













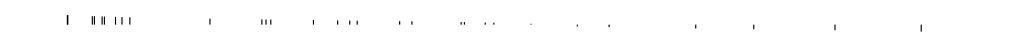









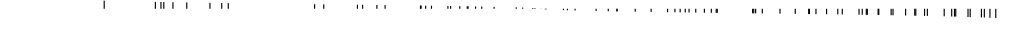

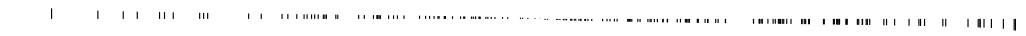















Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process		1.83	5.6e−05	3.3e−03
secondary metabolite biosynthetic process		1.38	7.5e−03	1.6e−01
ergot alkaloid biosynthetic process		1.62	7.7e−03	1.6e−01
protein refolding		1.57	2.2e−02	3.8e−01
copper ion binding		1.50	6.2e−02	7.3e−01
hydrolase activity. acting on glycosyl bonds		1.48	7.2e−02	8.0e−01
secondary metabolic process		1.33	9.2e−02	9.2e−01
asperthecin biosynthetic process		1.41	9.8e−02	9.2e−01
melanin biosynthetic process		1.42	1.1e−01	9.2e−01
pigment metabolic process involved in developmental pigmentation		1.38	1.3e−01	9.4e−01
protein–folding chaperone binding		1.34	1.4e−01	9.6e−01
sterol metabolic process		1.37	1.5e−01	9.7e−01
proteasomal ubiquitin–independent protein catabolic process		1.34	1.5e−01	9.8e−01
protein folding		1.28	1.8e−01	1.0e+00
negative regulation of DNA–templated transcription		1.33	1.8e−01	1.0e+00
proteasome core complex. alpha–subunit complex		1.34	1.8e−01	1.0e+00
proteasome–mediated ubiquitin–dependent protein catabolic process		1.23	2.0e−01	1.0e+00
cellulase activity		1.29	2.0e−01	1.0e+00
xylan catabolic process		1.25	2.3e−01	1.0e+00
cytosolic large ribosomal subunit		1.18	2.5e−01	1.0e+00
obsolete nucleosome positioning		−1.84	2.3e−03	7.2e−02
maturation of LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−1.91	1.8e−03	5.8e−02
cellular response to starvation		−1.59	1.2e−03	4.0e−02
filamentous growth of a population of unicellular organisms in response to starvation		−1.68	1.1e−03	4.0e−02
hyphal growth		−1.44	1.1e−03	4.0e−02
maturation of SSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−1.92	8.7e−04	3.5e−02
preribosome. small subunit precursor		−1.94	5.1e−04	2.2e−02
conidium formation		−1.61	4.4e−04	2.0e−02
fumitremorgin B biosynthetic process		−1.94	2.5e−04	1.2e−02
syncytium formation by plasma membrane fusion		−1.98	1.2e−04	6.7e−03
SSU–rRNA from 5.8S rRNA and LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−2.17	2.2e−05	1.4e−03
endonucleolytic cleavage in 5'–ETS of tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−2.18	6.7e−06	4.8e−04
endonucleolytic cleavage to generate mature 5'–end of SSU–rRNA from (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−2.18	6.2e−06	4.8e−04
small–subunit processome		−2.20	2.0e−06	1.8e−04
preribosome. large subunit precursor		−2.20	2.0e−06	1.8e−04
ribosomal large subunit biogenesis		−2.32	1.7e−06	1.8e−04
pseurotin A biosynthetic process		−2.06	2.7e−07	4.4e−05
rRNA processing		−2.43	1.2e−08	2.7e−06
fumagillin biosynthetic process		−2.54	1.6e−14	5.1e−12
nucleolus		−2.79	8.6e−19	5.6e−16