

Li-Jun

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3704274/publications.pdf>

Version: 2024-02-01

28
papers

4,228
citations

331670
21
h-index

477307
29
g-index

31
all docs

31
docs citations

31
times ranked

5338
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	2.2	107
2	TEfinder: A Bioinformatics Pipeline for Detecting New Transposable Element Insertion Events in Next-Generation Sequencing Data. <i>Genes</i> , 2021, 12, 224.	2.4	4
3	Metatranscriptomic Comparison of Endophytic and Pathogenic <i>Fusarium</i> "Arabidopsis" Interactions Reveals Plant Transcriptional Plasticity. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1071-1083.	2.6	25
4	Fusaric acid instigates the invasion of banana by <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> TR4. <i>New Phytologist</i> , 2020, 225, 913-929.	7.3	49
5	Accessory Chromosomes in <i>Fusarium oxysporum</i> . <i>Phytopathology</i> , 2020, 110, 1488-1496.	2.2	42
6	Chromosome-Scale Genome Assembly of <i>Fusarium oxysporum</i> Strain Fo47, a Fungal Endophyte and Biocontrol Agent. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1108-1111.	2.6	29
7	Genome Sequence of <i>Fusarium oxysporum</i> f. sp. <i>matthiolae</i> , a Brassicaceae Pathogen. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 569-572.	2.6	9
8	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.	4.4	55
9	Shuffling effector genes through mini-chromosomes. <i>PLoS Genetics</i> , 2019, 15, e1008345.	3.5	8
10	FoMyo5 motor domain substitutions (Val151 to Ala and Ser418 to Thr) cause natural resistance to fungicide phenamacril in <i>Fusarium oxysporum</i> . <i>Pesticide Biochemistry and Physiology</i> , 2018, 147, 119-126.	3.6	15
11	Improved Assembly of Reference Genome <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> Strain Fol4287. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	31
12	Kinome Expansion in the <i>Fusarium oxysporum</i> Species Complex Driven by Accessory Chromosomes. <i>MSphere</i> , 2018, 3, .	2.9	29
13	Deciphering Pathogenicity of <i>Fusarium oxysporum</i> From a Phylogenomics Perspective. <i>Advances in Genetics</i> , 2017, 100, 179-209.	1.8	26
14	Conservation and divergence of the cyclic adenosine monophosphate protein kinase A (cAMP-PKA) pathway in two plant-pathogenic fungi: <i>Fusarium graminearum</i> and <i>F. verticillioides</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 196-209.	4.2	23
15	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	2.8	109
16	Compartmentalized gene regulatory network of the pathogenic fungus <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2016, 211, 527-541.	7.3	48
17	Horizontal chromosome transfer and rational strategies to manage <i>Fusarium</i> vascular wilt diseases. <i>Molecular Plant Pathology</i> , 2014, 15, 763-766.	4.2	29
18	<i>Fusarium</i> Pathogenomics. <i>Annual Review of Microbiology</i> , 2013, 67, 399-416.	7.3	475

#	ARTICLE	IF	CITATIONS
19	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	21.4	840
20	Transposable elements in phytopathogenic <i>Verticillium</i> spp.: insights into genome evolution and inter- and intra-specific diversification. <i>BMC Genomics</i> , 2012, 13, 314.	2.8	62
21	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.	3.5	164
22	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.	4.7	477
23	Genome Sequencing and Comparative Transcriptomics of the Model Entomopathogenic Fungi <i>Metarhizium anisopliae</i> and <i>M. acridum</i> . <i>PLoS Genetics</i> , 2011, 7, e1001264.	3.5	542
24	Systematic discovery of regulatory motifs in <i>Fusarium graminearum</i> by comparing four <i>Fusarium</i> genomes. <i>BMC Genomics</i> , 2010, 11, 208.	2.8	16
25	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
26	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. <i>PLoS Genetics</i> , 2009, 5, e1000549.	3.5	332
27	Genomics of the fungal kingdom: Insights into eukaryotic biology. <i>Genome Research</i> , 2005, 15, 1620-1631.	5.5	269
28	Guest, a transposable element belonging to the Tc1/mariner superfamily is an ancient invader of <i>Neurospora</i> genomes. <i>Fungal Genetics and Biology</i> , 2004, 41, 52-61.	2.1	8