	amino acid metabolic process	aromatic amino acid metabolic process ornithine biosynthetic process methionine catabolic process citrulline biosynthetic process proline catabolic process 4-hydroxyproline catabolic process methionyl-tRNA aminoacylation			
	anatomical structure development	The level of the promoter involved in smooth muscle cell differentiation Compared to the promoter involved in smooth muscle cell differentiation		cargo recepto activity	-scavenger receptor activity
	carboh deriv meta proc	positive regulation of glycoprotein biosynthetic process		` =	
	nydrate vative abolic pess	glucose 6-phosphate metabolic process			
	carbohydrate metabolic process	positive regulation of glycogen biosynthetic process			Sulfide: quinone oxidoreductase activity I sulfide: quinone oxidoreductase activity I sulfide: quinone oxidore
	cell differentiation	positive regulation of macrophage derived foam cell differentiation		catal acti	sulfide: Quingne oxidore ductase activity I valide is a city in the construction of the construction of the construction of molecular oxygen I valide is a city in the construction of the construction of molecular oxygen I valide is a city in the construction of city in the city
	cell motility	skeletal muscle satellite cell migration		ytic vity	gluciokinase activity Fluctokinase activity buty/y
	detoxification	cellular detoxification of cadmium ion			Befoxidase activity metrionine—it Valigase activity metrionine—it Valigase activity metrionine—it Valigase activity gamma-gutamylcyclyotransferase activity grotein adenylytransferase activity boxide nydrolase activity -5—nucleotidase activity
	DNA replication	regulation of DNA endoreduplication			
	tem _l scrip	positive regulation of transcription of nucleolar large rRNA by RNA polymerase I positive regulation of transcription from RNA polymerase II promoter in response to stress		lipid binding	-lipoic acid binding
	immune system process	induced systemic resistance leukocyte migration involved in inflammatory response leukocyte chemotaxis complement activation, classical pathway T cell activation antigen transcytosis by M cells in mucosal-associated lymphoid tissue regulation of mast cell activation immune response			
	intra pı tra	positive regulation of protein insertion into mitochondrial outer membrane			
	lipid metabolic process	green leaf volatile biosynthetic process fatty acid biosynthetic process phosphatidic acid biosynthetic process fatty acid derivative biosynthetic process cardiolipin acyl-chain remodeling		molecula adaptor activity	-soluble NSF attachment protein activity
	ubule-k	retrograde neuronal dense core vesicle transport anterograde neuronal dense core vesicle transport protein transport along microtubule over_represented_pvalue		7	over_represented_pvalue
	muscle system process	regulation of the force of skeletal muscle contraction regulation of slow–twitch skeletal muscle fiber contraction muscle filament sliding			0.04 0.03 0.02 0.01
	nervous system process	sensory perception of taste		- 7	- ubiquitin-protein transferase activator activity
	med	negative regulation of hydrogen peroxide-mediated programmed cell death		olecular unction igulator activity	-guanylate cyclase activator activity
	protein catabolic process	anaphase-promoting complex-dependent catabolic process -ubiquitin-dependent protein catabolic process			-adenylate cyclase activator activity
	protein folding	negative regulation of chaperone-mediated protein folding			
	roteir turati	peptidyl-lysine modification to peptidyl-hypusine zymogen activation		molecular transducer activity	- acetylcholine receptor activity
	in-contai complex assembly	protein heterooligomerization protein homooligomerization protein homotrimerization positive regulation of protein–containing complex assembly			
	ss cti	male meiosis I positive regulation of meiotic cell cycle regulation of meiotic nuclear division			-acetylcholine–gated monoatomic cation–selective channel activity -sugar transmembrane transporter activity
		A PROPERTY OF THE PROPERTY OF		tran ac	-fructose transmembrane transporter activity -gated channel activity -dehydroascorbic acid transmembrane transporter activity -extracellular ligand-gated monoatomic ion channel activity
	sulfur compoun metaboli process	- hydrogen sulfide metabolic process - sulfide oxidation, using sulfide:quinone oxidoreductase - glucosinolate biosynthetic process		rter ty	- potassium channel activity - D–glucose transmembrane transporter activity - intracellular cAMP–activated cation channel activity - transmembrane transporter activity
	transmembra transport	fructose transmembrane transport glucose transmembrane transport carbohydrate transmembrane transport		-	- monoatomic ion channel activity - trehalose transmembrane transporter activity - phosphatidic acid transfer activity - glucose binding
	<	inorganic cation transmembrane transport negative regulation of regulated secretory pathway phagocytosis, engulfment endocytosis			FAD binding identical protein binding cargo receptor activity Wnt-protein binding low-density lipoprotein particle binding
	vitamin metabolic process	endocytosis -vitamin B6 metabolic process		NA	iron ion binding amyloid-beta binding Notch binding D5 dopamine receptor binding insulin-like growth factor II binding 3-phosphoinositide-dependent protein kinase binding
	NA	introballular auditories hamen stasis sage in transforming growth factor beta stimulus			- insulin–like growth factor I binding - PTB domain binding - PDZ domain binding - TORC2 complex binding - Hsp70 protein binding
BP			MF		- enżymė binding