GO: Day 7 WGCNA MEblue Ranslation rRNA processing SRP-dependent cotranslational protein targeting to membrane cytoplasmic translation mitochondrial translational elongation structural constituent of ribosome RNA binding mitochondrial translational elongation translational initiation mRNA splicing, via spliceosome mitochondrial translational termination protein folding ATP synthesis coupled proton transport
formation of cytoplasmic translation initiation complex regulation of transcription, DNA-templated mitochondrial translation RNA splicing mRNA processing nuclear-transcribed mRNA catabolic process, nonsense-mediated decay ribosomal large subunit biogenesis microtubule-based process microtubule-based process microtubule-based process microtubule-based process microtubule-based process microtubule-based process -DNA binding unfolded protein binding translation initiation factor activity mRNA binding rRNA binding translational elongation positive regulation of translation translation elongation factor activity viral transcription
chromatin remodeling
mRNA methylation
ribosomal small subunit assembly GTPase activity ribosomal small subunit assembly protein refolding ubiquitin-dependent ERAD pathway transcription by RNA polymerase II ribosomal large subunit assembly proteasomal ubiquitin-independent protein catabolic process mitochondrial respiratory chain complex I assembly positive regulation of transcription elongation from RNA polymerase II promoter negative regulation of intrinsic apoptotic signaling pathway maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) endoplasmic reticulum to Golgi vesicle-mediated transport mitochondrial proton-transporting ATP synthase complex assembly mitochondrial electron transport, NADH to ubiquinone regulation of megakaryocyte differentiation RNA methylation protein transport tRNA binding ribosome binding RNA helicase activity proton-transporting ATP synthase activity, rotational mechanism small ribosomal subunit rRNA binding transcription corepressor activity negative regulation of transcription by RNA polymerase II
positive regulation of DNA-templated transcription, elongation
response to endoplasmic reticulum stress
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
transcription elongation from RNA polymerase II promoter
tRNA methylation GTP binding threonine-type endopeptidase activity positive regulation of transcription by RNA polymerase II
nucleosome positioning
DNA repair
positive regulation of ATP-dependent microtubule motor activity, plus-end-directed mRNA 5'-UTR binding NADH dehydrogenase (ubiquinone) activity response to unfolded protein negative regulation of ATPase activity cysteine-type endopeptidase activity negative regulation of ATPase activity
toxin transport
intracellular protein transport
intracellular protein transport
negative regulation of apoptotic signaling pathway
ribosomal small subunit biogenesis
actin filament capping
cell redox homeostasis
positive regulation of establishment of protein localization to telomere metal ion binding protein-lysine N-methyltransferase activity proteas'omal protein catabolic process RNA polymerase II cis-regulatory region sequence-specific DNA binding proteasomal protein catabolic process apoptotic process apoptotic process positive regulation by host of viral transcription mitochondrial electron transport, ubiquinol to cytochrome catablishment of mitotic spindle orientation nucleosome assembly Golgi disassembly peptidyl-lysine methylation tRNA stabilization actin cytoskeleton organization wing disc development protein disulfide isomerase activity chaperone binding DNA-binding transcription factor activity maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA repressing transcription factor binding response to cytokine melanosome transport ubiquitin protein ligase binding positive regulation of telomere maintenance via telomerase regulation of mRNA export from nucleus mRNA 3 –end processing positive regulation of gluconeogenesis actin filament bundle assembly endopeptidase activator activity histone binding imaginal disc-derived wing morphogenesis mitochondrial electron transport, cytochrome c to oxygen immune system developmen methylated histone binding proteasome—mediated ubiquitin—dependent protein catabolic process posttranslational protein targeting to membrane, translocations proteolysis involved in cellular protein catabolic process mRNA transcription by RNA polymerase II ATP biosynthetic process positive regulation of embryonic development positive regulation of telomerase activity vesicle fusion sequence-specific DNA binding RNA polymerase II core promoter sequence-specific DNA binding protein heterodimerization activity vesicle fusion chaperone cofactor—dependent protein refolding regulation of transcription by RNA polymerase II positive regulation of B cell activation short—term memory snRNA transcription by RNA polymerase II peptidyl—lysine trimethylation L—alanine metabolic process protein-containing complex binding U2 snRNA binding GDP binding response to heat protein deubiquitination protein deubiquitination
