

Quanjia Chen

List of Publications by Year in descending order

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papers

284
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933447

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246
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#	ARTICLE	IF	CITATIONS
1	Neofunctionalization of a polyploidization-activated cotton long intergenic non-coding RNA <i></i> during drought stress regulation. <i>Plant Physiology</i> , 2021, 186, 2152-2168.	4.8	27
2	Genome-wide association reveals genetic variation of lint yield components under salty field conditions in cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 23.	3.6	26
3	CarNAC2, a novel NAC transcription factor in chickpea (<i>Cicer arietinum</i> L.), is associated with drought-response and various developmental processes in transgenic arabidopsis. <i>Journal of Plant Biology</i> , 2014, 57, 55-66.	2.1	24
4	Genome-wide identification of the DUF668 gene family in cotton and expression profiling analysis of GhDUF668 in <i>Gossypium hirsutum</i> under adverse stress. <i>BMC Genomics</i> , 2021, 22, 395.	2.8	21
5	Temporal salt stress-induced transcriptome alterations and regulatory mechanisms revealed by PacBio long-reads RNA sequencing in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2020, 21, 838.	2.8	19
6	Using Transcriptome Analysis to Screen for Key Genes and Pathways Related to Cytoplasmic Male Sterility in Cotton (<i>Gossypium hirsutum</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 5120.	4.1	16
7	Integrative Analysis of the lncRNA and mRNA Transcriptome Revealed Genes and Pathways Potentially Involved in the Anther Abortion of Cotton (<i>Gossypium hirsutum</i> L.). <i>Genes</i> , 2019, 10, 947.	2.4	14
8	Disequilibrium evolution of the Fructose-1,6-bisphosphatase gene family leads to their functional biodiversity in <i>Gossypium</i> species. <i>BMC Genomics</i> , 2020, 21, 379.	2.8	13
9	Genome-wide association analysis reveals loci and candidate genes involved in fiber quality traits in sea island cotton (<i>Gossypium barbadense</i>). <i>BMC Plant Biology</i> , 2020, 20, 289.	3.6	13
10	Identification and Characterization of the ERF Subfamily B3 Group Revealed GhERF13.12 Improves Salt Tolerance in Upland Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 705883.	3.6	12
11	Genome-wide association analysis reveals quantitative trait loci and candidate genes involved in yield components under multiple field environments in cotton (<i>Gossypium hirsutum</i>). <i>BMC Plant Biology</i> , 2021, 21, 250.	3.6	11
12	Integrative transcriptomic and gene co-expression network analysis of host responses upon <i>Verticillium dahliae</i> infection in <i>Gossypium hirsutum</i> . <i>Scientific Reports</i> , 2021, 11, 20586.	3.3	11
13	Detection of favorable alleles for yield and yield components by association mapping in upland cotton. <i>Genes and Genomics</i> , 2018, 40, 725-734.	1.4	8
14	Rapid Mining of Candidate Genes for <i>Verticillium</i> Wilt Resistance in Cotton Based on BSA-Seq Analysis. <i>Frontiers in Plant Science</i> , 2021, 12, 703011.	3.6	8
15	Transcriptome analysis and identification of genes associated with oil accumulation in upland cotton. <i>Physiologia Plantarum</i> , 2022, 174, e13701.	5.2	8
16	Quantitative Trait Locus Analysis and Identification of Candidate Genes for Micronaire in an Interspecific Backcross Inbred Line Population of <i>Gossypium hirsutum</i> × <i>Gossypium barbadense</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 763016.	3.6	7
17	QTL mapping for plant height and fruit branch number based on RIL population of upland cotton. <i>Journal of Cotton Research</i> , 2020, 3, .	2.5	6
18	Linkage and association analyses reveal that hub genes in energy-flow and lipid biosynthesis pathways form a cluster in upland cotton. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1841-1859.	4.1	6

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19	Identification of exogenous ABA and heat stress tolerance in various cotton genotypes. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 404-416.	0.8	5
20	Quantitative Trait Locus Mapping and Identification of Candidate Genes for Resistance to Fusarium Wilt Race 7 Using a Resequencing-Based High Density Genetic Bin Map in a Recombinant Inbred Line Population of <i>Gossypium barbadense</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 815643.	3.6	5
21	Quantitative Trait Loci and Transcriptome Analysis Reveal Genetic Basis of Fiber Quality Traits in CCRI70 RIL Population of <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 753755.	3.6	5
22	Functional examination of lncRNAs in allotetraploid <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2021, 22, 443.	2.8	4
23	Genome-Wide Comparative Analysis of Heat Shock Transcription Factors Provides Novel Insights for Evolutionary History and Expression Characterization in Cotton Diploid and Tetraploid Genomes. <i>Frontiers in Genetics</i> , 2021, 12, 658847.	2.3	4
24	GhLBDs Promote Callus Initiation and Act as Selectable Markers to Increase Transformation Efficiency. <i>Frontiers in Plant Science</i> , 2022, 13, 861706.	3.6	4
25	Multi-environment Evaluations Across Ecological Regions Reveal That the Kernel Oil Content of Cottonseed Is Equally Determined by Genotype and Environment. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 2529-2544.	5.2	3
26	Genome-wide identification and expression analysis of the 2OG-Fe(II) oxygenase gene family in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1969-1977.	3.1	2
27	Nanopore-Based Comparative Transcriptome Analysis Reveals the Potential Mechanism of High-Temperature Tolerance in Cotton (<i>Gossypium hirsutum</i> L.). <i>Plants</i> , 2021, 10, 2517.	3.5	2
28	Genetic dissection of QTLs linked with seedling, yield and fiber quality traits of upland cotton under salt stress field conditions. <i>Euphytica</i> , 2021, 217, 1.	1.2	0