF-mediated Glucocorticoid Regulation | 2.1 | 0.281 | turquoise | TLR4,PLA2G6,LY96,MIF,MAPK1,CD14,CD74,PTGS2,NR3C1 |
| Salvage Pathways of Pyrimidine Deoxyribonucleotides | 2.09 | 0.5 | turquoise | APOBEC3B,TYMP,APOBEC3G,APOBEC3A |
| GM-CSF Signaling | 2.08 | 0.212 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,CSF2RB,CAMK2D,RRAS2,GAB1,PIK3C3,PIK3R6,LYN,STAT5B,FRS2 |
| p53 Signaling | 2.06 | 0.195 | turquoise | HDAC9,PIK3C2B,PIK3CA,TP63,PERP,PIK3R5,CDK4,MDM2,BIRC5,FAS,PTEN,CHEK1,TP53I3,SCO2,MDM4,CCND2,GAB1,GADD45A,PIK3C3,PIK3R6,HIPK2,FRS2 |
| IGF-1 Signaling | 2.06 | 0.195 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,PXN,MAPK1,YWHAH,YWHAE,SOS2,PIK3R5,IGFBP7,PTK2,RRAS2,PRKCI,GAB1,FOXO1,PIK3C3,PIK3R6,SOCS2,SOCS5,FRS2 |
| Phosphatidylglycerol Biosynthesis II (Non-plastidic) | 2.06 | 0.296 | turquoise | AGPAT5,ABHD5,LPCAT2,LPCAT4,MBOAT1,GPAT3,AGPAT3,CDS2 |
| HGF Signaling | 2.05 | 0.192 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,MAP3K9,PIK3C2B,MAP3K14,PIK3CA,PXN,MAPK1,SOS2,PIK3R5,PTK2,RRAS2,PRKCI,GAB1,ETS2,PRKCD,PIK3C3,PIK3R6,PRKCE,PTGS2,FRS2 |
| SAPK/JNK Signaling | 2.03 | 0.196 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K9,PIK3C2B,PIK3CA,NFATC3,TRGV9,SOS2,PIK3R5,MINK1,TRADD,RRAS2,GAB1,GADD45A,PIK3C3,PIK3R6,FCER1G,DUSP4,GNG5,FRS2 |
| VEGF Family Ligand-Receptor Interactions | 2.03 | 0.202 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,FLT1,SOS2,PIK3R5,VEGFA,PLA2G6,RRAS2,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,FRS2 |
| Pancreatic Adenocarcinoma Signaling | 1.97 | 0.189 | turquoise | PIK3C2B,PIK3CA,PLD3,TFDP1,PA2G4,MAPK1,SMAD3,PIK3R5,CDK4,HBEGF,MDM2,BIRC5,VEGFA,PLD4,TGFBR2,HMOX1,GAB1,PIK3C3,E2F7,PIK3R6,PTGS2,FRS2,E2F2 |
| IL-6 Signaling | 1.95 | 0.184 | turquoise | RAP1B,RAP2B,CXCL8,PIK3C2B,MAP3K14,RAP2A,ABCB1,PIK3CA,MAPK1,IL6R,SOS2,PIK3R5,CEBPB,VEGFA,RRAS2,GAB1,IL1RN,PIK3C3,PIK3R6,IL1B,CD14,TNFRSF1B,TNF,FRS2,MCL1 |
| Choline Biosynthesis III | 1.94 | 0.385 | turquoise | PLD4,HMOX1,CEPT1,PLD3,PCYT1A |
| HER-2 Signaling in Breast Cancer | 1.93 | 0.198 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3C2B,PIK3CA,SOS2,PIK3R5,MDM2,ITGB7,PRKCI,RRAS2,GAB1,FOXO1,PRKCD,PIK3C3,PIK3R6,PRKCE,FRS2 |
| Gluconeogenesis I | 1.92 | 0.304 | turquoise | PGK1,ENO1,GPI,PGAM1,ALDOA,GAPDH,MDH2 |
| Antigen Presentation Pathway | 1.92 | 0.265 | turquoise | HLA-DOA,HLA-DMA,HLA-DMB,HLA-B,CIITA,CANX,HLA-DOB,CD74,PSMB6 |
| Pyridoxal 5'-phosphate Salvage Pathway | 1.91 | 0.219 | turquoise | BRAF,PDXK,MAP3K9,DAPK1,CDK5,MAPK1,PRPF4B,PRKCD,CDK4,CSNK1A1,PRKCE,ADPGK,LIMK1,IRAK1 |
| IL-3 Signaling | 1.9 | 0.2 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,PIK3R5,CSF2RB,PRKCI,RRAS2,FOXO1,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,STAT5B,FRS2 |
| Myc Mediated Apoptosis Signaling | 1.9 | 0.208 | turquoise | RAP1B,RAP2B,RAP2A,PIK3C2B,PIK3CA,YWHAE,YWHAH,SOS2,PIK3R5,FAS,RRAS2,GAB1,PIK3C3,PIK3R6,BID,FRS2 |
| Semaphorin Signaling in Neurons | 1.89 | 0.231 | turquoise | ITGB1,DPYSL2,PTK2,SEMA3A,CFL1,MAPK1,CDK5,RHOU,RHOF,RHOH,FNBP1,LIMK1 |
| HIF1α Signaling | 1.88 | 0.185 | turquoise | RAP2B,RAP1B,SLC2A5,RAP2A,PIK3C2B,PIK3CA,MAPK1,CREBBP,PIK3R5,MDM2,ELOB,ELOC,LDHB,ARNT,VEGFA,RRAS2,GAB1,RBX1,PIK3C3,PIK3R6,MMP11,LDHA,FRS2 |
| PI3K Signaling in B Lymphocytes | 1.88 | 0.183 | turquoise | RAP2B,RAP1B,RAP2A,IL4R,CD19,PIK3CA,CAMK4,MAPK1,CD79B,ATF5,NFATC3,ITPR1,PTEN,CALM1 (includes others),TLR4,RRAS2,CAMK2D,PRKCI,VAV3,LYN,PLCB1,PLEKHA2,PLEKHA1,CR2 |
| Pathogenesis of Multiple Sclerosis | 1.87 | 0.444 | turquoise | CCR1,CXCR3,CCL5,CCL3 |
| Neurotrophin/TRK Signaling | 1.87 | 0.202 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SPRY1,CREBBP,CREB3,SOS2,PIK3R5,CREB5,RRAS2,GAB1,PIK3C3,PIK3R6,FRS2 |
| ErbB4 Signaling | 1.85 | 0.205 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,FRS2 |
| Crosstalk between Dendritic Cells and Natural Killer Cells | 1.82 | 0.2 | turquoise | IL15RA,TYROBP,KLRD1,CD69,HLA-B,ITGAL,FAS,TLR4,CSF2RB,PRF1,CAMK2D,CD80,CD226,CD86,TNFRSF1B,TNF,IL2RB |
| IL-2 Signaling | 1.82 | 0.208 | turquoise | RAP2B,RAP1B,PIK3C2B,RAP2A,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,SOS2,PIK3R6,PIK3R5,STAT5B,FRS2,IL2RB |
| IL-9 Signaling | 1.82 | 0.234 | turquoise | PIK3C2B,PIK3CA,GAB1,IL9R,PIK3C3,PIK3R6,PIK3R5,SOCS2,STAT5B,TNF,FRS2 |
| Glioblastoma Multiforme Signaling | 1.81 | 0.173 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SOS2,CDK4,PIK3R5,FZD1,RHOH,PTEN,PIK3C3,RHOU,PLCB1,RHOF,FRS2,E2F2,PIK3C2B,MDM2,ITPR1,RRAS2,WNT10A,GAB1,FOXO1,PRKCD,E2F7,PIK3R6,PDGFD,FNBP1 |
| Growth Hormone Signaling | 1.77 | 0.198 | turquoise | PIK3C2B,PIK3CA,MAPK1,PIK3R5,RPS6KA6,PRKCI,GAB1,PIK3C3,PRKCD,CEBPA,PIK3R6,PRKCE,SOCS2,RPS6KA4,STAT5B,SOCS5,FRS2 |
| CNTF Signaling | 1.74 | 0.209 | turquoise | RAP2B,RAP1B,PIK3C2B,RAP2A,RPS6KA6,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,PIK3R6,PIK3R5,RPS6KA4,FRS2 |
| ERK5 Signaling | 1.74 | 0.209 | turquoise | RAP1B,RAP2B,RAP2A,YWHAE,YWHAH,CREB3,CREBBP,GNAQ,CREB5,RPS6KA6,RRAS2,GAB1,MEF2C,RPS6KA4 |
| T Cell Receptor Signaling | 1.73 | 0.184 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,CAMK4,MAPK1,NFATC3,CD4,SOS2,PIK3R5,CD8A,CALM1 (includes others),RRAS2,GAB1,PIK3C3,VAV3,LAT,PIK3R6,FRS2,LCP2 |
| Salvage Pathways of Pyrimidine Ribonucleotides | 1.71 | 0.191 | turquoise | MAP3K9,APOBEC3B,DAPK1,MAPK1,UPP1,CDK4,CSNK1A1,APOBEC3G,APOBEC3A,LIMK1,IRAK1,BRAF,CDK5,PRKCD,PRPF4B,PRKCE,AK9,ADPGK |
| Gap Junction Signaling | 1.71 | 0.165 | turquoise | RAP2B,RAP1B,RAP2A,TUBA1B,PIK3CA,MAPK1,GRIA1,SOS2,CSNK1A1,PIK3R5,TUBB,SP1,PIK3C3,CAV1,PLCB1,PRKCE,TUBA1C,FRS2,PIK3C2B,TUBB3,GNAS,TUBB4B,CSNK1G3,TUBG1,GNAQ,TUBA4A,ITPR1,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6 |
| Thrombin Signaling | 1.69 | 0.163 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MPRIP,CAMK4,CAMK1D,MYL6,MAPK1,PIK3R5,RHOH,PTK2,CAMK2D,PIK3C3,RHOU,PLCB1,PRKCE,RHOF,GNG5,FRS2,MYL12A,PIK3C2B,GNAS,GNAQ,ITPR1,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,GATA3,ARHGEF10,FNBP1 |
| Erythropoietin Signaling | 1.68 | 0.193 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,STAT5B,FRS2 |
| Inflammasome pathway | 1.68 | 0.3 | turquoise | TLR4,NLRP3,NLRP1,AIM2,PYCARD,IL1B |
| LPS-stimulated MAPK Signaling | 1.67 | 0.189 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,MAP3K14,PIK3CA,MAPK1,PIK3R5,TLR4,PRKCI,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,CD14,FRS2 |
| Apoptosis Signaling | 1.67 | 0.189 | turquoise | RAP2B,RAP1B,CAPN5,RAP2A,MAP3K14,MAPK1,FAS,BAK1,CAPNS1,RRAS2,BID,PRKCE,CAPN2,TNFRSF1B,BIRC3,TNF,MCL1,CAPN3 |
| eNOS Signaling | 1.64 | 0.169 | turquoise | PIK3CA,CAMK4,PIK3R5,HSPA5,VEGFA,AQP3,CCNA2,HSP90B1,STUB1,PIK3C3,CAV1,PRKCE,FRS2,DNM2,PIK3C2B,GNAS,FLT1,HSPA9,GNAQ,ITPR1,HSPA8,CALM1 (includes others),AQP9,PRKCI,GAB1,PRKCD,PIK3R6,ESR1 |
| CTLA4 Signaling in Cytotoxic T Lymphocytes | 1.63 | 0.188 | turquoise | PIK3C2B,PIK3CA,TRGV9,AP1S2,HLA-B,PIK3R5,AP1B1,CD8A,AP2S1,CD80,GAB1,PIK3C3,LAT,PIK3R6,FCER1G,CD86,FRS2,LCP2 |
| Glutathione Redox Reactions I | 1.58 | 0.286 | turquoise | GSTM1,MGST1,GSTM2,MGST2,GPX1,GSTK1 |
| Endoplasmic Reticulum Stress Pathway | 1.58 | 0.286 | turquoise | HSP90B1,ERN1,XBP1,DNAJC3,HSPA5,MBTPS2 |
| VDR/RXR Activation | 1.57 | 0.195 | turquoise | CCNC,CCL5,CEBPB,NCOA3,PRKCI,FOXO1,SP1,GADD45A,RUNX2,PRKCD,CEBPA,CD14,PRKCE,VDR,RXRA |
| Molecular Mechanisms of Cancer | 1.56 | 0.147 | turquoise | RAP2B,MAPK1,SMAD3,SOS2,PTK2,TGFBR2,CAMK2D,PLCB1,HIPK2,BIRC3,FRS2,E2F2,PIK3C2B,TFDP1,CREBBP,BMP8B,AURKA,CCND2,GAB1,RABIF,PRKCD,PIK3R6,CFLAR,ARHGEF10,FNBP1,RAP1B,RAP2A,PIK3CA,PA2G4,ARHGEF7,PIK3R5,CDK4,FZD1,RHOH,FAS,CHEK1,BRAF,CDK5,BMPR1A,PIK3C3,RHOU,PRKCE,BID,RHOF,ITGB1,GNAS,GNAQ,MDM2,BAK1,GNAI3,RRAS2,PRKCI,FOXO1,WNT10A,E2F7,BMP6,CTNND1 |
| Regulation of Actin-based Motility by Rho | 1.56 | 0.19 | turquoise | ITGB1,MPRIP,ARPC1B,MYL6,CFL1,ARPC5L,PIP4K2B,PIP5K1B,RHOH,LIMK1,ARPC2,RHOU,RHOF,ARPC4,FNBP1,MYL12A |
| GDNF Family Ligand-Receptor Interactions | 1.56 | 0.19 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,ITPR1,DOK3,RRAS2,PDLIM7,GAB1,PIK3C3,PIK3R6,FRS2 |
| Aldosterone Signaling in Epithelial Cells | 1.55 | 0.166 | turquoise | ICMT,PIK3CA,MAPK1,SOS2,PIK3R5,DNAJC3,PIP4K2B,PIP5K1B,HSPA5,HSP90B1,PIK3C3,HSPE1,PRKCE,PLCB1,FRS2,PIK3C2B,HSPA9,DNAJC1,ITPR1,HSPA8,PRKCI,GAB1,HSCB,DNAJB11,PRKCD,HSPB11,PIK3R6,DNAJC7 |
| Protein Kinase A Signaling | 1.55 | 0.147 | turquoise | MAPK1,YWHAH,MYL6,NFATC3,SMAD3,PTEN,PTK2,TGFBR2,CAMK2D,PDE7B,GDE1,PLCB1,DUSP7,EYA2,SMPDL3A,KDELR1,PTPRE,YWHAE,HIST1H3C,CREBBP,CREB3,PTPN18,ITPR1,CREB5,EPM2A,AKAP13,H3F3A/H3F3B,PTPRB,PRKCD,ANAPC5,DUSP4,KDELR2,SIRPA,RAP1B,FLNB,CAMK4,PDE7A,DUSP6,PDE4A,AKAP7,PTPN12,BRAF,PTPRJ,FLNA,PRKCE,PDE4D,GNG5,MYL12A,PXN,PTPRK,GNAS,GNAQ,CALM1 (includes others),GNAI3,PRKCI,PTGS2 |
| Melanocyte Development and Pigmentation Signaling | 1.54 | 0.181 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,GNAS,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,CREB5,RPS6KA6,RRAS2,GAB1,PIK3C3,PIK3R6,RPS6KA4,FRS2 |
| ErbB Signaling | 1.54 | 0.181 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,HBEGF,NCK2,PRKCI,RRAS2,GAB1,FOXO1,PRKCD,PIK3C3,PIK3R6,PRKCE,FRS2 |
| Caveolar-mediated Endocytosis Signaling | 1.54 | 0.197 | turquoise | ITGB1,COPZ1,FLNB,HLA-B,FLOT1,ITGAL,ITGB7,COPG1,ITGAM,FLNA,ITGAV,CAV1,DNM2,ITGAX |
| Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells | 1.54 | 0.259 | turquoise | PRF1,GZMB,TRGV9,HLA-B,FCER1G,BID,FAS |
| Granzyme B Signaling | 1.54 | 0.312 | turquoise | PRF1,NUMA1,GZMB,BID,LMNB1 |
| Dolichyl-diphosphooligosaccharide Biosynthesis | 1.53 | 0.364 | turquoise | ALG13,ALG14,ALG3,ALG1 |
| Endometrial Cancer Signaling | 1.49 | 0.194 | turquoise | RAP1B,RAP2B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,PTEN,RRAS2,GAB1,PIK3C3,PIK3R6,FRS2 |
| ERK/MAPK Signaling | 1.47 | 0.159 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,YWHAH,MAPK1,DUSP6,SOS2,PIK3R5,PTK2,BRAF,ETS2,PIK3C3,PRKCE,FRS2,ITGB1,PIK3C2B,PXN,HIST1H3C,CREB3,CREBBP,CREB5,PLA2G6,H3F3A/H3F3B,RRAS2,PRKCI,GAB1,PRKCD,PIK3R6,RPS6KA4,DUSP4,ESR1 |
| IL-17 Signaling | 1.47 | 0.183 | turquoise | RAP2B,RAP1B,RAP2A,CXCL8,PIK3C2B,MAP3K14,PIK3CA,MAPK1,PIK3R5,CEBPB,RRAS2,GAB1,TIMP1,PIK3C3,PIK3R6,PTGS2,FRS2 |
| TGF-β Signaling | 1.47 | 0.183 | turquoise | RAP2B,RAP1B,RAP2A,RUNX3,MAPK1,SMAD3,CREBBP,SOS2,ACVR1,TGIF1,TGFBR2,RRAS2,BMPR1A,RUNX2,SMURF2,VDR,PMEPA1 |
| Ascorbate Recycling (Cytosolic) | 1.44 | 0.667 | turquoise | GLRX,GSTO1 |
| Tryptophan Degradation to 2-amino-3-carboxymuconate Semialdehyde | 1.43 | 0.429 | turquoise | AFMID,KMO,KYNU |
| Small Cell Lung Cancer Signaling | 1.43 | 0.184 | turquoise | PIK3C2B,PIK3CA,TFDP1,PA2G4,CDK4,PIK3R5,PTEN,PTK2,GAB1,PIK3C3,PIK3R6,BID,PTGS2,TRAF5,RXRA,FRS2 |
| UVB-Induced MAPK Signaling | 1.41 | 0.194 | turquoise | PIK3C2B,PIK3CA,PRKCI,H3F3A/H3F3B,GAB1,MAPK1,PRKCD,PIK3C3,HIST1H3C,PIK3R6,PIK3R5,PRKCE,FRS2 |
| NGF Signaling | 1.4 | 0.171 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K9,PIK3C2B,MAP3K14,PIK3CA,MAPK1,CREBBP,CREB3,SOS2,PIK3R5,CREB5,RPS6KA6,RRAS2,GAB1,PRKCD,PIK3C3,PIK3R6,RPS6KA4,FRS2 |
| Docosahexaenoic Acid (DHA) Signaling | 1.4 | 0.204 | turquoise | PIK3C2B,PIK3CA,GAB1,FOXO1,PIK3C3,PIK3R6,PIK3R5,BIK,IL1B,BID,FRS2 |
| Telomerase Signaling | 1.4 | 0.172 | turquoise | RAP2B,RAP1B,RAP2A,HDAC9,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,TERF2,HSP90B1,RRAS2,GAB1,SP1,ETS2,PIK3C3,PIK3R6,TINF2,FRS2,IL2RB |
| Glutathione-mediated Detoxification | 1.39 | 0.261 | turquoise | GSTM1,MGST1,GSTM2,MGST2,GSTO1,GSTK1 |
| Gαq Signaling | 1.38 | 0.162 | turquoise | PIK3CA,CAMK4,MAPK1,NFATC3,PIK3R5,RHOH,HMOX1,PIK3C3,RHOU,PLCB1,PRKCE,RHOF,GNG5,FRS2,PIK3C2B,PLD3,GNAS,GNAQ,ITPR1,PLD4,CALM1 (includes others),PRKCI,GAB1,PRKCD,PIK3R6,FNBP1 |
| Nitric Oxide Signaling in the Cardiovascular System | 1.36 | 0.173 | turquoise | PIK3C2B,PIK3CA,CAMK4,MAPK1,FLT1,PIK3R5,ATP2A3,ITPR1,VEGFA,CALM1 (includes others),HSP90B1,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,CAV1,PRKCE,FRS2 |
| Endothelin-1 Signaling | 1.32 | 0.156 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,PIK3R5,BRAF,PLBD1,HMOX1,PIK3C3,PLCB1,PRKCE,FRS2,PLA2G16,PIK3C2B,GNAS,PLD3,GNAQ,ITPR1,PLD4,PLA2G6,GNAI3,PRKCI,RRAS2,GAB1,PRKCD,PIK3R6,RARRES3,PTGS2,PAFAH1B3 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 1.32 | 0.204 | turquoise | MDM4,GADD45A,YWHAE,YWHAH,WEE1,TOP2A,MDM2,AURKA,HIPK2,CHEK1 |
| α-Adrenergic Signaling | 1.31 | 0.178 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,GNAS,MAPK1,GNAQ,ITPR1,CALM1 (includes others),GNAI3,PRKCI,RRAS2,PRKCD,PRKCE,GNG5,SLC8A1 |
| Tumoricidal Function of Hepatic Natural Killer Cells | 1.31 | 0.25 | turquoise | PRF1,GZMB,SRGN,BID,ITGAL,FAS |
| Hereditary Breast Cancer Signaling | 1.31 | 0.162 | turquoise | RAP2B,RAP1B,RAP2A,HDAC9,PIK3C2B,PIK3CA,WEE1,CREBBP,TUBG1,PIK3R5,CDK4,SMARCD3,PTEN,CHEK1,RRAS2,GAB1,GADD45A,SMARCA2,PIK3C3,SMARCB1,PIK3R6,FRS2,POLR2L,PHF10 |
| Phagosome Maturation | 1.28 | 0.164 | turquoise | TUBA1B,TUBB3,ATP6V1D,VPS41,PRDX5,TUBB4B,PRDX1,HLA-B,TUBG1,TUBA4A,CANX,TUBB,ATP6V1A,VTI1B,DYNLRB1,ATP6V0A1,CTSA,DYNLL1,PIK3C3,TUBA1C,CTSC,NAPA |
| Leukotriene Biosynthesis | 1.28 | 0.308 | turquoise | MGST2,GGT1,ALOX5,DPEP2 |
| p38 MAPK Signaling | 1.26 | 0.168 | turquoise | MAPKAPK3,HIST1H3C,CREBBP,CREB3,CREB5,FAS,IRAK1,TGFBR2,TRADD,PLA2G6,RPS6KA6,H3F3A/H3F3B,IL1RN,IL1B,MEF2C,RPS6KA4,EEF2K,TNFRSF1B,TNF |
