

Maojun Wang

List of Publications by Year in descending order

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257450

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docs citations

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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.	4.4	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.	5.7	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.	8.8	18
4	Comparative genomic analyses reveal cis-regulatory divergence after polyploidization in cotton. <i>Crop Journal</i> , 2022, , .	5.2	0
5	Genomic insights into the recent chromosome reduction of autopolyploid sugarcane <i>Saccharum spontaneum</i> . <i>Nature Genetics</i> , 2022, 54, 885-896.	21.4	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.	8.3	2
7	Plant 3D genomics: the exploration and application of chromatin organization. <i>New Phytologist</i> , 2021, 230, 1772-1786.	7.3	23
8	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021, 22, 119.	8.8	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.	8.9	41
10	Genome-wide identification, evolutionary estimation and functional characterization of two cotton CKI gene types. <i>BMC Plant Biology</i> , 2021, 21, 229.	3.6	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.	7.3	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.	2.9	8
13	Disruption of topologically associating domains by structural variations in tetraploid cottons. <i>Genomics</i> , 2021, 113, 3405-3414.	2.9	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.	7.3	74
15	Phenomics-based GWAS analysis reveals the genetic architecture for drought resistance in cotton. <i>Plant Biotechnology Journal</i> , 2020, 18, 2533-2544.	8.3	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.	2.1	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.	8.3	88
18	Tracing the origin and evolution history of methylation-related genes in plants. <i>BMC Plant Biology</i> , 2019, 19, 307.	3.6	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.	12.8	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.	4.1	12
21	Population genomics reveals a fine-scale recombination landscape for genetic improvement of cotton. <i>Plant Journal</i> , 2019, 99, 494-505.	5.7	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.	21.4	468
23	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018, 4, 90-97.	9.3	137
24	Transcriptomic repertoires depict the initiation of lint and fuzz fibres in cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54	8.3	50
25	A global survey of alternative splicing in allopolyploid cotton: landscape, complexity and regulation. <i>New Phytologist</i> , 2018, 217, 163-178.	7.3	173
26	Long noncoding <i>scpr</i> RNA <i>s</i> involve in resistance to <i>Verticillium dahliae</i> , a fungal disease in cotton. <i>Plant Biotechnology Journal</i> , 2018, 16, 1172-1185.	8.3	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.	6.6	82
28	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017, 49, 579-587.	21.4	367
29	Interaction between calcium and potassium modulates elongation rate in cotton fiber cells. <i>Journal of Experimental Botany</i> , 2017, 68, 5161-5175.	4.8	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.	2.8	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.	3.3	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.	14.5	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.	4.8	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.	5.6	26
36	Long noncoding <i>scpr</i> RNA <i>s</i> and their proposed functions in fibre development of cotton (<i>Gossypium</i> spp.). <i>New Phytologist</i> , 2015, 207, 1181-1197.	7.3	160

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37	Down-regulating annexin gene GhAnn2 inhibits cotton fiber elongation and decreases Ca ²⁺ influx at the cell apex. Plant Molecular Biology, 2014, 85, 613-625.	3.9	58
38	Isolation and Characterization of a Conserved Domain in the Eremophyte H ⁺ -PPase Family. PLoS ONE, 2013, 8, e70099.	2.5	3
39	A Comparative Genome Analysis of PME and PME1 Families Reveals the Evolution of Pectin Metabolism in Plant Cell Walls. PLoS ONE, 2013, 8, e72082.	2.5	87
40	The Flavonoid Pathway Regulates the Petal Colors of Cotton Flower. PLoS ONE, 2013, 8, e72364.	2.5	43