## REVIGO Gene Ontology treemap

						Ocho On	gy	<u> </u>							
oxidation-reduction	process I	eneration of precursor netabolites nd energy	carboxylic acid metabolic process	respiratory electron transport cha	small molecule metabolic n process	negative regulation of mast ce activation antigen processing presentation of exogenous pept antigen process antigen process	cyclase signaling pathway  positive regulation of antigen receptor-mediated signaling pathway ide lass II	positive regulation of type I pre- interferon-mediated signaling pathway e:	mediated immunity  antigen cessing and second second antigen characteristics and second antigen cell—cell—cell—cell—cell—cell—cell—cell	in gamete generation	hydrogen ion	hydrogen transport	intracellular transport	al ribose phosphate biosynthetic process	mitochondrial transport chloride transmembrane transport
organic acid metabolic process	pentose biosynthetic process	single–organism metabolic process	catabolic m	etabolic met	ntose regulation o abolic lipid cataboli cess process	and presentation  peptide antige  MHC class	inoic glutamate receptor signaling	proliferation for B cell receptor r.	regulation of bioloid receptor signaling pathway	cell cytokine production  TRAM-dependent toll-like receptor 4	transmembrane transport mitochondrial	lactate transmembrane transport	ion ransport reg	anion Insport  ulation of ptic vesicle ocytosis	lasma membrane long-chain fatty acid transport  regulation of tochondrial membrane permeability involved programmed necrotic cell death
monosaccharide metabolic process	pigment catabolic process	compound metabolic process	catabolic cata process pro	enoid tetrapyrrole bolic metabolic cess process	biosynthetic process biosynthet process	bone	ptide de production involver in immune response diencephalon regu	of LIV/	e negative regulation	iral capsid econdary econdary neglopment negative regulation of enterferon—beta	coupled proton transport	lactate transport	transport along nicrotubule position of mitocholism respira	ndrial mi	smooth muscle nyperplasia tochondrial espiratory
small molecule	porphyrin–containing compound catabolic process		acid metabolism fatty a biosyntl process glycoside carbohydromath compound fatty a compound	netic biosynthetic process	cholestero cholestero catabolic process process	development	inhibition of cysteine-type regu	mber cyclohydrol lation l activity paraxia mesoderr rotein conylation commitm	y looping al mal pharynx e development	process  positive regulation of	response cellu	cotine jasmo aci stimu	onic d lasse  I asse  NADH dehydrogen complex	mbly I k	involved in
catabolic process	glutathione metabolic process	acid metabolic process galactose	catabolic process  ketone body	metabolic process cellular icosar	monophospha	regulation of apoptotic process involved in morphogenesis	n revise of	row develop ctory mitral layer regulatio of tongu muscle co	oment regulation of heart looping	sebaceous	to response cadmic special cadmic catal	enyl cellula	chain comitochon respirate	drial positive	assembly e regulation
cofactor metabolic process	lipid catabolic		biosynthetic process cellular ketone boo	process proces cellular derma	tan galactitol malonat		cell fate protein determination	positive regulation vascula wound hea	m of muscle fiber differentiation	zymogen inhibition P-dependent	to to lip	response respons platinum	e to compliant ion assem	assemb	assembly
tricarboxylic acid cycle	positive regulation of lipid catabolic process	catabolic process sulfide oxidation	metabolic process  regulation of cellular ketone metabolic process	metabolic Retone metabolic Retone metabolic by positive regular transcription from polymerase III par	process process thiamine sphingarine-1-phosphase diphosphia	regulation of hormone levels		nervous system myelin maintenance positive	excretion copro to	translational tein targeting membrane negative regulation	regulation of	regulation of respiratory burst f nitric-oxide	glucose (glucose metame	6-phospha tabolism	ide ate utilization SS
NADP metabolic process	valyl–tRNA aminoacylatio	sulfide oxidation, using sulfide:quinone oxidoreductase	cellular aldehyde lipid metabolic oxidatio process	branched-chain amino acid biosynthetic process process	thiamine tRNA-type intron splice site metabolic recognition	androgen biosynthetic process	regulation of	protein protein to an endoplasmic reticulum	of re	potential	regulation of - exidoreductase activity	reg	ulation GTP pydrolase ctivity protein sumoyiati	sumoylat	regulation of nitrogen utilization