

Pathway	Gene ranks	NES	pval	padj
mycotoxin biosynthetic process		1.80	3.9e-03	1.0e-01
secondary metabolic process		1.62	6.9e-03	1.6e-01
fumigaclavine C biosynthetic process		1.72	8.4e-03	1.8e-01
cellular response to iron ion starvation		1.71	1.1e-02	2.1e-01
gliotoxin biosynthetic process		1.63	1.3e-02	2.4e-01
peroxisomal membrane		1.59	2.3e-02	3.5e-01
secondary metabolite biosynthetic process		1.26	2.4e-02	3.5e-01
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process		1.57	2.5e-02	3.6e-01
xylan catabolic process		1.59	2.6e-02	3.6e-01
pigment metabolic process involved in developmental pigmentation		1.57	3.0e-02	4.0e-01
cytochrome-c oxidase activity		1.51	5.4e-02	6.3e-01
protein import into peroxisome matrix		1.45	5.7e-02	6.3e-01
proteasomal ubiquitin-independent protein catabolic process		1.48	5.8e-02	6.3e-01
proteasome storage granule		1.45	6.7e-02	6.6e-01
actin cortical patch organization		1.43	6.9e-02	6.7e-01
peroxisomal importomer complex		1.42	7.3e-02	6.9e-01
proteasome-mediated ubiquitin-dependent protein catabolic process		1.40	8.3e-02	7.1e-01
protein polyubiquitination		1.40	9.8e-02	7.2e-01
ergot alkaloid biosynthetic process		1.36	1.1e-01	7.2e-01
threonine catabolic process		1.36	1.1e-01	7.2e-01
ribosomal large subunit export from nucleus		-1.88	1.9e-03	6.1e-02
ribosome biogenesis		-1.93	1.7e-03	5.8e-02
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-1.92	1.4e-03	5.2e-02
obsolete polysome		-1.92	1.4e-03	5.2e-02
90S preribosome		-1.88	1.2e-03	5.0e-02
RNA polymerase I complex		-1.89	6.0e-04	2.6e-02
RNA polymerase I activity		-1.89	6.0e-04	2.6e-02
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.15	3.0e-04	1.5e-02
helvolic acid biosynthetic process		-2.00	2.0e-04	1.1e-02
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.32	7.6e-05	4.5e-03
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.18	3.3e-05	2.2e-03
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.18	3.3e-05	2.2e-03
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.36	2.5e-05	2.1e-03
preribosome. small subunit precursor		-2.15	1.4e-05	1.3e-03
ribosomal small subunit biogenesis		-2.21	1.1e-05	1.2e-03
rRNA processing		-2.41	8.1e-06	1.1e-03
ribosomal large subunit biogenesis		-2.45	5.9e-06	9.5e-04
preribosome. large subunit precursor		-2.51	1.9e-06	4.2e-04
small-subunit processome		-2.60	8.7e-08	2.8e-05
nucleolus		-2.83	2.1e-14	1.4e-11