Pathway	Gene ranks	NES	pval	padj
nucleolus	1. Name (1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	2.84	1.3e-18	8.2e-16
fumagillin biosynthetic process	N on-	2.48	1.1e-11	3.5e-09
rRNA processing	IMMETHEM TO THE TENED OF THE TE	2.48	1.1e-08	2.3e-06
ribosomal large subunit biogenesis	100 M (10310) ()	2.39	6.4e-07	1.0e-04
small-subunit processome		2.26	4.6e-06	5.6e-04
pseurotin A biosynthetic process		2.06	5.2e-06	5.6e-04
preribosome. large subunit precursor	100 H 100 H 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2.22	1.0e-05	9.5e-04
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	MERCHANICA CONTRACTOR	2.15	1.8e-05	1.5e-03
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.11	6.8e-05	4.9e-03
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.11	7.5e-05	4.9e-03
preribosome. small subunit precursor		2.03	8.2e-05	4.9e-03
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	tin notice of the second of	2.01	2.1e-04	1.1e-02
ribosomal small subunit biogenesis	tentro en la companya de la companya	1.92	1.3e-03	6.6e-02
filamentous growth of a population of unicellular organisms in response to starvation	THE COURT OF THE CONTROL OF THE CONT	1.61	2.6e-03	1.2e-01
hyphal growth	#1 HII - 11 1#1 / HIII HIIII HIIII HIIII HIIII HIIII HIIII HIIII HIII HIIII HIII	1.36	2.7e-03	1.2e-01
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	unu dan	1.86	3.1e-03	1.2e-01
syncytium formation by plasma membrane fusion	Microsoft Communication of the	1.80	3.3e-03	1.2e-01
conidium formation	To the terminal commence of the commence of th	1.48	3.4e-03	1.2e-01
poly(A)+ mRNA export from nucleus	The first of the second of the	1.82	5.1e-03	1.7e-01
helvolic acid biosynthetic process		1.79	5.5e-03	1.7e-01
pigment biosynthetic process		-1.20	2.8e-01	1.0e+00
xylan catabolic process	The second of th	-1.21	2.7e-01	1.0e+00
protein folding	And the second of the second o	– 1.16	2.7e-01	1.0e+00
DNA-binding transcription factor activity. RNA polymerase II-specific		-1.24	2.4e-01	1.0e+00
proteasome core complex. alpha-subunit complex		-1.27	2.2e-01	1.0e+00
protein-folding chaperone binding	en e	-1.29	2.1e-01	1.0e+00
proteasome storage granule		-1.27	2.0e-01	1.0e+00
negative regulation of DNA-templated transcription		-1.32	1.7e-01	1.0e+00
proteasomal ubiquitin-independent protein catabolic process		-1.31	1.7e-01	1.0e+00
proteasome-mediated ubiquitin-dependent protein catabolic process	the second of th	-1.29	1.5e-01	1.0e+00
melanin biosynthetic process		-1.34	1.5e-01	1.0e+00
sterol metabolic process		-1.36	1.3e-01	1.0e+00
hydrolase activity. acting on glycosyl bonds		-1.38	1.2e-01	1.0e+00
copper ion binding		-1.42	9.6e-02	1.0e+00
protein refolding		-1.43	8.8e-02	1.0e+00
secondary metabolite biosynthetic process		−1.24	7.2e-02	9.5e-01
pigment metabolic process involved in developmental pigmentation		-1.46	6.5e-02	9.3e-01
asperthecin biosynthetic process		-1.49	5.4e-02	9.1e-01
ergot alkaloid biosynthetic process		-1.60	1.7e-02	3.6e-01
fumigaclavine C biosynthetic process		-1.71	7.9e-03	2.3e-01
	0 2500 5000 7500			