

GO: Day 7 WGC			
term		term	
structural constituent of cytoskeleton		caveola assembly	
		microtubule-based process	
sphingolipid delta-4 desaturase activity		T cell costimulation	
		phosphocreatine biosynthetic process	
creatine kinase activity		lignin catabolic process	
		vesicle targeting, trans-Golgi to periciliary membrane compartment	
peptidase activity		regulation of cell division	
		heterotrimeric G-protein complex assembly	
hydroquinone:oxygen oxidoreductase activity		microtubule anchoring at centrosome	
		positive regulation of feeding behavior	
copper ion binding		aromatic compound catabolic process	
		negative regulation of transforming growth factor beta receptor signaling pathway	
alpha-tubulin binding		exocytic insertion of neurotransmitter receptor to postsynaptic membrane	
		glycogen biosynthetic process	
secondary active sulfate transmembrane transporter activity		negative regulation of myoblast differentiation	
		catechol-containing compound metabolic process	
chlorocatechol 1,2-dioxygenase activity		ventricular cardiac myofibril assembly	
		ERK5 cascade	
catechol 1,2-dioxygenase activity		sphinganine metabolic process	
		sulfate transmembrane transport	
sphingosine hydroxylase activity		peptidyl-tyrosine sulfation	
		peptidyl-glutamic acid modification	
protein-tyrosine sulfotransferase activity		taurine biosynthetic process	
		L-cysteine catabolic process to taurine	
methylene tetrahydrofolate reductase (NAD(P)H) activity		L-cysteine catabolic process to hypotaurine	
		regulation of histone methylation	
pseudophosphatase activity		heterochromatin maintenance	
		cellular heat acclimation	
H2A histone acetyltransferase activity		regulation of transcriptional start site selection at RNA polymerase II promoter	
		mitotic G1/S transition checkpoint	
peptidyl-cysteine S-nitrosylase activity		negative regulation of stress granule assembly	
		regulation of ribosomal DNA heterochromatin assembly	
glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity		protein polyglutamylation	
		regulation of aldosterone biosynthetic process	
taurocyamine kinase activity		cell differentiation involved in salivary gland development	
		apical constriction involved in gastrulation	
retinol O-fatty-acyltransferase activity		peptidyl-cysteine S-trans-nitrosylation	
		follicle-stimulating hormone secretion	
histone acetyltransferase activity (H4-K8 specific)		regulation of vitamin A metabolic process	
		regulation of intestinal lipid absorption	
histone acetyltransferase activity (H4-K5 specific)		regulation of eating behavior	
		ketone body metabolic process	
histone acetyltransferase activity (H4-K16 specific)		regulation of eye photoreceptor cell development	
		ribonucleoside monophosphate biosynthetic process	
N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity		regulation of action potential	
		pre-B cell differentiation	
(S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido)succinate AMP-lyase (fumarate-forming) activity		negative regulation of lung goblet cell differentiation	
		lung secretory cell differentiation	
sulfite oxidase activity		interleukin-21 secretion	
		innate vocalization behavior	
transketolase activity		regulation of Rho-dependent protein serine/threonine kinase activity	
		neuroanal-glial interaction involved in cerebral cortex radial glia guided migration	
glycogen debranching enzyme activity		regulation of mRNA 3'-end processing	
		triglyceride metabolic process	
beta-maltose 4-alpha-glucanotransferase activity		establishment of protein localization	
		negative regulation of protein refolding	
amyllo-alpha-1,6-glucosidase activity		protein transport to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	
		regulation of circadian sleep/wake cycle	
4-alpha-glucanotransferase activity		negative regulation of neuroinflammatory response	
		negative regulation of microglial cell activation	
serine-type endopeptidase inhibitor activity		negative regulation of astrocyte activation	
		protein maturation by [2Fe-2S] cluster transfer	
protein-containing complex binding		positive regulation of positive chemotaxis to cAMP	
		positive regulation of protein binding	
succinate dehydrogenase activity		embryo development ending in birth or egg hatching	
		regulation of ventricular cardiac muscle cell membrane depolarization	
nucleoside diphosphate kinase activity		regulation of signal transduction by receptor internalization	
		regulation of nerve growth factor receptor activity	
arginine kinase activity		negative regulation of sarcomere organization	
		negative regulation of membrane depolarization during cardiac muscle cell action potential	
myosin I binding		positive regulation of cholesterol efflux	
		glycerol ether metabolic process	
gamma-glutamylcyclotransferase activity		positive regulation of bile acid biosynthetic process	
		endoplasmic reticulum tubular network formation	
modified amino acid binding		rostrocaudal neural tube patterning	
		positive regulation of immature T cell proliferation in thymus	
