REVIGO Gene Ontology treemap

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anatomical structure morphogenesis	cardiovascular system development	brain development	regulation of tissue remodeling	nervous system development	hepaticobilia system developmen	minerali	nei deve	ulation of elopmental process	positive regulat biological prod	cess	julation of cell iferation	regulatio of cell communica	l ei	ulation of ignaling	cell projecti organizatio	of cellucon n biogen	ular project nent	jorganization
a alliula u	circulatory	tissue	granulocyte macrophage colony–stimulating factor production	cell aging	organ formation	epitheli developr	prog	elopmental grammed ell death	regulation of	regulation	negative reg	ulation proge	esterone	vitamin D	cell ce	cellu compo Il projectio		
cellular developmental process	development	System		ctor product	cranial nerve ion,pment	tissue emodeling ir	nvolved in n	endodermal digestive tract morphogenesis	intracellular signal transduction	of response apoptoti		f extrinsic receptor rotic signaling pathway pathway		receptor signaling pathway	ignaling athway		nance comp	lular ponent
vascular endothelial growth	cell	positive regulation of granulocyte	identity	cell	ell skin de	pidermis reg	positive regulation of multicellular	sitive ation of regulation	cell surface t	otor in regulation of cell f		proliferation ng		gulation of biological quality	actin filame bundle assembly	desmo: organiz	pr	component biogenesis ein merization
factor production	positive regulation	factor production	cell fate commitment	proliferation in forebrain	re	spiratory tube	organismal	of anoikis	pathway r	of ligand positive regulation or	i sianaiind	negative regulation biologic	way ve n of cal tran	signal siduction by sphorylation	response to lipid	respon	response phenylpropa	
single-multicellular organism process	vascular endothelia growth factor production	development	liver development	tube	anatomical structure	velopmen	cranial suture	outflow tract septum S morphogenesis	signal transduction	epithelial cel proliferation regulation of response to	pathway intracellula	G-protein coupled	regulation of chronic inflammatory	regulation of nucleotide–binding oligomerization	cellular	chemic		stimulus response to
positive regulation of cellular process	regulation of metabolic process loc	oositive egulation pro of degluta comotion positive regula		epiderma cells		regulation of res	lation sponse bio	egulation of lipid osynthetic orocess rrimidine	cellular response to biotic	extracellular stimulus regulation of response to nutrient levels	signal transductio	positive regulation of epithelial cell	regulation of toll-like receptor signaling	of biological	external	potass	ar response to	potassium ion cellular response to chemical
	of reactive oxygen species metabolic process	of ERK1 vitan 24–hyd act cascade negative	nin D nitric oxide biosynthet process	of catabolic process regulation of phosphorus	metabol process cellular amino aci	ic of phosphatid 3-kinase s transcr d from F	dylinositol signaling pription pription real state of the	atabolic process positive egulation	protein protein targeting mitoch in	otein ort into multice hondrial organis	llular smal stasis Ce	Ce	pathway Ikocyte ell-cell	regula	nse to	stimuliological dhesion		o signaling
glycosaminoglycan metabolic process	metabolic tra	CREI glycosam anscription proceedings of the procedure of the proceedings of the procedure	inoglycan met cess process	negative regulation of DNA	biosynthet process ethanolamine-containir compound metabolic process	II pron	reç II-3-phosphate process RNA I	gulation of scription from polymerase II		amate retion	in adhes	hetero adhes membra	philic cell-cell ion via plasma ne cell adhesion nolecules		stimulus	sulfur	death	myoblast
organonitrogen compound biosynthetic	regulation tri of response n	audation of .	ation phosphorylation	biosynthetic process positive regulation of histone	peptidyl–amii acid	acid metab	positive regulation of cellula	n protein autophosphorylation	inflammatory response	of respo	nse	pmental	cell	organ	bio	mpound synthesis	immune system	cell adhesion molecule
process positive regulation of macromolecule metabolic process	organonitrogen compound	positive egulation of proteo	glycan RNA bolic 3'-end	peptidyl-tyrosine ma		regulation regulation	on movement on 3'-UTR	nent .	inflammator	respor	ess se onse	cess pr	oliferation	sulfur co sulfur co meta meta	pholic	ological	process	production skeletal muscle satellite cell activation