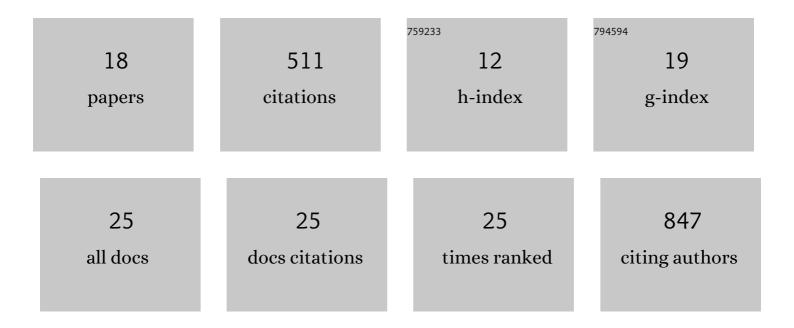
Baoxing Song

List of Publications by Year in descending order

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