connexin binding		mitotic cytokinesis	
		polyprenol catabolic process	
phosphatidic acid transfer activity		positive regulation of chromatin silencing	
		negative regulation of transcription by RNA polymerase II	
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		skin epidermis development	
		regulation of skeletal muscle tissue growth	
protein disulfide oxidoreductase activity		Notch signaling pathway involved in arterial endothelial cell fate commitment	
		negative regulation of epidermal cell differentiation	
activating transcription factor binding		negative regulation of cardiac muscle cell differentiation	
		endothelial tip cell fate specification	
sulfinoalanine decarboxylase activity		cerebellar molecular layer formation	
		astrocyte development	
aspartate 1-decarboxylase activity		very-low-density lipoprotein particle assembly	
		regulation of cardiac muscle cell proliferation	
protein-glutamic acid ligase activity		chaperone-mediated autophagy	
		cardiac chamber development	
phosphoenolpyruvate carboxykinase (GTP) activity		negative regulation of memory T cell differentiation	
		negative regulation of macrophage antigen processing and presentation	
polyprenol reductase activity		immunoglobulin production involved in immunoglobulin mediated immune response	
		mesoderm morphogenesis	
peptide-serine-N-acetyltransferase activity		Ran protein signal transduction	
		positive regulation of fatty acid oxidation	
2-acylglycerol O-acyltransferase activity		luteinizing hormone secretion	
		negative regulation of histone deacetylase activity	
SHG alpha-glucan phosphorylase activity		vulval cell fate specification	
		inner ear receptor cell differentiation	
linear malto-oligosaccharide phosphorylase activity		female genitalia development	
		regulation of type B pancreatic cell proliferation	
glycogen phosphorylase activity		spermatid nucleus elongation	
		sperm individualization	
heparan sulfate proteoglycan binding		positive regulation of neuron remodeling	
		positive regulation of immunoglobulin production	
cGMP-inhibited cyclic-nucleotide phosphodiesterase activity		positive regulation of cellular pH reduction	
		regulation of vulval development	
diacylglycerol O-acyltransferase activity		establishment of protein localization to vacuole	
		protein autoprocessing	
histone demethylase activity (H3-trimethyl-K4 specific)		response to leptin	
		multicellular organism reproduction	
glycosphingolipid binding		regulation of intrinsic apoptotic signaling pathway	
		protein localization to plasma membrane	
cytidylate kinase activity		methionine metabolic process	
		melanin biosynthetic process	
muscle alpha-actinin binding		'de novo' AMP biosynthetic process	
		membrane raft organization	
oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor		regulation of membrane depolarization during cardiac muscle cell action potential	
		regulation of sodium ion transmembrane transporter activity	
secondary active organic cation transmembrane transporter activity		negative regulation of calcium ion transport	
		regulation of cardiac muscle cell action potential involved in regulation of contraction	
ubiquitin activating enzyme activity		negative regulation of dendritic spine development	
		mitochondrion distribution	
low-density lipoprotein particle receptor activity		base-excision repair	
		circadian temperature homeostasis	
calcium ion binding		positive regulation of endocytosis	
		regulation of vascular endothelial growth factor signaling pathway	
SMAD binding		actin filament fragmentation	
		purine nucleotide metabolic process	
cholestenone 5-alpha-reductase activity		T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	
		mitotic chromosome movement towards spindle pole	
3-oxo-5-alpha-steroid 4-dehydrogenase activity		ciliary receptor clustering involved in smoothened signaling pathway	
		positive regulation of muscle cell differentiation	
Rab geranylgeranyltransferase activity		chaeta development	
		regulation of intracellular retrograde transport	
troponin I binding		positive regulation of skeletal muscle tissue growth	
		negative regulation of glial cell apoptotic process	
opioid receptor activity		cerebellar Purkinje cell layer structural organization	
		negative regulation of interleukin-10 production	
ferric iron binding		loop of Henle development	
		release of cytochrome c from mitochondria	
		heterochromatin organization	
		ceramide biosynthetic process	
		myelin maintenance	
		positive regulation of oocyte development	
		regulation of meiotic nuclear division	
		positive regulation of hepatic stellate cell activation	
		T follicular helper cell differentiation	
		AMP biosynthetic process	
		establishment of mitotic spindle orientation	
		retina development in camera-type eye	
		positive regulation of cell growth involved in cardiac muscle cell development	
		regulation of kinase activity	
		stem vascular tissue pattern formation	
		cotyledon vascular tissue pattern formation	
	MF		BP
	ontology		ontology