| Angiopoietin Signaling | 1.24 | 0.176 | turquoise | RAP1B,RAP2B,RAP2A,PIK3C2B,PIK3CA,PIK3R5,BIRC5,PTK2,RRAS2,FOXO1,GAB1,PIK3C3,PIK3R6,STAT5B,FRS2 |
| Cdc42 Signaling | 1.24 | 0.165 | turquoise | ITGB1,HLA-DOA,MPRIP,MAPK1,CFL1,MYL6,ARPC1B,ARPC5L,TRGV9,HLA-B,CLIP1,LIMK1,PRKCI,HLA-DMA,ARPC2,HLA-DMB,FCER1G,HLA-DOB,ARPC4,MYL12A |
| Signaling by Rho Family GTPases | 1.23 | 0.149 | turquoise | PIK3CA,ARPC1B,MYL6,MAPK1,ARHGEF7,PIK3R5,PIP4K2B,PIP5K1B,RHOH,CLIP1,LIMK1,PTK2,PIK3C3,RHOU,RHOF,GNG5,FRS2,MYL12A,ITGB1,MAP3K9,PIK3C2B,GNAS,CFL1,ARPC5L,GNAQ,RDX,VIM,CDC42EP3,GNAI3,PRKCI,GAB1,CYFIP1,ARPC2,PIK3R6,ARHGEF10,ARPC4,FNBP1 |
| iNOS Signaling | 1.23 | 0.205 | turquoise | TLR4,CALM1 (includes others),LY96,CAMK4,MAPK1,CREBBP,CD14,HMGA1,IRAK1 |
| Apelin Cardiomyocyte Signaling Pathway | 1.23 | 0.167 | turquoise | PIK3C2B,PIK3CA,MAPK1,MYL6,PIK3R5,ATP2A3,ITPR1,ARNT,GNAI3,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,PLCB1,SLC8A1,FRS2,MYL12A |
| Renin-Angiotensin Signaling | 1.22 | 0.163 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,GNAQ,PIK3R5,ITPR1,CCL5,PTK2,RRAS2,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,TNF,FRS2 |
| TR/RXR Activation | 1.21 | 0.17 | turquoise | PIK3C2B,PIK3CA,CAMK4,PIK3R5,MDM2,NCOA3,ENO1,KLF9,SLC16A3,LDLR,GAB1,PIK3C3,PIK3R6,STRBP,RXRA,THRB,FRS2 |
| GNRH Signaling | 1.19 | 0.156 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,MAPK1,SOS2,PTK2,CAMK2D,PLCB1,PRKCE,GNG5,MAP3K14,MAP3K9,PXN,GNAS,CREB3,CREBBP,GNAQ,HBEGF,ITPR1,CREB5,CALM1 (includes others),GNAI3,RRAS2,PRKCI,PRKCD |
| Ephrin Receptor Signaling | 1.18 | 0.154 | turquoise | RAP2B,RAP1B,RAP2A,ARPC1B,MAPK1,SOS2,LIMK1,PTK2,VEGFA,NCK2,GNG5,ITGB1,MAP3K14,PXN,GNAS,CFL1,ARPC5L,CXCR4,CREB3,CREBBP,GNAQ,CREB5,GNAI3,RRAS2,ARPC2,PDGFD,ARPC4 |
| Arsenate Detoxification I (Glutaredoxin) | 1.17 | 0.5 | turquoise | GLRX2,GSTO1 |
| Heme Biosynthesis from Uroporphyrinogen-III I | 1.17 | 0.5 | turquoise | PPOX,FECH |
| Spermine and Spermidine Degradation I | 1.17 | 0.5 | turquoise | SMOX,SAT1 |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 1.16 | 0.164 | turquoise | PIK3C2B,KCNN3,PIK3CA,KCNN4,CAMK4,MAPK1,CAMK1D,GRIA1,PIK3R5,ITPR1,PRKCI,CAMK2D,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,PLCB1,FRS2 |
| Estrogen-mediated S-phase Entry | 1.16 | 0.231 | turquoise | CCNA2,TFDP1,E2F7,CDK4,ESR1,E2F2 |
| Agrin Interactions at Neuromuscular Junction | 1.16 | 0.178 | turquoise | LAMC1,PTK2,ITGB1,RAP1B,RAP2B,GABPB1,RAP2A,PXN,RRAS2,MAPK1,ARHGEF7,UTRN,ITGAL |
| Antioxidant Action of Vitamin C | 1.15 | 0.167 | turquoise | SLC2A5,PLA2G16,PLD3,MAPK1,GLRX,GSTO1,PLBD1,PLD4,HMOX1,PLA2G6,CSF2RB,PLCB1,RARRES3,TXN,STAT5B,TNF,PAFAH1B3 |
| HMGB1 Signaling | 1.14 | 0.158 | turquoise | RAP2B,RAP1B,RAP2A,CXCL8,PIK3C2B,PIK3CA,MAPK1,PIK3R5,RHOH,TLR4,RRAS2,GAB1,SP1,PIK3C3,PIK3R6,RHOU,IL1B,TNFRSF1B,RHOF,TNF,FRS2,FNBP1 |
| P2Y Purigenic Receptor Signaling Pathway | 1.14 | 0.158 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,CREBBP,CREB3,GNAQ,PIK3R5,CREB5,GNAI3,RRAS2,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,PLCB1,GNG5,FRS2 |
| nNOS Signaling in Neurons | 1.13 | 0.196 | turquoise | CAPN5,CALM1 (includes others),CAMK4,PRKCI,CAPNS1,PRKCD,PRKCE,CAPN2,CAPN3 |
| CCR5 Signaling in Macrophages | 1.13 | 0.17 | turquoise | CAMK4,GNAS,MAPK1,CD4,TRGV9,CCL5,CCL3,FAS,CALM1 (includes others),GNAI3,PRKCI,PRKCD,FCER1G,PRKCE,GNG5 |
| Heme Biosynthesis II | 1.13 | 0.333 | turquoise | PPOX,FECH,ALAS1 |
| G-Protein Coupled Receptor Signaling | 1.12 | 0.144 | turquoise | RAP2B,RAP1B,RAP2A,HCAR3,PIK3CA,CAMK4,PDE7A,MAPK1,DUSP6,SOS2,TBXA2R,PIK3R5,PDE4A,BRAF,CAMK2D,PDE7B,GDE1,PIK3C3,RGS10,PLCB1,PRKCE,PDE4D,FRS2,SMPDL3A,PIK3C2B,HRH2,GNAS,CREB3,CREBBP,GNAQ,GABBR1,CREB5,FPR1,GNAI3,P2RY13,RRAS2,P2RY14,GAB1,PIK3R6,DUSP4 |
| Role of MAPK Signaling in the Pathogenesis of Influenza | 1.12 | 0.176 | turquoise | PLBD1,RAP2B,RAP1B,PLA2G16,PLA2G6,RAP2A,RRAS2,MAPK1,RARRES3,PTGS2,CCL5,TNF,PAFAH1B3 |
| MIF Regulation of Innate Immunity | 1.1 | 0.2 | turquoise | TLR4,PLA2G6,LY96,MIF,MAPK1,CD14,PTGS2,CD74 |
| OX40 Signaling Pathway | 1.08 | 0.191 | turquoise | HLA-DOA,HLA-DMA,TRGV9,CD4,HLA-DMB,HLA-B,FCER1G,HLA-DOB,TRAF5 |
| Ovarian Cancer Signaling | 1.08 | 0.154 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,TFDP1,PA2G4,MAPK1,FGF9,PIK3R5,CDK4,FZD1,PTEN,VEGFA,BRAF,RRAS2,ARRB1,WNT10A,GAB1,PIK3C3,PIK3R6,PTGS2,FRS2 |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 1.07 | 0.149 | turquoise | RAP1B,PIK3CA,MAPK1,APOA2,PIK3R5,RHOH,PIK3C3,RHOU,PRKCE,S100A8,SERPINA1,RHOF,TNFRSF1B,FRS2,MAP3K14,PIK3C2B,MAP3K9,CREBBP,TLR2,TLR4,NCF1,PRKCI,GAB1,PRKCD,PIK3R6,IRF8,TNF,FNBP1,SIRPA |
| Amyotrophic Lateral Sclerosis Signaling | 1.06 | 0.161 | turquoise | CAPN5,PIK3C2B,PIK3CA,GRIA1,GPX1,PIK3R5,SOD1,VEGFA,CAPNS1,GAB1,PIK3C3,PIK3R6,BID,CAPN2,BIRC3,FRS2,SSR4,CAPN3 |
| Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes | 1.05 | 0.169 | turquoise | RAP1B,RAP2B,RAP2A,CAMK4,MAPK1,NFATC3,SMAD3,SOS2,TGFBR2,CALM1 (includes others),RRAS2,CD80,VAV3,LAT |
| Role of IL-17F in Allergic Inflammatory Airway Diseases | 1.04 | 0.195 | turquoise | CXCL8,RPS6KA6,MAPK1,CREBBP,CREB3,IL1B,RPS6KA4,CREB5 |
| IL-10 Signaling | 1.04 | 0.174 | turquoise | CCR1,MAP3K14,HMOX1,IL4R,MAPK1,SP1,IL1RN,FCGR2A,BLVRA,IL1B,CD14,TNF |
| UVC-Induced MAPK Signaling | 1.04 | 0.188 | turquoise | BRAF,RAP1B,RAP2B,RAP2A,RRAS2,PRKCI,MAPK1,PRKCD,PRKCE |
| Ephrin A Signaling | 1.04 | 0.177 | turquoise | PTK2,PIK3C2B,PIK3CA,CFL1,GAB1,PIK3C3,VAV3,PIK3R6,PIK3R5,FRS2,LIMK1 |
| Neuregulin Signaling | 1.03 | 0.165 | turquoise | ITGB1,RAP1B,RAP2B,RAP2A,MAPK1,SOS2,HBEGF,PTEN,HSP90B1,PRKCI,RRAS2,CDK5,PRKCD,PRKCE,STAT5B |
| Antiproliferative Role of Somatostatin Receptor 2 | 1.02 | 0.167 | turquoise | BRAF,RAP2B,RAP1B,PIK3C2B,RAP2A,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,PIK3R6,PIK3R5,GNG5,FRS2 |
| Calcium Transport I | 1.01 | 0.3 | turquoise | ANXA5,ATP2A3,ATP2B4 |
| Pentose Phosphate Pathway | 1.01 | 0.3 | turquoise | PGD,TKT,TALDO1 |
| Melatonin Signaling | 1 | 0.171 | turquoise | BRAF,CALM1 (includes others),GNAI3,CAMK2D,CAMK4,PRKCI,MAPK1,RORA,PRKCD,GNAQ,PRKCE,PLCB1 |
| Eicosanoid Signaling | 0.996 | 0.175 | turquoise | PLA2G16,PLBD1,PLA2G6,TBXA2R,RARRES3,PTGS2,GGT1,ALOX5,TBXAS1,DPEP2,PAFAH1B3 |
| Pyruvate Fermentation to Lactate | 0.983 | 0.4 | turquoise | LDHA,LDHB |
| Tetrahydrofolate Salvage from 5,10-methenyltetrahydrofolate | 0.983 | 0.4 | turquoise | MTHFD2,MTHFD1 |
| Serine Biosynthesis | 0.983 | 0.4 | turquoise | PSAT1,PHGDH |
| Bladder Cancer Signaling | 0.971 | 0.161 | turquoise | RAP1B,RAP2B,RAP2A,CXCL8,DAPK1,TFDP1,MAPK1,PA2G4,FGF9,CDK4,MDM2,VEGFA,RRAS2,MMP11,RASSF1 |
| Iron homeostasis signaling pathway | 0.959 | 0.153 | turquoise | ATP6V1D,MAPK1,SMAD3,HSPA9,BMP8B,IL6R,SLC25A37,CD163,ATP6V1A,HMOX2,ATP6V0A1,ARNT,HMOX1,HSCB,BMPR1A,FECH,TFRC,BMP6,STAT5B,SLC11A1 |
| Phospholipases | 0.955 | 0.175 | turquoise | PLA2G16,PLD4,PLBD1,PLA2G6,HMOX1,PLD3,PLCB1,RARRES3,PLA1A,PAFAH1B3 |
| Complement System | 0.955 | 0.194 | turquoise | CFD,CD59,CR1,C5AR1,ITGAM,ITGAX,CR2 |
| Triacylglycerol Biosynthesis | 0.951 | 0.186 | turquoise | PLPP5,AGPAT5,ABHD5,LPCAT2,LPCAT4,MBOAT1,GPAT3,AGPAT3 |
| Methylthiopropionate Biosynthesis | 0.943 | 1 | turquoise | ADI1 |
| Reelin Signaling in Neurons | 0.939 | 0.16 | turquoise | ITGB1,PIK3C2B,MAP3K9,PIK3CA,PIK3R5,ITGAL,GAB1,CDK5,PIK3C3,LYN,PIK3R6,LRP8,FRS2,ARHGEF10,PAFAH1B3 |
| Pyrimidine Deoxyribonucleotides De Novo Biosynthesis I | 0.939 | 0.217 | turquoise | TYMS,DUT,RRM2,AK9,APOBEC3G |
| Ephrin B Signaling | 0.936 | 0.167 | turquoise | NCK2,PTK2,GNAI3,PXN,GNAS,CFL1,MAPK1,CXCR4,VAV3,GNAQ,GNG5,LIMK1 |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 0.932 | 0.152 | turquoise | CXCL8,PIK3C2B,PIK3CA,C5AR1,NLRP3,MAPK1,PIK3R5,CCL5,TLR2,TLR4,CLEC7A,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,IL1B,TNF,FRS2 |
| Adrenomedullin signaling pathway | 0.928 | 0.144 | turquoise | RAP2B,RAP1B,RAP2A,KCNN4,PIK3CA,KCNN3,CAMK4,MAPK1,SOS2,PIK3R5,ARNT,PTK2,BRAF,PIK3C3,PLCB1,FRS2,PIK3C2B,GNAS,GNAQ,CEBPB,ITPR1,CALM1 (includes others),RRAS2,GAB1,IL1RN,PIK3R6,IL1B,RXRA,TNF |
| Glucocorticoid Receptor Signaling | 0.917 | 0.136 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,YWHAH,MAPK1,NFATC3,SMAD3,SOS2,PIK3R5,CCL5,TAF10,CD163,HSPA5,CCL3,NR3C1,TGFBR2,HSP90B1,ANXA1,PIK3C3,SMARCB1,CEBPA,STAT5B,FRS2,POLR2L,MAP3K14,PIK3C2B,CXCL8,SRA1,CREBBP,HSPA9,CEBPB,NCOA3,SMARCD3,HSPA8,RRAS2,GAB1,SMARCA2,IL1RN,PIK3R6,IL1B,NRIP1,PTGS2,TNF,ESR1,PHF10 |
| PEDF Signaling | 0.91 | 0.158 | turquoise | RAP2B,RAP1B,PIK3C2B,RAP2A,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,PIK3R6,PIK3R5,CFLAR,TCF7,FRS2,FAS |
| Estrogen Receptor Signaling | 0.91 | 0.15 | turquoise | RAP2B,RAP1B,RAP2A,SRA1,MAPK1,CCNC,HIST1H3C,CREBBP,SOS2,TAF10,NR3C1,NCOA3,DDX5,RRAS2,H3F3A/H3F3B,THRAP3,RUNX2,NRIP1,ESR1,POLR2L |
| Role of p14/p19ARF in Tumor Suppression | 0.907 | 0.182 | turquoise | PIK3C2B,PIK3CA,GAB1,PIK3C3,PIK3R6,PIK3R5,MDM2,FRS2 |
| Mouse Embryonic Stem Cell Pluripotency | 0.886 | 0.153 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,ID2,MAPK1,CREBBP,SOS2,PIK3R5,FZD1,RRAS2,GAB1,BMPR1A,PIK3C3,PIK3R6,FRS2 |
| Tryptophan Degradation III (Eukaryotic) | 0.879 | 0.208 | turquoise | HSD17B10,AFMID,KMO,KYNU,HSD17B8 |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 0.87 | 0.15 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,BMP8B,SOS2,PIK3R5,FZD1,RRAS2,WNT10A,GAB1,BMPR1A,PIK3C3,PIK3R6,BMP6,FRS2,TCL1A |
| Role of NFAT in Cardiac Hypertrophy | 0.87 | 0.14 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,CAMK1D,MAPK1,SOS2,PIK3R5,CSNK1A1,TGFBR2,CAMK2D,PIK3C3,PRKCE,PLCB1,GNG5,FRS2,HDAC9,PIK3C2B,GNAS,GNAQ,ITPR1,CALM1 (includes others),GNAI3,RRAS2,PRKCI,GAB1,PRKCD,PIK3R6,MEF2C,SLC8A1 |
| MSP-RON Signaling Pathway | 0.87 | 0.162 | turquoise | TLR2,TLR4,CSF2RB,PIK3C2B,PIK3CA,ITGAM,GAB1,PIK3C3,PIK3R6,PIK3R5,TNF,FRS2 |
| PI3K/AKT Signaling | 0.87 | 0.15 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3CA,MAPK1,YWHAH,YWHAE,SOS2,MDM2,PTEN,HSP90B1,RRAS2,GAB1,FOXO1,LIMS1,PTGS2,MCL1,THEM4 |
| Thyroid Cancer Signaling | 0.863 | 0.178 | turquoise | RAP2B,RAP1B,BRAF,RAP2A,CXCL8,RRAS2,MAPK1,RXRA |
| RhoGDI Signaling | 0.863 | 0.144 | turquoise | ITGB1,ARHGAP6,GNAS,MYL6,CFL1,ARPC1B,ARPC5L,ARHGEF7,CREBBP,RDX,GNAQ,PIP4K2B,PIP5K1B,RHOH,LIMK1,GNAI3,ARPC2,RHOU,GNG5,RHOF,ESR1,ARHGEF10,ARPC4,FNBP1,MYL12A |
| Sertoli Cell-Sertoli Cell Junction Signaling | 0.863 | 0.144 | turquoise | RAP1B,RAP2B,ITGB1,SPTBN1,TUBA1B,MAP3K9,MAP3K14,RAP2A,TUBB3,MAPK1,TUBB4B,TGFBR3,TUBG1,TUBA4A,AFDN,YBX3,TUBB,PTEN,RRAS2,KEAP1,TUBA1C,VCL,ACTN4,TNF,ACTN1 |
| LPS/IL-1 Mediated Inhibition of RXR Function | 0.854 | 0.141 | turquoise | ABCG1,ALAS1,FMO5,ABCB9,IRAK1,GSTM2,ALDH1A1,PPARGC1B,FABP5,HS3ST1,TNFRSF1B,GSTK1,ABCB1,GSTM1,MGST1,GSTO1,TLR4,LY96,MGST2,IL1RN,SMOX,IL1B,CD14,SLC27A3,RXRA,TNF,ABCC4,NDST1,ACSL1 |
| Type II Diabetes Mellitus Signaling | 0.854 | 0.146 | turquoise | PIK3C2B,MAP3K14,PIK3CA,MAPK1,CD36,PKM,PIK3R5,CEBPB,TRADD,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,SOCS2,SLC27A3,TNFRSF1B,SOCS5,TNF,FRS2,ACSL1 |
| Endocannabinoid Developing Neuron Pathway | 0.848 | 0.148 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,CREBBP,CREB3,PIK3R5,CREB5,BRAF,GNAI3,RRAS2,GAB1,PIK3C3,PIK3R6,MGLL,GNG5,FRS2 |
| Induction of Apoptosis by HIV1 | 0.845 | 0.167 | turquoise | MAP3K14,TRADD,SLC25A4,CXCR4,BID,TNFRSF1B,TNF,BIRC3,FAS,BAK1 |
| Differential Regulation of Cytokine Production in Macrophages and T Helper Cells by IL-17A and IL-17F | 0.845 | 0.222 | turquoise | IL1B,CCL5,CCL3,TNF |
| Arginine Biosynthesis IV | 0.842 | 0.333 | turquoise | GLUD1,ASL |
| Urea Cycle | 0.842 | 0.333 | turquoise | ASL,ARG1 |
| Pentose Phosphate Pathway (Non-oxidative Branch) | 0.842 | 0.333 | turquoise | TKT,TALDO1 |
| Adenine and Adenosine Salvage III | 0.842 | 0.333 | turquoise | ADA2,ADA |
| Purine Ribonucleosides Degradation to Ribose-1-phosphate | 0.842 | 0.333 | turquoise | ADA2,ADA |
| GDP-mannose Biosynthesis | 0.842 | 0.333 | turquoise | GPI,PMM1 |
| Th17 Activation Pathway | 0.839 | 0.16 | turquoise | STAT4,HSP90B1,IRF4,NFATC3,RORA,TRGV9,IL21R,IL6R,FCER1G,IL1B,AHR,IRAK1 |
| PDGF Signaling | 0.83 | 0.153 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,RRAS2,GAB1,PIK3C3,CAV1,PIK3R6,PDGFD,FRS2 |
| Axonal Guidance Signaling | 0.827 | 0.131 | turquoise | DPYSL2,RAP2B,TUBA1B,MAPK1,MYL6,NFATC3,SOS2,TUBB,LIMK1,VEGFA,PTK2,NCK2,PLCB1,PLXNB2,TUBA1C,ABLIM2,FRS2,PIK3C2B,TUBB3,CFL1,BMP8B,GAB1,PRKCD,ARPC2,PIK3R6,RTN4,PDGFD,RAP1B,RAP2A,PIK3CA,ARPC1B,ARHGEF7,PIK3R5,FZD1,ABLIM1,CDK5,SRGAP1,PIK3C3,PRKCE,MMP11,PSMD14,SEMA4A,GNG5,MYL12A,ITGB1,PXN,GNAS,PLXNC1,ARPC5L,TUBB4B,CXCR4,TUBG1,TUBA4A,GNAQ,PLXND1,GNAI3,SEMA3A,PRKCI,RRAS2,WNT10A,BMP6,ARPC4 |
| Atherosclerosis Signaling | 0.807 | 0.148 | turquoise | PLA2G16,CXCL8,CXCR4,APOA2,CD36,SELPLG,PLBD1,PLA2G6,IL1RN,RARRES3,IL1B,S100A8,SERPINA1,PDGFD,COL18A1,ALOX5,TNF,PAFAH1B3 |
| CREB Signaling in Neurons | 0.801 | 0.138 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MAPK1,GRIA1,SOS2,PIK3R5,CAMK2D,PIK3C3,PRKCE,PLCB1,GNG5,FRS2,POLR2L,PIK3C2B,GNAS,CREB3,CREBBP,GNAQ,ITPR1,CREB5,GNAI3,CALM1 (includes others),RRAS2,PRKCI,GAB1,PRKCD,PIK3R6 |
| Colorectal Cancer Metastasis Signaling | 0.801 | 0.137 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,MAPK1,SMAD3,SOS2,PIK3R5,FZD1,RHOH,TGFBR2,BRAF,VEGFA,ARRB1,PIK3C3,RHOU,MMP11,RHOF,GNG5,FRS2,PIK3C2B,GNAS,GRK3,IL6R,BIRC5,TLR2,TLR4,RRAS2,WNT10A,GAB1,PIK3R6,PTGS2,TNF,FNBP1 |
