Pathway	Gene ranks	NES	pval	padj
secondary metabolite biosynthetic process	Minutes and the second of the	1.63	2.4e-04	7.8e-02
positive regulation of secondary metabolite biosynthetic process	m 1	1.71	1.2e-02	1.0e+00
negative regulation of G2/M transition of mitotic cell cycle		1.70	1.2e-02	1.0e+00
asperfuranone biosynthetic process		1.66	1.8e-02	1.0e+00
shamixanthone biosynthetic process	THE CONTRACTOR OF THE CONTRACT	1.59	3.2e-02	1.0e+00
cellular response to osmotic stress		1.57	4.2e-02	1.0e+00
membrane raft	The state of the s	1.55	4.9e-02	1.0e+00
prenyltransferase activity	m · · · · · · · · · · · · · · · · · · ·	1.50	5.7e-02	1.0e+00
cell wall-bounded periplasmic space		1.51	6.0e-02	1.0e+00
intracellular iron ion homeostasis		1.49	6.7e-02	1.0e+00
extracellular region	luminin annona i con caroni a	1.28	6.9e-02	1.0e+00
oxidoreductase activity		1.44	7.3e-02	1.0e+00
glutathione transferase activity		1.47	7.9e-02	1.0e+00
cellular response to hydrogen peroxide	termination of the second of t	1.43	8.4e-02	1.0e+00
glutathione metabolic process		1.45	8.7e-02	1.0e+00
asperthecin biosynthetic process	to the second of	1.42	8.9e-02	1.0e+00
protein homodimerization activity	The first control of the second of the secon	1.41	8.9e-02	1.0e+00
syncytium formation by plasma membrane fusion	The first of the contract of t	1.41	9.1e-02	1.0e+00
fibrinogen binding		1.43	9.7e-02	1.0e+00
o-orsellinic acid biosynthetic process		1.43	9.9e-02	1.0e+00
U1 snRNP		-1.44	9.9e-02	1.0e+00
vesicle-mediated transport	And the second of the second o	-1.37	9.6e-02	1.0e+00
negative regulation of septation initiation signaling		-1.46	9.1e-02	1.0e+00
protein targeting to ER		-1.47	8.6e-02	1.0e+00
endoplasmic reticulum to Golgi vesicle-mediated transport	C. C	-1.44	8.2e-02	1.0e+00
mitochondrial small ribosomal subunit	en e	-1.51	8.1e-02	1.0e+00
chaperonin-containing T-complex		-1.50	6.8e-02	1.0e+00
mRNA 3'-end processing		-1.51	6.5e-02	1.0e+00
U4/U6 x U5 tri-snRNP complex	On the second of	-1.52	6.2e-02	1.0e+00
poly(U) RNA binding		-1.56	4.9e-02	1.0e+00
RNA binding	the state of the s	-1.56	4.6e-02	1.0e+00
mitochondrial ribosome		-1.57	4.2e-02	1.0e+00
cytoplasmic translation		-1.79	3.3e-02	1.0e+00
protein glycosylation		-1.64	2.8e-02	1.0e+00
mitochondrial respiratory chain complex I assembly		-1.62	2.3e-02	1.0e+00
helvolic acid biosynthetic process		-1.70	1.5e-02	1.0e+00
obsolete rRNA export from nucleus		-1.73	1.0e-02	1.0e+00
cytosolic small ribosomal subunit		-2.08	8.4e-03	1.0e+00
cytosolic large ribosomal subunit	A compared to the compared to	-2.23	1.2e-03	2.5e-01
structural constituent of ribosome	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-2.28	1.8e-04	7.8e-02
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