REVIGO Gene Ontology treemap

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oxidation-red process		respiratory ele	ctron	generation of precursor metabolites		doxorubicin metabolic process		cellular ketone metabolic	mitochondri fusion		.K36	organiza	avage to		mitochondrial fragmentation involved in apoptotic process positive regulation of	cellular protei localization	hydroge transmen transp	nbrane	RP-dependent cotranslational rotein targeting to membrane
				and energy		C21-steroid hormone metabolic process		process	translational termination	al n	ranslation generate mature 3'-en SSU-IRNA (INCL) 5.85 IRNA, LSU-IRN release of otidyl-amitochondriak fu		u-rRNA, rRNA) ass	rial NADI	assembly	localization to	cellular	vesicl	
quinone metabolic process	terpenoio catabolio process	ARF GTPa		olic metab	oolic of	ositive gulation ligase	process, nonsense–mediated decay	negative regulation of autophagy	translationa initiation	modif	positive regulation of mitochon		s from chain complex I biogenesis con of ndrion histone ndrion H3_K36		rogenase organelle fusion positive regulation	hydrogen			ine single-organism cellular
glycoside metabolic	galactose catabolic process	1.090.00.00		regulation of cell cycle arrest	metaboli	C N-linke	metabolic	cellular amide metabolic process	translationa elongation	al single-c	embly organism brane	mitochond respirator chain comp	rial mitochon y proton-trans olex ATP synth	drial sporting rR	rediated integrin	single-organisi transport	n pyruvate transmembrane transport	establishn	regulation of lipid transport by positive regulation of transcription from RNA polymerase II promoter
process	isoprenoi catabolio process	ubiquitin dependent	itory electr	regulation of notice of transport biosynthetic	ucleotide t chain netabolic	nicotinate nucleotid salvage	e metabolic process	positive regulation of chromatin binding	cellular respo	acid re	esponse emonic a	e to	positive regulation of myotube ferentiation	cell migra involved vasculoge	in of DN nesis recombin at telom	regulation of mitochondrial DNA replication	presentation of p	antigen rocessing and resentation of	insulin catabolic process negative regulation
carboxylic acid metabolic process	regulation	homoostooio	cell redox putrescine homeostasis acetylation proce		single-organism cellular process aldehy metabo		regulation of NF-kappaB transcription	paB catabolic process	stimulus		regu	ulation m	tongue orphogenesis	regulation of apoptotic DNA fragmentation		regulation of fat cell proliferation	and presentation of exogenous peptide antigen processing and processing and		of interferon—beta insulin biosynthetic process
regulation of mitochondrial membrane	signal transductior involved in ce cycle checkpo	ell signaling	regulation of cellular ketone metabolic proces by positive regulation of transcription from RNA polymerase II promoter	metabolic pr	positive regulation of rotein kinase B signaling	endoplasm reticulum calcium io homeostas	nic tricarboxylic n acid n metabolic		cellular response to acid chemica cellu		resp	of ponse d	evelopment f secondary sexual	gulation regulation of DNA recombinat at telome	T cell homeostatic	tongue development	presentation of p	oresentation of peptide antigen	metabolic chromatin process silencing at rDNA
dicarboxylic	amine metabolio process	succinate metabolic process	regulation of glycolytic by positive regulation of transcription from RNA polymerase II promoter	alcohol re	guiation		cysteinyl-tRNA aminoacylation regula	process	response to	coxyge	cellular sponse to in-containing ompound ho	esponse to ho	aracteristics B cell omeostatic roliferation	skeletal muscle fik differentiat	male sexual	nuclear fragmentation involved in apoptotic uclear change	racute-phase racute-p	phase positive plant of the positive plant o	localization carbohydrate
acid metabolic process	ARF prote signal transduction	metabolic process	thiamine diphosphate biosynthetic process	catabolic _{bi}	ATD	egulation of nucleoside m	opionate of etabolic isoprer metabolic process proces	noid testosterone biosynthetic process	apoptotic signaling pathway	hydrogen peroxide catabolic	negative egulation of ose import in esponse to	response to interleukin-2	viral process	ess	interspecies interaction between ral process—	viral capsid secondary envelopment reaction	inflammato response nitrogen utilization	regu	utilization llation trogen
small molecule metabolic process	negative regula of endoplasm reticulum calci ion concentrat	metabolic	thiamine diphosphate metabolic process	I metabolic	acetate	metabolic glyco	cription from RNA	ine vitamin olic catabolic ess process	response of to amine	activation f membrane attack	retinal o	cell	nulti–orga ellular pro	nism mı	ulti-organism metabolic process		regulation carbohydra utilization	of single-	zation regulation of growth rate corganism occess