

Yong Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

14
papers

2,519
citations

9
h-index

16
g-index

16
ext. papers

2,939
ext. citations

6.4
avg, IF

3.88
L-index

#	Paper	IF	Citations
14	High-Throughput Screening Assays to Identify Plant Natural Products with Antifungal Properties Against <i>Fusarium oxysporum</i> . <i>Methods in Molecular Biology</i> , 2022 , 2391, 171-184	1.4	0
13	The genome of opportunistic fungal pathogen <i>Fusarium oxysporum</i> carries a unique set of lineage-specific chromosomes. <i>Communications Biology</i> , 2020 , 3, 50	6.7	26
12	Fusaric acid instigates the invasion of banana by <i>Fusarium oxysporum</i> f. sp. cubense TR4. <i>New Phytologist</i> , 2020 , 225, 913-929	9.8	19
11	Identifying TF Binding Motifs from a Partial Set of Target Genes and its Application to Regulatory Network Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 1211-1221	3.2	221
10	Genome-wide analysis of <i>Fusarium verticillioides</i> reveals inter-kingdom contribution of horizontal gene transfer to the expansion of metabolism. <i>Fungal Genetics and Biology</i> , 2019 , 128, 60-73	3.9	4
9	FoMyo5 motor domain substitutions (Val to Ala and Ser to Thr) cause natural resistance to fungicide phenamacril in <i>Fusarium oxysporum</i> . <i>Pesticide Biochemistry and Physiology</i> , 2018 , 147, 119-126	4.9	6
8	Kinome Expansion in the <i>Fusarium oxysporum</i> Species Complex Driven by Accessory Chromosomes. <i>MSphere</i> , 2018 , 3,	5	20
7	A Computational Protocol to Analyze Metatranscriptomic Data Capturing Fungal-Host Interactions. <i>Methods in Molecular Biology</i> , 2018 , 1848, 207-233	1.4	1
6	Deciphering Pathogenicity of <i>Fusarium oxysporum</i> From a Phylogenomics Perspective. <i>Advances in Genetics</i> , 2017 , 100, 179-209	3.3	14
5	A De Novo-Assembly Based Data Analysis Pipeline for Plant Obligate Parasite Metatranscriptomic Studies. <i>Frontiers in Plant Science</i> , 2016 , 7, 925	6.2	9
4	Differential expression profiling of the early response to <i>Ustilagoidea virens</i> between false smut resistant and susceptible rice varieties. <i>BMC Genomics</i> , 2015 , 16, 955	4.5	31
3	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus <i>Penicillium aurantiogriseum</i> NRRL 62431. <i>BMC Genomics</i> , 2014 , 15, 69	4.5	85
2	Specific adaptation of <i>Ustilagoidea virens</i> in occupying host florets revealed by comparative and functional genomics. <i>Nature Communications</i> , 2014 , 5, 3849	17.4	122
1	WEGO: a web tool for plotting GO annotations. <i>Nucleic Acids Research</i> , 2006 , 34, W293-7	20.1	2180