REVIGO Gene Ontology treemap

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pyrimidine nucleoside metabolic proces	signal peptid processing	I small brote	ein ca	rotein tabolic rocess	pyrimidine nucleoside monophosphate biosynthetic process	cell cycle	cell div	rision orgar	nelle fission r	nuclear division	synthase act	e oxidor ac ivity	lation of reductase ctivity	negative regulation of catalytic activity regulation of oxide synthas phosphatase		homeostasis
deoxyribonucleoside monophosphate biosynthetic process	negative regulation of peptidyl-cysteine S-nitrosylation	pyrimidine–containir compound metaboli process	nucle monopl meta	nosphate abolic	energy reserve metabolic process	mitotic cell cycl	protein–I le comple assemi	ex checkpoi	I complex	organiene	protein destabilizat	linase	ation of activity	activity hormone transport	regulation of translation elongation	voltage-gated calcium channel activity
cellular lipid biosynthetic process	peptidyl-cysteine modification	ether metabolic	nitric meta	coxide deoxyribonucleo abolic monophospha cess metabolic proc		caveola assemb	negativ regulation of prote depolymeriz	in sprouting in abs	inflammasor	RNA polymerase I transcriptional	peptide trans	porti	plasmic nsport	Golgi vesicle transport	chrom segre	egulation of
ether lipid biosynthetic process	long-chain fatty pyrimidin biosynthetic process	ne nucleoside m	xyribose etabolism etabolic rocess	D-amino acid catabolic process	glucosamine	protein–DNA complex subun organization	roft	proton-transpo V-type ATPa	se organizati		protein localization	cellular protein peptide complex localization	peption peptio	en transport	protein seri	ne/threonine ition of ^{/ay} osome gation
protein	nucleoside monophosphate metabolic process	of actin III b	orocess	ıroporphyrinoç III metabolic process	Ideoxyribonucleotide	spindle assemb checkpoint		on of regulation cytokine		on, chaperone-mediated protein complex assembly	post–Golgi vesicle–mediated transport	water transpor	cellul t localiza	l of cellular	apoptotic process cardiac n	nuscle cell
ubiquitination	DNA recombination	nucleoside monophosphate biosynthetic process of	energy erivation oxidation organic mpounds	deoxyribonucleos triphosphate metabolic proces	phosphatidylethanolamine metabolic process	anatomical for structure arrangement	oramen ovale closure	mediolateral regionalization	pulmonary valve formation	regulation of embryonic cell shape	response to	cellular response to	B cell cyto	l vasom	otion to	evasion or elerance by positive st
protein nitrosylation	post translational	activation of rotein kinase	V(D)J ombination	macromolect catabolic process	IIIKINA	forebrain morphogenesis	hepatic duct anatomical development	olfactory nerve structure arra structural organization	regulation of the matter of th	endothelial cell	respons	glucagon se toulus		and slow fibe posit fast regulati	ive imm	ell mediated positive une response punding of l tumor cell ell mediated une response
histone deubiquitination	polyamine biosynthetic process	phosphatidylethanolamine biosynthetic process	rcerolipid etabolic process	protein refolding	DNA conformation change	3	hepatoblast lifferentiation	otolith development	regulation of hematopoiet stem cell proliferation	endothelium development	to	esponse to glucagon	presenta peptide a	en processing ar ation of endogen ntigen via MHC o hway, TAP-depe	ous class I to	esponse o gamma adiation