

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

25 papers	1,283 citations	16 h-index	26 g-index
26 ext. papers	1,979 ext. citations	11 avg, IF	4.19 L-index

#	Paper	IF	Citations
25	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	36.3	266
24	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017 , 49, 579-587	36.3	229
23	Whole genome sequencing reveals rare off-target mutations and considerable inherent genetic or/and somaclonal variations in CRISPR/Cas9-edited cotton plants. <i>Plant Biotechnology Journal</i> , 2019 , 17, 858-868	11.6	96
22	A global survey of alternative splicing in allopolyploid cotton: landscape, complexity and regulation. <i>New Phytologist</i> , 2018 , 217, 163-178	9.8	95
21	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018 , 4, 90-97	11.5	82
20	GhABF2, a bZIP transcription factor, confers drought and salinity tolerance in cotton (<i>Gossypium hirsutum</i> L.). <i>Scientific Reports</i> , 2016 , 6, 35040	4.9	75
19	Transcriptome analysis reveals a comprehensive insect resistance response mechanism in cotton to infestation by the phloem feeding insect <i>Bemisia tabaci</i> (whitefly). <i>Plant Biotechnology Journal</i> , 2016 , 14, 1956-75	11.6	72
18	High-efficient and precise base editing of C to T in the allotetraploid cotton (<i>Gossypium hirsutum</i>) genome using a modified CRISPR/Cas9 system. <i>Plant Biotechnology Journal</i> , 2020 , 18, 45-56	11.6	63
17	Osmotin: A plant defense tool against biotic and abiotic stresses. <i>Plant Physiology and Biochemistry</i> , 2018 , 123, 149-159	5.4	48
16	Multi-omics analyses reveal epigenomics basis for cotton somatic embryogenesis through successive regeneration acclimation process. <i>Plant Biotechnology Journal</i> , 2019 , 17, 435-450	11.6	46
15	Comprehensive analysis of NAC transcription factors uncovers their roles during fiber development and stress response in cotton. <i>BMC Plant Biology</i> , 2018 , 18, 150	5.3	36
14	The JASMONATE ZIM-Domain Gene Family Mediates JA Signaling and Stress Response in Cotton. <i>Plant and Cell Physiology</i> , 2017 , 58, 2139-2154	4.9	34
13	The GhmiR157a-GhSPL10 regulatory module controls initial cellular dedifferentiation and callus proliferation in cotton by modulating ethylene-mediated flavonoid biosynthesis. <i>Journal of Experimental Botany</i> , 2018 , 69, 1081-1093	7	30
12	A transgenic strategy for controlling plant bugs (<i>Adelphocoris suturalis</i>) through expression of double-stranded RNA homologous to fatty acyl-coenzyme A reductase in cotton. <i>New Phytologist</i> , 2017 , 215, 1173-1185	9.8	26
11	The application of a heat-inducible CRISPR/Cas12b (C2c1) genome editing system in tetraploid cotton (<i>G. hirsutum</i>) plants. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2436-2443	11.6	20
10	Tracing the origin and evolution history of methylation-related genes in plants. <i>BMC Plant Biology</i> , 2019 , 19, 307	5.3	17
9	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021 , 22, 119	18.3	10

8	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	8.3	10
7	A Single-Nucleotide Mutation in a GLUTAMATE RECEPTOR-LIKE Gene Confers Resistance to Fusarium Wilt in. <i>Advanced Science</i> , 2021 , 8, 2002723	13.6	8
6	Red fluorescent protein (DsRed2), an ideal reporter for cotton genetic transformation and molecular breeding. <i>Crop Journal</i> , 2018 , 6, 366-376	4.6	7
5	Transcriptome and metabolome analysis reveal that oral secretions from <i>Helicoverpa armigera</i> and <i>Spodoptera litura</i> influence wound-induced host response in cotton. <i>Crop Journal</i> , 2020 , 8, 929-942	4.6	6
4	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,	6.3	6
3	Genomic interrogation of a MAGIC population highlights genetic factors controlling fiber quality traits in cotton.. <i>Communications Biology</i> , 2022 , 5, 60	6.7	0
2	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	18.3	0
1	Identification and Functional Analysis of lncRNA by CRISPR/Cas9 During the Cotton Response to Sap-Sucking Insect Infestation.. <i>Frontiers in Plant Science</i> , 2022 , 13, 784511	6.2	0