GO: Day 7 WGCNA MEyellow positive regulation of synapse assembly -T-helper 1 type immune response BMP signaling pathway small GTPase binding negative regulation of apoptotic process antimicrobial humoral response protein autophosphorylation SH3 domain binding I-kappaB kinase/NF-kappaB signaling protein ubiquitination atrial septum primum morphogenesis marginal zone B cell differentiation generation of catalytic spliceosome for second transesterification step DNA binding positive regulation of protein catabolic process cell morphogenesis involved in neuron differentiation X11-like protein binding BMP signaling pathway involved in heart development negative regulation of interleukin-6 production autophagy cell surface receptor signaling pathway RS domain binding T-helper 2 cell differentiation negative regulation of interleukin-8 biosynthetic process humoral immune response mediated by circulating immunoglobulin follicular dendritic cell differentiation beta-tubulin binding cell migration in utero embryonic development immune system process acetyltransferase activator activity activation of protein kinase activity mitral valve morphogenesis SREBP signaling pathway negative regulation of natural killer cell activation polysome binding response to angiotensin negative regulation of dephosphorylation actin cytoskeleton organization regulation of mitotic nuclear division aspartic endopeptidase activity, intramembrane cleaving positive regulation of filopodium assembly neurotransmitter receptor transport to postsynaptic membrane positive regulation of myoblast fusion phosphoserine residue binding germarium-derived oocyte fate determination regulation of synapse maturation positive regulation of transcription by RNA polymerase II regulation of lateral mesodermal cell fate specification transforming growth factor beta receptor activity, type I ER overload response positive regulation of transforming growth factor beta receptor signaling pathway positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity ubiquitin protein ligase activity positive regulation of interleukin–10 biosynthetic process negative regulation of inflammatory response microtubule organizing center organization SH2 domain binding intrinsic apoptotic signaling pathway in response to oxidative stress growth hormone receptor signaling pathway via JAK-STAT positive regulation of epithelial to mesenchymal transition involved in endocardial cushion formation positive regulation of determination of dorsal identity MRF binding positive regulation of alkaline phosphatase activity endocardial cushion cell fate commitment cardiac muscle cell fate commitment · regulation of DNA binding intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator -S100 protein binding vesicle-mediated transport in synapse negative regulation of tumor necrosis factor production pathway-restricted SMAD protein phosphorylation phosphotyrosine residue binding development of secondary female sexual characteristics regulation of RNA splicing macrophage chemotaxis transcription regulatory region sequence-specific DNA binding negative regulation of interleukin-12 production positive regulation of type I interferon production regulation of steroid metabolic process peptidyl-glutamate ADP-deribosylation protein serine/threonine kinase activity negative regulation of transcription, DNA-templated adherens junction assembly regulation of small GTPase mediated signal transduction positive regulation of catalytic activity ADP-ribosylglutamate hydrolase activity cellular response to organic cyclic compound positive regulation of peptidyl-tyrosine autophosphorylation protein K63-linked ubiquitination beta-N-acetylglucosaminidase activity innate immune response germinal center formation adenylate cyclase-activating G protein-coupled receptor signaling pathway phosphatidylinositol dephosphorylation protein domain specific binding microtubule cytoskeleton organization regulation of synapse organization regulation of cytokine production negative regulation of interleukin–2 production protein de–ADP–ribosylation phosphatidylinositol-3,4,5-trisphosphate binding neuron projection extension receptor signaling pathway via JAK-STAT
Golgi ribbon formation K63-linked polyubiquitin modification-dependent protein binding positive regulation of I-kappaB kinase/NF-kappaB signaling regulation of growth luteinization ubiquitin-protein transferase activity paraxial mesoderm development positive regulation of cardiac muscle cell proliferation positive regulation of MAP kinase activity mRNA processing structural constituent of postsynaptic actin cytoskeleton platelet-derived growth factor receptor signaling pathway proteasome—mediated ubiquitin—dependent protein catabolic process negative regulation of sodium ion transmembrane transporter activity satellite cell activation involved in skeletal muscle regeneration SMAD binding positive regulation of transcription by transcription factor localization myotube differentiation involved in skeletal muscle regeneration cell-cell signaling via exosome Rho guanyl-nucleotide exchange factor activity negative regulation of tumor necrosis factor biosynthetic process protein localization to cell cortex nucleologenesis regulation of epithelial cell differentiation transcription coactivator activity cell morphogenesis protein phosphorylation negative regulation of I-kappaB kinase/NF-kappaB signaling patched ligand maturation importin-alpha family protein binding regulation of establishment of cell polarity protein deubiquitination positive regulation of protein insertion into mitochondrial outer membrane protein tyrosine kinase activator activity negative regulation of chaperone-mediated protein folding negative regulation of erythrocyte differentiation thymidine biosynthetic process tolerance induction to lipopolysaccharide mRNA CDS binding negative regulation of toll-like receptor 5 signaling pathway negative regulation of nucleotide-binding oligomerization domain containing 1 signaling pathway negative regulation