REVIGO Gene Ontology treemap

							one ontology tree	<u> </u>								
nucleic acid metabolic process	cellular macı metabolic		RNA metabol	lic process	gene expression		regulation of metabolic process	cellular catabolic process	positive regulation of cellular process	regulation of RNA stability	regulation of mRNA stability	organelle or	ganization	regulation of organization organization covalent	on co	omolecular omplex ubunit anization regulation
						Holon	regulation of cellular catabolic process	autopriagy	cellular protein metabolic of catabolisn	metabolio process	gative	cellular co bioger	mponent ne organel	chromatin modification le organiza		of cellular component organization
cellular nitrogen compound metabolic process	cellular metabolic process	macron s biosyr	lular nolecule nthetic bi cess	macromole iosynthetic p		cellular nitrogen compound biosynthetic process	regulation of catabolic process	posttranscriptional regulation of gene expression	regulation of binding tregulation of molecular	regulation of transferase activity bio	egulation of regulation of iological transferase activity	chromosome	r ribonucleoprotein	ribonucleoprotein complex assembly	egulation o	protein
							cellular protein metabolic process	regulation of biological process	ubiquitin-dependent	metabolic process egulation of ytoplasmic ranslation of cellular translation of cellular process of cellular translation elongation of cellular translation of cellular trans		organization	complex I biogenesis	cellular component disassembly	nromosome rganizatior membrane organization	e complex disassembly mitochondrial
nucleobase–containing compound metabolic process	RNA processing	heterocycle biosynthetic process RNA proce	i combound i		obase–containing ound biosynthetic process	organic cyclic compound biosynthetic process	cellular response to stress	response to topologically incorrect protein signal transduction response to topologically incorrect protein signal response to topological response to topological response to the response to topological response to topological response to the response to topological response to the response to topological response to the response to th	piotic signaling mulus pathway conse chordate cygen embryonic	e ephrin c receptor g signaling / pathway cellular response	organic cyclonetabolic pro	ic compound metab	romolecule metabolism olic proces	Ce	ell cycle	negative
	regulation of cellular macromolecule biosynthetic	mRNA metabo	Olic macromolec modificatio	l metabo	olic from F	iption RNA rase II	regulation of cellular DNA-templated transcription in response to stress	response tresponse trespon		levels cellular response to nitrogen compound				mitoti	c cell cycl	е
heterocycle metabolic process	process organic substance	mRNA processing		modificati	vsine prote		response to response endoplasmic to reticulum unfolded	cellular response receptor	naling growth factor stimulus response to endogenous stimulus	to DNA damage intracellular	primary metabolic process – <mark>primary metabolism</mark>		nitrogen compound metabolism		metabolism	
cellular aromatic compound metabolic process	biosynthetic process	transcription from RNA	conjugation removal	in RNA polymera	metabolic process	phosphate-containing ncRNA compound metabolic process transcription	and the discount of a feet	ocalization	localization compound transport			substance lic process				catabolic
	cellular biosynthetic	polymerase II promoter RNA splicing	. protein deubiquitina	ation methylatio		amide metabolic process regulation of	cellula tr cellular	ransport	vesicle-m	import		biosy component ization or		nthesis	autophagy	catabolic catabolism process
	process		g protein metabol process	compoun metaboli	c polymerase p	RNA 3'-end DNA-templated transcription, elongation	localization	arriue	rclear organic substance transport		bioge	ogenesis v		rocess	establishment of tissue polarity	methylation