

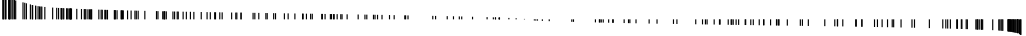
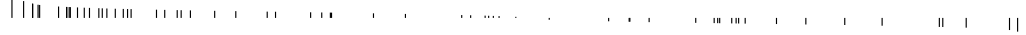
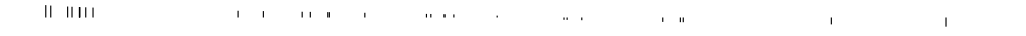
















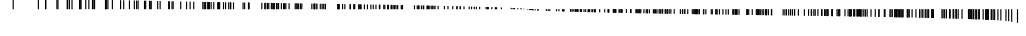




















Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process		2.10	1.2e-06	7.8e-05
ergot alkaloid biosynthetic process		1.75	5.9e-04	2.0e-02
secondary metabolite biosynthetic process		1.50	1.8e-03	5.7e-02
secondary metabolic process		1.62	1.0e-02	1.9e-01
protein folding		1.62	2.4e-02	3.5e-01
protein refolding		1.59	2.8e-02	3.8e-01
cytosolic small ribosomal subunit		1.55	4.0e-02	4.9e-01
protein-folding chaperone binding		1.53	4.2e-02	5.1e-01
asperthecin biosynthetic process		1.51	4.6e-02	5.3e-01
pigment metabolic process involved in developmental pigmentation		1.39	9.0e-02	6.5e-01
cytosolic large ribosomal subunit		1.35	1.0e-01	6.5e-01
hydrolase activity. acting on glycosyl bonds		1.40	1.0e-01	6.6e-01
proteasomal ubiquitin-independent protein catabolic process		1.39	1.0e-01	6.6e-01
cellular response to iron ion starvation		1.33	1.4e-01	7.6e-01
cytochrome-c oxidase activity		1.31	1.6e-01	8.2e-01
copper ion binding		1.32	1.7e-01	8.5e-01
proteasome core complex. alpha-subunit complex		1.30	1.8e-01	8.7e-01
cellulase activity		1.30	1.9e-01	8.9e-01
negative regulation of DNA-templated transcription		1.29	1.9e-01	8.9e-01
sterol metabolic process		1.29	1.9e-01	9.0e-01
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-1.91	2.2e-03	6.1e-02
nucleus		-1.23	2.2e-03	6.1e-02
syncytium formation by plasma membrane fusion		-1.99	7.2e-04	2.3e-02
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.04	3.8e-04	1.4e-02
90S preribosome		-2.03	3.1e-04	1.2e-02
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.05	1.4e-04	5.5e-03
ribosomal small subunit biogenesis		-2.10	8.8e-05	3.8e-03
conidium formation		-1.76	7.1e-05	3.3e-03
preribosome. small subunit precursor		-2.19	2.3e-05	1.1e-03
fumitremorgin B biosynthetic process		-2.14	1.8e-05	9.6e-04
pseurotin A biosynthetic process		-2.18	2.1e-06	1.2e-04
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.32	9.2e-07	6.7e-05
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.32	9.1e-07	6.7e-05
preribosome. large subunit precursor		-2.40	5.9e-07	5.5e-05
ribosomal large subunit biogenesis		-2.41	3.4e-07	3.7e-05
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.35	2.1e-07	2.7e-05
small-subunit processome		-2.45	2.0e-07	2.7e-05
rRNA processing		-2.63	3.3e-10	7.2e-08
fumagillin biosynthetic process		-2.55	1.2e-11	3.8e-09
nucleolus		-3.13	3.6e-23	2.4e-20