of granuloma formation negative regulation of chronic inflammatory response activin binding negative regulation of CD40 signaling pathway negative regulation of B cell activation B-1 B cell homeostasis regulation of histone acetylation phosphatidylserine binding negative regulation of innate immune response positive regulation of pri-miRNA transcription by RNA polymerase II aminomethyltransferase activity Sertoli cell proliferation 'de novo' actin filament nucleation filopodium assembly regulation of MyD88-dependent toll-like receptor signaling pathway actin binding negative regulation of regulatory T cell differentiation positive regulation of activated T cell proliferation mesenchymal cell differentiation endocardial cushion morphogenesis protein tyrosine/serine/threonine phosphatase activity regulation of NIK/NF-kappaB signaling histone H2A monoubiquitination regulation of apoptotic process RNA polymerase II cis-regulatory region sequence-specific DNA binding positive regulation of translation positive regulation of adipose tissue development response to wounding negative regulation of cytoplasmic translation nucleic acid binding protein polyubiquitination positive regulation of B cell differentiation intracellular signal transduction positive regulation of vascular endothelial growth factor production microtubule minus-end binding positive regulation of interferon-beta secretion positive regulation of interferon-alpha secretion sodium-dependent phosphate transport cellular response to DNA damage stimulus protein phosphatase binding macroautophagy cell adhesion natural killer cell differentiation protein kinase activity positive regulation of cytoplasmic mRNA processing body assembly negative regulation of interleukin–1 beta production negative regulation of intracellular estrogen receptor signaling pathway cytokine-mediated signaling pathway ubiquitin binding glomerular visceral epithelial cell development lipid storage positive regulation of synaptic transmission, dopaminergic sodium:phosphate symporter activity positive regulation of peptidase activity positive regulation of NMDA glutamate receptor activity positive regulation of free ubiquitin chain polymerization ATP binding negative regulation of hydrogen peroxide-induced neuron intrinsic apoptotic signaling pathway maintenance of protein location in mitochondrion establishment of protein localization to mitochondrion cellular response to hydrogen sulfide purine-nucleoside phosphorylase activity response to starvation negative regulation of transcription by RNA polymerase I protein K11–linked deubiquitination regulation of centrosome duplication retinoic acid receptor binding negative regulation of DNA replication regulation of protein ubiquitination protein deubiquitination involved in ubiquitin-dependent protein catabolic process TORC2 complex binding protein dephosphorylation cellular response to starvation lamellipodium assembly calcium-dependent protein kinase activity positive regulation of transcription, DNA-templated regulation of insulin receptor signaling pathway COP9 signalosome assemble positive regulation of interleukin-2 biosynthetic process cadherin binding negative regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway positive regulation of release of cytochrome c from mitochondria positive regulation of response to cytokine stimulus Rho GTPase binding protein localization to Golgi apparatus outflow tract morphogenesis cellular response to platelet-derived growth factor stimulus GTPase inhibitor activity cell migration involved in gastrulation positive regulation of interferon–gamma production DNA damage response, signal transduction by p53 class mediator positive regulation of multicellular organism growth DNA-binding transcription factor activity, RNA polymerase II-specific positive regulation of pathway-restricted SMAD protein phosphorylation regulation of proteasomal protein catabolic process chondrocyte differentiation glycine decarboxylation via glycine cleavage system protein kinase B binding T cell homeostasis positive regulation of phosphatidylinositol 3-kinase signaling response to immobilization stress transcription factor binding cytoskeleton organization cellular calcium ion homeostasis post-embryonic development kinase activity pharyngeal system development dorsal/ventral pattern formation immune response sternite morphogenesis prenylated protein tyrosine phosphatase activity leg disc pattern formation chitin-based larval cuticle pattern formation apoptotic chromosome condensation histone methyltransferase activity (H3–K36 specific) negative regulation of receptor signaling pathway via JAK-STAT protein retention in Golgi apparatus histone H2A-K15 ubiquitination nuclear hormone receptor binding histone H2A–K13 ubiquitination modulation by host of viral transcription transcription, DNA-templated embryonic heart tube morphogenesis histone methyltransferase activity (H3-K9 specific) negative régulation of mitochondrial fission negative regulation of autophagy of mitochondrion Rac GTPase binding response to UV-C activation of innate immune response response to exogenous dsRNA positive regulation of mitochondrial electron transport, NADH to ubiquinone type II transforming growth factor beta receptor binding positive regulation of cardiac ventricle development paraxial mesoderm structural organization neural plate mediolateral regionalization transforming growth factor beta receptor activity, type III Mullerian duct regression lateral mesoderm development fibrous ring of heart morphogenesis dorsal aorta morphogenesis steroid hormone receptor activity transforming growth factor beta receptor complex assembly response to luteinizing hormone epicardium-derived cardiac fibroblast cell development [protein]-3-O-(N-acetyl-D-glucosaminyl)-L-threonine O-N-acetyl-alpha-D-glucosaminase activity protein K33-linked deubiquitination positive regulation of cytosolic calcium ion concentration positive regulation of reactive oxygen species biosynthetic process regulation of