## REVIGO Gene Ontology treemap

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transcription fro		regulation of transcription of RNA polymera	rom	nucleic acid metabolic	aromation compound biosynthe	nd he tic bic	heterocycle biosynthetic	mitral valve morphogenes	regulation of monocytis differential	yte spin	nal cord lopment	auditory receptor cell fate ommitme	org	gan	regulation of cell fferentiation	smooth muscle cell differentiation	activation of innate immune response	e microg cell activat	intrinsic apoptor signaling pathw in response to D	ay response-regulating
		promoter		process	process		process	negative regulation of pro-B cell	embryonic ey morphogenes	is tate	he: develo	art regu	enniaet i	cellular triglycerid	compartme pattern is specification	involved	Fc-epsilon receptor signaling	regulation of I–kappaB kinase/NF–kapp	ephrin receptor aB signaling	basophil
regulation	regulation cellu						cellular	differentiation		commitr	ment	differ	entiation	nomeostas	ISTSPECIFICATIO	in female pregnancy	activation	signaling of innat		response
of nitrogen compound metabolic	nitro compo biosyn	gen ound thetic	nic cyclion pound synthetic rocess	metabolic	nucleobase-co compound me process	etabolic Co	compound metabolic	oculomotor nerve development	regulation of secondary heart field cardioblast proliferation	regulation of stem	renal regative renal interstitia stem cell development		interleukin–4 tissue production developm		ossificatio	skeletal n muscle cell differentiation	activation of immune response	degranulation	complement component C5a signaling pathway	receptor mediated signaling pathway
process	process proces						process	development	vascular	regulation	n of multicellu	ular plate		regulation of respiratory	skeletal	bone		basophil	phosphorelay sign transduction syste	-
organic cyclic compound	·		tion of	nitrogen compound	negative regulation	on  DNA	DNA-templated transcription,	procedio	smooth muscle cel developmen	problem		forma	ition gas	seous exchange y neurological	system developmen	development	I–kappaB kinase/NF–kappaB signaling	mediated immunity	positive regulate of adenosine recurrence signaling pathy	eptor
metabolic	·	process biosynthetic process		metabolic of gene process expression		9	initiation	natriuresis	labyrinthine	е	spinal co	syster	cardiac	septum comp	erior chondron developm involved tern endochondra	Harderian gland		fa	tty acid	vay
cellular	regulation	of regulation		guiation	sitive	. אואר	regulation of multicellular	myeloid cell	vessel developme	differentiat	differentia	ition	nent	$\perp$	nation morphoge	nesis	epoxygen P450 path		tabolic I	response to orticosterone
nitrogen compound	regulation process	proces		rocess pa	in profit in profit in the state of the stat	nylation	ion organismal process	development	tube developmen	organ	nervou	s latera	regulat foreb	tion of regulator	tion of regulation ondrial pancreat m ion cell	on of oligodendrocyte	e 	<u> </u>	rocess lucuronate	
metabolic ·		positive regulation	of	positive	positive regulation	viral				Milaevelopii	differentia		differen		ntration differentia	ation	epoxygen B4 catab	ase P450	nathway	response to orticosterone
process	regulation viral entry	oi   biologica	DN modific	"	of mRNA		gene t silencing	megakaryocyt development	<ul> <li>I circulatory</li> </ul>	regulation	n of developme	ental edge ce	linterleu	tion of regular ukin-4 neut	stomac neuroendo cell	nerve	proces	SS gluta	minvl–tRNA	esponse to metal ion
biosynthetic	into host co	ell DNA	posi	tive	process	cell regulation	n		developmer	nt angiogen	esis process		proc		differentia	ation	long-chair			
process	transcriptio initiation	process	regul of ce	ation regulation of endothelia cell migration		of immun	cellular macromolecule	myeloid cell differentiation	pregulation		Ive neurona stem ce	ıı involved	ion regula in of mas	ation of ten	ation vasculoge involved corona vascula	d in endothelial ry cell	acid catal	ooto	phatidylserine bolic process	response to methylglyoxal
	from RNA polymerase II promote	e regulation	pepulayi	cellular		5-methylcytosin metabolic	ER-associated	platelet	proliferation	n l	regulation of cyclin-depend	f DI	VA AV	G0 to G	regulation o	Golgi vesicle	entrainment of circadian	response to cell-matrix	chromosome	
gene expression	regulation of gene	process	modifi	process	process	process	catabolic process	alpha (	chromosome organization O	ssembly	protein serine/threoni kinase activit	ne chec	cation	transition of mitotic co			entrainr circadia	n clock	segregation	regulation
	expression epigenetion	cofactor-dependent	g promo	ion from DNA-template transcription in response to	histone H3–T6	regulation of cellular ketone metabolic proces by negative regulation of transcription from RNA polymerase II promotei	a II promoter				positive regulatet alphagi	regu ranule or	ganizati		of dense	positive regulation of tooth	to diacyl bacterial	response to potassium ion starvation	drug	
positive regulation of nitrogen compound	vitamin biosynthet	ic protein	nega	ative transmembral	in regulation	taurine	transcriptional activation by	homologous (chromosome	chromatin h	istone H3 cetylation	positive regulation	negative of cyclin-	regulation dependent	checkpoir platelet	biogenesis positive regulation	mineralizatior regulation o extracellular	response respor	n <b>se to</b>	_	meiotic prophase
metabolic process	process	ADP-ribosyla	of met	abolic kinase signali eess pathway	ne of histone Ing H3–K27 acetvlation	biosyntheti process	looping	segregation	oodoming		of mitotic	serine/t	hreonine n activity	norphogene	of mitotic cell cycle, embryonic	matrix assembly	radiation	to hypoxia	transpo	