REVIGO Gene Ontology treemap

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translational termination	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	multi–organism metabolic process		cellular component disassembly		translation		protein targeting		gle–organism cellular ocalization	mast cell	nitric oxide storage positive moral imm of IP-10	regulation of cardiac muscle adaptation of cerulation of c	regulation of la vessel odeling progulation of la vessel odeling progulation of regulation of regulation of lagen latabolic hist	gative gulation collagen tabolic ocess gulation of stolysis
SRP-dependent cotranslational protein targeting to membrane translational elongation protein localization to endoplasmic reticulum	translational initiation RNA catabolic process	single-organism localization	multi-orç cellular p		NA metaboli process	catabolic		substance	ngle-organism transport	cellular protein metabolic	positive regulation of interferon-beta production CD4-positive,	regulation of apoptosis involved in tissue homeostasis regulation of	fusion an	resentation of peptide antigen Che	to emical nmune
			extrac			maturation			nicotinamic		CD25-positive, alpha-beta regulatory T cell differentiation	blood vessel remodeling response to	death	n wound Pro	ffector ocess esicular
		membrane orga <mark>tization</mark> translation a	ribosoma small subu biogenes	unit organizat	tion	ation SSU-rRNA		omplement activation		ic localization	response to vitamin	inorganic substance	of cellula response drug	body so	sorting iway
			protein metaboli	mRNA processing body assemb	reactive oxygen species	involved in DNA repair	from RN/ polymeras	modified ami	regulation endopeptid activity	amino acid family catabolic process	regulation of response to drugespo	cellular response to aluminum ior onse to vit	sodium dode	multives body so	n of host sicular sorting
		protein complex subunit organization	regulation of transcription from RNA polymerase III promoter reputation reput	of catabolic	oxidative stress	post-translational protein modification peptide secretion		protein I	nega regulat ination lympho chemo	tion of peptide ocyte amidation	point	glucocorticoid mediated signaling pathway do	to to dium vitan decyl	patny	ative ition of
				multi-organis reproductive behavior	mating	peptide modification	regulation of chromatin disassembly regulation of	of DNA N-glycosylas activity	regulation of glycolytic process negative regulation from F polymerase II prom	peroxisome peroxisome	recognition response to drug	from RNA polymerase	respor to acellular mulus stero	regulation endocy	ost cell tion o
		interspecies interaction		protein	transport		superoxide dismutase activity	ejaculation biosynthetic	aromatic amin	component biogenesis C-terminal	integrin-mediated signaling pathway integrin-n	regulation of spindle	cellular compone		bolic
		between organisms	glycoprote cataboli		process	regulation of DNA N-glycosylase activity protection from		autopriagy	acid family metabolic process	protein amino acid modification	resignaling cell cycle checkpoint		organizatio	on catabol proce	olism
		macromolecular complex subunit organization	extracellu matrix organizati	lar reproductive	regulation o glycoproteir	cell mediated cytotoxicity f protein	cytoskeletororganization		regulation	actin cytoskeleton reorganization guanosine–containing compound biosynthetic process	multi-organis		localization	common m progenito prolifera reactive of specie metabol	or cell ation oxygen ies