REVIGO Gene Ontology treemap

cell cycle	cell-cell signaling	microtubule-based process	cell cycle G2/M phas transition morphogenes	e multicellula organisma process	of muscle	cellular amino acid metabolic process	intracellula		protein localization to synaps transmemb	on tra	dosomal ansport rograde insport,	mRNA metabolic process	protein modification to small protein conjugation of removal	RNA spli	macromolecul cing catabolic process
neurogenesis	head development	cell part morphogenesis	cell part norphogenesis cell cycle cell cycle hromosome segregation of an epithelium non-canonical Wnt signaling pathway	filament-based process	biosynthetic process	compound biosynthetic process	localization protein		protein	transport endo to C protein protein ocalization localization		protein modification by small	protein dephosphorylation	peptidyl-an acid modification	nino cellular amide metabolic on process
		cell cycle		cell growth	docking	secretion	within membrane	Cintracel	llular transp	ort:o cell	cytoskeleton-dependent intracellular transport	protein conjugation	mRNA me peptidyl–lysine modification	tRNA metabolic	DNA protein
		chromosome segregation		biosynthetic process	process devel	system development	mitochondrial transport	metal ion transport	ion transport	transport	receptor ocalization o synapse	RNA splicing, via transesterification reactions	regulation	process roncess	eplication acylation
cell cycle process	signal release	apoptotic process		camera-type eye development cellular ketone metabolic process	receptor protein signaling pathway	of cell polarity	vesicle localization	divalent inorganic cation transport	neurotransmitter receptor localization to postsynaptic specialization membrane	secretory granule localization vesicle-mediat transport in synapse	Golgi vesicle	DNA metabolic process	of catabolic process	metabolic process regulation of cellular catabolic process	protein protein maturation methylation DNA recombination
chromosome organization	cell projection organization	membrane organization	positive regulation of developmenta process	regulation of cellular component biogenesis	regulation of supramolecular fiber organization	covalent chromatin modification	homeosta process	atic regulation regulation	ulation red blecular bid	negative gulation of osynthetic process	cellula respons DNA dar stimul	respo nage oxyger	nse to topol	cellular	ephosphorylation
	organization	microtubule cytoskeleton organization	inclusion body assembly	complex subunit I	mitochondrion organization	chromatin organization involved in regulation of transcription	hormone transport	regulation of gene expression, epigenetic	filament-based process	regulation of synapse structure o activity			in-1 abiotic DNA gamage s	response to copologically incorrect stimulus ce	II-cell adhesion
regulation of organelle organization	organelle fission	regulation of cell projection	organelle assembly	endomembrane system organization	of postsynaptic structure	organization	anatomical	glucose homeostasis	of cell proliferation regulation	regulation of neurotransmitte levels	regulat of cellu respons	ular respon	rgen to oxidative stress	response to oxygen-containing compound	interaction with symbiont
chromatin organization	positive regulation of cellular component biogenesis	axonal transport	protein–DNA complex subunit organization	ribonucleoprotein complex biogenesis DNA replication-dependent nucleosome organization	fiber organization vesicle organization	of synaptic structure positive regulation	regulation of postsynaptic specialization membrane neurotransmitter receptor levels	regulation of gene expression carbohydrate		of gene silencing activation of GTPase activity	antigen p	rocessing antigen pro	drate carbohydra	positive regulation of lymphocyte	ological protein