

Pathway	Gene ranks	NES	pval	padj
nucleolus		3.20	4.0e-27	2.6e-24
fumagillin biosynthetic process		2.55	1.8e-12	5.7e-10
rRNA processing		2.73	1.5e-11	3.2e-09
small-subunit processosome		2.72	3.9e-11	6.3e-09
preribosome. large subunit precursor		2.65	2.9e-10	3.8e-08
ribosomal large subunit biogenesis		2.61	2.5e-09	2.8e-07
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.56	1.5e-08	1.4e-06
pseurotin A biosynthetic process		2.11	3.2e-08	2.6e-06
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.35	6.8e-08	4.4e-06
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.35	6.8e-08	4.4e-06
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.45	1.6e-07	9.6e-06
preribosome. small subunit precursor		2.29	6.7e-07	3.4e-05
ribosomal small subunit biogenesis		2.35	6.9e-07	3.4e-05
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.25	1.2e-05	5.7e-04
conidium formation		1.79	1.7e-05	7.6e-04
ribosome biogenesis		2.02	1.0e-04	4.2e-03
90S preribosome		1.93	1.7e-04	6.3e-03
filamentous growth of a population of unicellular organisms in response to starvation		1.74	3.7e-04	1.3e-02
hyphal growth		1.52	5.5e-04	1.8e-02
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.97	7.2e-04	2.2e-02
proteasome core complex. alpha-subunit complex		-1.35	1.5e-01	7.2e-01
protein refolding		-1.33	1.5e-01	7.2e-01
actin cortical patch organization		-1.36	1.4e-01	7.2e-01
proteasome storage granule		-1.32	1.4e-01	7.2e-01
peroxisomal membrane		-1.33	1.4e-01	7.2e-01
carbohydrate catabolic process		-1.38	1.2e-01	6.8e-01
copper ion binding		-1.40	1.2e-01	6.7e-01
cellulase activity		-1.39	1.1e-01	6.7e-01
proteasomal ubiquitin-independent protein catabolic process		-1.37	1.1e-01	6.7e-01
protein-folding chaperone binding		-1.42	1.0e-01	6.4e-01
xylan catabolic process		-1.41	9.6e-02	6.2e-01
protein folding		-1.38	9.5e-02	6.2e-01
proteasome-mediated ubiquitin-dependent protein catabolic process		-1.38	8.7e-02	6.0e-01
pigment metabolic process involved in developmental pigmentation		-1.44	8.2e-02	5.8e-01
secondary metabolic process		-1.37	6.3e-02	5.0e-01
hydrolase activity. acting on glycosyl bonds		-1.52	5.2e-02	4.4e-01
ergot alkaloid biosynthetic process		-1.57	3.7e-02	3.5e-01
asperthecin biosynthetic process		-1.64	3.3e-02	3.3e-01
secondary metabolite biosynthetic process		-1.36	1.8e-02	2.1e-01
fumigaclavine C biosynthetic process		-2.00	1.2e-04	4.5e-03