	anatomical structure development	Weight in smooth muscle cell differentiation with entail light that the horping the horping that the light that the horping the horping that the horping t				sulfide:quinone oxidoreductase activity 1—acylgiveerol—3—phosphate O—acyltransferase activity hydrolase activity, hydrolyzing N—glycosyl compounds oxidoreductase activity 2—methylthiopropyl glycosinolate S—oxygenase activity 4—methylthiopropyl glycosinolate S—oxygenase activity c—4 methylsterol oxidase activity ethanolaminephosphotransferase activity		
	carbohydra derivative metabolic process	positive regulation of glycoprotein biosynthetic process glucose 6-phosphate metabolic process		catalytic activity  DNA binding		sulfide; quinone oxidore ductase, activity particles of a guinone oxidore ductase activity particles of a guinone oxidore ductase activity particles of a guinone oxidore ductase activity particles oxidore oxido		
	Ω	positive regulation of glycogen biosynthetic process			catalytic activity			
	arbohydrate metabolic process	negative regulation of glycogen biosynthetic process						
	ation	positive regulation of macrophage derived foam cell differentiation skeletal muscle satellite cell migration				methionine—tRNA ligase activity gamma—giutamylcyclotransferase activity grotein adenylytransferase activity epoxide hydrolase activity epoxide hydrolase activity oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor oxidoreductase activity, acting on the CH–CH group of donors		
	cell	hematopoietic stem cell migration regulation of fibroblast migration				-RNA polymerase II cis-regulatory region sequence-specific DNA binding		
	cellula amino acid metabo proces	ornithine biosynthetic process methionine catabolic process citrulline biosynthetic process proline catabolic process 4-hydroxyproline catabolic process methionyl-tRNA aminoacylation						
	cytos orga				DNA binding			
	skeleton	mitotic spindle assembly				-RNA polymerase II intronic transcription regulatory region sequence-specific DNA binding		
	etoxification	cellular detoxification of cadmium ion						
	D Z	negative regulation of double-strand break repair via nonhomologous end joining  DNA double-strand break processing involved in repair via single-strand annealing						
	DNA replication	regulation of DNA endoreduplication						
	으 의	positive regulation of transcription of nucleolar large rRNA by RNA polymerase I positive regulation of transcription from RNA polymerase II promoter in response to heat stress			lipid binding	·lipoic acid binding		
	ed system proces	leukocyte migration involved in inflammatory response complement activation, classical pathway						
	intra p tra	regulation of mast cell activation  positive regulation of protein insertion into mitochondrial outer membrane						
	ular ort	rareen leaf volatile hiosynthetic process	over_represented_pvalue  0.04 0.03 0.02 0.01		molecular function regulator activity	ubiquitin-protein transferase activator activity		
	pid cro-	Phosphatidic acid biosynthetic process positive regulation of fatty acid oxidation fatty acid derivative biosynthetic process cardiolipin acyl—chain remodeling seriold metabolic process N—acylphosphatidylethanolamine metabolic process maintenance of ciliary planar beating movement pattern				guanylate cyclase activator activity		
	ubule-bas ovement	maintenance of ciliary planar beating movement pattern retrograde neuronal dense core vesicle transport anterograde neuronal dense core vesicle transport protein transport along microtubule				adenylate cyclase activator activity		
	mRNA metabolic process	positive regulation of mRNA polyadenylation				acetyltransferase activator activity over_represented_pvalue		
	nuscle system rocess	regulation of the force of skeletal muscle contraction regulation of slow–twitch skeletal muscle fiber contraction muscle filament sliding transition between fast and slow fiber				acetyltransierase activator activity	0.04 0.03 0.02 0.01	
	ne sy pr	sensory perception of taste						
	peroxisom organizati	peroxisome fission			molecular transducer activity	-acetylcholine receptor activity		
	program cell deat	negative regulation of hydrogen peroxide-mediated programmed cell death			ar xer			
	med proteir catabol proces	anaphase-promoting complex-dependent catabolic process						
	s for	negative regulation of chaperone-mediated protein folding						
	iion	zymogen activation regulation of myosin-light-chain-phosphatase activity			RNA binding	regulatory RNA binding		
	rotein dification ocess	histone acetylation protein adenylylation						
	n-contain complex	protein heterooligomerization protein homotrimerization radial spoke assembly protein tetramerization						
	reproc	multicellular organismal reproductive process male meiosis I				sugar transmembrane transporter activity fructose transmembrane transporter activity		
	ctive s	positive regulation of meiotic cell cycle regulation of meiotic nuclear division synaptic transmission involved in micturition by the complete receptor signaling pathway				gated channel activity dehydroascorbic acid transmembrane transporter activity		
	ignaling	The state of the s		activity	transpo	-acetylcholine-gated cation-selective channel activity -transmembrane transporter activity		
	sulfur compound metabolic process	positive regulation of meiotic cell cycle regulation of meiotic nuclear division  positive regulation of meiotic nuclear division  positive regulation of meiotic nuclear division  positive regulation of meiotic cell cycle  positive regulation of meiotic cell cycle  positive regulation of meiotic cell cycle  positive regulation pathway  positive regulation of meiotic cell cycle  positive regulation pathway  positive regulation of meiotic nuclear cell cycle  positive regulation pathway  positive regulation of meiotic nuclear cell cycle  positive regulation pathway  positive regulation pathwa				- D-glucose transmembrane transporter activity - trehalose transmembrane transporter activity		
						- phosphatidic acid transfer activity - extracellular ligand-gated ion channel activity		
	ransme n trans	telomeric D-loop disassembly fructose transmembrane transport glucose transmembrane transport				glucose binding -cargo receptor activity -FAD binding -low-density lipoprotein particle binding -amyloid-beta binding -Hsp90 protein binding -D5 dopamine receptor binding -translation elongation factor binding -insulin-like growth factor II binding -identical protein binding		
	mbrane port	carbohydrate transmembrane transport inorganic cation transmembrane transport norganic cation transmembrane transport negative regulation of regulated secretory pathway phagocytosis, engulfment						
	ediate port	-phagocytosis, engulfment -endocytosis -vesicle docking			Z A			
	vitamin metabolic process	vitamin B6 metabolic process				-3-phosphoinositide-dependent protein kinase binding -insulin-like growth factor I binding -PTB domain binding -Hsp70 protein binding		
	N A	Charles to transforming growth factor beta stimulus (mone)				TORC2 complex binding insulin–like growth factor receptor binding anaphase–promoting complex binding insulin binding		
BP		Personal and the second contraction of the s	_	MF		modili biridilig		