GO: Day 7 WGCNA MEbrown positive regulation of adiponectin secretion lipid transporter activity negative regulation of monocyte chemotactic protein-1 production cellular triglyceride homeostasis serine-type endopeptidase activity protein trimerization alcohol dehydrogenase (NAD+) activity negative regulation of interleukin-6 secretion retrograde transport, endosome to Golgi collagen binding positive regulation of cytokine secretion carnitine metabolic process, CoA-linked oleic acid binding intracellular protein transport sodium channel regulator activity transepithelial transport negative regulation of NIK/NF-kappaB signaling oxidoreductase activity lipid catabolic process plasminogen activation phosphatidylinositol binding positive regulation of sodium ion transmembrane transport carbon-carbon lyase activity positive regulation of fibrinolysis response to drug-S-(hydroxymethyl)glutathione dehydrogenase activity fatty acid alpha-oxidation oxidation-reduction process extracellular matrix binding neutrophil degranulation NAD binding melanosome assembly negative regulation of gluconeogenesis cholesterol binding proteolysis involved in cellular protein catabolic process early endosome to Golgi transport tripeptidyl-peptidase activity polysaccharide catabolic process scavenger receptor activity carnitine biosynthetic process ethanol oxidation carbohydrate binding early endosome to recycling endosome transport regulation of early endosome to recycling endosome transport glycerol-3-phosphate dehydrogenase [NAD+] activity cholesterol efflux hyaluronic acid binding fibrinolysis positive regulation of cell adhesion molecule production integrin binding D-xylose metabolic process toll-like receptor 3 signaling pathway chitinase activity Factor XII activation fatty acid binding negative regulation of ERK1 and ERK2 cascade fatty acid beta-oxidation using acyl-CoA dehydrogenase structural constituent of presynaptic active zone fatty acid oxidation chitin catabolic process acid sphingomyelin phosphodiesterase activity carbohydrate mediated signaling oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor growth plate cartilage chondrocyte morphogenesis positive regulation of histone H4 acetylation identical protein binding negative regulation of phosphatase activity sterol transport L-xylulose reductase (NAD+) activity negative regulation of protein localization to plasma membrane carotenoid dioxygenase activity glycerol-3-phosphate catabolic process regulation of interferon-beta production beta-carotene 15,15'-monooxygenase activity retinol metabolic process fatty acid beta-oxidation L-xylulose reductase (NADP+) activity phagocytosis, recognition carbonyl reductase (NADPH) activity proteolysis -NADP metabolic process long-chain fatty acid binding sphingomyelin metabolic process DNA demethylation icosatetraenoic acid binding clathrin coat assembly violaxanthin de-epoxidase activity synaptic vesicle priming tRNA transcription by RNA polymerase III acyl-CoA oxidase activity response to mineralocorticoid protein complex oligomerization mitogen-activated protein kinase p38 binding negative regulation of cell growth oxidoreductase activity, acting on CH-OH group of donors central nervous system development carotene catabolic process zinc ion binding negative regulation of fat cell differentiation blood coagulation, intrinsic pathway L-rhamnonate dehydratase activity regulation of phosphatidylcholine biosynthetic process positive regulation of phospholipid biosynthetic process sterol binding · positive regulation of long-chain fatty acid import into cell-L-methionine-(S)-S-oxide reductase activity intracellular lipid transport cell-matrix adhesion ADP-ribosylarginine hydrolase activity eye photoreceptor cell differentiation protein transport Rab GTPase binding regulation of early endosome to late endosome transport L-threonine 3-dehydrogenase activity negative regulation of macrophage derived foam cell differentiation synapse maturation triglyceride lipase activity xylulose metabolic process sporulation resulting in formation of a cellular spore cell adhesion molecule binding cholesterol metabolic process endopeptidase activity · high-density lipoprotein particle remodeling viral entry into host cellubiquitin-specific protease binding fatty acid catabolic process oxidative demethylation lipid binding protein targeting to peroxisome LRR domain binding response to bacterium negative regulation of fibroblast proliferation exopeptidase activity chondrocyte differentiation L-threonine catabolic process to glycine ATPase-coupled transmembrane transporter activity vesicle tethering to Golgi phospholipase activator activity immune response termination of signal transduction thiamine pyrophosphate binding