Pathway	G	Sene ranks	NES	pval	padj
intracellular anatomical structure	MILE TO THE THE TAX TO		2.01	3.9e-06	2.5e-03
cellular response to heat	Military and a second of the s		1.93	4.2e-04	9.2e-02
fungal-type cell wall	MITTER MI		1.59	5.8e-04	9.4e-02
protein-folding chaperone binding	1 100 1		1.80	3.0e-03	3.9e-01
protein refolding	No. 1		1.73	7.2e-03	7.8e-01
protein folding	11 100 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1.70	1.3e-02	1.0e+00
cellular response to osmotic stress	I to a constant of the constan	· · · · · · · · · · · · · · · · · · ·	1.61	2.3e-02	1.0e+00
chromosome segregation	CO C		1.63	2.3e-02	1.0e+00
positive regulation of DNA-templated transcription	to the second se		1.63	3.0e-02	1.0e+00
chromosome. centromeric region	to the control of the		1.54	3.6e-02	1.0e+00
regulation of fungal-type cell wall organization	Tit is a		1.52	3.8e-02	1.0e+00
mitotic spindle midzone	1 - 1 - 11 -		1.51	4.5e-02	1.0e+00
proteasome-mediated ubiquitin-dependent protein catabolic process	1 1 11 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	the second of th	1.47	4.5e-02	1.0e+00
positive regulation of G2/M transition of mitotic cell cycle	The state of the s		1.56	4.6e-02	1.0e+00
asperthecin biosynthetic process	Title is a management of	· · · · ·	1.51	5.4e-02	1.0e+00
protein homodimerization activity			1.51	6.0e-02	1.0e+00
negative regulation of G2/M transition of mitotic cell cycle	The second secon		1.50	6.9e-02	1.0e+00
protein import into peroxisome matrix	***************************************		1.47	7.2e-02	1.0e+00
positive regulation of protein import into nucleus	The state of the s		1.46	7.3e-02	1.0e+00
actin cortical patch organization			1.43	8.0e-02	1.0e+00
TOR signaling			-1.40	1.3e-01	1.0e+00
rRNA processing			-1.52	1.3e-01	1.0e+00
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	,	en e	-1.45	1.3e-01	1.0e+00
autolysis			-1.41	1.2e-01	1.0e+00
asperfuranone biosynthetic process			-1.48	1.1e-01	1.0e+00
emericellamide biosynthetic process			-1.51	1.1e-01	1.0e+00
xanthone-containing compound biosynthetic process		· · · · · · · · · · · · · · · · · · ·	<b>–1.56</b>	1.0e-01	1.0e+00
90S preribosome		0 0 0 0	<b>–1.47</b>	9.3e-02	1.0e+00
o-orsellinic acid biosynthetic process		"	<b>–1.48</b>	9.1e-02	1.0e+00
fumitremorgin B biosynthetic process			<b>–1.52</b>	9.0e-02	1.0e+00
fumagillin biosynthetic process		e e e e e e e e e e e e e e e e e e e	-1.64	8.8e-02	1.0e+00
negative regulation of sexual sporulation resulting in formation of a cellular spore			-1.68	8.5e-02	1.0e+00
dehydroaustinol biosynthetic process		и ц	-1.62	7.9e-02	1.0e+00
sexual sporulation resulting in formation of a cellular spore			<b>–1.65</b>	7.8e-02	1.0e+00
austinol biosynthetic process		и ц	-1.60	7.4e-02	1.0e+00
nucleolus			-1.49	6.4e-02	1.0e+00
oxidoreductase activity		en e	-1.77	5.3e-02	1.0e+00
helvolic acid biosynthetic process			-1.70	2.0e-02	1.0e+00
regulation of DNA-templated transcription	Name of the second seco		-1.88	8.5e-03	7.9e-01
secondary metabolite biosynthetic process	0 2500	5000 7500	-1.82	7.9e-05	2.6e-02
	0 2500	7000			