

Yingfeng Luo

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

2,353
citations

471371

17
h-index

580701

25
g-index

26
all docs

26
docs citations

26
times ranked

4095
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	13.7	603
2	The rubber tree genome reveals new insights into rubber production and species adaptation. <i>Nature Plants</i> , 2016, 2, 16073.	4.7	324
3	Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1375-1386.	1.4	206
4	Comparative transcriptome analysis of transporters, phytohormone and lipid metabolism pathways in response to arsenic stress in rice (<i>Oryza sativa</i>). <i>New Phytologist</i> , 2012, 195, 97-112.	3.5	193
5	The apricot (<i>Prunus armeniaca</i> L.) genome elucidates Rosaceae evolution and beta-carotenoid synthesis. <i>Horticulture Research</i> , 2019, 6, 128.	2.9	119
6	Rationally Designed APOBEC3B Cytosine Base Editors with Improved Specificity. <i>Molecular Cell</i> , 2020, 79, 728-740.e6.	4.5	104
7	The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , 2020, 21, 60.	3.8	104
8	Metagenomic Insights into the Fibrolytic Microbiome in Yak Rumen. <i>PLoS ONE</i> , 2012, 7, e40430.	1.1	98
9	PacBio full-length cDNA sequencing integrated with RNA-seq reads drastically improves the discovery of splicing transcripts in rice. <i>Plant Journal</i> , 2019, 97, 296-305.	2.8	90
10	Genome structure and evolution of <i>Antirrhinum majus</i> L. <i>Nature Plants</i> , 2019, 5, 174-183.	4.7	85
11	Genome-wide specificity of prime editors in plants. <i>Nature Biotechnology</i> , 2021, 39, 1292-1299.	9.4	80
12	Detection and genotyping of restriction fragment associated polymorphisms in polyploid crops with a pseudo-reference sequence: a case study in allotetraploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2013, 14, 346.	1.2	69
13	A genome and gene catalog of glacier microbiomes. <i>Nature Biotechnology</i> , 2022, 40, 1341-1348.	9.4	50
14	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. <i>Nature Communications</i> , 2016, 7, 12845.	5.8	43
15	The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. <i>Molecular Plant</i> , 2019, 12, 402-409.	3.9	41
16	BIGpre: A Quality Assessment Package for Next-Generation Sequencing Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 238-244.	3.0	26
17	An integrated RNA-Seq and network study reveals a complex regulation process of rice embryo during seed germination. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 176-181.	1.0	20
18	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 161-172.	3.0	18

#	ARTICLE	IF	CITATIONS
19	VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. <i>Nucleic Acids Research</i> , 2022, 50, D888-D897.	6.5	18
20	Transcriptional profiling of biomass degradation-related genes during <i>Trichoderma reesei</i> growth on different carbon sources. <i>Journal of Biotechnology</i> , 2014, 173, 59-64.	1.9	15
21	Identification of a G2-like transcription factor, OsPHL3, functions as a negative regulator of flowering in rice by co-expression and reverse genetic analysis. <i>BMC Plant Biology</i> , 2018, 18, 157.	1.6	15
22	Complete genome of <i>Phenylobacterium zucineum</i> “a novel facultative intracellular bacterium isolated from human erythroleukemia cell line K562. <i>BMC Genomics</i> , 2008, 9, 386.	1.2	12
23	BIGrat: a repeat resolver for pyrosequencing-based re-sequencing with Newbler. <i>BMC Research Notes</i> , 2012, 5, 567.	0.6	10
24	Genomic organization and promoter analysis of the <i>Trichomonas vaginalis</i> core histone gene families. <i>Parasitology International</i> , 2010, 59, 29-34.	0.6	8
25	Amplicon-based sequencing and co-occurrence network analysis reveals notable differences of microbial community structure in healthy and dandruff scalps. <i>BMC Genomics</i> , 2022, 23, 312.	1.2	2