mRNA splicing, via spliceosome -[protein]-3-O-(N-acetyl-D-glucosaminyl)-L-serine/L-threonine O-N-acetyl-alpha-D-glucosaminase activity Toll signaling pathway cardiac epithelial to mesenchymal transition small GTPase mediated signal transduction response to virus [protein]-3-O-(N-acetyl-D-glucosaminyl)-L-serine O-N-acetyl-alpha-D-glucosaminase activity bone mineralization positive regulation of mesenchymal cell proliferation negative regulation of mitochondrial membrane permeability ventricular trabecula myocardium morphogenesis thioesterase binding phosphatidylethanolamine catabolic process phosphatidylcholine catabolic process G protein-coupled receptor signaling pathway sodium:potassium-exchanging ATPase activity neutrophil migration response to fructose positive regulation of cellular protein localization regulation of immunoglobulin production C3HC4-type RING finger domain binding regulation of cell cycle regulation of low-density lipoprotein particle receptor catabolic process positive regulation of metallopeptidase activity lysyl-tRNA aminoacylation ubiquitin conjugating enzyme binding basophil activation involved in immune response endochondral ossification positive regulation of DNA-binding transcription factor activity metal ion binding inflammatory responsé regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation positive regulation of glutathione biosynthetic process lysine-tRNA ligase activity -PERK-mediated unfolded protein response negative regulation of translation in response to stress negative regulation of translation in response to endoplasmic reticulum stress cellular response to fatty acid ATP adenylyltransferase activity positive regulation of neutrophil apoptotic process ubiquitin-dependent protein catabolic process atrial septum secundum morphogenesis positive regulation of DNA repair DNA-binding transcription factor activity signal transduction by protein phosphorylation regulation of potassium ion transmembrane transporter activity positive regulation of nucleocytoplasmic transport N-acetyl-beta-D-galactosaminidase activity negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage glucocorticoid receptor signaling pathway development involved in symbiotic interaction positive regulation of mast cell chemotaxis nuclear receptor transcription coactivator activity negative regulation of actin filament depolymerization trans-synaptic signaling by endocannabinoid, modulating synaptic transmission regulation of intracellular calcium activated chloride channel activity sodium channel inhibitor activity phospholipase C-activating G protein-coupled glutamate receptor signaling pathway recombinational repair regulation of mitochondrion organization regulation of non-canonical Wnt signaling pathway rRNA (adenine–N6–)-methyltransferase activity activation of Janus kinase activity otic vesicle morphogenesis RNA 3'-end processing Golgi reassembly endoplasmic reticulum membrane fusion N-acetylgalactosamine kinase activity response to prolactin cellular response to anoxia negative regulation of protein kinase C signaling interleukin-4 receptor binding regulation of urea metabolic process regulation of carbohydrate metabolic process positive regulation of phosphatidic acid biosynthetic process positive regulation of glutamate metabolic process elongation factor-2 kinase activity positive regulation of ammonia assimilation cycle negative regulation of bile acid biosynthetic process -intracellular bile acid receptor signaling pathway chenodeoxycholic acid binding interleukin-17 secretion bile acid signaling pathway establishment of chromosome localization mitochondrial citrate transmembrane transport bile acid receptor activity covalent chromatin modification response to temperature stimulus fasciculation of sensory neuron axon citrate secondary active transmembrane transporter activity craniofacial suture morphogenesis ecdysis, collagen and cuticulin-based cuticle nuclear speck organization regulation of chromosome condensation Fc-gamma receptor I complex binding negative regulation of sister chromatid cohesion positive regulation of bone mineralization trigeminal ganglion development regulation of branch elongation involved in ureteric bud branching kringle domain binding positive regulation of ureteric bud formation olfactory placode formation negative regulation of satellite cell differentiation male sex differentiation phosphatidylinositol-3,5-bisphosphate 3-phosphatase activity fungiform papilla morphogenesis IMP biosynthetic process cyclic purine nucleotide metabolic process AMP deaminase activity positive regulation of interleukin-6 secretion odontogenesis transport response to carbohydrate acetyl-CoA carboxylase activity regulation of biological quality malonyl–CoA biosynthetic process -glomerular parietal epithelial cell differentiation small RNA loading onto RISC myosin light chain binding regulation of cytoplasmic translation positive regulation of viral translation positive regulation of polysome binding triplex DNA binding positive regulation of cytoplasmic translation DNA-templated viral transcription U2 snRNA 3'-end processing regulation of Ral protein signal transduction 3'-5' DNA/RNA helicase activity uterine gland development tarsal gland development negative regulation of acute inflammatory response interleukin-6 production glutamine-fructose-6-phosphate transaminase (isomerizing) activity positive regulation of phosphatidylinositol 3-kinase activity negative regulation of transcription by RNA polymerase III UDP–N–acetylglucosamine metabolic process uridylate kinase activity glucosamine biosynthetic process post-Golgi vesicle-mediated transport negative regulation of cell morphogenesis involved in differentiation regulation of phosphorylation of RNA polymerase II C-terminal domain thymidylate kinase activity dUDP biosynthetic process dTDP biosynthetic process cell maturation mesoderm formation protein kinase binding negative regulation of tooth mineralization dibenzo-p-dioxin metabolic process BP ontology ontology