| IL-12 Signaling and Production in Macrophages | 0.793 | 0.144 | turquoise | PIK3C2B,PIK3CA,MAPK1,APOA2,PIK3R5,CEBPB,TLR2,STAT4,TLR4,PRKCI,GAB1,PRKCD,PIK3C3,PIK3R6,PRKCE,S100A8,SERPINA1,IRF8,RXRA,TNF,FRS2 |
| Lymphotoxin β Receptor Signaling | 0.793 | 0.159 | turquoise | MAP3K14,PIK3C2B,PIK3CA,MAPK1,GAB1,PIK3C3,CREBBP,PIK3R6,PIK3R5,TRAF5,FRS2 |
| FGF Signaling | 0.785 | 0.152 | turquoise | PIK3C2B,PIK3CA,MAPK1,FGF9,SOS2,CREB3,CREBBP,PIK3R5,ITPR1,CREB5,GAB1,PIK3C3,PIK3R6,FRS2 |
| Synaptic Long Term Potentiation | 0.783 | 0.146 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,MAPK1,GRIA1,CREBBP,CREB3,GNAQ,ITPR1,CREB5,CALM1 (includes others),RRAS2,CAMK2D,PRKCI,PRKCD,PRKCE,PLCB1 |
| PXR/RXR Activation | 0.777 | 0.161 | turquoise | ABCB1,GSTM1,ALDH1A1,GSTM2,FOXO1,ALAS1,RXRA,TNF,NR3C1,ABCB9 |
| Oncostatin M Signaling | 0.777 | 0.175 | turquoise | MT2A,RAP1B,RAP2B,RAP2A,RRAS2,MAPK1,STAT5B |
| Circadian Rhythm Signaling | 0.77 | 0.182 | turquoise | ARNTL,NR1D1,BHLHE41,CREBBP,CREB3,CREB5 |
| Antiproliferative Role of TOB in T Cell Signaling | 0.77 | 0.192 | turquoise | TGFBR2,CCNA2,MAPK1,PABPC4,SMAD3 |
| Sperm Motility | 0.764 | 0.147 | turquoise | PLA2G16,GNAS,CAMK4,PDE4A,ITPR1,PLBD1,PTK2,PLA2G6,CALM1 (includes others),PRKCI,PRKCD,PRKCE,PLCB1,RARRES3,PDE4D,LTK,PAFAH1B3 |
| Role of IL-17A in Arthritis | 0.762 | 0.157 | turquoise | PIK3C2B,CXCL8,PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R6,PIK3R5,CCL5,PTGS2,FRS2 |
| cAMP-mediated signaling | 0.75 | 0.136 | turquoise | HCAR3,CAMK4,CAMK1D,PDE7A,MAPK1,DUSP6,TBXA2R,PDE4A,AKAP7,BRAF,CAMK2D,PDE7B,GDE1,RGS10,PDE4D,SMPDL3A,HRH2,GNAS,CREB3,CREBBP,GABBR1,CREB5,FPR1,P2RY13,GNAI3,CALM1 (includes others),AKAP13,P2RY14,DUSP4,PKIG |
| Role of IL-17A in Psoriasis | 0.745 | 0.231 | turquoise | CXCL8,S100A9,S100A8 |
| NAD biosynthesis II (from tryptophan) | 0.745 | 0.231 | turquoise | AFMID,KMO,KYNU |
| Cardiac Hypertrophy Signaling | 0.738 | 0.135 | turquoise | RAP2B,RAP1B,RAP2A,PIK3CA,CAMK4,MYL6,MAPK1,PIK3R5,RHOH,TGFBR2,PIK3C3,RHOU,PLCB1,RHOF,GNG5,FRS2,MYL12A,MAP3K14,PIK3C2B,MAP3K9,GNAS,MAPKAPK3,IL6R,CREBBP,GNAQ,GNAI3,CALM1 (includes others),RRAS2,GAB1,PIK3R6,MEF2C,FNBP1 |
| Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza | 0.738 | 0.171 | turquoise | CCR1,CXCL8,IL1RN,IL1B,CCL5,CCL3,TNF |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 0.735 | 0.135 | turquoise | PIK3CA,CAMK4,MAPK1,NFATC3,PIK3R5,CSNK1A1,FZD1,ACP5,TRADD,BMPR1A,RUNX2,PIK3C3,TRAF5,TNFRSF1B,BIRC3,FRS2,ITGB1,MAP3K14,PIK3C2B,BMP8B,IL7,CSF1R,CALM1 (includes others),FOXO1,GAB1,WNT10A,IL1RN,PIK3R6,IL1B,BMP6,TNF |
| Acute Phase Response Signaling | 0.73 | 0.139 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K14,PIK3CA,MAPK1,APOA2,IL6R,SOS2,CEBPB,NR3C1,HMOX2,IRAK1,TRADD,HMOX1,RRAS2,RBP7,IL1RN,IL1B,SOCS2,SERPINA1,TNFRSF1B,SOCS5,TNF |
| Sphingosine and Sphingosine-1-phosphate Metabolism | 0.728 | 0.286 | turquoise | SGPP2,SGPP1 |
| Superpathway of Serine and Glycine Biosynthesis I | 0.728 | 0.286 | turquoise | PSAT1,PHGDH |
| Phosphatidylcholine Biosynthesis I | 0.728 | 0.286 | turquoise | CEPT1,PCYT1A |
| Aspartate Degradation II | 0.728 | 0.286 | turquoise | GOT2,MDH2 |
| RhoA Signaling | 0.721 | 0.144 | turquoise | ARHGAP6,MPRIP,CFL1,MYL6,ARPC1B,ANLN,ARPC5L,RDX,CDC42EP3,PIP4K2B,RAPGEF6,PIP5K1B,LIMK1,PTK2,ARPC2,ARPC4,MYL12A |
| FcγRIIB Signaling in B Lymphocytes | 0.717 | 0.149 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,RRAS2,GAB1,CD79B,PIK3C3,PIK3R6,LYN,PIK3R5,FRS2 |
| PPARα/RXRα Activation | 0.714 | 0.138 | turquoise | RAP2B,RAP1B,RAP2A,MAP3K14,GNAS,MAPK1,APOA2,SMAD3,CD36,TGFBR3,CREBBP,SOS2,GNAQ,ACVR1,NCOA3,TGFBR2,HSP90B1,RRAS2,PLCB1,IL1B,MEF2C,GOT2,RXRA,STAT5B |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation | 0.714 | 0.137 | turquoise | CXCL8,COL19A1,IL4R,MYL6,FLT1,COL4A3,SMAD3,IL6R,CXCR3,CCL5,IFNAR2,FAS,VEGFA,TGFBR2,TLR4,LY96,TIMP1,IL1B,CD14,COL4A4,PDGFD,TNFRSF1B,COL18A1,TNF,TIMP2 |
| tRNA Splicing | 0.701 | 0.167 | turquoise | SMPDL3A,PDE7B,PDE7A,GDE1,TSEN54,PDE4A,PDE4D |
| CD40 Signaling | 0.697 | 0.15 | turquoise | MAP3K14,PIK3C2B,PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R6,PIK3R5,PTGS2,TRAF5,FRS2,FCER2 |
| Amyloid Processing | 0.682 | 0.16 | turquoise | CAPN5,CAPNS1,MAPK1,CDK5,CSNK1A1,PRKCE,CAPN2,CAPN3 |
| DNA Double-Strand Break Repair by Non-Homologous End Joining | 0.678 | 0.214 | turquoise | DCLRE1C,XRCC6,LIG4 |
| Phenylalanine Degradation IV (Mammalian, via Side Chain) | 0.678 | 0.214 | turquoise | SMOX,SLC27A3,GOT2 |
| Colanic Acid Building Blocks Biosynthesis | 0.678 | 0.214 | turquoise | GPI,PMM1,GALK2 |
| Polyamine Regulation in Colon Cancer | 0.67 | 0.19 | turquoise | PSME2,SAT1,OAZ1,PSME4 |
| UDP-D-xylose and UDP-D-glucuronate Biosynthesis | 0.666 | 0.5 | turquoise | UXS1 |
| Dolichol and Dolichyl Phosphate Biosynthesis | 0.666 | 0.5 | turquoise | DHDDS |
| β-alanine Degradation I | 0.666 | 0.5 | turquoise | ABAT |
| Spermine Biosynthesis | 0.666 | 0.5 | turquoise | SMS |
| Spermidine Biosynthesis I | 0.666 | 0.5 | turquoise | SRM |
| Sulfate Activation for Sulfonation | 0.666 | 0.5 | turquoise | PAPSS1 |
| Glutamate Biosynthesis II | 0.666 | 0.5 | turquoise | GLUD1 |
| Glutamate Degradation X | 0.666 | 0.5 | turquoise | GLUD1 |
| Granulocyte Adhesion and Diapedesis | 0.66 | 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 |
| Cell Cycle: G1/S Checkpoint Regulation | 0.66 | 0.152 | turquoise | HDAC9,CCND2,PA2G4,TFDP1,FOXO1,SMAD3,E2F7,CDK4,MDM2,E2F2 |
| Corticotropin Releasing Hormone Signaling | 0.658 | 0.139 | turquoise | RAP1B,GNAS,CAMK4,MAPK1,CREBBP,CREB3,GNAQ,CRH,ITPR1,CREB5,BRAF,VEGFA,CALM1 (includes others),GNAI3,PRKCI,PRKCD,PRKCE,MEF2C,PTGS2 |
| Toll-like Receptor Signaling | 0.654 | 0.149 | turquoise | TLR2,TLR4,MAP3K14,LY96,MAPK1,IL1RN,TICAM2,IL1B,CD14,TNF,IRAK1 |
| Airway Pathology in Chronic Obstructive Pulmonary Disease | 0.636 | 0.25 | turquoise | CXCL8,TNF |
| Sucrose Degradation V (Mammalian) | 0.636 | 0.25 | turquoise | TPI1,ALDOA |
| Histidine Degradation III | 0.636 | 0.25 | turquoise | MTHFD2,MTHFD1 |
| TNFR2 Signaling | 0.633 | 0.172 | turquoise | MAP3K14,TBK1,TNFRSF1B,TNF,BIRC3 |
| Sphingosine-1-phosphate Signaling | 0.62 | 0.138 | turquoise | PIK3C2B,PIK3CA,MAPK1,GNAQ,PIK3R5,RHOH,PTK2,GNAI3,GAB1,PIK3C3,RHOU,PIK3R6,PLCB1,PDGFD,RHOF,FRS2,FNBP1 |
| PTEN Signaling | 0.62 | 0.138 | turquoise | RAP2B,RAP1B,ITGB1,RAP2A,PIK3CA,MAPK1,FLT1,YWHAH,TGFBR3,SOS2,PIK3R5,PTEN,PTK2,TGFBR2,RRAS2,FOXO1,BMPR1A |
| Telomere Extension by Telomerase | 0.616 | 0.2 | turquoise | TERF2,XRCC6,TINF2 |
| Vitamin-C Transport | 0.616 | 0.2 | turquoise | TXN,GLRX,GSTO1 |
| Ceramide Signaling | 0.6 | 0.14 | turquoise | RAP1B,RAP2B,RAP2A,PIK3C2B,PIK3CA,CNKSR1,PIK3R5,RRAS2,GAB1,PIK3C3,PIK3R6,TNFRSF1B,FRS2,TNF |
| FAT10 Cancer Signaling Pathway | 0.599 | 0.156 | turquoise | TGFBR2,CXCR4,SMAD3,TGFBR3,ACVR1,TNFRSF1B,TNF |
| Fatty Acid β-oxidation I | 0.593 | 0.167 | turquoise | HSD17B10,SLC27A3,ACAA2,ACSL1,HSD17B8 |
| Opioid Signaling Pathway | 0.593 | 0.13 | turquoise | RAP2B,RAP1B,RAP2A,CAMK4,CAMK1D,MAPK1,SOS2,AP1B1,BRAF,ARRB1,CAMK2D,RGS10,PRKCE,PLCB1,GNG5,SIGMAR1,GNAS,GRK3,CREB3,CREBBP,ITPR1,CREB5,AP2S1,GNAI3,CALM1 (includes others),RPS6KA6,RRAS2,PRKCI,PRKCD,LYN,RPS6KA4 |
| Gα12/13 Signaling | 0.587 | 0.135 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,PXN,MAPK1,MYL6,TBXA2R,PIK3R5,PTK2,RRAS2,GAB1,PIK3C3,VAV3,PIK3R6,MEF2C,FRS2,MYL12A |
| tRNA Charging | 0.578 | 0.158 | turquoise | WARS,CARS,TARS,VARS,SARS,EPRS |
| Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F | 0.575 | 0.174 | turquoise | IL1B,CCL5,CCL3,TNF |
| RANK Signaling in Osteoclasts | 0.559 | 0.137 | turquoise | MAP3K14,PIK3C2B,MAP3K9,PIK3CA,CAMK4,MAPK1,PIK3R5,CALM1 (includes others),GAB1,PIK3C3,PIK3R6,TRAF5,FRS2,BIRC3 |
| Prostanoid Biosynthesis | 0.559 | 0.222 | turquoise | PTGS2,TBXAS1 |
| Folate Transformations I | 0.559 | 0.222 | turquoise | MTHFD2,MTHFD1 |
| EGF Signaling | 0.558 | 0.143 | turquoise | PIK3C2B,PIK3CA,MAPK1,GAB1,PIK3C3,SOS2,PIK3R6,PIK3R5,ITPR1,FRS2 |
| Relaxin Signaling | 0.545 | 0.131 | turquoise | SMPDL3A,RAP1B,PIK3C2B,PIK3CA,GNAS,MAPK1,PDE7A,GNAQ,PIK3R5,PDE4A,BRAF,VEGFA,GNAI3,GAB1,PDE7B,GDE1,PIK3C3,PIK3R6,PDE4D,GNG5,FRS2 |
| G Beta Gamma Signaling | 0.545 | 0.134 | turquoise | RAP2B,RAP1B,RAP2A,GNAS,MAPK1,SOS2,GNAQ,HBEGF,GNAI3,PRKCI,RRAS2,PRKCD,CAV1,PRKCE,GNG5,DNM2 |
| April Mediated Signaling | 0.545 | 0.154 | turquoise | MAP3K14,MAPK1,NFATC3,TNFRSF13B,TRAF5,TNFRSF17 |
| Gαi Signaling | 0.545 | 0.134 | turquoise | RAP2B,RAP1B,RAP2A,GNAS,MAPK1,SOS2,TBXA2R,GABBR1,FPR1,GNAI3,P2RY13,P2RY14,RRAS2,RGS10,CAV1,GNG5 |
| AMPK Signaling | 0.542 | 0.128 | turquoise | CAB39,PIK3CA,RAB1A,MAPK1,PIK3R5,CCNA2,TBC1D1,PIK3C3,SMARCB1,EEF2K,AK9,FRS2,PFKFB3,PIK3C2B,GNAS,AK3,CREB3,CREBBP,RAB8A,CREB5,SMARCD3,PPM1G,GAB1,FOXO1,SMARCA2,PIK3R6,CAMKK2,PHF10 |
| UVA-Induced MAPK Signaling | 0.542 | 0.135 | turquoise | RAP2B,RAP1B,PIK3C2B,RAP2A,RPS6KA6,PIK3CA,RRAS2,GAB1,MAPK1,PIK3C3,PIK3R6,PIK3R5,PLCB1,RPS6KA4,FRS2 |
| TCA Cycle II (Eukaryotic) | 0.533 | 0.167 | turquoise | SDHB,IDH3G,SUCLG1,MDH2 |
| LXR/RXR Activation | 0.527 | 0.133 | turquoise | APOA2,CD36,ABCG1,TLR4,LY96,LDLR,IL1RN,IL1B,CD14,SERPINA1,S100A8,PTGS2,TNFRSF1B,RXRA,TNF,CYP51A1 |
| L-carnitine Biosynthesis | 0.514 | 0.333 | turquoise | TMLHE |
| Diphthamide Biosynthesis | 0.514 | 0.333 | turquoise | DPH5 |
| NADH Repair | 0.514 | 0.333 | turquoise | GAPDH |
| Coenzyme A Biosynthesis | 0.514 | 0.333 | turquoise | PPCDC |
| S-methyl-5-thio-α-D-ribose 1-phosphate Degradation | 0.514 | 0.333 | turquoise | ADI1 |
| Glutathione Biosynthesis | 0.514 | 0.333 | turquoise | GCLC |
| L-cysteine Degradation III | 0.514 | 0.333 | turquoise | GOT2 |
| 4-hydroxyproline Degradation I | 0.514 | 0.333 | turquoise | GOT2 |
| Thiosulfate Disproportionation III (Rhodanese) | 0.514 | 0.333 | turquoise | TST |
| Glutamate Degradation II | 0.514 | 0.333 | turquoise | GOT2 |
| Tyrosine Biosynthesis IV | 0.514 | 0.333 | turquoise | PCBD1 |
| 4-aminobutyrate Degradation I | 0.514 | 0.333 | turquoise | ABAT |
| Aspartate Biosynthesis | 0.514 | 0.333 | turquoise | GOT2 |
| BMP signaling pathway | 0.514 | 0.138 | turquoise | RAP1B,RAP2B,RAP2A,RRAS2,CAMK4,MAPK1,BMPR1A,RUNX2,BMP8B,CREBBP,BMP6 |
| RAR Activation | 0.513 | 0.128 | turquoise | SRA1,PIK3CA,MAPK1,RDH10,SMAD3,SDR16C5,CREBBP,RARG,SMARCD3,PTEN,VEGFA,CSF2RB,RBP7,ALDH1A1,PRKCI,SMARCA2,PRKCD,SMARCB1,PRKCE,NRIP1,RXRA,STAT5B,CITED2,PHF10 |
| Granzyme A Signaling | 0.513 | 0.176 | turquoise | GZMA,PRF1,CREBBP |
| Glutamate Receptor Signaling | 0.511 | 0.143 | turquoise | CALM1 (includes others),SLC1A4,HOMER2,CAMK4,GRIA1,SLC38A1,HOMER3,GNG5 |
| Factors Promoting Cardiogenesis in Vertebrates | 0.498 | 0.135 | turquoise | TGFBR2,PRKCI,BMPR1A,PRKCD,TGFBR3,BMP8B,CDC6,ACVR1,PRKCE,MEF2C,FZD1,BMP6 |
| IL-17A Signaling in Gastric Cells | 0.495 | 0.16 | turquoise | CXCL8,MAPK1,CCL5,TNF |
| B Cell Activating Factor Signaling | 0.485 | 0.146 | turquoise | MAP3K14,MAPK1,NFATC3,TNFRSF13B,TRAF5,TNFRSF17 |
| Mechanisms of Viral Exit from Host Cells | 0.485 | 0.146 | turquoise | PRKCI,CHMP2A,PRKCD,PRKCE,SH3GLB1,LMNB1 |
| Stearate Biosynthesis I (Animals) | 0.485 | 0.146 | turquoise | SRD5A3,LPCAT4,SLC27A3,TBXAS1,ACSL1,THEM4 |
| Purine Nucleotides Degradation II (Aerobic) | 0.469 | 0.167 | turquoise | ADA2,IMPDH1,ADA |
| D-myo-inositol (1,3,4)-trisphosphate Biosynthesis | 0.469 | 0.167 | turquoise | ITPKB,INPP5A,PTEN |
| Fatty Acid α-oxidation | 0.469 | 0.167 | turquoise | TMLHE,ALDH1A1,PTGS2 |
| Apelin Pancreas Signaling Pathway | 0.463 | 0.138 | turquoise | PIK3C2B,PIK3CA,GAB1,ERN1,PIK3C3,PIK3R5,PIK3R6,FRS2 |
| Human Embryonic Stem Cell Pluripotency | 0.458 | 0.128 | turquoise | PIK3C2B,PIK3CA,GNAS,SMAD3,BMP8B,ACVR1,PIK3R5,FZD1,TGFBR2,FOXO1,GAB1,WNT10A,BMPR1A,PIK3C3,PIK3R6,PDGFD,BMP6,FRS2 |
| TWEAK Signaling | 0.458 | 0.147 | turquoise | TRADD,MAP3K14,TNFRSF25,BID,BIRC3 |
| Osteoarthritis Pathway | 0.455 | 0.125 | turquoise | ITGB1,CXCL8,SMAD3,CREBBP,CREB3,ANXA2,CEBPB,FZD1,CREB5,TLR2,VEGFA,TGFBR2,TLR4,S100A9,SP1,RUNX2,BMPR1A,ANXA5,IL1B,MEF2C,S100A8,NAMPT,PTGS2,TNFRSF1B,TNF |
| UDP-N-acetyl-D-galactosamine Biosynthesis II | 0.439 | 0.182 | turquoise | GPI,UAP1 |
| GADD45 Signaling | 0.428 | 0.158 | turquoise | CCND2,GADD45A,CDK4 |
| Putrescine Degradation III | 0.428 | 0.158 | turquoise | ALDH1A1,SMOX,SAT1 |
| D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis | 0.427 | 0.148 | turquoise | PLD4,PLCB1,PIP4K2B,PIP5K1B |
| 3-phosphoinositide Biosynthesis | 0.426 | 0.124 | turquoise | PIK3C2B,CD19,PIK3CA,PPFIBP2,PIK3R5,PIP4K2B,PAWR,PIP5K1B,ACP5,PPM1K,PTPN12,PTEN,ATP1A1,GAB1,PTPRJ,CD80,PIK3C3,SGPP2,PIK3R6,CD86,SGPP1,MTMR7,FRS2,SIRPA |
| Superpathway of Inositol Phosphate Compounds | 0.425 | 0.123 | turquoise | PIK3CA,PPFIBP2,PIK3R5,PIP4K2B,ACP5,PIP5K1B,INPP5A,PPM1K,PTPN12,PTEN,ATP1A1,ITPKB,PTPRJ,PIK3C3,SGPP2,PLCB1,FRS2,PIK3C2B,CD19,PAWR,PLD4,GAB1,CD80,PIK3R6,CD86,SGPP1,MTMR7,SIRPA |
| Airway Inflammation in Asthma | 0.415 | 0.25 | turquoise | TNF |
| Uracil Degradation II (Reductive) | 0.415 | 0.25 | turquoise | DPYSL2 |
| Retinoate Biosynthesis II | 0.415 | 0.25 | turquoise | RBP7 |
| Pentose Phosphate Pathway (Oxidative Branch) | 0.415 | 0.25 | turquoise | PGD |
| Eumelanin Biosynthesis | 0.415 | 0.25 | turquoise | MIF |
