Revigo TreeMap

proteasome-mediated ubiquitin-dependent	translation	histone	acetylation	positive regulation of transcription elongation by RNA polymerase II		apoptotic signaling pathway			aerobic respiration		
protein catabolic process proteasome-mediated	ubiquitin-dependent protein cat	abolic process		positive	regulation of trans	positiv	ositive regulation				
	protein deubiquitinatio	protein deubiquitination		DNA dama <mark>elongati</mark> response	on by RNA polym	ierase II	assembly		aerobic respiration mitochondrial electron transport, NADH to ubiquinone		
mitochondrial translation	protein polyubiquitinati	isoleucine catabolic process	cytoplasmic translation		positive regulat transcription ini by RNA polyme	tiation	positive regulation of nitochondrial translation				
			mRNA processing	regulation of DNA-templated transcription	regulation double-stra	nd '	positive regulation of telomerase activity		proton motive force–driven mitochondrial ATP synthesis		
mitochondrial respiratory mitochondria chain complex I assembly	rRNA processing I respiratory chain complex I ass	RNA splicing embly		intracellular pro	vesicle-med transport	chron seg	omosome nosome seg gregation	mitotic regation ytokinesis	cell cycle	rhythmic process	
	chromatin organization	RNA polymerase II preinitiation complex assembly	cellular component biogenesis		retrograd vesicle-med transport, (to endoplas reticulur	diated Golgi smic	cell divisio	n	termination of RNA polymerase transcription	in utero II embryonic development	