## MÃ;rton Miskei

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10817531/publications.pdf

Version: 2024-02-01

623188 676716 1,427 22 14 22 citations g-index h-index papers 22 22 22 2281 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	3.8	417
2	Fuzzy complexes: Specific binding without complete folding. FEBS Letters, 2015, 589, 2533-2542.	1.3	177
3	The 2008 update of the Aspergillus nidulans genome annotation: A community effort. Fungal Genetics and Biology, 2009, 46, S2-S13.	0.9	99
4	FuzDB: database of fuzzy complexes, a tool to develop stochastic structure-function relationships for protein complexes and higher-order assemblies. Nucleic Acids Research, 2017, 45, D228-D235.	6.5	96
5	Comparison of gene expression signatures of diamide, H2O2 and menadione exposed Aspergillus nidulans cultures – linking genome-wide transcriptional changes to cellular physiology. BMC Genomics, 2005, 6, 182.	1.2	79
6	AtfA bZIP-type transcription factor regulates oxidative and osmotic stress responses in Aspergillus nidulans. Molecular Genetics and Genomics, 2010, 283, 289-303.	1.0	78
7	Sequence-Based Prediction of Fuzzy Protein Interactions. Journal of Molecular Biology, 2020, 432, 2289-2303.	2.0	77
8	Annotation of stress–response proteins in the aspergilli. Fungal Genetics and Biology, 2009, 46, S105-S120.	0.9	76
9	Transcriptome changes initiated by carbon starvation in Aspergillus nidulans. Microbiology (United) Tj ETQq1 1 (	0.784314	rgBT_/Overloc
10	Fuzziness enables context dependence of protein interactions. FEBS Letters, 2017, 591, 2682-2695.	1.3	60
11	Sequence-based prediction of protein binding mode landscapes. PLoS Computational Biology, 2020, 16, e1007864.	1.5	41
12	Comparison of transcriptional and translational changes caused by long-term menadione exposure in Aspergillus nidulans. Fungal Genetics and Biology, 2011, 48, 92-103.	0.9	38
13	Insights into Adaptations to a Near-Obligate Nematode Endoparasitic Lifestyle from the Finished Genome of Drechmeria coniospora. Scientific Reports, 2016, 6, 23122.	1.6	32
14	Protein phosphatase Z modulates oxidative stress response in fungi. Fungal Genetics and Biology, 2012, 49, 708-716.	0.9	26
15	The polymorphism of protein phosphatase Z1 gene in <i>Candida albicans</i> . Journal of Basic Microbiology, 2010, 50, S74-82.	1.8	13
16	Molecular Evolution of Phosphoprotein Phosphatases in Drosophila. PLoS ONE, 2011, 6, e22218.	1.1	11
17	Study on the glutathione metabolism of the filamentous fungus Aspergillus nidulans. Acta Microbiologica Et Immunologica Hungarica, 2017, 64, 255-272.	0.4	11
18	The phosphatome of opportunistic pathogen Candida species. Fungal Biology Reviews, 2021, 35, 40-51.	1.9	9

#	Article	IF	CITATIONS
19	Conservation of male-specific expression of novel phosphoprotein phosphatases in Drosophila. Development Genes and Evolution, 2010, 220, 123-128.	0.4	8
20	Stress tolerances of nullmutants of functionâ€unknown genes encoding menadione stressâ€responsive proteins in <i>Aspergillus nidulans</i> . Journal of Basic Microbiology, 2016, 56, 827-833.	1.8	3
21	Genome-wide mapping of binding sites of the transposase-derived SETMAR protein in the human genome. Computational and Structural Biotechnology Journal, 2021, 19, 4032-4041.	1.9	3
22	Two Targets, One Hit: new Anticancer Therapeutics to Prevent Tumorigenesis Without Cardiotoxicity. Frontiers in Pharmacology, 2020, 11, 569955.	1.6	1