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nucleolus		2.56	5.1e-13	3.3e-10
fumagillin biosynthetic process		2.53	3.3e-12	1.1e-09
pseurotin A biosynthetic process		2.10	2.9e-07	6.4e-05
rRNA processing		2.27	1.1e-05	1.8e-03
ribosomal large subunit biogenesis		2.16	8.6e-05	1.1e-02
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.02	4.8e-04	4.5e-02
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.02	4.9e-04	4.5e-02
preribosome. large subunit precursor		1.94	1.3e-03	1.1e-01
preribosome. small subunit precursor		1.93	1.6e-03	1.2e-01
small-subunit processome		1.88	2.3e-03	1.5e-01
poly(A)+ mRNA export from nucleus		1.86	3.8e-03	2.3e-01
protein transmembrane transporter activity		1.79	6.3e-03	3.4e-01
ribosomal small subunit biogenesis		1.74	7.3e-03	3.7e-01
obsolete nucleosome positioning		1.79	8.3e-03	3.7e-01
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.70	8.8e-03	3.7e-01
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.74	9.0e-03	3.7e-01
cellular response to starvation		1.36	1.8e-02	6.4e-01
90S preribosome		1.70	2.6e-02	8.3e-01
fumitremorgin B biosynthetic process		1.62	2.6e-02	8.3e-01
filamentous growth of a population of unicellular organisms in response to starvation		1.38	2.7e-02	8.3e-01
proteasome-mediated ubiquitin-dependent protein catabolic process		-1.16	2.8e-01	1.0e+00
protein targeting to membrane		-1.23	2.7e-01	1.0e+00
proteasome core complex. beta-subunit complex		-1.23	2.7e-01	1.0e+00
proteasome core complex. alpha-subunit complex		-1.23	2.7e-01	1.0e+00
proteasome storage granule		-1.24	2.4e-01	1.0e+00
secondary metabolite biosynthetic process		-1.12	2.4e-01	1.0e+00
proteasomal ubiquitin-independent protein catabolic process		-1.26	2.3e-01	1.0e+00
cellulase activity		-1.27	2.3e-01	1.0e+00
DNA-binding transcription factor activity. RNA polymerase II-specific		-1.29	2.2e-01	1.0e+00
protein folding		-1.23	2.1e-01	1.0e+00
negative regulation of DNA-templated transcription		-1.33	1.7e-01	1.0e+00
sterol metabolic process		-1.34	1.7e-01	1.0e+00
protein-folding chaperone binding		-1.33	1.7e-01	1.0e+00
cytosolic large ribosomal subunit		-1.26	1.7e-01	1.0e+00
ergot alkaloid biosynthetic process		-1.41	1.1e-01	1.0e+00
asperthecin biosynthetic process		-1.38	1.1e-01	1.0e+00
copper ion binding		-1.40	9.9e-02	1.0e+00
hydrolase activity. acting on glycosyl bonds		-1.38	9.8e-02	1.0e+00
protein refolding		-1.46	5.9e-02	1.0e+00
fumigaclavine C biosynthetic process		-1.58	1.6e-02	6.1e-01