| Glutathione Redox Reactions II | 0.415 | 0.25 | turquoise | GLRX |
| Thymine Degradation | 0.415 | 0.25 | turquoise | DPYSL2 |
| Melatonin Degradation II | 0.415 | 0.25 | turquoise | SMOX |
| Arginine Degradation I (Arginase Pathway) | 0.415 | 0.25 | turquoise | ARG1 |
| Trans, trans-farnesyl Diphosphate Biosynthesis | 0.415 | 0.25 | turquoise | IDI1 |
| NAD Biosynthesis III | 0.415 | 0.25 | turquoise | NAMPT |
| L-cysteine Degradation I | 0.415 | 0.25 | turquoise | GOT2 |
| Phenylalanine Degradation I (Aerobic) | 0.415 | 0.25 | turquoise | PCBD1 |
| Acetate Conversion to Acetyl-CoA | 0.415 | 0.25 | turquoise | ACSL1 |
| Role of PI3K/AKT Signaling in the Pathogenesis of Influenza | 0.413 | 0.13 | turquoise | PIK3C2B,GNAI3,PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R6,PIK3R5,CCL5,FRS2 |
| Adipogenesis pathway | 0.405 | 0.125 | turquoise | HDAC9,ARNTL,DGKD,SMAD3,XBP1,CEBPD,FBXW7,FZD1,CEBPB,FOXO1,CDK5,BMPR1A,CEBPA,TCF7,STAT5B,TNF |
| autophagy | 0.393 | 0.132 | turquoise | ATG13,CTSA,VPS41,PIK3C3,WIPI1,ATG4A,CTSC |
| Glycogen Degradation II | 0.39 | 0.167 | turquoise | PGM1,TYMP |
| Mevalonate Pathway I | 0.39 | 0.167 | turquoise | PMVK,IDI1 |
| Pregnenolone Biosynthesis | 0.39 | 0.167 | turquoise | MICAL2,MICAL3 |
| ATM Signaling | 0.378 | 0.125 | turquoise | RNF168,MDM4,GADD45A,RAD17,CREB3,CREBBP,BID,MDM2,CREB5,CBX5,SMC1A,CHEK1 |
| Role of BRCA1 in DNA Damage Response | 0.362 | 0.125 | turquoise | ABRAXAS1,GADD45A,SMARCA2,E2F7,SMARCB1,BRIP1,E2F2,SMARCD3,PHF10,CHEK1 |
| Hepatic Cholestasis | 0.351 | 0.12 | turquoise | CXCL8,MAP3K14,ABCB1,SLC22A7,IRAK1,TLR4,LY96,PRKCI,SLCO3A1,ABCB4,IL1RN,PRKCD,PRKCE,IL1B,CD14,TNFRSF1B,RXRA,TNF,ESR1 |
| Fatty Acid Activation | 0.349 | 0.154 | turquoise | SLC27A3,ACSL1 |
| γ-glutamyl Cycle | 0.349 | 0.154 | turquoise | GCLC,GGT1 |
| G Protein Signaling Mediated by Tubby | 0.342 | 0.133 | turquoise | GNAS,GNAQ,PLCB1,GNG5 |
| Tetrapyrrole Biosynthesis II | 0.341 | 0.2 | turquoise | ALAS1 |
| CMP-N-acetylneuraminate Biosynthesis I (Eukaryotes) | 0.341 | 0.2 | turquoise | NANS |
| Citrulline-Nitric Oxide Cycle | 0.341 | 0.2 | turquoise | ASL |
| Rapoport-Luebering Glycolytic Shunt | 0.341 | 0.2 | turquoise | PGAM1 |
| Galactose Degradation I (Leloir Pathway) | 0.341 | 0.2 | turquoise | GALK2 |
| Lactose Degradation III | 0.341 | 0.2 | turquoise | PSAP |
| dTMP De Novo Biosynthesis | 0.341 | 0.2 | turquoise | TYMS |
| Glutamate Degradation III (via 4-aminobutyrate) | 0.341 | 0.2 | turquoise | ABAT |
| Folate Polyglutamylation | 0.341 | 0.2 | turquoise | MTHFD1 |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 0.339 | 0.119 | turquoise | GNAS,CAMK4,CSNK1G3,CREBBP,CREB3,GNAQ,CSNK1A1,ATP2A3,PAWR,ITPR1,CREB5,CALM1 (includes others),GNAI3,PRKCI,CDK5,PRKCD,PRKCE,PLCB1,CAMKK2 |
| Cell Cycle Control of Chromosomal Replication | 0.334 | 0.125 | turquoise | MCM6,CDK5,CDT1,CDC6,TOP2A,CDK4,MCM4 |
| Synaptic Long Term Depression | 0.332 | 0.119 | turquoise | RAP2B,RAP1B,PLA2G16,RAP2A,GNAS,MAPK1,GRIA1,GNAQ,CRH,ITPR1,PLBD1,PLA2G6,GNAI3,RRAS2,PRKCI,PRKCD,LYN,PRKCE,PLCB1,RARRES3,PAFAH1B3 |
| Retinoate Biosynthesis I | 0.318 | 0.129 | turquoise | RBP7,ALDH1A1,RDH10,SDR16C5 |
| Death Receptor Signaling | 0.312 | 0.12 | turquoise | MAP3K14,TRADD,TNFRSF25,BID,TBK1,CFLAR,TNFRSF1B,TNF,BIRC3,FAS,LIMK1 |
| Chondroitin Sulfate Degradation (Metazoa) | 0.312 | 0.143 | turquoise | CEMIP2,HEXDC |
| Isoleucine Degradation I | 0.312 | 0.143 | turquoise | HSD17B10,BCAT1 |
| Glycogen Degradation III | 0.312 | 0.143 | turquoise | PGM1,TYMP |
| Superpathway of D-myo-inositol (1,4,5)-trisphosphate Metabolism | 0.302 | 0.13 | turquoise | ITPKB,INPP5A,PTEN |
| Inhibition of Angiogenesis by TSP1 | 0.295 | 0.125 | turquoise | TGFBR2,VEGFA,MAPK1,CD36 |
| Role of JAK2 in Hormone-like Cytokine Signaling | 0.295 | 0.125 | turquoise | SOCS2,STAT5B,SOCS5,SIRPA |
| Apelin Adipocyte Signaling Pathway | 0.292 | 0.118 | turquoise | GSTM1,GNAI3,MGST1,GSTM2,MAPK1,MGST2,GPX1,SOD1,GSTK1 |
| Triacylglycerol Degradation | 0.291 | 0.122 | turquoise | PNPLA7,ABHD2,MGLL,NDST1,PLA1A |
| Chondroitin and Dermatan Biosynthesis | 0.286 | 0.167 | turquoise | CHPF |
| Arginine Degradation VI (Arginase 2 Pathway) | 0.286 | 0.167 | turquoise | ARG1 |
| Glycine Cleavage Complex | 0.286 | 0.167 | turquoise | GLDC |
| Selenocysteine Biosynthesis II (Archaea and Eukaryotes) | 0.286 | 0.167 | turquoise | SARS |
| UDP-N-acetyl-D-glucosamine Biosynthesis II | 0.286 | 0.167 | turquoise | UAP1 |
| Zymosterol Biosynthesis | 0.286 | 0.167 | turquoise | CYP51A1 |
| Glycogen Biosynthesis II (from UDP-D-Glucose) | 0.286 | 0.167 | turquoise | GYG1 |
| Endocannabinoid Cancer Inhibition Pathway | 0.281 | 0.115 | turquoise | PIK3C2B,PIK3CA,MAPK1,CREBBP,CREB3,GNAQ,PIK3R5,VIM,CREB5,PTK2,VEGFA,GNAI3,CCND2,GAB1,PIK3C3,PIK3R6,FRS2,CAMKK2 |
| Superpathway of Citrulline Metabolism | 0.279 | 0.133 | turquoise | ASL,ARG1 |
| Dermatan Sulfate Degradation (Metazoa) | 0.279 | 0.133 | turquoise | CEMIP2,HEXDC |
| Adenosine Nucleotides Degradation II | 0.279 | 0.133 | turquoise | ADA2,ADA |
| Histidine Degradation VI | 0.279 | 0.133 | turquoise | MICAL2,MICAL3 |
| Parkinson's Signaling | 0.279 | 0.133 | turquoise | UCHL1,MAPK1 |
| Leptin Signaling in Obesity | 0.264 | 0.115 | turquoise | PIK3C2B,PIK3CA,MAPK1,GAB1,FOXO1,PIK3C3,PIK3R6,PIK3R5,PLCB1,FRS2 |
| Sumoylation Pathway | 0.263 | 0.115 | turquoise | SP1,STUB1,CREBBP,CEBPA,RHOU,MDM2,RHOF,RHOH,NR3C1,FAS,FNBP1 |
| CD27 Signaling in Lymphocytes | 0.255 | 0.115 | turquoise | MAP3K9,MAP3K14,CD70,BID,TRAF5,CD27 |
| Role of JAK family kinases in IL-6-type Cytokine Signaling | 0.253 | 0.12 | turquoise | MAPK1,IL6R,STAT5B |
| RAN Signaling | 0.251 | 0.125 | turquoise | KPNA2,KPNA1 |
| Glutaryl-CoA Degradation | 0.251 | 0.125 | turquoise | HSD17B10,HSD17B8 |
| Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate) | 0.251 | 0.125 | turquoise | PMVK,IDI1 |
| Thioredoxin Pathway | 0.242 | 0.143 | turquoise | TXN |
| Glycoaminoglycan-protein Linkage Region Biosynthesis | 0.242 | 0.143 | turquoise | XYLT1 |
| Apelin Liver Signaling Pathway | 0.233 | 0.115 | turquoise | COL18A1,TNF,FAS |
| Ubiquinol-10 Biosynthesis (Eukaryotic) | 0.225 | 0.118 | turquoise | MICAL2,MICAL3 |
| γ-linolenate Biosynthesis II (Animals) | 0.225 | 0.118 | turquoise | SLC27A3,ACSL1 |
| Mitochondrial L-carnitine Shuttle Pathway | 0.225 | 0.118 | turquoise | SLC27A3,ACSL1 |
| Oxidative Ethanol Degradation III | 0.225 | 0.118 | turquoise | ALDH1A1,ACSL1 |
| Phosphatidylethanolamine Biosynthesis II | 0.206 | 0.125 | turquoise | CEPT1 |
| Superoxide Radicals Degradation | 0.206 | 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 | 0.0848 | turquoise | TIAM1,MYL6,CDK4,AFDN,YBX3,VTI1B,PTEN,TGFBR2,PRKCI,CEBPA,VCL,TNFRSF1B,TNF,NAPA |
| 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 | 0.0625 | turquoise | MAP3K14,MAPK1 |
| 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 |
| Cellular Effects of Sildenafil (Viagra) | 0 | 0.103 | turquoise | CALM1 (includes others),KCNN4,KCNN3,CAMK4,MPRIP,GNAS,MYL6,PABPC4,PDE4A,PLCB1,PDE4D,ITPR1,MYL12A |
| Cardiomyocyte Differentiation via BMP Receptors | 0 | 0.105 | turquoise | BMPR1A,MEF2C |
| CDK5 Signaling | 0 | 0.0865 | turquoise | ITGB1,LAMC1,RAP1B,RAP2B,RAP2A,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 | 0.0952 | turquoise | HSP90B1,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 | 0.0702 | turquoise | RAD17,E2F7,E2F2,CHEK1 |
| DNA Methylation and Transcriptional Repression Signaling | 0 | 0.1 | turquoise | CHD3,H3F3A/H3F3B,ARID4B |
| Androgen Signaling | 0 | 0.0963 | turquoise | GNAI3,CALM1 (includes others),PRKCI,GNAS,CAMK4,MAPK1,PRKCD,SMAD3,CREBBP,GNAQ,PRKCE,GNG5,POLR2L |
| Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency | 0 | 0.0889 | turquoise | ETS2,PHC3,JARID2,SH3GLB1 |
| Basal Cell Carcinoma Signaling | 0 | 0.0588 | turquoise | WNT10A,BMP8B,FZD1,BMP6 |
| Cleavage and Polyadenylation of Pre-mRNA | 0 | 0.0833 | turquoise | PAPOLA |
| Retinoic acid Mediated Apoptosis Signaling | 0 | 0.0847 | turquoise | BID,TNFRSF10C,CFLAR,RXRA,RARG |
| IL-1 Signaling | 0 | 0.0769 | turquoise | MAP3K14,GNAI3,GNAS,MAPK1,GNAQ,GNG5,IRAK1 |
| 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 | 0.0694 | turquoise | WNT10A,CSNK1G3,CSNK1A1,FZD1,NCOA3 |
| TNFR1 Signaling | 0 | 0.104 | turquoise | TRADD,MAP3K14,BID,TNF,BIRC3 |
| Intrinsic Prothrombin Activation Pathway | 0 | 0.0244 | turquoise | COL18A1 |
| Cyclins and Cell Cycle Regulation | 0 | 0.112 | turquoise | CCNA2,HDAC9,CCND2,PA2G4,TFDP1,WEE1,E2F7,CDK4,E2F2 |
| Assembly of RNA Polymerase II Complex | 0 | 0.04 | turquoise | TAF10,POLR2L |
| IL-17A Signaling in Airway Cells | 0 | 0.112 | turquoise | PIK3C2B,PIK3CA,MAPK1,GAB1,PIK3C3,PIK3R6,PIK3R5,FRS2,PTEN |
| 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 |
| Hematopoiesis from Multipotent Stem Cells | 0 | 0.0833 | turquoise | IL7 |
| Transcriptional Regulatory Network in Embryonic Stem Cells | 0 | 0.04 | turquoise | H3F3A/H3F3B,SKIL |
| nNOS Signaling in Skeletal Muscle Cells | 0 | 0.075 | turquoise | CALM1 (includes others),CAMK4,CAPN3 |
| Netrin Signaling | 0 | 0.0769 | turquoise | NCK2,NFATC3,ABLIM2,ABLIM1,ENAH |
| Heparan Sulfate Biosynthesis | 0 | 0.0923 | turquoise | PNPLA7,XYLT1,EXT1,HS3ST1,NDST1,PLA1A |
| Bupropion Degradation | 0 | 0.0833 | turquoise | CYP51A1,CYP1B1 |
| Glucose and Glucose-1-phosphate Degradation | 0 | 0.1 | turquoise | PGM1 |
| Nicotine Degradation III | 0 | 0.0465 | turquoise | CYP51A1,CYP1B1 |
| Dopamine Degradation | 0 | 0.0714 | turquoise | ALDH1A1,SMOX |
| Heparan Sulfate Biosynthesis (Late Stages) | 0 | 0.0862 | turquoise | PNPLA7,EXT1,HS3ST1,NDST1,PLA1A |
| Pyrimidine Ribonucleotides De Novo Biosynthesis | 0 | 0.0465 | turquoise | SLC25A42,AK9 |
| Androgen Biosynthesis | 0 | 0.0833 | turquoise | SRD5A3 |
| Acyl-CoA Hydrolysis | 0 | 0.1 | turquoise | THEM4 |
| The Visual Cycle | 0 | 0.105 | turquoise | RBP7,RDH10 |
| D-myo-inositol-5-phosphate Metabolism | 0 | 0.0974 | turquoise | PPFIBP2,PIP4K2B,PAWR,ACP5,PPM1K,PTPN12,PTEN,PLD4,ATP1A1,PTPRJ,SGPP2,PLCB1,MTMR7,SGPP1,SIRPA |
| Melatonin Degradation I | 0 | 0.04 | turquoise | CYP51A1,CYP1B1 |
| NAD Salvage Pathway II | 0 | 0.0476 | turquoise | ACP5 |
| 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 | 0.0769 | turquoise | XYLT1,CHPF,HS3ST1,NDST1 |
| Dermatan Sulfate Biosynthesis | 0 | 0.0741 | turquoise | XYLT1,CHPF,HS3ST1,NDST1 |
| Cholesterol Biosynthesis I | 0 | 0.0769 | turquoise | CYP51A1 |
| 1D-myo-inositol Hexakisphosphate Biosynthesis II (Mammalian) | 0 | 0.111 | turquoise | ITPKB,INPP5A |
| Urate Biosynthesis/Inosine 5'-phosphate Degradation | 0 | 0.0769 | turquoise | IMPDH1 |
| NAD Phosphorylation and Dephosphorylation | 0 | 0.1 | turquoise | ACP5 |
| Dermatan Sulfate Biosynthesis (Late Stages) | 0 | 0.0488 | turquoise | HS3ST1,NDST1 |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0 | 0.0882 | turquoise | ATP1A1,PTPRJ,SGPP2,PPFIBP2,SGPP1,MTMR7,PAWR,ACP5,PPM1K,PTPN12,SIRPA,PTEN |
| Nicotine Degradation II | 0 | 0.0612 | turquoise | FMO5,CYP51A1,CYP1B1 |
| Citrulline Biosynthesis | 0 | 0.111 | turquoise | ARG1 |
| Valine Degradation I | 0 | 0.111 | turquoise | BCAT1,ABAT |
| Serotonin Degradation | 0 | 0.0364 | turquoise | ALDH1A1,SMOX |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0 | 0.0882 | turquoise | ATP1A1,PTPRJ,SGPP2,PPFIBP2,SGPP1,MTMR7,PAWR,ACP5,PPM1K,PTPN12,SIRPA,PTEN |
| Leucine Degradation I | 0 | 0.111 | turquoise | BCAT1 |
| 3-phosphoinositide Degradation | 0 | 0.1 | turquoise | PPFIBP2,MTMR1,PAWR,ACP5,PPM1K,PTPN12,PTEN,INPP4A,ATP1A1,PTPRJ,SGPP2,MTM1,MTMR7,SGPP1,SIRPA |
| D-myo-inositol (1,4,5)-trisphosphate Degradation | 0 | 0.0588 | turquoise | INPP5A |
| 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 | 0.0682 | turquoise | CHPF,HS3ST1,NDST1 |
| Cholesterol Biosynthesis III (via Desmosterol) | 0 | 0.0769 | turquoise | CYP51A1 |
| Superpathway of Melatonin Degradation | 0 | 0.0545 | turquoise | SMOX,CYP51A1,CYP1B1 |
| 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 |
| 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 | 0.0865 | turquoise | BRAF,HCAR3,HRH2,GNAS,MAPK1,CREB3,CREBBP,GNG5,CREB5 |
| Inhibition of Matrix Metalloproteases | 0 | 0.0789 | turquoise | TIMP1,MMP11,TIMP2 |
| Agranulocyte Adhesion and Diapedesis | 0 | 0.111 | turquoise | ITGB1,CXCL8,CD99,C5AR1,MYL6,CXCR4,CKLF,RDX,CCL5,CCL3,ITGB7,SELPLG,GNAI3,IL1RN,IL1B,PODXL,MMP11,CXCL2,TNF |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 0 | 0.111 | turquoise | RAP2B,RAP1B,RAP2A,PIK3C2B,PIK3CA,ID2,MAPK1,FGF9,SMAD3,SOS2,PIK3R5,FZD1,TGFBR2,BRAF,RRAS2,WNT10A,GAB1,PIK3C3,PIK3R6,PDGFD,FRS2 |
| HIPPO signaling | 0 | 0.0714 | turquoise | YWHAE,YWHAH,RASSF6,SMAD3,TEAD2,RASSF1 |
| PCP pathway | 0 | 0.0862 | turquoise | WNT10A,VANGL1,DAAM1,FZD1,PRICKLE1 |
| Wnt/Ca+ pathway | 0 | 0.0984 | turquoise | NFATC3,CREBBP,CREB3,PLCB1,FZD1,CREB5 |
| Nucleotide Excision Repair Pathway | 0 | 0.0286 | turquoise | POLR2L |
| Cardiac β-adrenergic Signaling | 0 | 0.101 | turquoise | SMPDL3A,GNAS,PDE7A,GRK3,PDE4A,ATP2A3,AKAP7,AKAP13,PDE7B,GDE1,PDE4D,GNG5,SLC8A1,PKIG |
| Interferon Signaling | 0 | 0.0556 | turquoise | IFNAR2,BAK1 |
| GABA Receptor Signaling | 0 | 0.0753 | turquoise | KCNN4,KCNN3,GNAS,ABAT,GABBR1,AP1B1,AP2S1 |