terminal branching, open tracheal system
cellular response to tumor necrosis factor
protein stabilization
response to type I interferon
negative regulation of transcription, DNA-templated
negative regulation of B cell apoptotic process
response to oxidative stress
negative regulation by host of viral transcription
cellular response to interleukin-1
hyaluronan metabolic process
regulated exocytosis actin filament binding cytochrome-c oxidase activity nucleosomal DNA binding heat shock protein binding hyaluronan metabolic process regulated exocytosis liver development constitutive secretory pathway pentose - phosphate shunt protein targeting to ER spermatid nucleus elongation sperm individualization positive regulation of neuron remodeling primary miRNA processing autophagosome assembly -ADP binding snoRNA binding L-alanine:2-oxoglutarate aminotransferase activity motor activity primary miRNA processing autophagosome assembly skeletal muscle tissue regeneration leg disc development. NIK/NF-kappaB signaling autophagy of mitochondrion proton transmembrane transport retrograde transport, endosome to Golgi seryl-tRNA aminoacylation regulation of gene expression regulation of MAP kinase activity blood vessel maturation. peptide disulfide oxidoreductase activity actin binding large ribosomal subunit rRNA binding superoxide dismutase activity insulin secretion involved in cellular response to glucose stimulus Golgi organization actin filament severing dolichyl-diphosphooligosaccharide-protein glycotransferase activity retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum positive regulation of dendritic spine morphogenesis RNA processing protein kinase inhibitor activity cellular response to organic substance
mRNA export from nucleus
mitochondrial cytochrome c oxidase assembly
endoplasmic reticulum unfolded protein response ribonucleoprotein complex binding peptidyl-prolyl cis-trans isomerase activity endoplasmic reticulum unfolded protein response chitin metabolic process chromatin silencing process chromatin silencing pteridine biosynthetic process acrosome assembly enucleate erythrocyte differentiation regulation of DNA replication negative regulation of protein ubiquitination piecemeal microautophagy of the nucleus positive regulation of NF-kappaB transcription factor activity negative regulation of smooth muscle cell differentiation phospholipid transport sequence-specific double-stranded DNA binding translation initiation factor binding RNA polymerase II complex binding nucleosome binding mRNA 3'-UTR binding transcription coactivator activity cyclosporin A binding supercoiled DNA binding serine-tRNA ligase activity L-alanine catabolic respiration
L-alanine catabolic process
regulation of fatty acid metabolic process
release of sequestered calcium ion into cytosol by endoplasmic reticulum
endosomal lumen acidification
negative regulation of chromatin silencing proteasome-activating ATPase activity mannosyl-oligosaccharide 1,2-alpha-mannosidase activity aslective autophagy selective autophagy selective autophagy selective autophagy 3'-UTR-mediated mRNA stabilization positive regulation of androgen receptor activity negative regulation of cell motility cellular response to laminar fluid shear stress pericentric heterochromatin assembly chaperone-mediated protein complex assembly cerebellar Purkinje cell layer development cellular response to DNA damage stimulus macroautophagy RNA export from nucleus -RNA polymerase II C-terminal domain phosphoserine binding 7SK snRNA binding mRNA (cytidine-5-)-methyltransferase activity macroautophagy
RNA export from nucleus
positive regulation of viral transcription
peptidyl—lysine monomethylation
CENP—A containing nucleosome assembly
regulation of anion transport
regulation of mRNA processing
positive regulation of gene expression
caveolin—mediated endocytosis
histone H3—K4 methylation
te—sensitive calcium—release channel activity mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity DNA-directed 5'-3' RNA polymerase activity protein tag regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity COPII vesicle coating protein peptidyl-prolyl isomerization regulation of translation of lipid metabolic process positive regulation of hypothemical process of translation to Cajal body positive regulation of telomerase RNA localization to Cajal body proteasome assembly regulation of oxidative phosphorylation mucosal immune response actomyosin structure organization regulation of histone modification convergent extension involved in gastrulation regulation of Arp2/3 complex-mediated actin nucleation chaperone-mediated protein folding axo-dendritic transport plasma membrane tubulation