
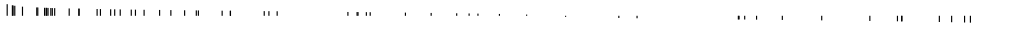















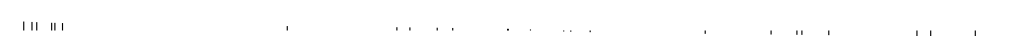


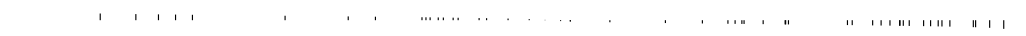
















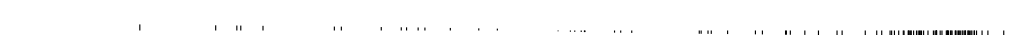



Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process		2.07	1.4e−04	1.3e−02
secondary metabolic process		1.92	1.4e−04	1.3e−02
ergot alkaloid biosynthetic process		1.86	1.4e−04	1.3e−02
structural constituent of ribosome		1.80	4.6e−04	3.2e−02
helvolic acid biosynthetic process		1.83	1.8e−03	7.9e−02
mycotoxin biosynthetic process		1.85	2.1e−03	8.7e−02
cytochrome−c oxidase activity		1.74	2.5e−03	9.7e−02
cytosolic large ribosomal subunit		1.81	3.0e−03	1.1e−01
secondary metabolite biosynthetic process		1.45	3.8e−03	1.3e−01
cytosolic small ribosomal subunit		1.81	4.9e−03	1.6e−01
gliotoxin biosynthetic process		1.75	1.1e−02	3.0e−01
cellular response to iron ion starvation		1.78	1.5e−02	3.8e−01
protein−folding chaperone binding		1.66	2.0e−02	4.3e−01
protein folding		1.60	2.1e−02	4.3e−01
fungal−type cell wall		1.39	2.4e−02	5.0e−01
prenyltransferase activity		1.60	2.5e−02	5.0e−01
pigment metabolic process involved in developmental pigmentation		1.56	3.1e−02	5.9e−01
melanin biosynthetic process		1.56	3.5e−02	6.4e−01
ergosterol biosynthetic process		1.56	4.2e−02	7.3e−01
asperthecin biosynthetic process		1.60	4.4e−02	7.3e−01
oxidoreductase activity		−1.61	4.8e−02	7.5e−01
nuclear periphery		−1.54	4.4e−02	7.3e−01
fumitremorgin B biosynthetic process		−1.63	4.3e−02	7.3e−01
poly(A)+ mRNA export from nucleus		−1.71	1.9e−02	4.3e−01
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		−1.79	1.8e−02	4.2e−01
ribosomal small subunit biogenesis		−1.80	1.7e−02	4.1e−01
cellular response to farnesol		−1.74	1.5e−02	3.8e−01
ribosomal large subunit export from nucleus		−1.77	9.3e−03	2.6e−01
RNA helicase activity		−1.75	9.0e−03	2.6e−01
SSU−rRNA from 5.8S rRNA and LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		−2.03	7.1e−03	2.2e−01
preribosome. small subunit precursor		−1.91	1.5e−03	6.8e−02
90S preribosome		−1.92	1.2e−03	6.1e−02
maturation of LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		−2.10	1.0e−03	5.5e−02
small−subunit processome		−2.01	6.4e−04	3.8e−02
preribosome. large subunit precursor		−2.05	5.0e−04	3.2e−02
ribosomal large subunit biogenesis		−2.32	3.1e−04	2.6e−02
endonucleolytic cleavage to generate mature 5'−end of SSU−rRNA from (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		−2.22	1.1e−04	1.3e−02
endonucleolytic cleavage in 5'−ETS of tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		−2.22	1.1e−04	1.3e−02
rRNA processing		−2.37	1.5e−05	4.8e−03
nucleolus		−2.68	4.8e−12	3.1e−09