Pathway	Gene ranks	NES	pval	padj
cytosolic large ribosomal subunit		2.96	4.0e−15	2.6e−12
structural constituent of ribosome		2.71	1.3e−12	4.4e−10
nucleolus		2.40	3.2e−09	7.0e−07
cytosolic small ribosomal subunit		2.50	4.4e−08	7.2e−06
cytoplasmic translation		2.42	7.2e−07	9.4e−05
rRNA processing		2.21	1.8e−05	2.0e−03
maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		2.24	2.9e−05	2.7e−03
small−subunit processome		2.18	5.4e−05	4.4e−03
ribosomal large subunit biogenesis		2.16	7.0e−05	5.0e−03
preribosome. large subunit precursor		2.15	9.5e−05	6.2e−03
cytoplasm		1.44	1.2e−04	6.8e−03
mitochondrial ribosome		2.09	1.3e−04	6.8e−03
SSU−rRNA from 5.8S rRNA and LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		2.06	2.5e−04	1.3e−02
ribosomal small subunit assembly		1.96	3.7e−04	1.7e−02
ribosomal large subunit assembly		2.06	4.7e−04	2.0e−02
obsolete rRNA export from nucleus		1.98	5.8e−04	2.3e−02
RNA binding		1.89	1.6e−03	6.1e−02
protein import into nucleus		1.89	2.6e−03	9.5e−02
maturation of LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.90	3.3e−03	1.1e−01
chaperonin−containing T−complex		1.80	4.0e−03	1.3e−01
sterigmatocystin biosynthetic process		−1.41	1.2e−01	6.5e−01
prenyltransferase activity		−1.44	1.2e−01	6.5e−01
peptidase activity		−1.42	1.2e−01	6.5e−01
intracellular calcium ion homeostasis		−1.42	1.1e−01	6.3e−01
secondary metabolic process		−1.47	1.1e−01	6.3e−01
monodictyphenone biosynthetic process		−1.46	9.6e−02	6.1e−01
emericellamide biosynthetic process		−1.52	9.2e−02	6.1e−01
nitrogen compound metabolic process		−1.48	8.4e−02	6.1e−01
fatty acid catabolic process		−1.53	8.2e−02	6.1e−01
dehydroaustinol biosynthetic process		−1.56	8.0e−02	6.0e−01
fibrinogen binding		−1.54	7.2e−02	5.9e−01
austinol biosynthetic process		−1.59	7.0e−02	5.9e−01
glutathione transferase activity		−1.54	6.8e−02	5.9e−01
zinc ion binding		−1.59	5.5e−02	5.3e−01
xanthone−containing compound biosynthetic process		−1.61	5.4e−02	5.2e−01
chitinase activity		−1.65	4.1e−02	4.3e−01
autolysis		−1.67	3.7e−02	4.1e−01
gliotoxin biosynthetic process		−1.92	3.6e−02	4.1e−01
mycotoxin biosynthetic process		−1.85	1.8e−02	3.2e−01
secondary metabolite biosynthetic process		−1.57	1.5e−02	2.9e−01