REVIGO Gene Ontology treemap

									ology tioo									
nucleic acid metabolic process	gene expressior	macromo biosynt	cellular macromolecule biosynthetic process		cellular aromatic compound metabolic process		I metabolic process I		anic cyclic mpound olic process		el embry	in utero reg embryonic of development diffe		inner cell mass cell proliferation	cellula respons to stres	r apo se sigr ss pat	naling Is	cellular response to aminar fluid shear stress
										fat cell differentiatior	lamellipodium	fat pad development	atrioventricul node developmer	pacemaker	ER-nucleu signaling	receptor	intracellula receptor signaling	stress–activated protein kinase signaling
transcription from RNA polymerase II promoter	cellular nitrogen compound metabolic	regulation of gene expressio	n RNA	orocessing	prima metabo proce	olic	RNA splici	process		cardiac pacemaker cell differentiation	epithelial cell maturation involved in prostate gland of	glandular epithelial cell differentiation		neuron fate	of cellular	toll-like receptor	NIK/NF-kappa	reticulum
	process		positive organi		ic cyclic			positive		positivplacenta blood ve		d vessel d	developn		stresscell	lular respons	nse to str	ess stress
		cellular	regulation	n of com	boulla i	NA-templ	I DIOSVI	ımeucı	regulation of	_	regulation of	spinal cord	adipose	nervous	501622			
	regulation	metabolic process	protein kir activity	nase biosy	nthetic	transcripti terminatio	ion, proc	ļi.	nterferon-beta biosynthetic	of neuron	osteoblast differentiation	motor neuron differentiation	tissue developmer	system t neuron differentiation	SMAD protein	hippo	negative regulation of translational initiation in	epidermal growth factor-activated receptor transactivation by G-protein coupled receptor signaling pathway
	of nitrogen	process	activity	y process				process		left/right		axial		prostato	signal	signaling	response to stress	
cellular macromolecule	compound			ncRN/	Α , , ,		DNA	DNIA		pattern	regulation of monocyte		spinal cord	l dland	transduction -	regulation of	response	regulation of
metabolic process	metabolic process	organic	peptidyl–arginine N–methylation	I MATANA	lic interleu	l m	netabolic	DNA	macromorcoale	formation	,	development	development axial	developmen	t endoplasmic	intrinsic apoptotic signaling pathway	to growth	response to
		substance		nrooo	produ	ction	process re	eplication						T	reticulum	in response to DNA		DINA damage
	trans	scription from I	KNA poly	polymerase II promoter						regulation of stem cell		mitral valve	mesoderm	endocardium morphogenesi	unfolded _ s protein	damage	factor	stimulus cellular
RNA metabolic process	positive regulation of RNA biosynthetic process	termination of RNA polymerase II transcription	egulation of nterleukin–6	macromolecule modification	vitamin biosynthe	Litt-associated 1.09		lation of logical		stem cell differentiation	differentiation		morphogenesi	mmary	response no	necroptotic process	response to interferon—be	response to mechanical
			production		process	S pr	rocess pr	ocess	cleavage		definitive notochord		keratinocyte development	duct positive regulation o		response to	intracellular steroid hormon	regulation of
			negative regulation	positive regulation of	histone arginine	rRNA metabol	mRNA lic metabolic	peptidyl-arg	protein		emopoiesis morphoge	morphogenesis	en	end bud fission growth		topologically ncorrect protein	receptor signal	I translational
			of RNA	interleukin–2 production	l mothydation l	proces			antylation			vesicle		p	ositive	egulation of	rogulation	modulation of transcription in other
nucleobase–containing compound metabolic process	regulation of	i oimeianonci i	metabolic process regulation	guanosine–containing compound metabolic process	transduction by		positive	regulati		RNA	transpo	nucleocyto	oomno.		julation of	ransferase	regulation	organism involved in
	transcription					interferon-gam secretion	regulation of 1 cell cytokine	of DN/	IA gene	localization			JOIT	prote	positive reg	ulation		ation of
	from RNA		of vascular smooth		phosphorylation	ו	production				microtub				of protein b	oinding	viral positive	process
	polymerase II		muscle	regulation	cellular	transcription cellular		process			negative	/e rendosomal		tubule		Price-specific regulation of phospholipase phospholipase	regulation	response to peptidoglycan
	promoter		contraction	of cellular	protein	initiation from RNA	A protein	~	P 10	mRNA transport	regulation	gulation of transport transport NA localization		oring at	•	nscription C activity	cellular proce	
	promotor	regulation of	positive	process	modification process	polymeras	se metabolic				RNA lo			_	activity .			
heterocycle metabolic process	nitrogen	RNA splicing	or motabolio	activation of	regulation of DNA						early endoso		negative re of norepin		romatin	nromosome	metaboli metabolis	regulation of cholesterol
				Rho GTPase		DNA-templated transcription,		peptidyl-methic modificatio	biosynthetic		to late	imnor	secre	tion	dification	rganization	process	homeostasis
	compound metabolic process	chaperone-mediated protein folding	GTP	activity	production	initiation	modification	modification	process		endosome transport	, Impor	regulat store-op	on or	romatin mo	dification		
				DNA methylation	histone	chanara	L-fucose	proteasomal	protoin	nuclear	negative	negative regulation			ucleoprotein riboni	ucleoprotein histone		DNA
				involved in	mRNA	chaperone mediated protein	tein Catabolic		ndent alvacevilation	transport	regulation	ľ	retrograde	de protein	Comp	plex subunit H3-K36 ganization demethylation	methylatio	
			process	gamete generation	metabolic process	folding requiri	namy rodaming		in Golgi		exocytos	import int	o transport	, ER to bio	ogenesis			checkpoint
					PIOCESS		1					Hucieus	l Gylo.					