Yingfeng Luo

List of Publications by Year
in descending order

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	VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. Nucleic Acids Research, 2022, 50, D888-D897.	6.5	18
2	Amplicon-based sequencing and co-occurence network analysis reveals notable differences of microbial community structure in healthy and dandruff scalps. BMC Genomics, 2022, 23, 312.	1.2	2
3	A genome and gene catalog of glacier microbiomes. Nature Biotechnology, 2022, 40, 1341-1348.	9.4	50
4	Genome-wide specificity of prime editors in plants. Nature Biotechnology, 2021, 39, 1292-1299.	9.4	80
5	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. Genomics, Proteomics and Bioinformatics, 2020, 18, 161-172.	3.0	18
6	Rationally Designed APOBEC3B Cytosine Base Editors with Improved Specificity. Molecular Cell, 2020, 79, 728-740.e6.	4.5	104
7	The genome evolution and domestication of tropical fruit mango. Genome Biology, 2020, 21, 60.	3.8	104
8	Genome structure and evolution of Antirrhinum majus L. Nature Plants, 2019, 5, 174-183.	4.7	85
9	The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. Molecular Plant, 2019, 12, 402-409.	3.9	41
10	The apricot (Prunus armeniaca L.) genome elucidates Rosaceae evolution and beta-carotenoid synthesis. Horticulture Research, 2019, 6, 128.	2.9	119
11	PacBio full‐length <scp>cDNA</scp> sequencing integrated with <scp>RNA</scp>‐seq reads drastically improves the discovery of splicing transcripts in rice. Plant Journal, 2019, 97, 296-305.	2.8	90
12	Identification of a G2-like transcription factor, OsPHL3, functions as a negative regulator of flowering in rice by co-expression and reverse genetic analysis. BMC Plant Biology, 2018, 18, 157.	1.6	15
13	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. Nature Communications, 2016, 7, 12845.	5.8	43
14	The rubber tree genome reveals new insights into rubber production and species adaptation. Nature Plants, 2016, 2, 16073.	4.7	324
15	An integrated RNA-Seq and network study reveals a complex regulation process of rice embryo during seed germination. Biochemical and Biophysical Research Communications, 2015, 464, 176-181.	1.0	20
16	Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. Applied and Environmental Microbiology, 2015, 81, 1375-1386.	1.4	206
17	Transcriptional profiling of biomass degradation-related genes during Trichoderma reesei growth on different carbon sources. Journal of Biotechnology, 2014, 173, 59-64.	1.9	15
18	Detection and genotyping of restriction fragment associated polymorphisms in polyploid crops with a pseudo-reference sequence: a case study in allotetraploid Brassica napus. BMC Genomics, 2013, 14, 346.	1.2	69

#	Article	IF	Citations
19	The genomes of four tapeworm species reveal adaptations to parasitism. Nature, 2013, 496, 57-63.	13.7	603
20	Comparative transcriptome analysis of transporters, phytohormone and lipid metabolism pathways in response to arsenic stress in rice (*Oryza sativa*). New Phytologist, 2012, 195, 97-112.	3.5	193
21	BIGrat: a repeat resolver for pyrosequencing-based re-sequencing with Newbler. BMC Research Notes, 2012, 5, 567.	0.6	10
22	Metagenomic Insights into the Fibrolytic Microbiome in Yak Rumen. PLoS ONE, 2012, 7, e40430.	1.1	98
23	BIGpre: A Quality Assessment Package for Next-Generation Sequencing Data. Genomics, Proteomics and Bioinformatics, 2011, 9, 238-244.	3.0	26
24	Genomic organization and promoter analysis of the Trichomonas vaginalis core histone gene families. Parasitology International, 2010, 59, 29-34.	0.6	8
25	Complete genome of Phenylobacterium zucineum â€" a novel facultative intracellular bacterium isolated from human erythroleukemia cell line K562. BMC Genomics, 2008, 9, 386.	1.2	12