## REVIGO Gene Ontology treemap

								KEVIG	o Gene Unit	nogy treem	ap						
activation		protein activation	pept cross-l		crost via complement 4 activation pepti		eptide ss-linking hondroitin -sulfate aminoglycan	T call chamatavia	response to auditory stimulus	viral latency	arsenate ion transmembrane transport	calcium-mediated signaling using extracellular calcium source	canalicular bile acid transport	1	small molection biosynthe process	tic antibiotic metabolic	
complex a	ctivity	cascade	Cross-i	illiking a			dyl-amino nodification		response to lead ion	cellular response to staurosporine	protein localization to chromosome, centromeric region	protein secretion by platelet	pyrimidine nucleobase transport	Biodynarioae	protein mannösylation glycosylation		
anaphase-promoting complex-dependent protes ubsystem-dependent protein catalodic proce	regula astro	tion of cvte	arboxylic acid netabolic	regula peptidyl-		citrulline metabolic	positive regulation of cell morphogenesis involved in	response to mercury ion	response to	Fas signaling T cell che	nemotaxis	spermine transport	positive regulation of ion transport	process steroid		UDP-glucosylation	
	differer	differentiation pr		phospho	orylation	process	differentiation	protein	other organism		ne	regulation of	julation of Rap	biosynthetic process	omega-oxidation	phosphorylation	
keratinocyte differentiation	biosynthe	eta-alanine beta-alar piosynthetic metabol process process		e bone mineralization involved in bone maturation		double-strand ak processing blyed in repair single-strand annealing	heart tube anterior/posterio pattern		response to toxic substance	glycerol transport	response to staurosporine	signaling nathway in	ransduction	hormone	positive regulation systemic arte	The second secon	
tissue	fasciculati	positi on regulatio	ive on of steine	positive	regul	positive lation of Rho yl-nucleotide	positive regulation of Wnt signaling pathway by BMP signaling	negative regulation of viral entry into host cell	positive regulation of calcium ion transport	polyamine transport	response to vitamin B6		oonse to lymphocyte eron-beta migration	metabolic process <b>hor</b> i	blood press mone metab maturatio	olism <sup>regulation</sup> of	
dicarboxylic acid	neuron ax	prote	ess a ein tor	regulation o	re	activity	substance P catabolic		spindle stabilizat	tion cytoskele organizat	ion H3–K4	microtubule cytoskeletor	ton nuclear	protein destabilization	relaxation cardiac mus		
biosynthetic process	process	cess removal thymidine		egative	diffe	negative regulation	.	disassembly	negative regulat		demethylat	ion organizatior	division parallel	pyridine-containing	vitamin B6	single-organism	
peptide catabolic process	fructoselysi metabolio process	ne catabo	olic regu	ulation of opeptidase activity	substrate adhesion-depend cell spreading		riated le cell metabolic	protein	of organelle	actir cytoskel	l snind		actin ne filament		_	process	
of woodbar	negative regulation mitochond RNA catab	of catabo	olic sy	napse turation r		of prote	electron transport	depolymerization		regulat	ion positi	ve on of organello	chain	indole-containing compound		single-organism metabolism	
recycling anthranilate	process ovarian	tryptoph		podium	process positive regulatio	positive positive regulation	chain e regulation	oi spinale	cellular proteir	organiza n phagose	proce	mitochondri	assembly  NADH	process single-orga	re	esponse o biotic microtubule-based process	
metabolic process	follicle atresia	process acetyl-0	s to ass	assembly	of fibroblas proliferati	of generation of epigeneration	on, healing	organization	complex assemb	priagosor			dehydrogenase c complex assembly	cellular pro		stimulus process	