REVIGO Gene Ontology treemap

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mRNA met		RNA splicing	double-stran break repair via homologous	regulation of DNA metabolic	leukocyte migration involved in inflammatory	adenylate cyclase–activating dopamine receptor signaling pathway	regulation of cellular catabolic process	regulation of catabolic process	epithelial cell proliferation involved in renal tubule morphogenesi	programr cell dea induced s symbio	med regulath motor	or neuron	neural crest cell fate commitment	morphogenesis	of zinc ion	esophagus smooth muscle contraction	zinc ion homeostasis	maintenance of location
signal transduct		ular nolecule F	recombinatio	n process	DNA metabolic	- f (regulation of skeletal muscle fiber development	proteasome-mediated ubiquitin-dependent protein catabolic process	regulation of canonical Wnt signaling pathway involved in controlling type B pancreatic cell proliferation	regulati of grow	vth deaden	lear-transcribed RNA catabolic process, nylation-dependent decay	cellular ketone metabolic process	positive regulation of sequence–specific DNA binding transcription factor activity	positive regulation of systemic	transport sequestering	sensory perception of smell	D-aspartate import
DNA damage checkpoint		bolic prod cess	cessing	linkage	process	activation of	corticosteroid	regulation	stromal-epithelia cell signaling	transducti	invo	hymal stem	signaling pathway involved in osteoblast	cell fate	arterial blood pressure	of metal ion	or smell	
cellular response to DNA damage	l respons	l translesio		double-strand	Involved in	cysteine-type endopeptidase activity	adenylate cy signaling pathway	clase-active cyclase activity	prostate gland development intrinsic	activation JAK2 kina	of silence	matin mir cing at	neralocorticoid receptor signaling	negative	gluconeogenesi		UDP=N-acetylgalactosamine metabolic process	carbohydrate biosynthetic process
stimulus	to fungu	S '	negative	negative regulation	DNA replication		regulation of Rap GTPase	of cyclase	apoptotic signaling	activity	d exoge		neural of	sitive regulation growth hormone ceptor signaling	monoterpenoio	gamma-aminobutyric gluconeogen process secondary		vitamin
primary metabolic process	extension involved ir somitogene	break processing involved in repair via single–strand	determination of dorsal	of Wnt signaling pathway involved ir dorsal/ventral axis specification	peptidyl-asparagine hydroxylation	signaling pathway	signal	activity	regulation of	cataboli	s prod	abolic fo	optic cup	pathway lation of ce-specific negative regulation of transmembrane receptor	metabolic process	alcohol metabolic process	proteoglycan metabolic process	biosynthetic process
cellular metabolic process	peptidyl-histic	ine replication	linflammator	y postreplication repair	DNA packaging	outophom/	transduction by p53 class mediator			autocrin signalin	neuro	receptor cam	nyolyed in tran	binding protein serinethrecone kinase signaling pathway	neutrophil	leukocyte	antigen processing and	antigen processing and presentation of peptide
negative regulation of ubiquitin–protein ligase activity	peptidyl-pyrrometl		organic substance metabolic	negative regulation of digestive	negative regulation of low-density lipoprotein particle	ATP-dependen chromatin remodeling	dense gra organiza	inule organiz	ISOMAI	-Y41 sigr	TCR nalosome ssembly		n cell junctio	n insertion		aggregation	antigen pro and prese of exogo peptide a	entation enous
involved in mitotic cell cycle	positive	recombination	acid	peptidyl-aspartic	K29-IINKed	filopodium	cellular	111131	NA histone	-tyrosine	ecretory granule	establishm of proteir	ent localization within		epithelial cell-cell adhesion	endothelial cell-cell adhesion	rocessing and resentation of exogenous eptide antigen	processing and presentation of exogenous antigen
protein polyubiquitination	regulation of deoxyribonucleas activity	********	protein K33-linked	response	deubiquitination signal transduction	assembly	· · · · · · · · · · · · · · · · · · ·	complex from assembly ATP-depe		ora	ganization modelin	localizatio	membrar	organization	mechanosensory	of negative regulation	lation COM	llular ponent
DNA replication	protein K27-linke	DNA-templated transcription	deubiquitination organic cyclic compound	to fungus response to	in response to DNA damage cellular aromatic	protein insertion into ER membra		eton actin file	ament nucle zation mobil	eosome ribor lization	nucleoprotein complex assembly	chromosome organization	spliceosome	assembly		msory behavion response to have to hav	ypoxia 0 - 3 0 - 1	nization genesis
cellular response to	regulation of	stress f heterocycle	metabolic	starvation nucleic acid	compound metabolic process	cellular compone	ent	IIIIIIace	allular a		omembrane	actin filament	of intracelli	t intra-Golgi vesicle-mediated	response to	respor prostaglandir	nse meta	totic aphase
amino acid	acid anterior/posterior	i process i	mRNA 3'-end processing	metabolic process	nucleobase–containing compound metabolic process	organization	complex su organizati	bunit trans	port bu		system ganization	notwork	rcellular comp	onent	E	ion		cycle