## REVIGO Gene Ontology treemap

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translational elongation		translational termination		translational initiation		nuclear–transcribed mRNA catabolic process, nonsense–mediated decay		SRP-dependent cotranslational protein targeting to membrane	cellular component disassembly		nembrane ganization	single–org intracel transp	ganism Iular	nacromolecular complex subunit organization	brain renin-angiotensi system  positive regulation of mitochondria	negative regulation o	f post-embryo	positive regulation sis of gastrulation surfactant homeostasis
translation		RNA catabolic process		nucleobase–containing compound catabolic process		synthetic	organic cyclic compound biosynthetic	endoplasmic reticulum	of protein		sport mem rep				depolarization reminimation post-embryonic camera-type		regulation of ion homeostasis	ystem multicellular organismal metabolic process post–embryonic organ
positive	aromatic		metabolic process cellu	lar nega	biosynthet via lath negative p				protein complex ch	regula choles stors	age remo	ticle ti	cholesterol transport regulation made	cell receptor signaling pathway acromolecular	regulation of development heterochron	t, erythrocyte differentiation		development epidermis development
regulation of metabolic process positive	compound biosynthet process	biosynth	etic compositions biosyn	hetic biosyn	thetic me	cleotide etabolic rocess	pyrimidine dimer repair by nucleotide–excision repair	single-organism	organization regulation of	regul of me	ation regula phago	of tion of cytosis bio	genesis	complex remodeling negative regulation f NF-kappaB import into nucleus	biosyntheti process	organic o c compou metabo proces	ind detect	detection of endogenous
regulation of cAMP metabolic process	positive regulation of response to stimulu	tion negative regulation of protein dephosphorylation dephosphorylation norepind		hrine regulation of of i of i cholesterol		gulation immune system process	positive regulation of activin receptor signaling pathway	cellular localization	protein complex assembly	phospl effl	holipid ood lux matu	oocyte microtub nucleati		regulation of DNA-templated transcription, initiation positive	catabolic proc <mark>bios</mark>	protei metabo ynthesis proces	stimu	otimarao
positive regulation of nucleobase–containing compound metabolic process	nucleobase–contai compound metabo process		n of regulati	on of regula	DNA transion of progenesis	A-templated nscriptional reinitiation	pyrimidine dimer repair	multi-organism	single-organi localization		macromolec localizatio	or	ganelle anization	regulation of trophoblast cell migration	aromatic het	erocycle etabolic expre	P 0.1. 0.	otein lipoprotein
negative regulation of SMAD protein complex assembly	collagen catabolic	transcription	from comporate sponse tress	acid metabo	pro meta prod	otein abolic p	regulation of rotein kinase B signaling cellular	metabolic process	multi- <mark>լուննո</mark> լ	rdanis	viral budding			regulation of cellular component movement	process	rocess	thyroid h	ar response to normone stimulus cellular
positive regulation of amyloid precursor protein biosynthetic process	mRNA metabolio	steroi	donhoenhor	positive regular	response- signaling ubiquitin- protein	nune -regulating g pathway -dependent catabolic	response to organic substance regulation of cellular		cellular proce		cellular localization	single-orga transpor		ell of cellular	B cell B cell prolit proliteration	regulation Feration proliferation	ti-organism process	component organization or biogenesis
positive regulation of RNA polymerase Il transcriptional preinitiation complex assembly	N-termina protein myristoylat	regulation immune sy	<sub>n of</sub>  nucleo <sup>stem</sup>  metab	tide protein	multivesic sorting lipop x meta	ss via the cicular body pathway protein abolic cess	process protein kinase B signaling	viral life cycle	interspecies inter between organ		organic substance transport	regulation microtubule-b movemen	pased	positive regulation	positive reg of cyclic-nu phosphodie activit	cleotide estat	of cell	onse IV-B