REVIGO Gene Ontology treemap

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microtubule cytoskeleton organization	organelle fission	negative regulation of organelle organization	regulation of dendrite development cellular protein	mitochondrial respiratory chain complex I assembly	respiratory chain complex I biogenesis	NADH dehydrogenase complex assembly	mitotic cell c	ycle cell	l cycle	single-organisr metabolic process	mitotic nuclear envelope disassembly	cell division	disassembly	protein localization to chromosome		transport
regulation	histone H3–K4 demethylation micro	microtubule bundle formation otubule cytos	complex assembly	modification	regulation on gliogenesis	assembly	microtubule-b process	pr	on-reduction rocess	demethylation	positive regulation of cell cycle process	vitamin biosynthetic process	cellular alcohol metabolic process	glycerol transpo		transmembrane transport
	organelle	cellular component	mobilization parallel actin	of organell organizatio	e anchoring	choring H3-S28 phosphorylation positive	process	po regul	positive mitotic gammacid acid		metabolic metabolites		cell cycle	to chromosome, centromeric region transport		compound transport
microtubule	organization	disassembly	filament bund assembly	respiratory	ex organization	regulation of exit from mitosis	spindle check	point gent	tamycin	regulation of secondar	y hepoxilin	phenol-containing compound	polar body extrusion	mercury ion	response to	response to staurosporine
depolymerization	cytoskeleton organization	phagosome maturation	regulation of histone H3–K methylation	Ichromosom		maintenance	respiratory electron	y monot	ocess terpenoid	metabolic process secondary alcohol	process	catabolic process meiotic	after meiotic divisions small		se to mercury to drug	ion to parathyroid hormone stimulus
activation of	arsenate ion transmembrane	positive regulation of Rho guanyl-nucleotide exchange factor	aminoglycan catabolic	carboxylic acid metabolic	amyloid precursor protein metabolic	positive regulation of neural precursor	transport ch	ain me	tabolic ocess /e	metabolic	metabolic process	cell cycle	molecule biosynthetic process	response to lead ion	response to testosterone	response to potassium ion
anaphase–promoti complex activity	canalicular bile	activity protein	antalolu	process egulation of Rho uanyl-nucleotide exchange factor activity	process sodium-dependent phosphate transport	regulation of gene expression,	hormone metabolic process	regulatio system arterial bl pressu	nic of lood s	protein	epidermal cell fferentiation	skin evelopment	synapse maturation	compound m	indole etabolic signal	rine negative regulation of
anaphase-promoting complex-dependent protea ubiquitin-dependent protein catabolic proces	DNA double-strand break processing in activation via single-strand	of anaphase-p	D-aspartate	negative regulation of mplex activit	mplement D-am ctivation, Yectin activations atthway	d of	estrogen metabolic process	sensory perceptio of sound	n regu dig syster	gestive m process	asciculation of motor euron askin	canonical Wnt signaling pathway involved in mesenchymal stem	canonical Wnt signaling pathway involved in osteoblast	nicotinamide nu	abolism sicleotide positiv	ignaling ve regulation of aptic plasticity
peptide positive regulatic regulatic of ion transmemb transpo	regulation of	phosphorylation positive regulation of transmembrane		protein redealkylation o	positive egulation regulation lipop	activity activity regulation of sulfur or succeptor receptor receptor	sensory perception	negative regulation of low–density lipoprotein particle		water	arian follicle	dentinogenesis	free ubiquitin chain polymerization	single-organis	release from vira	cellular component organization or biogenesis
negative regulation		transport regulation of natural killer cell activation	regulation of dopamine metabolic process	regulation regulation of Rac cel	gulation of lular amide h	ydrogen ion nsmembrane transport	protein destabilization		phagosome acidification	retina homeostasis	regulation of primitive erythrocyte fferentiation	optic cup formation involved in camera-type eye development	catagen	single–organis process	auditory behavior	methylation