

Li Guo

List of Publications by Year in descending order

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34
papers

1,541
citations

623734

14
h-index

454955

30
g-index

48
all docs

48
docs citations

48
times ranked

2769
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
2	The opium poppy genome and morphinan production. <i>Science</i> , 2018, 362, 343-347.	12.6	225
3	Application of Metagenomic Next-Generation Sequencing in the Diagnosis of Pulmonary Infectious Pathogens From Bronchoalveolar Lavage Samples. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 541092.	3.9	72
4	Basil Downy Mildew (<i>Peronospora belbahrii</i>): Discoveries and Challenges Relative to Its Control. <i>Phytopathology</i> , 2015, 105, 885-894.	2.2	64
5	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
6	MSIsensor-pro: Fast, Accurate, and Matched-normal-sample-free Detection of Microsatellite Instability. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 65-71.	6.9	53
7	Three chromosome-scale <i>Papaver</i> genomes reveal punctuated patchwork evolution of the morphinan and noscapine biosynthesis pathway. <i>Nature Communications</i> , 2021, 12, 6030.	12.8	51
8	Compartmentalized gene regulatory network of the pathogenic fungus <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2016, 211, 527-541.	7.3	48
9	Kinome Expansion in the <i>Fusarium oxysporum</i> Species Complex Driven by Accessory Chromosomes. <i>MSphere</i> , 2018, 3, .	2.9	29
10	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
11	A Chromosome-Scale Genome Assembly for the <i>Fusarium oxysporum</i> Strain Fo5176 To Establish a Model <i>Arabidopsis</i> -Fungal Pathosystem. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3549-3555.	1.8	28
12	Metatranscriptomic Comparison of Endophytic and Pathogenic <i>Fusarium</i> <i>Arabidopsis</i> Interactions Reveals Plant Transcriptional Plasticity. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1071-1083.	2.6	25
13	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>Fusarium verticillioides</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 196-209.	4.2	23
14	Malectin/Malectin-like domain-containing proteins: A repertoire of cell surface molecules with broad functional potential. <i>Cell Surface</i> , 2021, 7, 100056.	3.0	23
15	FvSO regulates vegetative hyphal fusion, asexual growth, fumonisin B1 production, and virulence in <i>Fusarium verticillioides</i> . <i>Fungal Biology</i> , 2015, 119, 1158-1169.	2.5	20
16	Split-Read Indel and Structural Variant Calling Using PINDEL. <i>Methods in Molecular Biology</i> , 2018, 1833, 95-105.	0.9	20
17	Genomic insights into longan evolution from a chromosome-level genome assembly and population genomics of longan accessions. <i>Horticulture Research</i> , 2022, 9, .	6.3	14
18	A De Novo-Assembly Based Data Analysis Pipeline for Plant Obligate Parasite Metatranscriptomic Studies. <i>Frontiers in Plant Science</i> , 2016, 7, 925.	3.6	10

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19	Predicting Virulence of <i>Fusarium oxysporum</i> f. sp. <i>Cubense</i> Based on the Production of Mycotoxin Using a Linear Regression Model. <i>Toxins</i> , 2020, 12, 254.	3.4	10
20	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.	2.1	8
21	Dynamic network inference and association computation discover gene modules regulating virulence, mycotoxin and sexual reproduction in <i>Fusarium graminearum</i> . <i>BMC Genomics</i> , 2020, 21, 179.	2.8	8
22	A Chromosome-Level Reference Genome of Chinese Balloon Flower (<i>Platycodon grandiflorus</i>). <i>Frontiers in Genetics</i> , 2022, 13, 869784.	2.3	7
23	Mako: A Graph-based Pattern Growth Approach to Detect Complex Structural Variants. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 205-218.	6.9	6
24	A global survey of the transcriptome of the opium poppy (<i>Papaver somniferum</i>) based on single-molecule long-read isoform sequencing. <i>Plant Journal</i> , 2022, 110, 607-620.	5.7	5
25	Cerebrospinal Fluid from Healthy Pregnant Women Does Not Harbor a Detectable Microbial Community. <i>Microbiology Spectrum</i> , 2021, 9, e0076921.	3.0	5
26	Chromosome-Scale Genome Assembly of <i>Talaromyces rugulosus</i> W13939, a Mycoparasitic Fungus and Promising Biocontrol Agent. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1446-1450.	2.6	4
27	Transportation, germs, culture: a dynamic graph model of COVID-19 outbreak. <i>Quantitative Biology</i> , 2020, 8, 238-244.	0.5	4
28	<i>Fusarium graminearum</i> Genomics and Beyond. , 2014, , 103-122.		4
29	Mating type and spore killing characterization of <i>Fusarium verticillioides</i> strains. <i>Mycological Progress</i> , 2015, 14, 1.	1.4	2
30	Inferring regulatory networks through orthologous gene mapping. , 2013, , .		1
31	A Computational Protocol to Analyze Metatranscriptomic Data Capturing Fungal-Host Interactions. <i>Methods in Molecular Biology</i> , 2018, 1848, 207-233.	0.9	1
32	Mapping Genome Variants Sheds Light on Genetic and Phenotypic Differentiation in Chinese. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 226-228.	6.9	1
33	Identifying TF Binding Motifs from Partial Set of Target Genes and its Application to Regulatory Network Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	0
34	Transportation, Germs, Culture: A Dynamic Graph Model of COVID-19 Outbreak. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0