| Wnt/β-catenin Signaling | 0 | 0.0719 | turquoise | TGFBR2,WNT10A,TGFBR3,CSNK1G3,CREBBP,CSNK1A1,GNAQ,TLE3,ACVR1,MDM2,FZD1,RARG |
| Serotonin Receptor Signaling | 0 | 0.05 | turquoise | SMOX,PCBD1 |
| Insulin Receptor Signaling | 0 | 0.112 | turquoise | RAP1B,RAP2B,RAP2A,PIK3C2B,PIK3CA,MAPK1,SOS2,PIK3R5,PTEN,PRKCI,RRAS2,GAB1,FOXO1,PIK3C3,PIK3R6,FRS2 |
| Dopamine Receptor Signaling | 0 | 0.0263 | turquoise | SMOX,PCBD1 |
| Notch Signaling | 0 | 0.108 | turquoise | FURIN,DTX1,DTX4,MAML3 |
| GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell | 0 | 0.0694 | turquoise | GNAI3,GNAS,GNAQ,PLCB1,ITPR1 |
| GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells | 0 | 0.102 | turquoise | GNAI3,GNAS,PRKCI,PRKCD,GPBAR1,GNAQ,PRKCE,PLCB1,ITPR1,GNG5,FFAR1 |
| 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 | 0.0918 | turquoise | H3F3A/H3F3B,UBE2N,RBX1,LIG4,COPS6,TOP2A,COPS8,POLD4,POLR2L |
| Apelin Muscle Signaling Pathway | 0 | 0.0556 | turquoise | GNAS |
| Calcium Signaling | 0 | 0.113 | turquoise | RAP2B,RAP1B,RAP2A,HDAC9,CAMK4,TP63,MAPK1,MYL6,CAMK1D,NFATC3,GRIA1,CREB3,CREBBP,ATP2A3,ITPR1,CREB5,CALM1 (includes others),CAMK2D,MEF2C,SLC8A1,ATP2B4,CAMKK2 |
| Gαq Signaling | 1.91 | 0.014 | grey | CALCR,PRKCB |
| CDP-diacylglycerol Biosynthesis I | 1.72 | 0.0625 | grey | CDS1 |
| mTOR Signaling | 1.7 | 0.0108 | grey | EIF3E,PRKCB |
| Phosphatidylglycerol Biosynthesis II (Non-plastidic) | 1.69 | 0.0588 | grey | CDS1 |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 1.58 | 0.00939 | grey | WNT7B,CALCR |
| G-Protein Coupled Receptor Signaling | 1.43 | 0.00775 | grey | CALCR,PRKCB |
| Mechanisms of Viral Exit from Host Cells | 1.36 | 0.027 | grey | PRKCB |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 1.36 | 0.00709 | grey | WNT7B,PRKCB |
| nNOS Signaling in Neurons | 1.32 | 0.0244 | grey | PRKCB |
| UVC-Induced MAPK Signaling | 1.25 | 0.0208 | grey | PRKCB |
| PCP pathway | 1.23 | 0.02 | grey | WNT7B |
| Calcium-induced T Lymphocyte Apoptosis | 1.22 | 0.0192 | grey | PRKCB |
| Protein Kinase A Signaling | 1.22 | 0.0059 | grey | PTPN14,PRKCB |
| Basal Cell Carcinoma Signaling | 1.18 | 0.0175 | grey | WNT7B |
| Molecular Mechanisms of Cancer | 1.17 | 0.00554 | grey | WNT7B,PRKCB |
| UVB-Induced MAPK Signaling | 1.13 | 0.0156 | grey | PRKCB |
| Melatonin Signaling | 1.12 | 0.0154 | grey | PRKCB |
| Role of Wnt/GSK-3β Signaling in the Pathogenesis of Influenza | 1.12 | 0.0152 | grey | WNT7B |
| Thrombopoietin Signaling | 1.1 | 0.0145 | grey | PRKCB |
| ErbB4 Signaling | 1.08 | 0.0137 | grey | PRKCB |
| Chemokine Signaling | 1.08 | 0.0137 | grey | PRKCB |
| GM-CSF Signaling | 1.06 | 0.0133 | grey | PRKCB |
| Axonal Guidance Signaling | 1.06 | 0.00477 | grey | WNT7B,PRKCB |
| VDR/RXR Activation | 1.05 | 0.013 | grey | PRKCB |
| CCR5 Signaling in Macrophages | 1.03 | 0.0122 | grey | PRKCB |
| Growth Hormone Signaling | 1.03 | 0.0122 | grey | PRKCB |
| Erythropoietin Signaling | 1.02 | 0.0119 | grey | PRKCB |
| α-Adrenergic Signaling | 1.01 | 0.0118 | grey | PRKCB |
| Macropinocytosis Signaling | 1.01 | 0.0118 | grey | PRKCB |
| IL-3 Signaling | 1.01 | 0.0116 | grey | PRKCB |
| Neuregulin Signaling | 1 | 0.0115 | grey | PRKCB |
| Factors Promoting Cardiogenesis in Vertebrates | 1 | 0.0115 | grey | PRKCB |
| Prolactin Signaling | 1 | 0.0115 | grey | PRKCB |
| VEGF Family Ligand-Receptor Interactions | 1 | 0.0114 | grey | PRKCB |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 0.991 | 0.0112 | grey | PRKCB |
| LPS-stimulated MAPK Signaling | 0.983 | 0.011 | grey | PRKCB |
| NF-κB Activation by Viruses | 0.983 | 0.011 | grey | PRKCB |
| HER-2 Signaling in Breast Cancer | 0.983 | 0.011 | grey | PRKCB |
| GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells | 0.983 | 0.011 | grey | PRKCB |
| Sumoylation Pathway | 0.979 | 0.0109 | grey | CBX4 |
| PDGF Signaling | 0.967 | 0.0105 | grey | PRKCB |
| Cholecystokinin/Gastrin-mediated Signaling | 0.951 | 0.0101 | grey | PRKCB |
| ErbB Signaling | 0.947 | 0.01 | grey | PRKCB |
| Sperm Motility | 0.932 | 0.00971 | grey | PRKCB |
| VEGF Signaling | 0.928 | 0.00962 | grey | PRKCB |
| Apelin Cardiomyocyte Signaling Pathway | 0.928 | 0.00962 | grey | PRKCB |
| Nitric Oxide Signaling in the Cardiovascular System | 0.924 | 0.00952 | grey | PRKCB |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 0.921 | 0.00943 | grey | PRKCB |
| Phagosome Formation | 0.91 | 0.00917 | grey | PRKCB |
| Synaptic Long Term Potentiation | 0.903 | 0.00901 | grey | PRKCB |
| Virus Entry via Endocytic Pathways | 0.903 | 0.00901 | grey | PRKCB |
| G Beta Gamma Signaling | 0.896 | 0.00885 | grey | PRKCB |
| Glioma Signaling | 0.889 | 0.0087 | grey | PRKCB |
| Cellular Effects of Sildenafil (Viagra) | 0.886 | 0.00862 | grey | MYH11 |
| HGF Signaling | 0.886 | 0.00862 | grey | PRKCB |
| GP6 Signaling Pathway | 0.883 | 0.00855 | grey | PRKCB |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 0.879 | 0.00847 | grey | WNT7B |
| Apelin Endothelial Signaling Pathway | 0.879 | 0.00847 | grey | PRKCB |
| Fc Epsilon RI Signaling | 0.873 | 0.0084 | grey | PRKCB |
| Natural Killer Cell Signaling | 0.87 | 0.00833 | grey | PRKCB |
| fMLP Signaling in Neutrophils | 0.87 | 0.00833 | grey | PRKCB |
| CCR3 Signaling in Eosinophils | 0.866 | 0.00826 | grey | PRKCB |
| PI3K Signaling in B Lymphocytes | 0.866 | 0.00826 | grey | PRKCB |
| Renin-Angiotensin Signaling | 0.863 | 0.0082 | grey | PRKCB |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 0.86 | 0.00813 | grey | PRKCB |
| P2Y Purigenic Receptor Signaling Pathway | 0.854 | 0.008 | grey | PRKCB |
| 14-3-3-mediated Signaling | 0.851 | 0.00794 | grey | PRKCB |
| p70S6K Signaling | 0.848 | 0.00787 | grey | PRKCB |
| Corticotropin Releasing Hormone Signaling | 0.845 | 0.00781 | grey | PRKCB |
| Human Embryonic Stem Cell Pluripotency | 0.845 | 0.00781 | grey | WNT7B |
| Androgen Signaling | 0.842 | 0.00775 | grey | PRKCB |
| Type II Diabetes Mellitus Signaling | 0.815 | 0.00725 | grey | PRKCB |
| Ovarian Cancer Signaling | 0.81 | 0.00714 | grey | WNT7B |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 0.81 | 0.00714 | grey | PRKCB |
| IL-12 Signaling and Production in Macrophages | 0.804 | 0.00704 | grey | PRKCB |
| Epithelial Adherens Junction Signaling | 0.804 | 0.00704 | grey | MYH11 |
| Aldosterone Signaling in Epithelial Cells | 0.801 | 0.00699 | grey | PRKCB |
| Hepatic Cholestasis | 0.799 | 0.00694 | grey | PRKCB |
| Tight Junction Signaling | 0.783 | 0.00667 | grey | MYH11 |
| Regulation of eIF4 and p70S6K Signaling | 0.783 | 0.00667 | grey | EIF3E |
| Wnt/β-catenin Signaling | 0.775 | 0.00658 | grey | WNT7B |
| Glioblastoma Multiforme Signaling | 0.772 | 0.00654 | grey | WNT7B |
| eNOS Signaling | 0.772 | 0.00654 | grey | PRKCB |
| GNRH Signaling | 0.764 | 0.00641 | grey | PRKCB |
| Tec Kinase Signaling | 0.764 | 0.00641 | grey | PRKCB |
| Agranulocyte Adhesion and Diapedesis | 0.759 | 0.00633 | grey | MYH11 |
| Synaptic Long Term Depression | 0.754 | 0.00625 | grey | PRKCB |
| CXCR4 Signaling | 0.754 | 0.00625 | grey | PRKCB |
| PPARα/RXRα Activation | 0.745 | 0.0061 | grey | PRKCB |
| NF-κB Signaling | 0.733 | 0.00592 | grey | PRKCB |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation | 0.73 | 0.00588 | grey | MYH11 |
| Endothelin-1 Signaling | 0.73 | 0.00588 | grey | PRKCB |
| B Cell Receptor Signaling | 0.73 | 0.00588 | grey | PRKCB |
| RAR Activation | 0.728 | 0.00581 | grey | PRKCB |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 0.721 | 0.00571 | grey | WNT7B |
| ILK Signaling | 0.717 | 0.00565 | grey | MYH11 |
| Calcium Signaling | 0.714 | 0.00562 | grey | MYH11 |
| NRF2-mediated Oxidative Stress Response | 0.71 | 0.00556 | grey | PRKCB |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 0.706 | 0.00549 | grey | PRKCB |
| ERK/MAPK Signaling | 0.697 | 0.00538 | grey | PRKCB |
| Gap Junction Signaling | 0.695 | 0.00535 | grey | PRKCB |
| IL-8 Signaling | 0.688 | 0.00526 | grey | PRKCB |
| Thrombin Signaling | 0.686 | 0.00524 | grey | PRKCB |
| Breast Cancer Regulation by Stathmin1 | 0.684 | 0.00521 | grey | PRKCB |
| Leukocyte Extravasation Signaling | 0.68 | 0.00515 | grey | PRKCB |
| CREB Signaling in Neurons | 0.672 | 0.00505 | grey | PRKCB |
| Role of NFAT in Cardiac Hypertrophy | 0.666 | 0.00498 | grey | PRKCB |
| Phospholipase C Signaling | 0.664 | 0.00495 | grey | PRKCB |
| EIF2 Signaling | 0.656 | 0.00483 | grey | EIF3E |
| Actin Cytoskeleton Signaling | 0.65 | 0.00476 | grey | MYH11 |
| Opioid Signaling Pathway | 0.631 | 0.00455 | grey | PRKCB |
| Huntington's Disease Signaling | 0.616 | 0.00437 | grey | PRKCB |
| Colorectal Cancer Metastasis Signaling | 0.611 | 0.00431 | grey | WNT7B |
| Xenobiotic Metabolism Signaling | 0.583 | 0.004 | grey | PRKCB |
| Glucocorticoid Receptor Signaling | 0.498 | 0.00317 | grey | KRT76 |
| Protein Kinase A Signaling | 2.52 | 0.0263 | brown | PRKACB,PPP1R3D,DUSP5,PTPRJ,CDC14B,ADD1,TGFB2,UBASH3B,NFATC4,PLCL2 |
| Wnt/β-catenin Signaling | 2.32 | 0.0359 | brown | SOX4,TGFB2,TLE3,CD44,TLE1,BMPR2 |
| FAT10 Cancer Signaling Pathway | 2.07 | 0.0667 | brown | ACKR3,TGFB2,BMPR2 |
| Epithelial Adherens Junction Signaling | 1.95 | 0.0347 | brown | CTNNA1,TGFB2,BMPR2,WASF1,JUP |
| Glycine Degradation (Creatine Biosynthesis) | 1.73 | 0.5 | brown | GATM |
| Germ Cell-Sertoli Cell Junction Signaling | 1.63 | 0.0287 | brown | PIK3CA,RHOB,CTNNA1,TGFB2,JUP |
| RhoGDI Signaling | 1.63 | 0.0287 | brown | RHOB,ARHGEF7,CD44,WASF1,PIP5K1B |
| Cardiac Hypertrophy Signaling | 1.63 | 0.0253 | brown | PRKACB,PIK3CA,RHOB,TGFB2,NFATC4,PLCL2 |
| Phagosome Formation | 1.58 | 0.0331 | brown | PIK3CA,RHOB,IGHG1,PLCL2 |
| Rac Signaling | 1.55 | 0.0325 | brown | PIK3CA,CD44,WASF1,PIP5K1B |
| Molecular Mechanisms of Cancer | 1.54 | 0.0207 | brown | PRKACB,PIK3CA,RHOB,ARHGEF7,BMP3,TGFB2,CTNNA1,BMPR2 |
| Glioma Invasiveness Signaling | 1.44 | 0.0385 | brown | PIK3CA,RHOB,CD44 |
| Molybdenum Cofactor Biosynthesis | 1.44 | 0.25 | brown | GPHN |
| BMP signaling pathway | 1.41 | 0.0375 | brown | PRKACB,BMP3,BMPR2 |
| Human Embryonic Stem Cell Pluripotency | 1.37 | 0.0284 | brown | PIK3CA,BMP3,TGFB2,BMPR2 |
| Regulation of Actin-based Motility by Rho | 1.36 | 0.0357 | brown | RHOB,WASF1,PIP5K1B |
| Leptin Signaling in Obesity | 1.32 | 0.0345 | brown | PRKACB,PIK3CA,PLCL2 |
| Factors Promoting Cardiogenesis in Vertebrates | 1.3 | 0.0337 | brown | BMP3,TGFB2,BMPR2 |
| AMPK Signaling | 1.27 | 0.0229 | brown | PRKACB,PIK3CA,TBC1D1,RAB39A,PFKFB2 |
| Role of NFAT in Cardiac Hypertrophy | 1.25 | 0.0226 | brown | PRKACB,PIK3CA,TGFB2,NFATC4,PLCL2 |
| TGF-β Signaling | 1.25 | 0.0323 | brown | TGFB2,BMPR2,PMEPA1 |
| Neuroinflammation Signaling Pathway | 1.22 | 0.0201 | brown | PIK3CA,TGFB2,BMPR2,NFATC4,BACE2,IRAK2 |
| Tight Junction Signaling | 1.16 | 0.0242 | brown | PRKACB,JAM3,TGFB2,CTNNA1 |
| Tec Kinase Signaling | 1.16 | 0.0242 | brown | TNFRSF21,PIK3CA,RHOB,TNFRSF10B |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 1.16 | 0.0195 | brown | PIK3CA,IL15,NFATC4,IGHG1,PLCL2,IRAK2 |
| Gαs Signaling | 1.14 | 0.0288 | brown | PRKACB,CNR1,ADD1 |
| FAK Signaling | 1.12 | 0.0283 | brown | PIK3CA,ASAP1,ARHGEF7 |
| Axonal Guidance Signaling | 1.12 | 0.0168 | brown | MME,PRKACB,PIK3CA,ARHGEF7,BMP3,ADAM23,PLCL2,NFATC4 |
| Amyloid Processing | 1.1 | 0.04 | brown | PRKACB,BACE2 |
| Phototransduction Pathway | 1.1 | 0.04 | brown | PRKACB,GUCY2C |
| PPARα/RXRα Activation | 1.1 | 0.023 | brown | PRKACB,TGFB2,BMPR2,PLCL2 |
| Sertoli Cell-Sertoli Cell Junction Signaling | 1.1 | 0.023 | brown | PRKACB,JAM3,CTNNA1,JUP |
| Prostanoid Biosynthesis | 1.09 | 0.111 | brown | PTGES3 |
| Nitric Oxide Signaling in the Cardiovascular System | 1.08 | 0.0273 | brown | PRKACB,PIK3CA,GUCY2C |
| Signaling by Rho Family GTPases | 1.08 | 0.0201 | brown | PIK3CA,RHOB,ARHGEF7,WASF1,PIP5K1B |
| Dendritic Cell Maturation | 1.07 | 0.0225 | brown | PIK3CA,IL15,IGHG1,PLCL2 |
| p53 Signaling | 1.05 | 0.0265 | brown | PIK3CA,GADD45B,TNFRSF10B |
| IGF-1 Signaling | 1.05 | 0.0265 | brown | PRKACB,IGFBP4,PIK3CA |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 1.03 | 0.0259 | brown | PRKACB,PIK3CA,PLCL2 |
| Telomerase Signaling | 1.03 | 0.0259 | brown | PIK3CA,ELK3,PTGES3 |
| Apelin Pancreas Signaling Pathway | 0.991 | 0.0345 | brown | PRKACB,PIK3CA |
| Cleavage and Polyadenylation of Pre-mRNA | 0.975 | 0.0833 | brown | PABPN1 |
| Hematopoiesis from Multipotent Stem Cells | 0.975 | 0.0833 | brown | IL15 |
| Synaptic Long Term Potentiation | 0.971 | 0.0244 | brown | PRKACB,PPP1R3D,PLCL2 |
| Sphingosine-1-phosphate Signaling | 0.971 | 0.0244 | brown | PIK3CA,RHOB,PLCL2 |
| 3-phosphoinositide Biosynthesis | 0.967 | 0.0206 | brown | DUSP5,PIK3CA,PTPRJ,PIP5K1B |
| Wnt/Ca+ pathway | 0.955 | 0.0328 | brown | NFATC4,PLCL2 |
| Cellular Effects of Sildenafil (Viagra) | 0.947 | 0.0238 | brown | PRKACB,GUCY2C,PLCL2 |
| Actin Nucleation by ARP-WASP Complex | 0.943 | 0.0323 | brown | RHOB,WASF1 |
| Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency | 0.939 | 0.0236 | brown | PIK3CA,BMP3,BMPR2 |
| Gap Junction Signaling | 0.932 | 0.02 | brown | PRKACB,PIK3CA,GUCY2C,PLCL2 |
| Adipogenesis pathway | 0.932 | 0.0234 | brown | XBP1,BMPR2,NFATC4 |
| Endocannabinoid Developing Neuron Pathway | 0.932 | 0.0234 | brown | PRKACB,PIK3CA,CNR1 |
| ERK/MAPK Signaling | 0.924 | 0.0199 | brown | PRKACB,PPP1R3D,PIK3CA,ELK3 |
