## REVIGO Gene Ontology treemap

					, in the control of t	•					
translation		mRNA splicing, via spliceosome			macropinoc <mark>macropinocytosis</mark>		intracellular protein transport	sodium ion transport	response to cad	dmium ion	response to salt stress
		rRNA processing					protein targeting to plasma membrane				
translational initiation		nucleotide metabolic	abolic peptidyl-pro				sodium ion transmembran transport	calcium ion e import into cell	defense response	nse to cadmiu defense resp to bacteriu	l arsenic-containing
cytoplasmic translation <b>mR</b> l	protein		isomerization mitochondrial electron				ion tra	ansport	abscisic	response to	ethylene–activated signaling pathway
RNA secondary	catabolic process	proteolysis	cytoo	nsport, juinol to chrome c		sporulation resulting	I Sorocaro	development	acid–activated signaling pathway	brassinostero mediated signaling pathway	response to ethylene
structure unwinding	peptidyl–proline hydroxylation to 4–hydroxy–L–proline	mitotic recombination	n ca	eptide tabolic ocess	embryo development ending in seed dormancy					paima	
DNA topological change	chromosome segregation	lysine biosynthetic process via diaminopimelate		DNA-dependent DNA replication	embryo developme	nt ending in seed dorr	nancy cell redox homeostasis	long-term synaptic potentiation	microtubule-based movement microtubule-ba	assembly	protein folding
RNA splicing	chromosome organization	regulation of translation	tRNA me	ethylation	pollen development	neuronal action potential	negative regulation of meiotic cell cycle	pollen tube growth	cilium movem in cell m		reproduction