	anatomical structure development	GERTINA REQUISITION OF SYNASTIC GROWTH At neuromuscular junction development		cytoskeleta protein binding	· myosin light chain binding	
	process	positive regulation of transcription of nucleolar large rRNA by RNA polymerase I cytokinin biosynthetic process dopamine biosynthetic process S-adenosylmethionine biosynthetic process		<u>a</u>		
	catabolic	hydrogen peroxide catabolic process ubiquitin-dependent protein catabolic process positive regulation of proteasomal ubiquitin-dependent protein catabolic process putrescine catabolic process positive regulation of autophagy of mitochondrion in response to mitochondrial depolarization		enzyme binding	-DNA topoisomerase binding	
	cell population proliferation	positive regulation of cardiac muscle myoblast proliferation			guanylate cyclase activator activity	
	cell- signa	synaptic transmission, cholinergic synaptic transmission involved in micturition neuromuscular synaptic transmission		enzyme regulator activity	-adenylate cyclase activator activity	
	ng - (chemical synaptic transmission polyphosphate-mediated signaling negative regulation of lateral pseudopodium assembly			acetyltransferase activator activity	
	cellular omponen	caveola assembly positive regulation of non-motile cilium assembly		hydro activ actino carb	-N-formylglutamate deformylase activity	
	- 9	spermine acetylation putrescine acetylation nor-spermidine metabolic process		lase vity, g on o	To impigrate mate delormy lase delivity	
	- ;	nor-spermidine metabolic process spermidine acetylation protein ubiquitination				
	cellular protein modification	histone H3–K23 acetylation histone H3–K14 acetylation histone H4–K12 acetylation positive regulation of protein polyubiquitination		hydrolase activity, acting on glyco	hydrolase activity, hydrolyzing N-glycosyl compounds	
	cytoskeleton organization	actin cytoskeleton organization			FAD binding	
	develo _l matu			ion binding	phosphatidylinositol phosphate binding	
	pmental	synaptic vesicle maturation			spermidine binding	
	extracellular matrix organization	collagen fibril organization			glutamate 5-kinase activity insulin-activated receptor activity mannokinase activity	
	homeos			-	hexokinase activity glucokinase activity	
	ostatic	positive regulation of cellular pH reduction over_represented_pvalue			-fructokinase activity	over_represented_pvalue
	immune system process	B cell activation - 0.04 - 0.03 - 0.02 - 0.01		ligase activity	RNA-3'-phosphate cyclase activity methionine-tRNA ligase activity	0.04 0.03 0.02 0.01
	lipid etabol	regulation of lipid metabolic process cardiolipin acyl-chain remodeling			carbonate dehydratase activity	
		positive regulation of positive chemotaxis to cAMP		lyase activity	glutathione specific gamma-glutamylcyclotransferase activity tryptophanase activity	
	motion -	hematopoietic stem cell migration regulation of fibroblast migration			gamma-glutamylcyclotransferase activity	
	nervo syste	sensory perception of pain sensory perception of chemical stimulus cognition		-	sulfide:quinone oxidoreductase activity polyprenol reductase activity - Note that the second	
	- 0	associative learning		ductase	· peroxidase activity · isovaleryl–CoA dehydrogenase activity · peptide–methionine (R)–S–oxide reductase activity	
	protein folding	negative regulation of chaperone-mediated protein folding			proline dehydrogenase activity 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 -3-oxo-5-alpha-steroid 4-dehydrogenase activity	
	orotein	positive regulation of protein processing		phosphata activity	transmembrane receptor protein tyrosine phosphatase activity	
	гері	negative regulation of protein processing		SΦ		
	oduction	asexual reproduction		trai	-Tat protein binding	
	respons to stres	response to water deprivation response to oxidative stress response to hypoxia positive regulation of behavioral fear response melanotic encapsulation of foreign target		scription factor pinding	cAMP response element binding protein binding	
	- 1	response to ischemia			-1-acylglycerol-3-phosphate O-acyltransferase activity	
	ignal sduction	insulin receptor signaling pathway acetylcholine receptor signaling pathway regulation of adenylate cyclase—activating G protein—coupled receptor signaling pathway positive regulation of TORC2 signaling Interleukin—18—mediated signaling pathway negative regulation of Wnt signaling pathway Notch signaling pathway angiotensin—activated signaling pathway negative regulation of Notch signaling pathway angiotensin—activated signaling pathway		ransferas activity, ransferrir	alpha-1,6-mannosylglycoprotein 4-beta-N-acetylglucosaminyltransferase activity mycocerosate synthase activity	
	small molecule metabolic	In the control of Notch signaling pathway One chain fatty acid biosynthetic process Out to the control of Notch signaling pathway Out to the control of Notch signa			diamine N-acetyltransferase activity methionine adenosyltransferase activity	
		hydrogen sulfide metabolic process		trar t	acetylcholine-gated cation-selective channel activity fructose transmembrane transporter activity carbohydrate:proton symporter activity dehydroascorbic acid transmembrane transporter activity aromatic amino acid transmembrane transporter activity	
	sulfur mpound etabolic	sulfide oxidation, using sulfide:quinone oxidoreductase		embrane sporter tivity	thyroid hormone transmembrane transporter activity glucose transmembrane transporter activity potassium ion antiporter activity monocarboxylic acid transmembrane transporter activity	
	transpor	Tyroid stimulating hormone secretion Stimulating hormone secretion into mitochondrial outer membrane			- amino acid transmembrane transporter activity - nucleic acid transmembrane transporter activity - acetylcholine receptor activity - glucose binding	
	†	Egylatien et alle faith and to the morane transport egylatien et alle transport egylatien et alle faith et alle fa		_	quinone binding - D5 dopamine receptor binding - leukotriene–A4 hydrolase activity - PTB domain binding	
	NA	Hamber of the state of the stat			- heme binding - TORC2 complex binding - epoxide hydrolase activity - hydroxymethyl–, formyl– and related transferase activity - insulin binding - anaphase–promoting complex binding	
ВР		.cc. iccomotory somether	MF			