Pathway	Gene ranks	NES	pval	padj
cytosolic large ribosomal subunit		3.48	7.3e−27	4.7e−24
structural constituent of ribosome		3.32	3.3e−22	1.1e−19
cytosolic small ribosomal subunit		2.80	8.4e−13	1.8e−10
cytoplasmic translation		2.75	7.8e−11	1.3e−08
mitochondrial ribosome		2.62	7.3e−09	9.5e−07
obsolete rRNA export from nucleus		2.45	1.0e−08	1.1e−06
RNA binding		2.43	3.5e−06	2.8e−04
fungal biofilm matrix		2.13	1.4e−05	1.0e−03
mitochondrial large ribosomal subunit		2.28	2.1e−05	1.4e−03
hyphal cell wall		2.18	6.7e−05	3.9e−03
chaperonin−containing T−complex		2.00	1.1e−04	5.7e−03
mitochondrial membrane		1.87	2.4e−04	1.2e−02
eukaryotic translation initiation factor 3 complex		2.01	2.9e−04	1.3e−02
maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		2.08	3.4e−04	1.4e−02
induction by symbiont of host defense response		2.10	3.4e−04	1.4e−02
mitochondrial small ribosomal subunit		2.02	5.5e−04	2.1e−02
cell surface		1.69	6.4e−04	2.2e−02
mitotic spindle pole body		2.04	6.6e−04	2.2e−02
ribosomal small subunit assembly		1.94	7.9e−04	2.6e−02
ribosomal large subunit assembly		1.97	9.3e−04	2.8e−02
mycotoxin biosynthetic process		−1.56	7.0e−02	4.6e−01
glutathione transferase activity		−1.50	6.4e−02	4.4e−01
negative regulation of sexual sporulation resulting in formation of a cellular spore		−1.68	5.6e−02	4.1e−01
sexual sporulation resulting in formation of a cellular spore		−1.70	4.7e−02	3.6e−01
emericellamide biosynthetic process		−1.72	3.9e−02	3.1e−01
regulation of DNA−templated transcription		−1.77	3.4e−02	3.0e−01
fumitremorgin B biosynthetic process		−1.67	2.0e−02	2.3e−01
prenyltransferase activity		−1.64	2.0e−02	2.3e−01
helvolic acid biosynthetic process		−1.70	1.7e−02	2.2e−01
o−orsellinic acid biosynthetic process		−1.66	1.7e−02	2.2e−01
sterigmatocystin biosynthetic process		−1.70	1.5e−02	2.0e−01
asperfuranone biosynthetic process		−1.74	1.3e−02	1.8e−01
syncytium formation by plasma membrane fusion		−1.80	5.8e−03	1.0e−01
monodictyphenone biosynthetic process		−1.87	5.2e−03	9.6e−02
austinol biosynthetic process		−1.84	4.1e−03	8.0e−02
autolysis		−1.85	3.7e−03	7.4e−02
chitinase activity		−1.85	3.6e−03	7.4e−02
dehydroaustinol biosynthetic process		−1.84	1.7e−03	4.1e−02
secondary metabolic process		−1.80	1.1e−03	3.2e−02
secondary metabolite biosynthetic process		−1.79	1.3e−08	1.2e−06