	anatomical structure development	BEGETIVE REQUISITION OF A VINANTIA ASSEMBLY AT PEUROPHISCULAR INDITION VELOPMENT  RECEIVE REQUISITION OF A VINANTIA RECEIVE REPORTS VELOPMENT OF A VINANTIA RECEIVE REPORTS VELOPMENT OF A VINANTIA REPORTS VELOPMENT OF A VIN			Buffide Quinons oxidoreductase activity    Fig. 1	
	carbohydrate derivative metabolic process	glucose 6-phosphate metabolic process		catalytic activity	cliuramate 5-kinase activity file provided activity file provided activity perioded	
	cell motility	- hematopoietic stem cell migration - regulation of fibroblast migration			Birding of the sterious wat in the cities of the substituted phosphate groups by identified the sterious of th	n
	cellular amino acid metabolic process	ornithine biosynthetic process citrulline biosynthetic process leucine metabolic process proline metabolic process 4-hydroxyproline catabolic process proline biosynthetic process proline biosynthetic process proline catabolic process proline catabolic process methionyl-tRNA aminoacylation				
		-thyroid hormone generation		cytoskeletal protein binding	myosin light chain binding	
	cilium organization	- positive regulation of non-motile cilium assembly				
	cytoskeleton organization	- actin cytoskeleton organization			sequence-specific single stranded DNA binding	
	DNA repair	negative regulation of double-strand break repair via nonhomologous end joining		DNA	sequence-specific DNA binding  RNA polymerase II cis-regulatory region sequence-specific DNA binding	
	DNA-templated transcription	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 mRNA transcription			RNA polymerase II transcription regulatory region sequence-specific DNA binding	
	immune system process	positive regulation of DNA-binding transcription factor activity  - B cell activation				
		melanotic encapsulation of foreign target  long-chain fatty acid biosynthetic process lipoxin biosynthetic process regulation of lipid metabolic process		lipid binding	phosphatidylinositol phosphate binding	
	d oolic ess	lipoxygenase pathway cardiolipin acyl-chain remodeling phosphatidylethanolamine biosynthetic process  positive regulation of protein insertion into mitochondrial outer membrane negative regulation of mitochondrial membrane permeability				
	membrane micro	- caveola assembly - Golgi vesicle fusion to target membrane			guanylate cyclase activator activity	
	otubule-based movement	axo-dendritic transport  over_represented_pvalue  0.04 0.03		moleci functi regula	adenylate cyclase activator activity	over_represented_pvalue  0.04 0.03
	mitochondrion organization	- 0.02 - positive regulation of autophagy of mitochondrion in response to mitochondrial depolarization 0.01	ty		acetyltransferase activator activity	0.02
	mRNA metabolic process	-positive regulation of mRNA polyadenylation				
	nervous system process	sensory perception of pain sensory perception of chemical stimulus		tr n		
	peroxisome organization	cognition  peroxisome membrane biogenesis		molecular transducer activity	acetylcholine receptor activity	
	me programn cell death	regulation of programmed cell death positive regulation of mitochondrial membrane permeability involved in apoptotic process				
	ned	positive regulation of apoptotic DNA fragmentation				
	protein catabolic process	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	Converse	transcription regulator activity	DNA-binding transcription factor activity, RNA polymerase II-specific	
	protein folding	negative regulation of chaperone-mediated protein folding				
	protein modification process	<ul> <li>histone H3–K23 acetylation</li> <li>histone H3–K14 acetylation</li> <li>histone H4–K12 acetylation</li> <li>protein ubiquitination</li> <li>positive regulation of protein polyubiquitination</li> </ul>			acetylcholine-gated cation-selective channel activity fructose transmembrane transporter activity carbohydrate:proton symporter activity	
	reproductive process	regulation of female receptivity		transpo activ	dehydroascorbic acid transmembrane transporter activity aromatic amino acid transmembrane transporter activity thyroid hormone transmembrane transporter activity	
	signaling	Synaptic transmission, cholinergic tion  Synaptic transmission, cholinergic transmission  Synaptic transmission, cholinergic transmission  Synaptic transmission, cholinergic transmission  Synaptic transmissi		7	glucose transmembrane transporter activity solute:potassium antiporter activity monocarboxylic acid transmembrane transporter activity	
	sulfur compound metabolic process	hydrogen sulfide metabolic process sulfide oxidation, using sulfide:quinone oxidoreductase glucosinolate biosynthetic process			ramino acid transmembrane transporter activity  FAD binding reglucose binding theme binding reglucose binding regliage binding regliage binding regliage binding regliage binding regulars binding regular binding re	
	d transmembra	S-adenosylmethionine biosynthetic process  fructose transmembrane transport glucose transmembrane transport ion transmembrane transport		z	quinone binding D5 dopamine receptor binding translation elongation factor binding spermidine binding Tat protein binding	
	nbrane	positive regulation of dipeptide transmembrane transport regulation of glucose import  heterical content in the		Α .	PTB domain binding TORC2 complex binding insulin binding DNA topoisomerase binding anaphase–promoting complex binding	
BP	N <sub>A</sub>	Segments with the state of the	MF		cAMP response element binding protein binding Hsp90 protein binding promoter-specific chromatin binding	