GO: Day 7 WG(translation structural constituent of ribosome cytoplasmic translation ATP synthesis coupled proton transport SRP-dependent cotranslational protein targeting to membrane rRNA binding viral transcription microtubule-based process translational initiation proton-transporting ATP synthase activity, rotational mechanism mitochondrial translational termination actin nucleation RNA binding nuclear-transcribed mRNA catabolic process, nonsense-mediated decay translational elongation structural constituent of cytoskeleton mitochondrial electron transport, ubiquinol to cytochrome c mitochondrial respiratory chain complex I assembly cytochrome-c oxidase activity mitochondrial electron transport, cytochrome c to oxyger cell redox homeostasis ribosomal large subunit biogenesis nucleosomal DNA binding mitochondrial translational elongation actin filament capping L-alanine metabolic process L-alanine:2-oxoglutarate aminotransferase activity spleen development actin filament severing transaminase activity spermatid nucleus elongation sperm individualization positive regulation of neuron remodeling mRNA 5'-UTR binding mitochondrial translation histone H4-K16 acetylation GTP binding regulation of protein catabolic process mitochondrial electron transport, NADH to ubiquinone chitin metabolic process translation elongation factor activity positive regulation of early endosome to late endosome transport cytoplasmic actin-based contraction involved in cell motility aerobic respiration small ribosomal subunit rRNA binding regulation of innate immune response 2-oxoglutarate metabolic process oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, another compound as one donor, and incorporation of one atom of oxygen ATP metabolic process melanin biosynthetic process L-alanine catabolic process pyridoxal phosphate binding positive regulation of ATP-dependent microtubule motor activity, plus-end-directed protein ubiquitination ADP binding positive regulation of translation chaeta development histone H4-K8 acetylation MDM2/MDM4 family protein binding histone H4-K5 acetylation retina layer formation negative regulation of chromatin silencing RNA polymerase II transcription regulatory region sequence-specific DNA binding cochlea morphogenesis salivary gland cell autophagic cell death serine-type endopeptidase inhibitor activity endocytosis microtubule anchoring at centrosome protein polyubiquitination GTPase activity negative regulation of transcription by RNA polymerase II common myeloid progenitor cell proliferation phosphatidylinositol transfer activity actin filament polymerization regulation of protein catabolic process at postsynapse, modulating synaptic transmission mitochondrial ATP synthesis coupled proton transport DNA-binding transcription factor activity, RNA polymerase II-specific cellular response to organic substance wing disc development response to cytokine superoxide dismutase activity electron transport chain glycerol ether metabolic process DNA-binding transcription activator activity, RNA polymerase II-specific proton transmembrane transport regulation of BMP signaling pathway ribosomal small subunit assembly phosphoenolpyruvate carboxykinase (GTP) activity muscle cell differentiation ribosomal large subunit assembly misfolded RNA binding dendritic spine development response to 2,3,7,8-tetrachlorodibenzodioxine hyaluronan metabolic process succinate dehydrogenase (ubiquinone) activity -IRES-dependent viral translational initiation regulation of sorocarp development acetate CoA-transferase activity activation of protein kinase activity negative regulation of muscle organ development propionate metabolic process, methylcitrate cycle acetyl-CoA hydrolase activity acetate metabolic process cellular response to hepatocyte growth factor stimulus positive regulation of embryonic development NADH dehydrogenase (ubiquinone) activity -T-helper 2 cell differentiation negative regulation of interleukin-8 biosynthetic process copper ion binding humoral immune response mediated by circulating immunoglobulin follicular dendritic cell differentiation smooth endoplasmic reticulum calcium ion homeostasis tRNA binding -ATP biosynthetic process establishment of cell polarity involved in ameboidal cell migration actin cortical patch localization angiostatin binding actin cortical patch assembly regulation of centrosome cycle epidermal growth factor binding signaling modification of postsynaptic actin cytoskeleton vulval cell fate specification lysophosphatidic acid binding regulation of wound healing regulation of organelle assembly actin binding regulation of lamellipodium morphogenesis regulation of actin nucleation positive regulation of transcription by RNA polymerase II histone demethylase activity (H3-K36 specific) cellular response to tumor necrosis factor cellular response to angiotensin short-term memory isopentenyl-diphosphate delta-isomerase activity histone H3-K36 demethylation isopentenyl diphosphate biosynthetic process protein kinase activator activity dimethylallyl diphosphate biosynthetic process regulation of apoptotic process antimicrobial humoral response Ala-tRNA(Pro) hydrolase activity positive regulation of branching involved in ureteric bud morphogenesis positive regulation of vascular endothelial growth factor production proton transmembrane transporter activity microtubule cytoskeleton organization synaptic target inhibition positive regulation of protein phosphorylation MAP kinase activity bone resorption biosynthetic process galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity protein arginylation regulation of fatty acid metabolic process endosomal vesicle fusion phosphoserine residue binding -C-terminal protein lipidation regulation of vulval development basement membrane disassembly large ribosomal subunit rRNA binding antigen processing and presentation of peptide antigen positive regulation by symbiont of host autophagy motor activity positive regulation of proteasomal ubiquitin-dependent protein catabolic process positive regulation of Arp2/3 complex-mediated actin nucleation phosphatidylserine decarboxylase activity positive regulation of endothelial cell proliferation response to muscle stretch nucleoside-triphosphate diphosphatase activity positive regulation of gluconeogenesis tRNA 3'-end processing positive regulation of cellular protein catabolic process poly(U) RNA binding tRNA 5'-leader removal 'de novo' AMP biosynthetic process establishment of mitotic spindle orientation proteoglycan binding subtelomeric heterochromatin assembly regulation of centromere complex assembly DNA binding, bending negative regulation of chromosome condensation positive regulation of ubiquitin-protein transferase activity positive regulation of G protein-coupled receptor signaling pathway transcription coactivator binding positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage nucleosome positioning Toll signaling pathway protein heterodimerization activity ubiquitin-dependent SMAD protein catabolic process Golgi vesicle transport TIR domain binding regulation of cellular pH negative regulation of TOR signaling tricarboxylic acid cycle cysteine-type endopeptidase activator activity involved in apoptotic process -RNA transport proteolysis involved in cellular protein catabolic process chemoattractant activity actin filament fragmentation cellular detoxification positive regulation of gastrulation phosphatidylinositol-3,4-bisphosphate binding ameboidal-type cell migration regulation of neuron remodeling instar larval or pupal development phosphoprotein binding regulation of transcription from RNA polymerase II promoter in response to hypoxia complement activation, classical pathway 2 iron, 2 sulfur cluster binding positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity positive regulation of interleukin–10 biosynthetic process positive regulation of DNA biosynthetic process selenocysteine insertion sequence binding pinocytosis stem cell division laminin binding regulation of collateral sprouting in absence of injury cilium assembly negative regulation of RNA splicing xylan 1,4-beta-xylosidase activity suppression by virus of host apoptotic process response to erythropoietin alpha-L-arabinofuranosidase activity negative regulation of execution phase of apoptosis cellular response to prolactin cellular response to astaxanthin cadherin binding apoptotic process in bone marrow cell negative regulation of protein kinase B signaling negative regulation of cell size RNA polymerase II C-terminal domain phosphoserine binding protein deubiquitination cellular protein-containing complex assembly BH3 domain binding aggregation involved in sorocarp development complement activation, alternative pathway actin filament binding gastrulation with mouth forming second antimicrobial humoral immune response mediated by antimicrobial peptide negative regulation of protein secretion electron transfer activity pentose-phosphate shunt lignin catabolic process ethanolamine-phosphate phospho-lyase activity regulation of dendrite morphogenesis central nervous system neuron differentiation positive regulation of oxidative stress-induced neuron death actinin binding negative regulation of ATPase activity positive regulation of dendritic spine morphogenesis structural constituent of musclepiecemeal microautophagy of the nucleus cytoskeleton-dependent cytokinesis hyperosmotic response bHLH transcription factor binding positive regulation of histone deacetylation hippo signaling