REVIGO Gene Ontology treemap

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complement activation, alternative pathway		regulation of triglyceride biosynthetic process	positive regul of lipid stora	regu)n i		egulation eptidase vity	ERK1 and ERK2		positive gulation of otein coupled optor protein ling pathway	oxidation-reduct	tion process	tricarboxylic acid cycle	2-oxoglutarate metabolic process	
		response to		negative regulation	respo	onse to ve stress cell migra		blood	inte	ernal protein				transsulfuration	
		peptide hormone	chemotaxis	of apoptotic process				coagulat	ion a	cellular	succinate metabolic	mitochondria electron transport,	oxaloacetate metabolic boxylic acid cyc	metabolic process to	
complement activation, classical pathway		positive regulation of fat cell	positive regulation of B cell proliferation	regulation of autophagy		processing reginated reginated reduction reduction reduction reginated reduction reduc		ative cell ation of respondance	nse to	response to potassium ion	process	NADH to ubiquinone cysteine	mitochondrial asp	artate A1	saccharopine ate ATP glutathione lic metabolic metabolic
		lipopolysaccharide	positive regulation	cellular response to	positive regulation due	presenta	positive regulation	response gly to activity		starvation thrombin ate receptor signaling pathway		biosynthetic process via cystathionine	folic acid pu	rine tetrahydro	homocysteine
			of vascular plement activati endotrienal growth factor production	on, alternativ stimulus	e pathway localization to nucleus	transmembran transport	alpha biosynthe process		cycle				metabolic metabolic process	eobase tetrahydro interconve cess rine	i metanolic
			B cell receptor signaling	interferon-gamma	phosphatidylinositol 3-kinase signaling	3'-UTR-mediated mRNA destabilization	fatty acid metabolic process	zymogen p	_	id signaling pathway		lipid metaboli process	sulfide fa amii biosynthetic mei	mily GMP histidine catabolic metabolic	histidine malate metabolic metabolic process process
positive regulation of apoptotic cell clearance	inflammatory response	fatty acid beta-oxidation using acyl-CoA dehydrogenase	response to hypoxia	positive regulation of collagen biosynthetic	renin secretion into blood prod	steroid metabolic process	gluconeogenesi	signaling	protein	dration phosphate-L-lysine	mitochondrial respiratory	protein homotetramerization	cell-matrix ce cell-matrix adhes adhesion adhes	immu	ne system
				DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	receptor signaling	positive regulation of interleukin–6 secretion	cholesterol homeostasis	regulation of	ery long-chain fatty acid metabolic process glutamate catabolic process to aspartate negative regulation of	production involved in immune response ate interleukin–17 production ate	chain complex mitochondrial r lassembly chain complex		4411001011		
			response to stress	neuron projection	response to drug	tolerance	response to interferon-gamn	proepicardium development e alpha-linolenic			cristae establishment of synaptic mitochondrial specificity at translational neuromuscular elongation		aging	cytolys	cytolysis nuclear-transcribed mRNA catabolism, deadenylation-independence
positive regulation of activation of membrane attack complex		lipid homeostasis	response to biotic stimulus	immunologica		cell surface receptor	homeostasis	acid metabolic process	transforming growth factor oeta1 production positive regulation of double–strand		metabolism		or-sperm putrescine retaine retaine	polic	
				synapse formation		signaling pathway	of PERK-mediate unfolded protein response	d cofactor–dependent protein refolding	break repair via nonhomologous en joining	phosphorylation of STAT protein			proces acetylation of	cell p	cell proliferation