protein localization to perinuclear region of cytoplasm ATP binding transferase activity, transferring sulfur-containing groups pyrimidodiazepine synthase activity proton-exporting ATPase activity, phosphorylative mechanism MAP kinase kinase activity histone-lysine N-methyltransferase activity histone acetyltransferase activity RNA polymerase II cis-regulatory region sequence-specific DNA binding, bending GTP-dependent protein binding rRNA (guanine) methyltransferase activity chaperone—mediated protein lording axo—dendritic transport—plasma membrane tubulation—protein localization to perinuclear region of cytoplasm—DNA replication—independent nucleosome assembly—positive regulation of MDA—5 signaling pathway—complement activation, classical pathway—complement activation, classical pathway—cytoplasmic translational initiation—negative regulation of endoplasmic reticulum stress—induced eIF2 alpha phosphorylation—negative regulation of extrinsic apoptotic signaling pathway—nuclear inner membrane organization—early endosome to late endosome transport—formation of translation preinitiation complex—embryonic skeletal joint morphogenesis—isopentenyl diphosphate biosynthetic process—dimethylallyl diphosphate biosynthetic process—response to mitochondrial depolarisation—mRNA destabilization—response to jschemia tRNA (cytosine–5–)–methyltransferase activity U3 snoRNA binding glutathione dehydrogenase (ascorbate) activity RNA polymerase II transcription regulatory region sequence-specific DNA binding p53 binding serine-type endopeptidase inhibitor activity ATPase inhibitor activity response to ischemia regulation of mRNA stability endodermal cell fate commitment regulation of cyclin–dependent protein serine/threonine kinase activity protein import into mitochondrial intermembrane space DNA-binding transcription activator activity, RNA polymerase II-specific glucan 1,3-alpha-glucosidase activity androgen receptor signaling pathway androgen receptor signaling pathway zygote asymmetric cell division first cell cycle pseudocleavage asymmetric protein localization involved in cell fate determination positive regulation of DNA repair cleavage involved in rRNA processing negative regulation of transposon integration cell differentiation regulation of protein depolymerization alpha-glucosidase activity phosphatase regulator activity regulation of protein depolymerization regulation of protein depolymerization negative regulation of DNA binding histone methylation negative regulation of histone acetylation negative regulation of muscle organ development intracellular transport response to cAMP cellular response to nitrogen starvation IRES—dependent viral translational initiation positive regulation of NAD(P)H oxidase activity vesicle transport along microtubule transcription factor binding S-adenosyl-L-methionine binding purine-rich negative regulatory element binding isopentenyl-diphosphate delta-isomerase activity cysteine-type peptidase activity vesicle transport along microtubule regulation of stem cell differentiation protein destabilization tyrosyl–tRNA aminoacylation vesicle transport along actin filament enzyme regulator activity electron fransport chain protein localization to chromosome, telomeric region mitochondrial ribosome assembly retrograde transport, endosome to plasma membrane tRNA (guanine–N1–)–methyltransferase activity RNA stem-loop binding retrograde transport, endosome to plasma membrane regulation of macrophage activation binding of sperm to zona pellucida anterior/posterior axon guidance substrate—dependent cell migration, cell extension negative regulation of sequestering of triglyceride regulation of protein catabolic process at postsynapse, modulating synaptic transmission vesicle—mediated transport de novo' posttranslational protein folding ruffle assembly regulation of cell cycle process cytoskeleton—dependent cytokinesis positive regulation of I—kappaB kinase/NF—kappaB signaling regulation of multicellular organism growth negative regulation of IRE1—mediated unfolded protein response positive regulation of protein localization to nucleolus ERK1 and ERK2 cascade autophagosome maturation regulation of protein localization to cell surface regulation of protein localization to cell surface regulation of protein localization to move the localization to move the protein localization to cell surface regulation of protein localization to move ment protein localization to move ment protein localization to move ment protein K63—linked ubiquitination embryonic process involved in female pregnancy chromatin binding SNAP receptor activity identical protein binding peptidyl-aspartic acid 3-dioxygenase activity peptide-aspartate beta-dioxygenase activity protein kinase C binding proton transmembrane transporter activity MDM2/MDM4 family protein binding embryonic process involved in female pregnancy autophagy endoplasmic