tRNA wobble position uridine thiolation transcription corepressor activity mRNA cis splicing, via spliceosome negative regulation of cell growth ubiquitin-protein transferase activity positive regulation of feeding behavior extrinsic apoptotic signaling pathway in absence of ligand positive regulation of cell growth involved in cardiac muscle cell development structural constituent of postsynaptic actin cytoskeleton neutrophil activation involved in immune response regulation of insulin secretion involved in cellular response to glucose stimulus ubiquitin-ubiquitin ligase activity chromatin organization adenosine catabolic process peptide biosynthetic process mRNA binding actin filament-based movement receptor catabolic process glycolytic process translation activator activity positive regulation of epithelial cell migration synaptic target recognition calcium-dependent phospholipase A2 activity inosine biosynthetic process ribosomal small subunit biogenesis DNA damage response, signal transduction by p53 class mediator ATPase binding regulation of protein secretion protein retention in ER lumen threonine racemase activity artery development formation of primary germ layer peptidyl-lysine methylation serine racemase activity muscle cell cellular homeostasi positive regulation of caveolin-mediated endocytosis cellular response to mechanical stimulus mitogen-activated protein kinase binding negative regulation of intrinsic apoptotic signaling pathway chaeta morphogenesis L-malate dehydrogenase activity hypotonic response positive regulation of protein metabolic process anatomical structure morphogenesis p53 binding negative regulation of phosphatidylinositol 3-kinase signaling D-serine biosynthetic process translation initiation factor activity negative regulation of cell motility regulation of DNA binding positive regulation of transcription elongation from RNA polymerase II promoter CD4 receptor binding arginine transport cerebellar Purkinje cell layer development acetylgalactosaminyltransferase activity negative regulation of RNA polymerase II transcription preinitiation complex assembly negative regulation of antimicrobial humoral response early endosome to late endosome transport siRNA binding response to tumor cell regulation of embryonic pattern specification positive regulation of antifungal peptide production protein-lysine N-methyltransferase activity antifungal innate immune response polysaccharide catabolic process pyruvate transmembrane transporter activity positive regulation of mesenchymal cell proliferation T-helper 1 type immune response cellular response to hydrogen peroxide calcium-release channel activity positive regulation of receptor-mediated endocytosis selenocysteine incorporation transcription coactivator activity mitochondrial proton-transporting ATP synthase complex assembly response to interleukin-1 inorganic anion exchanger activity glycosaminoglycan metabolic process regulation of transcription, DNA-templated regulation of imaginal disc-derived wing size cis-trans isomerase activity R8 cell fate specification progesterone receptor signaling pathway D-serine ammonia-lyase activity cellular response to steroid hormone stimulus DNA-templated transcription, termination regulation of intracellular pH adenosine deaminase activity fat pad development B cell receptor signaling pathway pheromone activity retrograde protein transport, ER to cytosol face morphogenesis neuron apoptotic process kynurenine-oxoglutarate transaminase activity negative regulation of systemic arterial blood pressure membrane invagination positive regulation of chemokine biosynthetic process MAP kinase kinase activity kynurenine metabolic process collagen binding regulation of small GTPase mediated signal transduction smooth muscle tissue development regulation of extracellular exosome assembly protein transmembrane transporter activity modulation of excitatory postsynaptic potential regulation of mRNA splicing, via spliceosome cytokine receptor activity anoikis autophagosome maturation germinal center formation protein-disulfide reductase activity chondrocyte differentiation positive regulation of engulfment of apoptotic cell positive regulation of NF-kappaB transcription factor activity protein serine/threonine kinase activity specification of segmental identity, head Malpighian tubule stellate cell differentiation transcription factor binding negative regulation of insulin receptor signaling pathway L-aspartate import across plasma membrane response to drug hydroquinone:oxygen oxidoreductase activity epidermal growth factor receptor signaling pathway endodermal cell fate commitment sodium:bicarbonate symporter activity regulation of synapse structure or activity MF BP ontology ontology