

Baoxing Song

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

511
citations

759233

12
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

847
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	9.3	90
2	Parallel-META 2.0: Enhanced Metagenomic Data Analysis with Functional Annotation, High Performance Computing and Advanced Visualization. <i>PLoS ONE</i> , 2014, 9, e89323.	2.5	70
3	Sequence Polymorphisms at the <i>REDUCED DORMANCY5</i> Pseudophosphatase Underlie Natural Variation in <i>Arabidopsis</i> Dormancy. <i>Plant Physiology</i> , 2016, 171, 2659-2670.	4.8	52
4	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185.	8.8	47
5	Prediction and characterization of protein-protein interaction networks in swine. <i>Proteome Science</i> , 2012, 10, 2.	1.7	33
6	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021, 31, 1245-1257.	5.5	29
7	AnchorWave: Sensitive alignment of genomes with high sequence diversity, extensive structural polymorphism, and whole-genome duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	29
8	Gene expression evolution in pattern-triggered immunity within <i>Arabidopsis thaliana</i> and across Brassicaceae species. <i>Plant Cell</i> , 2021, 33, 1863-1887.	6.6	27
9	Mutagenesis of a Quintuple Mutant Impaired in Environmental Responses Reveals Roles for <i>CHROMATIN REMODELING4</i> in the <i>Arabidopsis</i> Floral Transition. <i>Plant Cell</i> , 2020, 32, 1479-1500.	6.6	17
10	Recovery of novel association loci in <i>Arabidopsis thaliana</i> and <i>Drosophila melanogaster</i> through leveraging INDELS association and integrated burden test. <i>PLoS Genetics</i> , 2018, 14, e1007699.	3.5	16
11	MetaSee: An Interactive and Extendable Visualization Toolbox for Metagenomic Sample Analysis and Comparison. <i>PLoS ONE</i> , 2012, 7, e48998.	2.5	14
12	QTL mapping and genomic analyses of earliness and fruit ripening traits in a melon recombinant inbred lines population supported by <i>de novo</i> assembly of their parental genomes. <i>Horticulture Research</i> , 2022, 9, .	6.3	12
13	Complement Genome Annotation Lift Over Using a Weighted Sequence Alignment Strategy. <i>Frontiers in Genetics</i> , 2019, 10, 1046.	2.3	9
14	Transcriptome profiling analysis of tea plant (<i>Camellia sinensis</i>) using Oxford Nanopore long-read RNA-Seq technology. <i>Gene</i> , 2021, 769, 145247.	2.2	7
15	Prediction and Analysis of the Protein-Protein Interaction Networks for Chickens, Cattle, Dogs, Horses and Rabbits. <i>Current Bioinformatics</i> , 2016, 11, 131-142.	1.5	5
16	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants. <i>Plant Genome</i> , 2022, 15, e20204.	2.8	5
17	Protein-protein interaction network-based detection of functionally similar proteins within species. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1736-1743.	2.6	4
18	PPIPP: an online protein-protein interaction network prediction and analysis platform. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 14, 305.	0.1	1