





































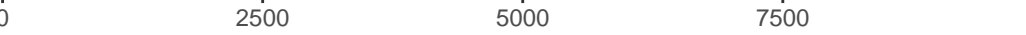


Pathway	Gene ranks	NES	pval	padj
nucleolus		2.10	1.6e−06	1.0e−03
fumagillin biosynthetic process		2.10	6.0e−06	1.9e−03
pseurotin A biosynthetic process		1.89	1.7e−05	3.7e−03
ribosomal large subunit biogenesis		2.01	1.2e−04	1.6e−02
rRNA processing		2.00	1.2e−04	1.6e−02
prenyltransferase activity		1.83	2.2e−04	2.0e−02
fumitremorgin B biosynthetic process		1.88	2.3e−04	2.0e−02
secondary metabolite biosynthetic process		1.59	2.4e−04	2.0e−02
secondary metabolic process		1.92	4.0e−04	2.9e−02
preribosome. large subunit precursor		1.90	8.2e−04	5.4e−02
SSU−rRNA from 5.8S rRNA and LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.81	3.0e−03	1.8e−01
preribosome. small subunit precursor		1.67	6.1e−03	3.2e−01
maturation of LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.70	6.4e−03	3.2e−01
small−subunit processome		1.73	7.4e−03	3.4e−01
shamixanthone biosynthetic process		1.76	9.0e−03	3.9e−01
ribosomal small subunit biogenesis		1.71	9.9e−03	4.0e−01
endonucleolytic cleavage in 5'−ETS of tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.73	1.2e−02	4.5e−01
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.72	1.3e−02	4.5e−01
endonucleolytic cleavage to generate mature 5'−end of SSU−rRNA from (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.72	1.3e−02	4.5e−01
helvolic acid biosynthetic process		1.65	1.6e−02	5.3e−01
proteasome core complex. beta−subunit complex		−1.34	1.6e−01	1.0e+00
cytoplasm to vacuole targeting by the Cvt pathway		−1.30	1.6e−01	1.0e+00
extrinsic component of membrane		−1.32	1.5e−01	1.0e+00
protein targeting to vacuole		−1.35	1.5e−01	1.0e+00
actin cytoskeleton organization		−1.34	1.4e−01	1.0e+00
phagophore assembly site		−1.35	1.4e−01	1.0e+00
proteasomal ubiquitin−independent protein catabolic process		−1.37	1.3e−01	1.0e+00
SCF ubiquitin ligase complex		−1.37	1.2e−01	1.0e+00
cellular response to pH		−1.37	1.2e−01	1.0e+00
obsolete integral component of Golgi membrane		−1.39	1.1e−01	1.0e+00
actin cortical patch		−1.40	1.1e−01	1.0e+00
negative regulation of DNA−templated transcription		−1.40	1.1e−01	1.0e+00
macroautophagy		−1.42	1.0e−01	1.0e+00
cellular response to hydrogen peroxide		−1.45	9.5e−02	1.0e+00
late endosome to vacuole transport		−1.42	8.9e−02	1.0e+00
cellular response to farnesol		−1.45	8.9e−02	1.0e+00
intracellular anatomical structure		−1.34	8.7e−02	1.0e+00
cytosolic small ribosomal subunit		−1.48	7.6e−02	1.0e+00
proteasome−mediated ubiquitin−dependent protein catabolic process		−1.53	6.6e−02	1.0e+00
peroxisome		−1.65	3.6e−02	8.7e−01