reticulum–Golgi intermediate compartment organization rescue of stalled ribosome salivary gland cell autophagic cell death posttranslational protein targeting to endoplasmic reticulum membrane microtubule sliding cortical microtubule organization positive regulation of G1/S transition of mitotic cell cycle spindle localization tyrosine-tRNA ligase activity Ala-tRNA(Pro) hydrolase activity bHLH transcription factor binding positive regulation of G1/S transition of mitotic cell cycle spindle localization spindle localization positive regulation of adherens junction organization mammary gland epithelial cell proliferation positive regulation of mitotic centrosome separation histone H4–K8 acetylation histone H4–K5 acetylation histone H4–K5 acetylation triglyceride biosynthetic process lipid droplet organization regulation of rRNA processing negative regulation of stress-activated MAPK cascade dendritic spine development microtubule anchoring at centrosome protein localization to nucleolus propionate metabolic process, methylcitrate cycle acetate metabolic process trachea formation regulation of mitotic cell cycle positive regulation of inclusion body assembly mannose trimming involved in glycoprotein ERAD pathway postreplication repair nt proteasomal ubiquitin-dependent protein catabolic process cytokine activity protein kinase A binding GTPase binding epidermal growth factor binding phosphatase inhibitor activity O-methyltransferase activity membrane insertase activity mannose trimming involved in glycoprotein ERAD pathway postreplication repair sostreplication repair postreplication repair postreplication of repair postreplication of regulation of signal transduction by p53 class mediator regulation of endocytic recycling regulation of histone H3–K9 trimethylation synaptic vesicle budding from endosome actin filament depolymerization chromatin organization regulation of toll–like receptor signaling pathway mitochondrial respiratory chain complex III assembly DNA damage response, detection of DNA damage negative regulation of release of cytochrome c from mitochondria positive regulation of protein modification process negative regulation of mRNA polyadenylation co-translational protein modification regulation of cellular hyperosmotic salinity response calcium export from the mitochondrion mesodermal cell fate determination chromatin assembly positive regulation assembly positive regulation and cell fate determination chromatin assembly positive regulation and collidation assembly positive regulation assembly positive regulation and collidation assembly positive regulation assembly and collidation assembly assembly and collidation assembly and collidation assembly and collidation assembly and collidation assembly assembly and collidation assembly assembly and collidation assembly assembly and collidation assembly succinate dehydrogenase (ubiquinone) activity phosphatidylserine decarboxylase activity voltage-gated anion channel activity histone methyltransferase activity (H3-K4 specific) double-stranded DNA binding nucleosomal histone binding class I DNA-(apurinic or apyrimidinic site) endonuclease activity hyaluronan synthase activity chromatin assembly positive regulation of CD8-positive, alpha-beta T cell differentiation negative regulation of CD4-positive, alpha-beta T cell differentiation acetate CoA-transferase activity regulation of CD4-positive, alpha-beta in tell uniferential in nuclear migration nucleas meganization nucleosome organization regulation of epidermal growth factor—activated receptor activity negative regulation of bone resorption Sertoli cell development facial nucleus development facial nucleus development RNA methyltransferase activity signal recognition particle binding facial nucleus development motor neuron migration aminophospholipid transport lymphocyte proliferation glutaminyl-tRNA aminoacylation hydrogen sulfide biosynthetic process cysteine biosynthetic process via cystathionine adult chitin-containing cuticle pigmentation adult chitin-based cuticle development negative regulation of netrin-activated signaling pathway cell projection morphogenesis long-term strengthening of neuromuscular junction Fc-epsilon receptor signaling pathway cellular copper ion homeostasis positive regulation of neurophil chemotaxis positive regulation of neurophil chemotaxis positive regulation by p53 class mediator protein secretion subtelomeric beterochymatin assembly poly(U) RNA binding Hsp70 protein binding nucleic acid binding NEDD8 activating enzyme activity rRNA primary transcript binding transition metal ion binding protein secretion subtelomeric heterochromatin assembly H4K20me3 modified histone binding regulation of centromere complex assembly negative regulation of chromosome condensation positive regulation of meiosis I negative regulation of collateral sprouting stress—activated MAPK cascade determination of adult lifespan glutamine-tRNA ligase activity mitochondrial promoter sequence-specific DNA binding protein catabolic process erythrocyte differentiation cAMP response element binding cellular response to testosterone stimulus