| Adrenomedullin signaling pathway | 0.921 | 0.0198 | brown | PRKACB,PIK3CA,GUCY2C,PLCL2 |
| PI3K Signaling in B Lymphocytes | 0.91 | 0.0229 | brown | PIK3CA,NFATC4,PLCL2 |
| Netrin Signaling | 0.91 | 0.0308 | brown | PRKACB,NFATC4 |
| Iron homeostasis signaling pathway | 0.91 | 0.0229 | brown | BMP3,BMPR2,ATP6V0E1 |
| Leukocyte Extravasation Signaling | 0.9 | 0.0194 | brown | PIK3CA,JAM3,CTNNA1,CD44 |
| Breast Cancer Regulation by Stathmin1 | 0.883 | 0.0191 | brown | PRKACB,PPP1R3D,PIK3CA,ARHGEF7 |
| Corticotropin Releasing Hormone Signaling | 0.866 | 0.0219 | brown | PRKACB,GUCY2C,CNR1 |
| Melatonin Signaling | 0.86 | 0.0286 | brown | PRKACB,PLCL2 |
| Integrin Signaling | 0.86 | 0.0188 | brown | PIK3CA,RHOB,ASAP1,ARHGEF7 |
| RAN Signaling | 0.857 | 0.0625 | brown | RANBP2 |
| HMGB1 Signaling | 0.854 | 0.0216 | brown | PIK3CA,RHOB,TGFB2 |
| P2Y Purigenic Receptor Signaling Pathway | 0.854 | 0.0216 | brown | PRKACB,PIK3CA,PLCL2 |
| Endometrial Cancer Signaling | 0.839 | 0.0278 | brown | PIK3CA,CTNNA1 |
| GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell | 0.839 | 0.0278 | brown | PRKACB,PLCL2 |
| Insulin Receptor Signaling | 0.827 | 0.021 | brown | PRKACB,PPP1R3D,PIK3CA |
| Th17 Activation Pathway | 0.81 | 0.0267 | brown | NFATC4,IRAK2 |
| Actin Cytoskeleton Signaling | 0.804 | 0.0179 | brown | PIK3CA,ARHGEF7,WASF1,PIP5K1B |
| Role of JAK1 and JAK3 in γc Cytokine Signaling | 0.801 | 0.0263 | brown | PIK3CA,IL15 |
| Dopamine Receptor Signaling | 0.801 | 0.0263 | brown | PRKACB,PPP1R3D |
| Phospholipase C Signaling | 0.796 | 0.0177 | brown | RHOB,ARHGEF7,NFATC4,IGHG1 |
| Ovarian Cancer Signaling | 0.79 | 0.0201 | brown | PRKACB,PIK3CA,CD44 |
| Cardiomyocyte Differentiation via BMP Receptors | 0.788 | 0.0526 | brown | BMPR2 |
| GADD45 Signaling | 0.788 | 0.0526 | brown | GADD45B |
| Communication between Innate and Adaptive Immune Cells | 0.785 | 0.0256 | brown | IL15,IGHG1 |
| Superpathway of Inositol Phosphate Compounds | 0.785 | 0.0175 | brown | DUSP5,PIK3CA,PTPRJ,PIP5K1B |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 0.78 | 0.0175 | brown | PIK3CA,BMP3,BMPR2,NFATC4 |
| Endoplasmic Reticulum Stress Pathway | 0.75 | 0.0476 | brown | XBP1 |
| Endocannabinoid Cancer Inhibition Pathway | 0.75 | 0.0192 | brown | PRKACB,PIK3CA,CNR1 |
| Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes | 0.742 | 0.0241 | brown | TGFB2,NFATC4 |
| Hepatic Cholestasis | 0.738 | 0.019 | brown | PRKACB,TGFB2,IRAK2 |
| IL-15 Signaling | 0.735 | 0.0238 | brown | PIK3CA,IL15 |
| Antiproliferative Role of Somatostatin Receptor 2 | 0.735 | 0.0238 | brown | PIK3CA,GUCY2C |
| HIPPO signaling | 0.735 | 0.0238 | brown | PPP1R3D,CD44 |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 0.733 | 0.0189 | brown | PRKACB,PPP1R3D,PLCL2 |
| Apelin Cardiac Fibroblast Signaling Pathway | 0.73 | 0.0455 | brown | TGFB2 |
| Relaxin Signaling | 0.728 | 0.0188 | brown | PRKACB,PIK3CA,GUCY2C |
| Gαq Signaling | 0.728 | 0.0188 | brown | PIK3CA,RHOB,NFATC4 |
| IL-7 Signaling Pathway | 0.703 | 0.0227 | brown | PIK3CA,IGHG1 |
| TCA Cycle II (Eukaryotic) | 0.697 | 0.0417 | brown | SDHA |
| Macropinocytosis Signaling | 0.697 | 0.0225 | brown | PIK3CA,RAB34 |
| Colorectal Cancer Metastasis Signaling | 0.693 | 0.0161 | brown | PRKACB,PIK3CA,RHOB,TGFB2 |
| Glioblastoma Multiforme Signaling | 0.686 | 0.0179 | brown | PIK3CA,RHOB,PLCL2 |
| Glucocorticoid Receptor Signaling | 0.682 | 0.0148 | brown | PRKACB,PIK3CA,TGFB2,NFATC4,PTGES3 |
| IL-1 Signaling | 0.682 | 0.022 | brown | PRKACB,IRAK2 |
| Aldosterone Signaling in Epithelial Cells | 0.68 | 0.0178 | brown | PIK3CA,PIP5K1B,PLCL2 |
| IL-4 Signaling | 0.676 | 0.0217 | brown | PIK3CA,NFATC4 |
| Death Receptor Signaling | 0.676 | 0.0217 | brown | TNFRSF21,TNFRSF10B |
| T Cell Exhaustion Signaling Pathway | 0.676 | 0.0176 | brown | PIK3CA,BMPR2,NFATC4 |
| Th1 and Th2 Activation Pathway | 0.67 | 0.0175 | brown | PIK3CA,BMPR2,NFATC4 |
| Antiproliferative Role of TOB in T Cell Signaling | 0.666 | 0.0385 | brown | TGFB2 |
| Reelin Signaling in Neurons | 0.662 | 0.0213 | brown | PIK3CA,CNR1 |
| D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis | 0.652 | 0.037 | brown | PIP5K1B |
| Sumoylation Pathway | 0.648 | 0.0208 | brown | RANBP2,RHOB |
| Acute Myeloid Leukemia Signaling | 0.642 | 0.0206 | brown | PIK3CA,JUP |
| IL-15 Production | 0.636 | 0.0357 | brown | IL15 |
| NF-κB Signaling | 0.627 | 0.0167 | brown | PRKACB,PIK3CA,BMPR2 |
| Sonic Hedgehog Signaling | 0.623 | 0.0345 | brown | PRKACB |
| Neuroprotective Role of THOP1 in Alzheimer's Disease | 0.604 | 0.0194 | brown | MME,PRKACB |
| RAR Activation | 0.597 | 0.016 | brown | PRKACB,PIK3CA,TGFB2 |
| CDK5 Signaling | 0.597 | 0.0192 | brown | PRKACB,PPP1R3D |
| B Cell Receptor Signaling | 0.597 | 0.016 | brown | PIK3CA,NFATC4,IGHG1 |
| Melanocyte Development and Pigmentation Signaling | 0.592 | 0.019 | brown | PRKACB,PIK3CA |
| Endothelin-1 Signaling | 0.575 | 0.0156 | brown | PIK3CA,GUCY2C,PLCL2 |
| PAK Signaling | 0.575 | 0.0185 | brown | PIK3CA,ARHGEF7 |
| GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells | 0.575 | 0.0185 | brown | PRKACB,PLCL2 |
| ILK Signaling | 0.572 | 0.0155 | brown | PIK3CA,LIMS2,RHOB |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 0.564 | 0.0154 | brown | PPP1R3D,PIK3CA,RHOB |
| Mouse Embryonic Stem Cell Pluripotency | 0.558 | 0.018 | brown | PIK3CA,BMPR2 |
| UVA-Induced MAPK Signaling | 0.558 | 0.018 | brown | PIK3CA,PLCL2 |
| Autoimmune Thyroid Disease Signaling | 0.554 | 0.0286 | brown | IGHG1 |
| Hematopoiesis from Pluripotent Stem Cells | 0.554 | 0.0286 | brown | IGHG1 |
| Chronic Myeloid Leukemia Signaling | 0.553 | 0.0179 | brown | PIK3CA,TGFB2 |
| Systemic Lupus Erythematosus Signaling | 0.551 | 0.0152 | brown | PIK3CA,NFATC4,IGHG1 |
| p38 MAPK Signaling | 0.547 | 0.0177 | brown | TGFB2,IRAK2 |
| T Cell Receptor Signaling | 0.542 | 0.0175 | brown | PIK3CA,NFATC4 |
| Apelin Cardiomyocyte Signaling Pathway | 0.542 | 0.0175 | brown | PIK3CA,PLCL2 |
| mTOR Signaling | 0.541 | 0.0149 | brown | PIK3CA,RHOB,EIF4B |
| iCOS-iCOSL Signaling in T Helper Cells | 0.536 | 0.0174 | brown | PIK3CA,NFATC4 |
| IL-8 Signaling | 0.533 | 0.0148 | brown | PIK3CA,RHOB,IRAK2 |
| Sperm Motility | 0.532 | 0.0172 | brown | PRKACB,PLCL2 |
| Allograft Rejection Signaling | 0.524 | 0.0263 | brown | IGHG1 |
| RhoA Signaling | 0.521 | 0.0169 | brown | WASF1,PIP5K1B |
| Paxillin Signaling | 0.521 | 0.0169 | brown | PIK3CA,ARHGEF7 |
| Gαi Signaling | 0.517 | 0.0168 | brown | PRKACB,CNR1 |
| Thrombin Signaling | 0.514 | 0.0144 | brown | PIK3CA,RHOB,PLCL2 |
| April Mediated Signaling | 0.514 | 0.0256 | brown | NFATC4 |
| HGF Signaling | 0.511 | 0.0167 | brown | PIK3CA,ELK3 |
| Pancreatic Adenocarcinoma Signaling | 0.502 | 0.0164 | brown | PIK3CA,TGFB2 |
| Th1 Pathway | 0.502 | 0.0164 | brown | PIK3CA,NFATC4 |
| PTEN Signaling | 0.498 | 0.0163 | brown | PIK3CA,BMPR2 |
| B Cell Activating Factor Signaling | 0.496 | 0.0244 | brown | NFATC4 |
| Primary Immunodeficiency Signaling | 0.496 | 0.0244 | brown | IGHG1 |
| Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza | 0.496 | 0.0244 | brown | IL15 |
| CD28 Signaling in T Helper Cells | 0.493 | 0.0161 | brown | PIK3CA,NFATC4 |
| CREB Signaling in Neurons | 0.483 | 0.0138 | brown | PRKACB,PIK3CA,PLCL2 |
| fMLP Signaling in Neutrophils | 0.475 | 0.0156 | brown | PIK3CA,NFATC4 |
| Renin-Angiotensin Signaling | 0.471 | 0.0155 | brown | PRKACB,PIK3CA |
| iNOS Signaling | 0.471 | 0.0227 | brown | IRAK2 |
| Role of p14/p19ARF in Tumor Suppression | 0.471 | 0.0227 | brown | PIK3CA |
| Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency | 0.463 | 0.0222 | brown | PHC1 |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 0.457 | 0.0152 | brown | PIK3CA,TGFB2 |
| STAT3 Pathway | 0.457 | 0.0152 | brown | TGFB2,BMPR2 |
| Cancer Drug Resistance By Drug Efflux | 0.456 | 0.0217 | brown | PIK3CA |
| Phagosome Maturation | 0.45 | 0.0149 | brown | CTSH,ATP6V0E1 |
| IL-9 Signaling | 0.449 | 0.0213 | brown | PIK3CA |
| Aryl Hydrocarbon Receptor Signaling | 0.445 | 0.0148 | brown | TGFB2,PTGES3 |
| 14-3-3-mediated Signaling | 0.441 | 0.0147 | brown | PIK3CA,PLCL2 |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0.441 | 0.0147 | brown | DUSP5,PTPRJ |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0.441 | 0.0147 | brown | DUSP5,PTPRJ |
| Nicotine Degradation II | 0.434 | 0.0204 | brown | FMO1 |
| p70S6K Signaling | 0.429 | 0.0144 | brown | PIK3CA,PLCL2 |
| Cardiac β-adrenergic Signaling | 0.429 | 0.0144 | brown | PRKACB,PPP1R3D |
| Th2 Pathway | 0.429 | 0.0144 | brown | PIK3CA,BMPR2 |
| Gustation Pathway | 0.418 | 0.0141 | brown | PRKACB,P2RX1 |
| Role of Cytokines in Mediating Communication between Immune Cells | 0.413 | 0.0192 | brown | IL15 |
| Semaphorin Signaling in Neurons | 0.413 | 0.0192 | brown | RHOB |
| autophagy | 0.408 | 0.0189 | brown | CTSH |
| IL-12 Signaling and Production in Macrophages | 0.403 | 0.0137 | brown | PIK3CA,TGFB2 |
| Docosahexaenoic Acid (DHA) Signaling | 0.401 | 0.0185 | brown | PIK3CA |
| Hereditary Breast Cancer Signaling | 0.396 | 0.0135 | brown | PIK3CA,GADD45B |
| Unfolded protein response | 0.395 | 0.0182 | brown | XBP1 |
| SPINK1 Pancreatic Cancer Pathway | 0.395 | 0.0182 | brown | CPM |
| 3-phosphoinositide Degradation | 0.389 | 0.0133 | brown | DUSP5,PTPRJ |
| Phospholipases | 0.383 | 0.0175 | brown | PLCL2 |
| D-myo-inositol-5-phosphate Metabolism | 0.376 | 0.013 | brown | DUSP5,PTPRJ |
| Retinoic acid Mediated Apoptosis Signaling | 0.372 | 0.0169 | brown | TNFRSF10B |
| PKCθ Signaling in T Lymphocytes | 0.366 | 0.0127 | brown | PIK3CA,NFATC4 |
| Mitochondrial Dysfunction | 0.36 | 0.0126 | brown | SDHA,BACE2 |
| PXR/RXR Activation | 0.356 | 0.0161 | brown | PRKACB |
| Ephrin A Signaling | 0.356 | 0.0161 | brown | PIK3CA |
| Melanoma Signaling | 0.351 | 0.0159 | brown | PIK3CA |
| Remodeling of Epithelial Adherens Junctions | 0.346 | 0.0156 | brown | CTNNA1 |
| eNOS Signaling | 0.338 | 0.012 | brown | PRKACB,PIK3CA |
| Cell Cycle: G1/S Checkpoint Regulation | 0.336 | 0.0152 | brown | TGFB2 |
| CNTF Signaling | 0.332 | 0.0149 | brown | PIK3CA |
| UVB-Induced MAPK Signaling | 0.332 | 0.0149 | brown | PIK3CA |
| Basal Cell Carcinoma Signaling | 0.327 | 0.0147 | brown | BMP3 |
| Xenobiotic Metabolism Signaling | 0.327 | 0.0109 | brown | PIK3CA,FMO1,PTGES3 |
| CXCR4 Signaling | 0.324 | 0.0117 | brown | PIK3CA,RHOB |
| Lymphotoxin β Receptor Signaling | 0.322 | 0.0145 | brown | PIK3CA |
| Role of IL-17A in Arthritis | 0.318 | 0.0143 | brown | PIK3CA |
| EGF Signaling | 0.318 | 0.0143 | brown | PIK3CA |
| G-Protein Coupled Receptor Signaling | 0.318 | 0.0108 | brown | PRKACB,PIK3CA,CNR1 |
| Caveolar-mediated Endocytosis Signaling | 0.313 | 0.0141 | brown | CD48 |
| Thrombopoietin Signaling | 0.309 | 0.0139 | brown | PIK3CA |
| IL-2 Signaling | 0.309 | 0.0139 | brown | PIK3CA |
| SPINK1 General Cancer Pathway | 0.309 | 0.0139 | brown | PIK3CA |
| Synaptic Long Term Depression | 0.307 | 0.0113 | brown | GUCY2C,PLCL2 |
| Agrin Interactions at Neuromuscular Junction | 0.305 | 0.0137 | brown | ARHGEF7 |
| MSP-RON Signaling Pathway | 0.301 | 0.0135 | brown | PIK3CA |
| Toll-like Receptor Signaling | 0.301 | 0.0135 | brown | IRAK2 |
| Role of NFAT in Regulation of the Immune Response | 0.298 | 0.011 | brown | PIK3CA,NFATC4 |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation | 0.295 | 0.011 | brown | IGFBP4,TGFB2 |
| ErbB2-ErbB3 Signaling | 0.292 | 0.0132 | brown | PIK3CA |
| Apelin Adipocyte Signaling Pathway | 0.292 | 0.0132 | brown | PRKACB |
| VDR/RXR Activation | 0.289 | 0.013 | brown | TGFB2 |
| Myc Mediated Apoptosis Signaling | 0.289 | 0.013 | brown | PIK3CA |
| Role of PI3K/AKT Signaling in the Pathogenesis of Influenza | 0.289 | 0.013 | brown | PIK3CA |
| Altered T Cell and B Cell Signaling in Rheumatoid Arthritis | 0.285 | 0.0128 | brown | IL15 |
| ErbB4 Signaling | 0.285 | 0.0128 | brown | PIK3CA |
| CD40 Signaling | 0.277 | 0.0125 | brown | PIK3CA |
| Cyclins and Cell Cycle Regulation | 0.277 | 0.0125 | brown | TGFB2 |
| IL-17A Signaling in Airway Cells | 0.277 | 0.0125 | brown | PIK3CA |
| GM-CSF Signaling | 0.277 | 0.0125 | brown | PIK3CA |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 0.276 | 0.0105 | brown | PIK3CA,TGFB2 |
| Calcium Signaling | 0.264 | 0.0103 | brown | PRKACB,NFATC4 |
| Estrogen-Dependent Breast Cancer Signaling | 0.264 | 0.0119 | brown | PIK3CA |
| GDNF Family Ligand-Receptor Interactions | 0.264 | 0.0119 | brown | PIK3CA |
| Neurotrophin/TRK Signaling | 0.264 | 0.0119 | brown | PIK3CA |
| Angiopoietin Signaling | 0.26 | 0.0118 | brown | PIK3CA |
| Non-Small Cell Lung Cancer Signaling | 0.26 | 0.0118 | brown | PIK3CA |
| Crosstalk between Dendritic Cells and Natural Killer Cells | 0.26 | 0.0118 | brown | IL15 |
| NRF2-mediated Oxidative Stress Response | 0.26 | 0.0102 | brown | PIK3CA,FMO1 |
| Growth Hormone Signaling | 0.256 | 0.0116 | brown | PIK3CA |
| FcγRIIB Signaling in B Lymphocytes | 0.253 | 0.0115 | brown | PIK3CA |
| Renal Cell Carcinoma Signaling | 0.253 | 0.0115 | brown | PIK3CA |
| Small Cell Lung Cancer Signaling | 0.253 | 0.0115 | brown | PIK3CA |
| Osteoarthritis Pathway | 0.253 | 0.01 | brown | CTNNA1,BMPR2 |
| Erythropoietin Signaling | 0.25 | 0.0114 | brown | PIK3CA |
