anatomical structure structure development process carbohydrate carbohydrate metabolic process differentiation	positive regulation of glycogen biosynthetic process positive regulation of macrophage derived foam cell differentiation positive regulation of macrophage derived foam cell differentiation		activity	catalytic	Sulfide: quinone exidore ductase activity Control C	
p m a m c	Ŀł methionyl-tRNA aminoacylation — — — — — — — — — — — — — — — — — — —		binding	DNA	RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II intronic transcription regulatory region sequence-specific DNA binding	
detoxification DNA repair PNA replication transcription	regulation of double–strand break repair via nonhomologous end joining regulation of DNA endoreduplication 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 positive regulation of transcription from RNA polymerase II promoter in response to stress		pinding	lipid binding	ipoic acid binding	
immune intracellular system protein process transport process intracellular process intracellular process intracellular metabolic movement	regulation of leukocyte chemotaxis Intil 1648 sixtem 164 existance Edition of the intil 1648 sixtem 164 existance Edition of the intil 1648 sixtem 164 existance Intil 1648 sixtem 1648 sixtem 164 existance Intil 1648 sixtem 164 existance Intil 1648 sixtem 164 existance Intil 1648 sixtem 1648 sixtem 164 existance Intil 1648 sixtem 1648 sixtem 164 existance Intil 1648 sixtem 1648 sixt	er_represented_pvalue 0.04 0.03	activity	molecular adaptor	over_represented_pva	⁄alue
mRNA muscle nervous programmed system system process process process death	(Control of the DNIA control of the Control o	0.02 0.01	activity	molecular function regulator	abiquitin-protein transferase activator activity guanylate cyclase activator activity adenylate cyclase activator activity	
protein protein protein protein protein process process	anaphase–promoting complex–dependent catabolic process negative regulation of chaperone–mediated protein folding zymogen activation histone ubiquitination positive regulation of protein oxidation regulation of myosin light–protein hose activity positive regulation of myosin light–protein kinase activity pepticy agrining N_methy ation behildy light modification to peptidyl–hypusine protein adenylylation		activity	molecular	acetylcholine receptor activity	
ă	protein adenity lation protein heterooligomerization actin filament polymerization involved in mitotic actomyosin contractile ring assembly protein homotrimerization positive regulation of protein—containing complex assembly regulation of barbed—end actin filament capping cytogamy multicellular organismal reproductive process male meiosis I positive regulation of meiotic cell cycle regulation of meiotic nuclear division synaptic transmission involved in mitotic actomyosin contractile ring assembly regulation of barbed—end actin filament capping cytogamy multicellular organismal reproductive process male meiosis I positive regulation of meiotic cell cycle regulation of meiotic nuclear division synaptic transmission involved in mitotic actomyosin contractile ring assembly positive regulation of meiotic cell cycle regulation of meiotic process sulfide oxidation, using sulfide: guinone oxidoreductase glutathione biosynthetic process glucosinolate biosynthetic process		activity	transporter activity	acetylcholine–gated cation–selective channel activity sugar transmembrane transporter activity ructose transmembrane transporter activity gated channel activity dehydroascorbic acid transmembrane transporter activity ransmembrane transporter activity extracellular ligand–gated ion channel activity potassium channel activity Deglucose transmembrane transporter activity intracellular cAMP–activated cation channel activity rehalose transmembrane transporter activity othosphatidic acid transfer activity	
ransmembrane esicle-mediate transport vitamin metabolic process NA P	fructose transmembrane transport glucose transmembrane transport carbohydrate transmembrane transport inorganic cation transmembrane transport negative regulation of regulated secretory pathway phagocytosis, engulfment vitamin B6 metabolic process Interest a secretory pathway activity involved in apoptotic process glassesembly glassesembl		ΛF	NA - - - - - - - - - -	glucose binding pargo receptor activity AD binding ow—density lipoprotein particle binding dentical protein binding amyloid—beta binding D5 dopamine receptor binding ranslation elongation factor binding rasulin—like growth factor II binding rasulin—like growth factor II binding PTB domain binding PTB domain binding PDZ domain binding rORC2 complex binding rORC9 protein binding ron ion binding ron ion binding renzyme binding	