COPII–coated vesicle cargo loading
negative regulation of maintenance of mitotic sister chromatid cohesion, telomeric
regulation of neuron apoptotic process translation activator activity cell cycle melanin biosynthetic process bone resorption Rho GTPase binding positive regulation of protein kinase B signaling mRNA transport regulation of neuron remodeling instar larval or pupal development chromatin DNA binding TBP-class protein binding cellular response to hydrogen peroxide snRNA 3'-end processing protein targeting to lysosome cellular response to arsenic-containing substance peptidyl-lysine dimethylation positive regulation of plasma cell differentiation positive regulation of lactation post-Golgi vesicle-mediated transport histone acetylation positive regulation of cell drowth protein folding chaperone misfolded protein binding ATPase activator activity myosin V binding positive regulation of cell growth cellular response to dexamethasone stimulus transsulfuration natural killer cell mediated cytotoxicity regulation of collateral sprouting in absence of injury negative regulation of I-kappaB kinase/NF-kappaB signaling ubiquitin-dependent protein catabolic process intra-Golgi vesicle-mediated transport positive regulation of immunoglobulin production positive regulation of immunoglobulin production response to interleukin-1 reactive oxygen species metabolic process regulation of I-kappaB kinase/NF-kappaB signaling retrograde protein transport, ER to cytosol inflammatory cell apoptotic process suppression by virus of host aboptotic process suppression by virus of host aboptotic process cellular response to erythropoietin cellular response to prolactin cellular response to actaxanthin apoptotic process in bone marrow cell prolyI-tRNA aminoacylation postsynaptic actin cytoskeleton organization postive regulation of protein phosphorylation positive regulation of AIP biosynthetic process positive regulation of AIP biosynthetic process negative regulation of protein phosphorylation positive regulation of protein phosphorylation inhate immune response in mucosa C-terminal protein lipidation I-kappaB kinase/NF-kappaB signaling regulation of phosphoryletion phosphorylation of ph positive regulation of cell growth cellular response to dexamethasone stimulus cadherin binding BH3 domain binding proline-tRNA ligase activity protein phosphatase inhibitor activity double-stranded RNA binding non-membrane spanning protein tyrosine kinase activity methyl-CpG binding cyclin-dependent protein serine/threonine kinase activator activity galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity thiol-dependent ubiquitin-specific protease activity tRNA methyltransferase activity low-density lipoprotein particle receptor binding mitochondrial ribosome binding DNA binding, bending Rab GTPase binding positive regulation by symbiont of host autophagy actin nucleation transported to the process of kinesin binding thiol-dependent ubiquitinyl hydrolase activity phosphorylase kinase regulator activity laminin binding phosphoprotein binding xylosyltransferase activity translation regulator activity endopeptidase inhibitor activity historie H4-R3 methylation prostate gland growth programmed cell death prostative regulation of G0 to G1 transition aggrephagy digestive tract morphogenesis protein maturation by protein folding mRNA cis splicing, via spliceosome protein modification by small protein conjugation histone H3-K36 dimethylation positive regulation of monocyte chemotaxis peptidyl-aspartic acid hydroxylation enzyme-directed rRNA 2-O-methylation cristae formation -DNA-binding transcription factor activity, RNA polymerase II-specific rRNA (uridine-2'-O-)-methyltransferase activity RNA 2'-O-methyltransferase activity cysteine-type endopeptidase activator activity involved in apoptotic process superoxide-generating NADPH oxidase activity enzyme-directed rRNA 2"-O-methylation cristae formation myeloid cell differentiation myeloid cell differentiation not cell differentiation with the cell protein amino acid acetylation somite rostral/caudal axis specification spermatogenesis, exchange of chromosomal proteins retinal cell programmed cell death protein import into peroxisome matrix, translocation positive regulation of telomere capping antimicrobial humoral immune response mediated by antimicrobial peptide platelet degranulation positive regulation of cell-substrate adhesion definitive hemopoiesis positive regulation of angiogenesis AT DNA binding structural constituent of cytoskeleton protein domain specific binding chemoattractant activity ADP-ribosylation factor binding positive regulation of angiogenesis BP ontology ontology