| FLT3 Signaling in Hematopoietic Progenitor Cells | 0.25 | 0.0114 | brown | PIK3CA |
| α-Adrenergic Signaling | 0.244 | 0.0111 | brown | PRKACB |
| IL-3 Signaling | 0.244 | 0.0111 | brown | PIK3CA |
| Prolactin Signaling | 0.241 | 0.011 | brown | PIK3CA |
| JAK/Stat Signaling | 0.241 | 0.011 | brown | PIK3CA |
| FGF Signaling | 0.238 | 0.0109 | brown | PIK3CA |
| IL-17 Signaling | 0.235 | 0.0108 | brown | PIK3CA |
| GABA Receptor Signaling | 0.235 | 0.0108 | brown | GPHN |
| VEGF Family Ligand-Receptor Interactions | 0.232 | 0.0106 | brown | PIK3CA |
| LPS-stimulated MAPK Signaling | 0.229 | 0.0105 | brown | PIK3CA |
| NF-κB Activation by Viruses | 0.229 | 0.0105 | brown | PIK3CA |
| PEDF Signaling | 0.229 | 0.0105 | brown | PIK3CA |
| CTLA4 Signaling in Cytotoxic T Lymphocytes | 0.226 | 0.0104 | brown | PIK3CA |
| ATM Signaling | 0.226 | 0.0104 | brown | GADD45B |
| HER-2 Signaling in Breast Cancer | 0.226 | 0.0104 | brown | PIK3CA |
| Oxidative Phosphorylation | 0.221 | 0.0102 | brown | SDHA |
| PDGF Signaling | 0.221 | 0.0102 | brown | PIK3CA |
| Ceramide Signaling | 0.215 | 0.01 | brown | PIK3CA |
| TR/RXR Activation | 0.215 | 0.01 | brown | PIK3CA |
| Prostate Cancer Signaling | 0.213 | 0.0099 | brown | PIK3CA |
| RANK Signaling in Osteoclasts | 0.21 | 0.0098 | brown | PIK3CA |
| Antioxidant Action of Vitamin C | 0.21 | 0.0098 | brown | PLCL2 |
| Cholecystokinin/Gastrin-mediated Signaling | 0.203 | 0.00952 | brown | RHOB |
| ErbB Signaling | 0.203 | 0.00952 | brown | PIK3CA |
| SAPK/JNK Signaling | 0.198 | 0.00935 | brown | PIK3CA |
| Natural Killer Cell Signaling | 0 | 0.008 | brown | PIK3CA |
| Amyotrophic Lateral Sclerosis Signaling | 0 | 0.00893 | brown | PIK3CA |
| Fc Epsilon RI Signaling | 0 | 0.008 | brown | PIK3CA |
| Huntington's Disease Signaling | 0 | 0.0081 | brown | SDHA,PIK3CA |
| LPS/IL-1 Mediated Inhibition of RXR Function | 0 | 0.00485 | brown | FMO1 |
| Acute Phase Response Signaling | 0 | 0.00578 | brown | PIK3CA |
| Clathrin-mediated Endocytosis Signaling | 0 | 0.00483 | brown | PIK3CA |
| CCR3 Signaling in Eosinophils | 0 | 0.00763 | brown | PIK3CA |
| Virus Entry via Endocytic Pathways | 0 | 0.00847 | brown | PIK3CA |
| HIF1α Signaling | 0 | 0.00806 | brown | PIK3CA |
| GNRH Signaling | 0 | 0.00599 | brown | PRKACB |
| Androgen Signaling | 0 | 0.00741 | brown | PRKACB |
| Glioma Signaling | 0 | 0.00826 | brown | PIK3CA |
| Type II Diabetes Mellitus Signaling | 0 | 0.00662 | brown | PIK3CA |
| Gα12/13 Signaling | 0 | 0.00709 | brown | PIK3CA |
| G Beta Gamma Signaling | 0 | 0.0084 | brown | PRKACB |
| EIF2 Signaling | 0 | 0.00465 | brown | PIK3CA |
| Regulation of eIF4 and p70S6K Signaling | 0 | 0.00633 | brown | PIK3CA |
| Role of Tissue Factor in Cancer | 0 | 0.00781 | brown | PIK3CA |
| NGF Signaling | 0 | 0.00813 | brown | PIK3CA |
| Agranulocyte Adhesion and Diapedesis | 0 | 0.00585 | brown | JAM3 |
| Granulocyte Adhesion and Diapedesis | 0 | 0.00621 | brown | JAM3 |
| PI3K/AKT Signaling | 0 | 0.00787 | brown | PIK3CA |
| cAMP-mediated signaling | 0 | 0.00909 | brown | PRKACB,CNR1 |
| VEGF Signaling | 0 | 0.00926 | brown | PIK3CA |
| IL-6 Signaling | 0 | 0.00735 | brown | PIK3CA |
| GP6 Signaling Pathway | 0 | 0.00758 | brown | PIK3CA |
| Sirtuin Signaling Pathway | 0 | 0.00733 | brown | SDHA,GADD45B |
| Opioid Signaling Pathway | 0 | 0.00418 | brown | PRKACB |
| Apelin Endothelial Signaling Pathway | 0 | 0.00806 | brown | PIK3CA |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 4.63 | 0.0761 | blue | FYN,ARPC2,HCK,RAB11A,PLCG1,PRKD3,ACTG1 |
| Tec Kinase Signaling | 3.06 | 0.0424 | blue | FYN,HCK,PLCG1,GNG3,PRKD3,ACTG1,TNFRSF10A |
| Calcium-induced T Lymphocyte Apoptosis | 2.78 | 0.0727 | blue | HLA-DOA,CHP1,PLCG1,PRKD3 |
| Protein Kinase A Signaling | 2.54 | 0.0263 | blue | AKAP2,AKAP13,CHP1,PPP1R14A,PLCG1,UBASH3B,LEF1,GNG3,PRKD3,TTN |
| Clathrin-mediated Endocytosis Signaling | 2.5 | 0.0338 | blue | LYZ,ARPC2,CHP1,AAK1,RAB11A,HIP1,ACTG1 |
| Phospholipase C Signaling | 2.29 | 0.031 | blue | FYN,CHP1,PPP1R14A,PLCG1,GNG3,FCGR2B,PRKD3 |
| CD28 Signaling in T Helper Cells | 2.23 | 0.0403 | blue | FYN,HLA-DOA,ARPC2,CHP1,PLCG1 |
| Fc Epsilon RI Signaling | 2.21 | 0.04 | blue | FYN,PLCG1,MAP2K3,OCRL,PRKD3 |
| Role of NFAT in Regulation of the Immune Response | 2.17 | 0.0331 | blue | FYN,HLA-DOA,CHP1,PLCG1,GNG3,FCGR2B |
| nNOS Signaling in Neurons | 2.05 | 0.0652 | blue | CHP1,CAPN7,PRKD3 |
| Glutamine Biosynthesis I | 2.03 | 1 | blue | GLUL |
| Prolactin Signaling | 2 | 0.044 | blue | FYN,PLCG1,SOCS5,PRKD3 |
| HER-2 Signaling in Breast Cancer | 1.91 | 0.0417 | blue | CDK6,PLCG1,MAP3K5,PRKD3 |
| Integrin Signaling | 1.84 | 0.0282 | blue | FYN,ARPC2,PLCG1,CAPN7,ACTG1,TTN |
| Type I Diabetes Mellitus Signaling | 1.83 | 0.0392 | blue | HLA-DOA,MAP2K3,MAP3K5,SOCS5 |
| PKCθ Signaling in T Lymphocytes | 1.81 | 0.0318 | blue | FYN,HLA-DOA,CHP1,PLCG1,MAP3K5 |
| Dopamine-DARPP32 Feedback in cAMP Signaling | 1.79 | 0.0314 | blue | CHP1,PLCG1,PPP1R14A,PAWR,PRKD3 |
| FAK Signaling | 1.77 | 0.0377 | blue | FYN,PLCG1,CAPN7,ACTG1 |
| Actin Cytoskeleton Signaling | 1.74 | 0.0268 | blue | ABI2,IQGAP2,ARPC2,LIMK2,ACTG1,TTN |
| eNOS Signaling | 1.72 | 0.0301 | blue | AQP3,HSP90AB1,PLCG1,ESR2,PRKD3 |
| Pyridoxal 5'-phosphate Salvage Pathway | 1.67 | 0.0469 | blue | CDK6,MAP2K3,LIMK2 |
| T Cell Receptor Signaling | 1.67 | 0.0351 | blue | FYN,PAG1,RASGRP1,PLCG1 |
| RhoGDI Signaling | 1.64 | 0.0287 | blue | ARPC2,LIMK2,GNG3,ESR2,ACTG1 |
| Ephrin Receptor Signaling | 1.63 | 0.0286 | blue | FYN,ARPC2,LIMK2,EPHA4,GNG3 |
| Virus Entry via Endocytic Pathways | 1.62 | 0.0339 | blue | FYN,PLCG1,ACTG1,PRKD3 |
| RhoA Signaling | 1.62 | 0.0339 | blue | ARPC2,LIMK2,ACTG1,TTN |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 1.61 | 0.0227 | blue | IL16,TRAF3IP2,CHP1,PLCG1,LEF1,MAP2K3,PRKD3 |
| Glioma Signaling | 1.58 | 0.0331 | blue | CDK6,CDKN2C,PLCG1,PRKD3 |
| Cdc42 Signaling | 1.58 | 0.0331 | blue | IQGAP2,HLA-DOA,ARPC2,LIMK2 |
| Melatonin Signaling | 1.57 | 0.0429 | blue | PLCG1,MAP2K3,PRKD3 |
| Synaptic Long Term Potentiation | 1.56 | 0.0325 | blue | CHP1,PLCG1,PPP1R14A,PRKD3 |
| Rac Signaling | 1.56 | 0.0325 | blue | ABI2,IQGAP2,ARPC2,LIMK2 |
| Tyrosine Biosynthesis IV | 1.56 | 0.333 | blue | PCBD2 |
| Molecular Mechanisms of Cancer | 1.56 | 0.0207 | blue | FYN,RASGRP1,CDK6,CDKN2C,LEF1,MAP2K3,MAP3K5,PRKD3 |
| Natural Killer Cell Signaling | 1.54 | 0.032 | blue | FYN,PLCG1,OCRL,PRKD3 |
| Hypoxia Signaling in the Cardiovascular System | 1.53 | 0.0417 | blue | UBE2J1,UBE2H,HSP90AB1 |
| RAR Activation | 1.52 | 0.0267 | blue | MAP3K5,REL,PRKD3,ZBTB16,SMARCA4 |
| B Cell Receptor Signaling | 1.52 | 0.0267 | blue | PAG1,MAP2K3,MAP3K5,FCGR2B,OCRL |
| fMLP Signaling in Neutrophils | 1.51 | 0.0312 | blue | ARPC2,CHP1,GNG3,PRKD3 |
| G Protein Signaling Mediated by Tubby | 1.5 | 0.0667 | blue | PLCG1,GNG3 |
| Axonal Guidance Signaling | 1.48 | 0.0189 | blue | FYN,ADAM28,ARPC2,CHP1,PLCG1,LIMK2,EPHA4,GNG3,PRKD3 |
| PI3K Signaling in B Lymphocytes | 1.47 | 0.0305 | blue | FYN,CHP1,PLCG1,FCGR2B |
| Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 1.45 | 0.0256 | blue | LYZ,PLCG1,PPP1R14A,MAP3K5,PRKD3 |
| Phenylalanine Degradation I (Aerobic) | 1.44 | 0.25 | blue | PCBD2 |
| Aryl Hydrocarbon Receptor Signaling | 1.43 | 0.0296 | blue | HSP90AB1,CDK6,ESR2,SMARCA4 |
| Cardiac β-adrenergic Signaling | 1.39 | 0.0288 | blue | AKAP2,AKAP13,PPP1R14A,GNG3 |
| Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes | 1.38 | 0.0361 | blue | FYN,CHP1,PLCG1 |
| Xenobiotic Metabolism Signaling | 1.37 | 0.0219 | blue | ABCB1,HSP90AB1,UST,MAP2K3,MAP3K5,PRKD3 |
| Leukocyte Extravasation Signaling | 1.37 | 0.0243 | blue | TIMP3,RASGRP1,PLCG1,ACTG1,PRKD3 |
| HIPPO signaling | 1.37 | 0.0357 | blue | SAV1,PPP1R14A,PATJ |
| Neurotrophin/TRK Signaling | 1.37 | 0.0357 | blue | PLCG1,MAP2K3,MAP3K5 |
| Non-Small Cell Lung Cancer Signaling | 1.35 | 0.0353 | blue | FHIT,CDK6,PLCG1 |
| Epithelial Adherens Junction Signaling | 1.35 | 0.0278 | blue | NOTCH4,ARPC2,LEF1,ACTG1 |
| Growth Hormone Signaling | 1.34 | 0.0349 | blue | PLCG1,PRKD3,SOCS5 |
| CCR5 Signaling in Macrophages | 1.32 | 0.0341 | blue | PLCG1,GNG3,PRKD3 |
| α-Adrenergic Signaling | 1.29 | 0.0333 | blue | PLCG1,GNG3,PRKD3 |
| Neuregulin Signaling | 1.28 | 0.033 | blue | HSP90AB1,PLCG1,PRKD3 |
| FGF Signaling | 1.27 | 0.0326 | blue | PLCG1,MAP2K3,MAP3K5 |
| Death Receptor Signaling | 1.27 | 0.0326 | blue | MAP3K5,ACTG1,TNFRSF10A |
| Role of NFAT in Cardiac Hypertrophy | 1.26 | 0.0226 | blue | CHP1,PLCG1,MAP2K3,GNG3,PRKD3 |
| D-myo-inositol-5-phosphate Metabolism | 1.26 | 0.026 | blue | PLCG1,PPP1R14A,PAWR,OCRL |
| Mechanisms of Viral Exit from Host Cells | 1.26 | 0.0488 | blue | ACTG1,PRKD3 |
| Salvage Pathways of Pyrimidine Ribonucleotides | 1.25 | 0.0319 | blue | CDK6,MAP2K3,LIMK2 |
| LPS-stimulated MAPK Signaling | 1.24 | 0.0316 | blue | MAP2K3,MAP3K5,PRKD3 |
| Apoptosis Signaling | 1.24 | 0.0316 | blue | PLCG1,CAPN7,MAP3K5 |
| Superpathway of Inositol Phosphate Compounds | 1.21 | 0.0219 | blue | FYN,PLCG1,PPP1R14A,PAWR,OCRL |
| Gαq Signaling | 1.21 | 0.025 | blue | CHP1,PLCG1,GNG3,PRKD3 |
| Phosphatidylcholine Biosynthesis I | 1.2 | 0.143 | blue | CHPT1 |
| Cardiac Hypertrophy Signaling | 1.16 | 0.0211 | blue | CHP1,PLCG1,MAP2K3,MAP3K5,GNG3 |
| Nur77 Signaling in T Lymphocytes | 1.14 | 0.0417 | blue | HLA-DOA,CHP1 |
| Cholecystokinin/Gastrin-mediated Signaling | 1.13 | 0.0286 | blue | MAP2K3,EPHA4,PRKD3 |
| ErbB Signaling | 1.13 | 0.0286 | blue | PLCG1,MAP2K3,PRKD3 |
| Germ Cell-Sertoli Cell Junction Signaling | 1.11 | 0.023 | blue | MAP2K3,LIMK2,MAP3K5,ACTG1 |
| GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells | 1.1 | 0.0278 | blue | PLCG1,GNG3,PRKD3 |
| CD27 Signaling in Lymphocytes | 1.08 | 0.0385 | blue | MAP2K3,MAP3K5 |
| Semaphorin Signaling in Neurons | 1.08 | 0.0385 | blue | FYN,LIMK2 |
| iCOS-iCOSL Signaling in T Helper Cells | 1.04 | 0.0261 | blue | HLA-DOA,CHP1,PLCG1 |
| Cell Cycle Control of Chromosomal Replication | 1.02 | 0.0357 | blue | TOP2A,CDK6 |
| G Beta Gamma Signaling | 1.01 | 0.0252 | blue | PLCG1,GNG3,PRKD3 |
| HGF Signaling | 1 | 0.025 | blue | PLCG1,MAP3K5,PRKD3 |
| Phagosome Formation | 0.991 | 0.0248 | blue | PLCG1,FCGR2B,PRKD3 |
| 3-phosphoinositide Biosynthesis | 0.975 | 0.0206 | blue | FYN,PPP1R14A,PAWR,OCRL |
| Guanosine Nucleotides Degradation III | 0.975 | 0.0833 | blue | NT5E |
| Regulation of Cellular Mechanics by Calpain Protease | 0.971 | 0.0333 | blue | CDK6,CAPN7 |
| NRF2-mediated Oxidative Stress Response | 0.955 | 0.0203 | blue | MAP2K3,MAP3K5,ACTG1,PRKD3 |
| Ephrin A Signaling | 0.951 | 0.0323 | blue | FYN,EPHA4 |
| Choline Biosynthesis III | 0.943 | 0.0769 | blue | CHPT1 |
| Urate Biosynthesis/Inosine 5'-phosphate Degradation | 0.943 | 0.0769 | blue | NT5E |
| PI3K/AKT Signaling | 0.943 | 0.0236 | blue | HSP90AB1,MAP3K5,OCRL |
| Osteoarthritis Pathway | 0.939 | 0.02 | blue | SIK3,TIMP3,LEF1,OCRL |
| Role of Tissue Factor in Cancer | 0.936 | 0.0234 | blue | FYN,HCK,LIMK2 |
| mTOR Signaling | 0.932 | 0.0199 | blue | RPS20,FKBP1A,PRR5L,PRKD3 |
| Remodeling of Epithelial Adherens Junctions | 0.924 | 0.0312 | blue | ARPC2,ACTG1 |
| CCR3 Signaling in Eosinophils | 0.914 | 0.0229 | blue | LIMK2,GNG3,PRKD3 |
| GP6 Signaling Pathway | 0.907 | 0.0227 | blue | FYN,COL9A1,PRKD3 |
| Cell Cycle: G1/S Checkpoint Regulation | 0.903 | 0.0303 | blue | CDK6,CDKN2C |
| Breast Cancer Regulation by Stathmin1 | 0.889 | 0.0191 | blue | PPP1R14A,LIMK2,GNG3,PRKD3 |
| Adenosine Nucleotides Degradation II | 0.886 | 0.0667 | blue | NT5E |
| 14-3-3-mediated Signaling | 0.879 | 0.0221 | blue | PLCG1,MAP3K5,PRKD3 |
| D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis | 0.879 | 0.0221 | blue | PPP1R14A,PAWR,OCRL |
| D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis | 0.879 | 0.0221 | blue | PPP1R14A,PAWR,OCRL |
| IL-10 Signaling | 0.873 | 0.029 | blue | MAP2K3,FCGR2B |
| TREM1 Signaling | 0.863 | 0.0286 | blue | PLCG1,FCGR2B |
| P2Y Purigenic Receptor Signaling Pathway | 0.86 | 0.0216 | blue | PLCG1,GNG3,PRKD3 |
| Caveolar-mediated Endocytosis Signaling | 0.854 | 0.0282 | blue | FYN,ACTG1 |
| Thrombopoietin Signaling | 0.845 | 0.0278 | blue | PLCG1,PRKD3 |
| D-myo-inositol (1,4,5)-trisphosphate Degradation | 0.836 | 0.0588 | blue | OCRL |
| Insulin Receptor Signaling | 0.833 | 0.021 | blue | FYN,PPP1R14A,OCRL |
| Role of MAPK Signaling in the Pathogenesis of Influenza | 0.824 | 0.027 | blue | MAP2K3,MAP3K5 |
| Chemokine Signaling | 0.824 | 0.027 | blue | PLCG1,LIMK2 |
| IL-12 Signaling and Production in Macrophages | 0.815 | 0.0205 | blue | LYZ,REL,PRKD3 |
| 1D-myo-inositol Hexakisphosphate Biosynthesis II (Mammalian) | 0.812 | 0.0556 | blue | OCRL |
| Purine Nucleotides Degradation II (Aerobic) | 0.812 | 0.0556 | blue | NT5E |
| D-myo-inositol (1,3,4)-trisphosphate Biosynthesis | 0.812 | 0.0556 | blue | OCRL |
| 3-phosphoinositide Degradation | 0.79 | 0.02 | blue | PPP1R14A,PAWR,OCRL |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 0.788 | 0.0175 | blue | CHP1,LEF1,MAP2K3,MAP3K5 |
| ErbB4 Signaling | 0.788 | 0.0256 | blue | PLCG1,PRKD3 |
| Type II Diabetes Mellitus Signaling | 0.783 | 0.0199 | blue | MAP3K5,PRKD3,SOCS5 |
| Cyclins and Cell Cycle Regulation | 0.772 | 0.025 | blue | CDK6,CDKN2C |
| NAD Salvage Pathway II | 0.752 | 0.0476 | blue | NT5E |
