

Maojun Wang

List of Publications by Year in descending order

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40
papers

3,035
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257357

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docs citations

42
times ranked

3047
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic interrogation of a MAGIC population highlights genetic factors controlling fiber quality traits in cotton. <i>Communications Biology</i> , 2022, 5, 60.	2.0	8
2	Introgression from <i>Gossypium hirsutum</i> is a driver for population divergence and genetic diversity in <i>Gossypium barbadense</i> . <i>Plant Journal</i> , 2022, 110, 764-780.	2.8	16
3	Dynamic 3D genome architecture of cotton fiber reveals subgenome-coordinated chromatin topology for 4-staged single-cell differentiation. <i>Genome Biology</i> , 2022, 23, 45.	3.8	18
4	Comparative genomic analyses reveal cis-regulatory divergence after polyploidization in cotton. <i>Crop Journal</i> , 2022, , .	2.3	0
5	Genomic insights into the recent chromosome reduction of autopolyploid sugarcane <i>Saccharum spontaneum</i> . <i>Nature Genetics</i> , 2022, 54, 885-896.	9.4	33
6	Multi-omics mapping of chromatin interaction resolves the fine hierarchy of 3D genome in allotetraploid cotton. <i>Plant Biotechnology Journal</i> , 2022, 20, 1639-1641.	4.1	2
7	Plant 3D genomics: the exploration and application of chromatin organization. <i>New Phytologist</i> , 2021, 230, 1772-1786.	3.5	23
8	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021, 22, 119.	3.8	76
9	Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. <i>Molecular Biology and Evolution</i> , 2021, 38, 3621-3636.	3.5	41
10	Genome-wide identification, evolutionary estimation and functional characterization of two cotton CKI gene types. <i>BMC Plant Biology</i> , 2021, 21, 229.	1.6	1
11	A combination of genome-wide and transcriptome-wide association studies reveals genetic elements leading to male sterility during high temperature stress in cotton. <i>New Phytologist</i> , 2021, 231, 165-181.	3.5	33
12	<i>Gossypium tomentosum</i> genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. <i>Genomics</i> , 2021, 113, 1999-2009.	1.3	8
13	Disruption of topologically associating domains by structural variations in tetraploid cottons. <i>Genomics</i> , 2021, 113, 3405-3414.	1.3	6
14	Combined GWAS and eQTL analysis uncovers a genetic regulatory network orchestrating the initiation of secondary cell wall development in cotton. <i>New Phytologist</i> , 2020, 226, 1738-1752.	3.5	74
15	Phenomics-based GWAS analysis reveals the genetic architecture for drought resistance in cotton. <i>Plant Biotechnology Journal</i> , 2020, 18, 2533-2544.	4.1	49
16	Mapping and validation of a fiber length QTL on chromosome D11 using two independent F2 populations of upland cotton. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	6
17	Multi-omics analyses reveal epigenomics basis for cotton somatic embryogenesis through successive regeneration acclimation process. <i>Plant Biotechnology Journal</i> , 2019, 17, 435-450.	4.1	88
18	Tracing the origin and evolution history of methylation-related genes in plants. <i>BMC Plant Biology</i> , 2019, 19, 307.	1.6	59

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19	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019, 10, 4702.	5.8	115
20	Genome-Wide Analysis of Cotton miRNAs During Whitefly Infestation Offers New Insights into Plant-Herbivore Interaction. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5357.	1.8	12
21	Population genomics reveals a fine-scale recombination landscape for genetic improvement of cotton. <i>Plant Journal</i> , 2019, 99, 494-505.	2.8	31
22	Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019, 51, 224-229.	9.4	468
23	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018, 4, 90-97.	4.7	137
24	Transcriptomic repertoires depict the initiation of lint and fuzz fibres in cotton (<i>Gossypium</i>). <i>Transcriptomics</i> , 2018, 10, 50-54.	4.1	50
25	A global survey of alternative splicing in allopolyploid cotton: landscape, complexity and regulation. <i>New Phytologist</i> , 2018, 217, 163-178.	3.5	173
26	Long noncoding RNAs involve in resistance to <i>Verticillium dahliae</i> , a fungal disease in cotton. <i>Plant Biotechnology Journal</i> , 2018, 16, 1172-1185.	4.1	121
27	Disrupted Genome Methylation in Response to High Temperature Has Distinct Affects on Microspore Abortion and Anther Indehiscence. <i>Plant Cell</i> , 2018, 30, 1387-1403.	3.1	82
28	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017, 49, 579-587.	9.4	367
29	Interaction between calcium and potassium modulates elongation rate in cotton fiber cells. <i>Journal of Experimental Botany</i> , 2017, 68, 5161-5175.	2.4	37
30	Genome-wide SSR-based association mapping for fiber quality in nation-wide upland cotton inbred cultivars in China. <i>BMC Genomics</i> , 2016, 17, 352.	1.2	124
31	The genome sequence of Sea-Island cotton (<i>Gossypium barbadense</i>) provides insights into the allopolyploidization and development of superior spinnable fibres. <i>Scientific Reports</i> , 2016, 5, 17662.	1.6	294
32	Multi-omics maps of cotton fibre reveal epigenetic basis for staged single-cell differentiation. <i>Nucleic Acids Research</i> , 2016, 44, 4067-4079.	6.5	46
33	Fibre elongation requires normal redox homeostasis modulated by cytosolic ascorbate peroxidase in cotton (<i>Gossypium hirsutum</i>). <i>Journal of Experimental Botany</i> , 2016, 67, 3289-3301.	2.4	54
34	Genome Sequencing. <i>Agronomy</i> , 2015, , 289-302.	0.2	3
35	A cotton fiber-preferential promoter, PGbEXPA2, is regulated by GA and ABA in Arabidopsis. <i>Plant Cell Reports</i> , 2015, 34, 1539-1549.	2.8	26
36	Long noncoding RNAs and their proposed functions in fibre development of cotton (<i>Gossypium</i> spp.). <i>New Phytologist</i> , 2015, 207, 1181-1197.	3.5	160

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37	Down-regulating annexin gene GhAnn2 inhibits cotton fiber elongation and decreases Ca ²⁺ influx at the cell apex. <i>Plant Molecular Biology</i> , 2014, 85, 613-625.	2.0	58
38	Isolation and Characterization of a Conserved Domain in the Eremophyte H ⁺ -PPase Family. <i>PLoS ONE</i> , 2013, 8, e70099.	1.1	3
39	A Comparative Genome Analysis of PME and PME1 Families Reveals the Evolution of Pectin Metabolism in Plant Cell Walls. <i>PLoS ONE</i> , 2013, 8, e72082.	1.1	87
40	The Flavonoid Pathway Regulates the Petal Colors of Cotton Flower. <i>PLoS ONE</i> , 2013, 8, e72364.	1.1	43