REVIGO Gene Ontology treemap

								cric Oritology							
complemen activation, alternative	inflamma	ntory	retinoid metabolic process	negative regulation o nucleotide metabolic	metabolic	phototransduction, visible light	negative regulation of mitochondrial DNA replication	vocal learning	carbohydrate transport	regulation of ribosome biogenesis regulation	process	regulation	regulation of mitochondrial fusion	pyrimidine–containii compound salvage	ŭ l
pathway	one PNA	snoRNA catabolic process		process	protoin	mitochondrial genome maintenance positive regulation of phagocytosis	positive regulation of fat cell proliferation positive regulation of mesenchymal stem cell proliferation	detection of external stimulus	lipid localization	of response	hormone a metabolic	and bile responsible responsib	onse neurotransmitter catabolic process	cytosine	negative regulation
dITP catabolic process	catabolic			aldehyde netabolic process	protein activation cascade			negative regulation of glucose import	otransduction,	response to visible light stimulus	oocyte rematuration of	negative regulation regulation regulation	sitive response	nucleoside biosynthetic process	I DIOSVINITATIO
activation of membrane	adenosine to galactosylce		eramide ac	a-aminobutyne	negative regulation of nucleoside				fat cell			response secr	etion positive		
nitric oxide production	cellular lipid	cellular lipid acetate metabolic metabol		ľ	metabolic process	mesenchymal stem cell		insulin stimulus negative regulation	proliferation regulation of inositol 1,4,5-trisphosphate-sensitive	by electric by electric cou		development local plasm	ablishment of protein alization to na membrane resorption	regulation of ATP biosynthetic process	pyrimidine-containing compound metabolic process
involved in inflammatory response	complement ac	proce ctivation,	sul , alterņativ		metabolic process	proliferation		regulation of rRNA processing	calcium-release channel	i i c uulalloii i	calcium ion	radiation positive regulation of lipid storage		response to organophosphoru	cellular response to
peptidyl-aspartic acid hydroxylation	metabolic	flammatory response	triglycerid biosynthet process	e lipid ic metabolic process	nucleobase–containing small molecule catabolic process	lipid digestion	skeleta	al brain renin-angioten: iber system	paramesonephric sin duct development	head developmen	tube left/right pattern formation	substrate-depende cell migration, cell extension	digestion	respon	cellular se to
peptidyl-aspartic	activating a	platelet activating factor	chitin catabolic	doxorubicin metabolic metabolic process	hydroxylation		transforn growth fa	determination of digestive tract	e body	lung vasculature developmen	phagocytosi recognitior	l valve	system is process	organopho	stimulus
	positive	netabolic process positive	process			lung saccule development	beta activ	ation left/right asymmetr		regulation of tionsenchyma stem cell	I mesenchyma	development	eyelid development in camera–type eye	ot nitrogen	response to jasmonic acid
snoRNA metabolic process	nucleoside dou	egulation of uble-strand reak repair	nucleobase metabolic process		catabolic process	muscle filame sliding	face nt morphoge		morphogenesis	differentiation bone morphogenesi	tongue	negative regulation of bone mineralization	velopment system	detection of detection of s	external
valine catabolic process	oxidation-reduction process	humoral immune esponse	of response	nitrosative s	of process	epiboly involved gastrulation wit	th developn	01 5611501	uterus morphogenesis	cell migration involved in	actin	embryonic camera-type	macrophage		stimulus etimulus
p100033	16	response	to stress	response		mouth forming sec	cond	Tiouron axe		gastrulation	movement	formation	chemotaxis	cell recognition	