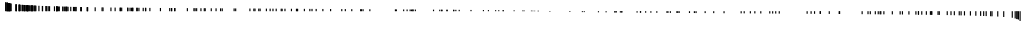









































Pathway	Gene ranks	NES	pval	padj
secondary metabolite biosynthetic process		2.01	2.8e-06	1.8e-03
pseurotin A biosynthetic process		1.83	3.4e-04	1.1e-01
helvolic acid biosynthetic process		1.82	9.8e-04	1.8e-01
cytosolic large ribosomal subunit		2.03	1.1e-03	1.8e-01
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.91	1.5e-03	1.8e-01
fumagillin biosynthetic process		2.02	1.7e-03	1.8e-01
preribosome. large subunit precursor		1.87	2.6e-03	1.9e-01
ribosomal large subunit biogenesis		1.84	2.7e-03	1.9e-01
small-subunit processome		1.84	3.1e-03	1.9e-01
cytosolic small ribosomal subunit		1.79	3.6e-03	1.9e-01
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.71	3.7e-03	1.9e-01
rRNA processing		1.81	3.8e-03	1.9e-01
asperfuranone biosynthetic process		1.71	6.6e-03	3.1e-01
structural constituent of ribosome		1.83	1.0e-02	4.3e-01
nucleolus		1.89	1.0e-02	4.3e-01
o-orsellinic acid biosynthetic process		1.63	1.3e-02	4.9e-01
ribosomal small subunit biogenesis		1.64	1.5e-02	5.5e-01
secondary metabolic process		1.63	1.6e-02	5.5e-01
monodictyphenone biosynthetic process		1.68	1.7e-02	5.5e-01
preribosome. small subunit precursor		1.65	1.9e-02	5.7e-01
DNA-directed DNA polymerase activity		-1.26	2.0e-01	1.0e+00
xylan catabolic process		-1.26	2.0e-01	1.0e+00
peroxisomal membrane		-1.26	2.0e-01	1.0e+00
protein deneddylation		-1.29	1.9e-01	1.0e+00
sulfate assimilation		-1.30	1.9e-01	1.0e+00
proteasomal ubiquitin-independent protein catabolic process		-1.30	1.8e-01	1.0e+00
COP9 signalosome		-1.31	1.8e-01	1.0e+00
mitotic actomyosin contractile ring. intermediate layer		-1.33	1.7e-01	1.0e+00
proteasome storage granule		-1.29	1.7e-01	1.0e+00
positive regulation of G2/M transition of mitotic cell cycle		-1.34	1.6e-01	1.0e+00
vacuolar transport		-1.36	1.6e-01	1.0e+00
fatty acid beta-oxidation		-1.36	1.5e-01	1.0e+00
Arp2/3 protein complex		-1.40	1.3e-01	1.0e+00
Arp2/3 complex-mediated actin nucleation		-1.40	1.3e-01	1.0e+00
fatty acid metabolic process		-1.42	1.2e-01	1.0e+00
positive regulation of asexual sporulation resulting in formation of a cellular spore		-1.40	1.2e-01	1.0e+00
negative regulation of sexual sporulation resulting in formation of a cellular spore		-1.48	1.0e-01	1.0e+00
protein autophosphorylation		-1.48	9.0e-02	1.0e+00
septin ring assembly		-1.53	7.3e-02	1.0e+00
fumitremorgin B biosynthetic process		-1.92	2.0e-03	1.8e-01