

Haifei Hu

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

448
citations

1039406

9
h-index

1125271

13
g-index

17
all docs

17
docs citations

17
times ranked

492
citing authors

#	ARTICLE	IF	CITATIONS
1	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
2	The Chicken Pan-Genome Reveals Gene Content Variation and a Promoter Region Deletion in <i>IGF2BP1</i> Affecting Body Size. <i>Molecular Biology and Evolution</i> , 2021, 38, 5066-5081.	3.5	70
3	Advances in Integrating Genomics and Bioinformatics in the Plant Breeding Pipeline. <i>Agriculture (Switzerland)</i> , 2018, 8, 75.	1.4	55
4	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2022, 15, e20109.	1.6	53
5	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1677-1690.	1.8	38
6	Single-Cell Genomic Analysis in Plants. <i>Genes</i> , 2018, 9, 50.	1.0	25
7	<i>Amborella</i> gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. <i>New Phytologist</i> , 2022, 233, 1548-1555.	3.5	16
8	Wheat Panache: A pangenome graph database representing presence-absence variation across sixteen bread wheat genomes. <i>Plant Genome</i> , 2022, 15, .	1.6	16
9	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction. <i>BMC Plant Biology</i> , 2022, 22, 180.	1.6	15
10	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus <i>cqProt-003</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 1443-1455.	1.8	13
11	Mapping of partial resistance to <i>Phytophthora sojae</i> in soybean PIs using whole-genome sequencing reveals a major QTL. <i>Plant Genome</i> , 2022, 15, e20184.	1.6	11
12	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. <i>Methods in Molecular Biology</i> , 2020, 2107, 35-47.	0.4	7
13	Genome-Wide Identification and Expansion Patterns of SULTR Gene Family in Gramineae Crops and Their Expression Profiles under Abiotic Stress in <i>Oryza sativa</i> . <i>Genes</i> , 2021, 12, 634.	1.0	6