| Endoplasmic Reticulum Stress Pathway | 0.752 | 0.0476 | blue | MAP3K5 |
| Opioid Signaling Pathway | 0.742 | 0.0167 | blue | FYN,HCK,MAP2K3,PRKD3 |
| GDNF Family Ligand-Receptor Interactions | 0.738 | 0.0238 | blue | PLCG1,DOK3 |
| Small Cell Lung Cancer Signaling | 0.714 | 0.023 | blue | FHIT,CDK6 |
| Superpathway of D-myo-inositol (1,4,5)-trisphosphate Metabolism | 0.714 | 0.0435 | blue | OCRL |
| Huntington's Disease Signaling | 0.708 | 0.0162 | blue | HIP1,GNG3,CAPN7,PRKD3 |
| Erythropoietin Signaling | 0.708 | 0.0227 | blue | PLCG1,PRKD3 |
| Factors Promoting Cardiogenesis in Vertebrates | 0.701 | 0.0225 | blue | LEF1,PRKD3 |
| Macropinocytosis Signaling | 0.701 | 0.0225 | blue | PLCG1,PRKD3 |
| Signaling by Rho Family GTPases | 0.699 | 0.0161 | blue | ARPC2,LIMK2,GNG3,ACTG1 |
| GNRH Signaling | 0.695 | 0.018 | blue | MAP2K3,MAP3K5,PRKD3 |
| IL-3 Signaling | 0.693 | 0.0222 | blue | CHP1,PRKD3 |
| Glioblastoma Multiforme Signaling | 0.69 | 0.0179 | blue | CDK6,PLCG1,LEF1 |
| Aldosterone Signaling in Epithelial Cells | 0.686 | 0.0178 | blue | HSP90AB1,PLCG1,PRKD3 |
| IL-1 Signaling | 0.686 | 0.022 | blue | MAP2K3,GNG3 |
| CDP-diacylglycerol Biosynthesis I | 0.682 | 0.04 | blue | LPCAT2 |
| IL-4 Signaling | 0.68 | 0.0217 | blue | HLA-DOA,OCRL |
| IL-17 Signaling | 0.672 | 0.0215 | blue | TRAF3IP2,MAP2K3 |
| Estrogen-mediated S-phase Entry | 0.668 | 0.0385 | blue | ESR2 |
| Acute Phase Response Signaling | 0.666 | 0.0173 | blue | MAP2K3,MAP3K5,SOCS5 |
| Reelin Signaling in Neurons | 0.666 | 0.0213 | blue | FYN,HCK |
| VEGF Family Ligand-Receptor Interactions | 0.666 | 0.0213 | blue | PLCG1,PRKD3 |
| PPARα/RXRα Activation | 0.662 | 0.0172 | blue | HSP90AB1,PLCG1,MAP2K3 |
| Sertoli Cell-Sertoli Cell Junction Signaling | 0.662 | 0.0172 | blue | MAP2K3,MAP3K5,ACTG1 |
| B Cell Development | 0.654 | 0.037 | blue | HLA-DOA |
| D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis | 0.654 | 0.037 | blue | PLCG1 |
| Phosphatidylglycerol Biosynthesis II (Non-plastidic) | 0.654 | 0.037 | blue | LPCAT2 |
| CTLA4 Signaling in Cytotoxic T Lymphocytes | 0.652 | 0.0208 | blue | FYN,PLCG1 |
| Sumoylation Pathway | 0.652 | 0.0208 | blue | MYB,MAP3K5 |
| Protein Ubiquitination Pathway | 0.648 | 0.0153 | blue | UBE2J1,HSP90AB1,UBE2H,PSMD13 |
| Acute Myeloid Leukemia Signaling | 0.646 | 0.0206 | blue | MAP2K3,LEF1 |
| Dendritic Cell Maturation | 0.642 | 0.0169 | blue | HLA-DOA,PLCG1,FCGR2B |
| PDGF Signaling | 0.638 | 0.0204 | blue | PLCG1,OCRL |
| Thyroid Hormone Metabolism II (via Conjugation and/or Degradation) | 0.625 | 0.0345 | blue | LARGE1 |
| Prostate Cancer Signaling | 0.62 | 0.0198 | blue | HSP90AB1,LEF1 |
| DNA Methylation and Transcriptional Repression Signaling | 0.613 | 0.0333 | blue | MBD2 |
| RANK Signaling in Osteoclasts | 0.613 | 0.0196 | blue | CHP1,MAP3K5 |
| Gαs Signaling | 0.602 | 0.0192 | blue | HCK,GNG3 |
| 4-1BB Signaling in T Lymphocytes | 0.588 | 0.0312 | blue | MAP3K5 |
| Inhibition of Angiogenesis by TSP1 | 0.588 | 0.0312 | blue | FYN |
| Role of JAK2 in Hormone-like Cytokine Signaling | 0.588 | 0.0312 | blue | SOCS5 |
| Regulation of the Epithelial-Mesenchymal Transition Pathway | 0.588 | 0.0158 | blue | NOTCH4,MAP2K3,LEF1 |
| VEGF Signaling | 0.578 | 0.0185 | blue | PLCG1,ACTG1 |
| ILK Signaling | 0.577 | 0.0155 | blue | LEF1,ACTG1,NACA |
| Nitric Oxide Signaling in the Cardiovascular System | 0.567 | 0.0182 | blue | HSP90AB1,PRKD3 |
| Antigen Presentation Pathway | 0.567 | 0.0294 | blue | HLA-DOA |
| Amyotrophic Lateral Sclerosis Signaling | 0.556 | 0.0179 | blue | GLUL,CAPN7 |
| Autoimmune Thyroid Disease Signaling | 0.556 | 0.0286 | blue | HLA-DOA |
| IL-17A Signaling in Fibroblasts | 0.556 | 0.0286 | blue | TRAF3IP2 |
| p38 MAPK Signaling | 0.551 | 0.0177 | blue | MAP2K3,MAP3K5 |
| Gap Junction Signaling | 0.548 | 0.015 | blue | PLCG1,ACTG1,PRKD3 |
| ERK/MAPK Signaling | 0.545 | 0.0149 | blue | FYN,PLCG1,PPP1R14A |
| Apelin Cardiomyocyte Signaling Pathway | 0.545 | 0.0175 | blue | PLCG1,PRKD3 |
| Adrenomedullin signaling pathway | 0.541 | 0.0149 | blue | PLCG1,MAP2K3,TTN |
| IL-8 Signaling | 0.538 | 0.0148 | blue | LIMK2,GNG3,PRKD3 |
| Notch Signaling | 0.536 | 0.027 | blue | NOTCH4 |
| Neuropathic Pain Signaling In Dorsal Horn Neurons | 0.535 | 0.0172 | blue | PLCG1,PRKD3 |
| Sperm Motility | 0.535 | 0.0172 | blue | PLCG1,PRKD3 |
| Allograft Rejection Signaling | 0.526 | 0.0263 | blue | HLA-DOA |
| Inhibition of Matrix Metalloproteases | 0.526 | 0.0263 | blue | TIMP3 |
| Neuroinflammation Signaling Pathway | 0.526 | 0.0134 | blue | HLA-DOA,CHP1,PLCG1,GLUL |
| Thrombin Signaling | 0.519 | 0.0144 | blue | PLCG1,GNG3,PRKD3 |
| Graft-versus-Host Disease Signaling | 0.517 | 0.0256 | blue | HLA-DOA |
| Oncostatin M Signaling | 0.507 | 0.025 | blue | TIMP3 |
| nNOS Signaling in Skeletal Muscle Cells | 0.507 | 0.025 | blue | SNTB1 |
| Th1 Pathway | 0.506 | 0.0164 | blue | HLA-DOA,NOTCH4 |
| NGF Signaling | 0.502 | 0.0163 | blue | PLCG1,MAP3K5 |
| Role of PKR in Interferon Induction and Antiviral Response | 0.499 | 0.0244 | blue | MAP2K3 |
| Role of IL-17F in Allergic Inflammatory Airway Diseases | 0.499 | 0.0244 | blue | TRAF3IP2 |
| Triacylglycerol Degradation | 0.499 | 0.0244 | blue | ABHD6 |
| Dermatan Sulfate Biosynthesis (Late Stages) | 0.499 | 0.0244 | blue | UST |
| EIF2 Signaling | 0.493 | 0.014 | blue | RPL13,RPS20,RPL3 |
| Cellular Effects of Sildenafil (Viagra) | 0.487 | 0.0159 | blue | PLCG1,ACTG1 |
| CREB Signaling in Neurons | 0.487 | 0.0138 | blue | PLCG1,GNG3,PRKD3 |
| AMPK Signaling | 0.484 | 0.0138 | blue | RAB11A,MAP2K3,SMARCA4 |
| Nicotine Degradation III | 0.481 | 0.0233 | blue | LARGE1 |
| Triacylglycerol Biosynthesis | 0.481 | 0.0233 | blue | LPCAT2 |
| Adipogenesis pathway | 0.479 | 0.0156 | blue | TXNIP,EZH2 |
| Renin-Angiotensin Signaling | 0.474 | 0.0155 | blue | PLCG1,PRKD3 |
| Chondroitin Sulfate Biosynthesis (Late Stages) | 0.474 | 0.0227 | blue | UST |
| Thyroid Cancer Signaling | 0.466 | 0.0222 | blue | LEF1 |
| Cancer Drug Resistance By Drug Efflux | 0.458 | 0.0217 | blue | ABCB1 |
| Estrogen Receptor Signaling | 0.457 | 0.015 | blue | ESR2,SMARCA4 |
| OX40 Signaling Pathway | 0.451 | 0.0213 | blue | HLA-DOA |
| Androgen Signaling | 0.449 | 0.0148 | blue | GNG3,PRKD3 |
| IL-6 Signaling | 0.445 | 0.0147 | blue | ABCB1,MAP2K3 |
| UVC-Induced MAPK Signaling | 0.444 | 0.0208 | blue | PRKD3 |
| Corticotropin Releasing Hormone Signaling | 0.44 | 0.0146 | blue | PLCG1,PRKD3 |
| Nicotine Degradation II | 0.437 | 0.0204 | blue | LARGE1 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 0.437 | 0.0204 | blue | TOP2A |
| p70S6K Signaling | 0.433 | 0.0144 | blue | PLCG1,PRKD3 |
| Th2 Pathway | 0.433 | 0.0144 | blue | HLA-DOA,NOTCH4 |
| Melatonin Degradation I | 0.429 | 0.02 | blue | LARGE1 |
| Amyloid Processing | 0.429 | 0.02 | blue | CAPN7 |
| Chondroitin Sulfate Biosynthesis | 0.416 | 0.0192 | blue | UST |
| Dermatan Sulfate Biosynthesis | 0.403 | 0.0185 | blue | UST |
| Hereditary Breast Cancer Signaling | 0.399 | 0.0135 | blue | CDK6,SMARCA4 |
| Serotonin Degradation | 0.397 | 0.0182 | blue | LARGE1 |
| Superpathway of Melatonin Degradation | 0.397 | 0.0182 | blue | LARGE1 |
| Unfolded protein response | 0.397 | 0.0182 | blue | MAP3K5 |
| Glutamate Receptor Signaling | 0.391 | 0.0179 | blue | GLUL |
| Role of CHK Proteins in Cell Cycle Checkpoint Control | 0.385 | 0.0175 | blue | TLK1 |
| Phospholipases | 0.385 | 0.0175 | blue | PLCG1 |
| Heparan Sulfate Biosynthesis (Late Stages) | 0.38 | 0.0172 | blue | UST |
| Retinoic acid Mediated Apoptosis Signaling | 0.374 | 0.0169 | blue | TNFRSF10A |
| Endocannabinoid Cancer Inhibition Pathway | 0.372 | 0.0128 | blue | MAP2K3,LEF1 |
| Induction of Apoptosis by HIV1 | 0.369 | 0.0167 | blue | MAP3K5 |
| Hepatic Cholestasis | 0.366 | 0.0127 | blue | ABCB1,PRKD3 |
| Wnt/Ca+ pathway | 0.364 | 0.0164 | blue | PLCG1 |
| PXR/RXR Activation | 0.358 | 0.0161 | blue | ABCB1 |
| Actin Nucleation by ARP-WASP Complex | 0.358 | 0.0161 | blue | ARPC2 |
| Mitotic Roles of Polo-Like Kinase | 0.353 | 0.0159 | blue | HSP90AB1 |
| T Helper Cell Differentiation | 0.348 | 0.0156 | blue | HLA-DOA |
| Tight Junction Signaling | 0.344 | 0.0121 | blue | PATJ,ACTG1 |
| Netrin Signaling | 0.343 | 0.0154 | blue | CHP1 |
| Heparan Sulfate Biosynthesis | 0.343 | 0.0154 | blue | UST |
| Wnt/β-catenin Signaling | 0.338 | 0.012 | blue | SOX4,LEF1 |
| UVB-Induced MAPK Signaling | 0.333 | 0.0149 | blue | PRKD3 |
| T Cell Exhaustion Signaling Pathway | 0.33 | 0.0118 | blue | HLA-DOA,PLCG1 |
| Basal Cell Carcinoma Signaling | 0.329 | 0.0147 | blue | LEF1 |
| CXCR4 Signaling | 0.327 | 0.0117 | blue | GNG3,PRKD3 |
| Th1 and Th2 Activation Pathway | 0.327 | 0.0117 | blue | HLA-DOA,NOTCH4 |
| Role of IL-17A in Arthritis | 0.32 | 0.0143 | blue | MAP2K3 |
| EGF Signaling | 0.32 | 0.0143 | blue | PLCG1 |
| Synaptic Long Term Depression | 0.311 | 0.0113 | blue | PLCG1,PRKD3 |
| Endometrial Cancer Signaling | 0.311 | 0.0139 | blue | LEF1 |
| Role of Wnt/GSK-3β Signaling in the Pathogenesis of Influenza | 0.311 | 0.0139 | blue | LEF1 |
| Ephrin B Signaling | 0.311 | 0.0139 | blue | GNG3 |
| GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell | 0.311 | 0.0139 | blue | PLCG1 |
| Agrin Interactions at Neuromuscular Junction | 0.307 | 0.0137 | blue | ACTG1 |
| MSP-RON Signaling Pathway | 0.303 | 0.0135 | blue | ACTG1 |
| Toll-like Receptor Signaling | 0.303 | 0.0135 | blue | MAP2K3 |
| Th17 Activation Pathway | 0.298 | 0.0133 | blue | HSP90AB1 |
| Dopamine Receptor Signaling | 0.295 | 0.0132 | blue | PPP1R14A |
| VDR/RXR Activation | 0.291 | 0.013 | blue | PRKD3 |
| Altered T Cell and B Cell Signaling in Rheumatoid Arthritis | 0.287 | 0.0128 | blue | HLA-DOA |
| Glioma Invasiveness Signaling | 0.287 | 0.0128 | blue | TIMP3 |
| Role of BRCA1 in DNA Damage Response | 0.279 | 0.0125 | blue | SMARCA4 |
| CD40 Signaling | 0.279 | 0.0125 | blue | MAP2K3 |
| IL-17A Signaling in Airway Cells | 0.279 | 0.0125 | blue | TRAF3IP2 |
| BMP signaling pathway | 0.279 | 0.0125 | blue | MAGED1 |
| GM-CSF Signaling | 0.279 | 0.0125 | blue | HCK |
| Endothelin-1 Signaling | 0.273 | 0.0104 | blue | PLCG1,PRKD3 |
| Regulation of Actin-based Motility by Rho | 0.265 | 0.0119 | blue | ARPC2 |
| IL-15 Signaling | 0.265 | 0.0119 | blue | PLCG1 |
| Antiproliferative Role of Somatostatin Receptor 2 | 0.265 | 0.0119 | blue | GNG3 |
| Crosstalk between Dendritic Cells and Natural Killer Cells | 0.262 | 0.0118 | blue | ACTG1 |
| Systemic Lupus Erythematosus Signaling | 0.26 | 0.0101 | blue | PLCG1,FCGR2B |
| FcγRIIB Signaling in B Lymphocytes | 0.255 | 0.0115 | blue | FCGR2B |
| Leptin Signaling in Obesity | 0.255 | 0.0115 | blue | PLCG1 |
| IL-7 Signaling Pathway | 0.252 | 0.0114 | blue | FYN |
| LPS/IL-1 Mediated Inhibition of RXR Function | 0.243 | 0.00971 | blue | ABCB1,UST |
| JAK/Stat Signaling | 0.243 | 0.011 | blue | SOCS5 |
| TGF-β Signaling | 0.237 | 0.0108 | blue | MAP2K3 |
| NF-κB Activation by Viruses | 0.231 | 0.0105 | blue | PRKD3 |
| ATM Signaling | 0.228 | 0.0104 | blue | TLK1 |
| PPAR Signaling | 0.223 | 0.0102 | blue | HSP90AB1 |
| NER Pathway | 0.223 | 0.0102 | blue | TOP2A |
| Antioxidant Action of Vitamin C | 0.212 | 0.0098 | blue | PLCG1 |
| CDK5 Signaling | 0.207 | 0.00962 | blue | PPP1R14A |
| Melanocyte Development and Pigmentation Signaling | 0.205 | 0.00952 | blue | PLCG1 |
| SAPK/JNK Signaling | 0.2 | 0.00935 | blue | MAP3K5 |
| PAK Signaling | 0.197 | 0.00926 | blue | LIMK2 |
| Glucocorticoid Receptor Signaling | 0 | 0.00888 | blue | HSP90AB1,CHP1,SMARCA4 |
| p53 Signaling | 0 | 0.00885 | blue | TNFRSF10A |
| LXR/RXR Activation | 0 | 0.00833 | blue | LYZ |
| Hepatic Fibrosis / Hepatic Stellate Cell Activation | 0 | 0.00549 | blue | COL9A1 |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 0 | 0.00758 | blue | PRKD3 |
| Relaxin Signaling | 0 | 0.00625 | blue | GNG3 |
| HMGB1 Signaling | 0 | 0.00719 | blue | MAP2K3 |
| Human Embryonic Stem Cell Pluripotency | 0 | 0.00709 | blue | LEF1 |
| Chronic Myeloid Leukemia Signaling | 0 | 0.00893 | blue | CDK6 |
| Gα12/13 Signaling | 0 | 0.00709 | blue | MAP3K5 |
| Colorectal Cancer Metastasis Signaling | 0 | 0.00803 | blue | LEF1,GNG3 |
| Sphingosine-1-phosphate Signaling | 0 | 0.00813 | blue | PLCG1 |
| Ovarian Cancer Signaling | 0 | 0.00671 | blue | LEF1 |
| Atherosclerosis Signaling | 0 | 0.0082 | blue | LYZ |
| Regulation of eIF4 and p70S6K Signaling | 0 | 0.00633 | blue | RPS20 |
| Paxillin Signaling | 0 | 0.00847 | blue | ACTG1 |
| Telomerase Signaling | 0 | 0.00862 | blue | HSP90AB1 |
| Mouse Embryonic Stem Cell Pluripotency | 0 | 0.00901 | blue | LEF1 |
| Gαi Signaling | 0 | 0.0084 | blue | GNG3 |
| Agranulocyte Adhesion and Diapedesis | 0 | 0.00585 | blue | ACTG1 |
| UVA-Induced MAPK Signaling | 0 | 0.00901 | blue | PLCG1 |
| STAT3 Pathway | 0 | 0.00758 | blue | SOCS5 |
| PTEN Signaling | 0 | 0.00813 | blue | OCRL |
| IGF-1 Signaling | 0 | 0.00885 | blue | SOCS5 |
| cAMP-mediated signaling | 0 | 0.00909 | blue | AKAP2,AKAP13 |
| G-Protein Coupled Receptor Signaling | 0 | 0.00719 | blue | FYN,RASGRP1 |
| Endocannabinoid Developing Neuron Pathway | 0 | 0.00781 | blue | MAP2K3 |
| Apelin Endothelial Signaling Pathway | 0 | 0.00806 | blue | PRKD3 |
| Calcium Signaling | 0 | 0.00513 | blue | CHP1 |