long-chain fatty acid transport internal peptidyl-lysine acetylation 3-hydroxyacyl-CoA dehydrogenase activity positive regulation of blood pressure retromer complex binding natural killer cell degranulation Golgi to plasma membrane transport D-cysteine desulfhydrase activity nucleotide-excision repair, DNA damage recognition extracellular matrix organization peptidyl-dipeptidase activity intracellular cholesterol transport dipeptidyl-peptidase activity cellular response to potassium iontumor necrosis factor-mediated signaling pathway dodecenoyl-CoA delta-isomerase activity regulation of systemic arterial blood pressure by renin-angiotensin mismatch repair cysteine-type endopeptidase activity arachidonic acid secretion BLOC-2 complex binding negative regulation of inflammatory response response to stimulus AP-3 adaptor complex binding developmental process involved in reproduction mRNA cis splicing, via spliceosome trans-aconitate 3-methyltransferase activity fatty acid beta-oxidation using acyl-CoA oxidase chloride ion binding monoacylglycerol catabolic process receptor-mediated endocytosis cellulase activity oligosaccharide biosynthetic process negative regulation of early endosome to late endosome transport monooxygenase activity vitamin A biosynthetic process methionine adenosyltransferase activity regulation of response to osmotic stress carnitine metabolic process enoyl-CoA hydratase activity lysosomal transport endosome organization mitogen-activated protein kinase binding positive regulation of systemic arterial blood pressure magnesium ion binding transcription-coupled nucleotide-excision repair production of molecular mediator involved in inflammatory response cellulose binding · cellulose catabolic process regulation of platelet-derived growth factor receptor signaling pathway phospholipase activity Arp2/3 complex-mediated actin nucleation decidualization protein kinase C activity glycerophospholipid metabolic process galactose binding regulation of adaptive immune response positive regulation of regulatory T cell differentiation transporter activity negative regulation of respiratory burst involved in inflammatory response tropinone reductase activity negative regulation of epithelium regeneration cleavage furrow ingression mismatched DNA binding positive regulation of AMPA glutamate receptor clustering endosome to plasma membrane protein transport hydrolase activity lipid metabolic process response to fatty acid-G/U mismatch-specific uracil-DNA glycosylase activity cellular response to thyroid hormone stimulus oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen positive regulation of NIK/NF-kappaB signaling tropane alkaloid biosynthetic process hydrolase activity, hydrolyzing O-glycosyl compounds protein localization to endosome digestion glutathione peroxidase activity regulation of DNA N-glycosylase activity 3-oxo-lignoceroyl-CoA reductase activity prostaglandin metabolic process regulation of alternative mRNA splicing, via spliceosome 3-oxo-cerotoyl-CoA reductase activity Golgi vesicle transport toxin transport 3-oxo-behenoyl-CoA reductase activity negative regulation of MAP kinase activity 3-oxo-arachidoyl-CoA reductase activity positive regulation of receptor recycling maintenance of DNA repeat elements single thymine insertion binding malonate catabolic process sphingomyelin catabolic process single guanine insertion binding regulation of autophagosome maturation malonyl-CoA synthetase activity carnitine catabolic process cellular stress response to acidic pH phosphatase activity cellular response to benomyl cellular response to linoleic acid adenosylhomocysteinase activity vesicle-mediated transport palmitoyl-CoA oxidase activity response to cold regulation of retinal cone cell fate specification carnitine O-acetyltransferase activity positive regulation of protein binding positive regulation of sodium ion transport xylose isomerase activity branching involved in ureteric bud morphogenesis stearic acid binding cellular response to exogenous dsRNA response to vitamin D linoleic acid binding positive regulation of protein dephosphorylation induction of bacterial agglutination protein carboxyl O-methyltransferase activity positive regulation of polynucleotide adenylyltransferase activity peptide-methionine (S)-S-oxide reductase activity synaptic vesicle exocytosis negative regulation of ATPase activity selenium binding cholesterol transport cellular response to osmotic stress SNAP receptor activity retinoid metabolic process raffinose alpha-galactosidase activity Golgi to secretory granule transport negative regulation of membrane protein ectodomain proteolysis long-chain fatty acid transporter activity retinoic acid metabolic process BP ontology ontology