

# Chaozhu Xing

## List of Publications by Year in descending order

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29  
papers

533  
citations

623188

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713013

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34  
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34  
docs citations

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times ranked

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#	ARTICLE	IF	CITATIONS
1	Integrated analysis of small RNA, transcriptome and degradome sequencing reveals that micro-RNAs regulate anther development in CMS cotton. <i>Industrial Crops and Products</i> , 2022, 176, 114422.	2.5	3
2	The cotton mitochondrial chimeric gene orf610a causes male sterility by disturbing the dynamic balance of ATP synthesis and ROS burst. <i>Crop Journal</i> , 2022, , .	2.3	11
3	Comparative performance of hybrid generations reveals the potential application of F2 hybrids in upland cotton. <i>Journal of Cotton Research</i> , 2022, 5, .	1.0	7
4	Physical mapping and InDel marker development for the restorer gene Rf2 in cytoplasmic male sterile CMS-D8 cotton. <i>BMC Genomics</i> , 2021, 22, 24.	1.2	16
5	The cellulose synthase (CesA) gene family in four <i>Gossypium</i> species: phylogenetics, sequence variation and gene expression in relation to fiber quality in Upland cotton. <i>Molecular Genetics and Genomics</i> , 2021, 296, 355-368.	1.0	9
6	Single-molecule real-time transcript sequencing of developing cotton anthers facilitates genome annotation and fertility restoration candidate gene discovery. <i>Genomics</i> , 2021, 113, 4245-4253.	1.3	5
7	Single-base resolution methylomes of cotton CMS system reveal epigenomic changes in response to high-temperature stress during anther development. <i>Journal of Experimental Botany</i> , 2020, 71, 951-969.	2.4	31
8	A genome-wide analysis of pentatricopeptide repeat (PPR) protein-encoding genes in four <i>Gossypium</i> species with an emphasis on their expression in floral buds, ovules, and fibers in upland cotton. <i>Molecular Genetics and Genomics</i> , 2020, 295, 55-66.	1.0	8
9	Development and utilization of an InDel marker linked to the fertility restorer genes of CMS-D8 and CMS-D2 in cotton. <i>Molecular Biology Reports</i> , 2020, 47, 1275-1282.	1.0	10
10	Comparative transcriptome analysis between inbred and hybrids reveals molecular insights into yield heterosis of upland cotton. <i>BMC Plant Biology</i> , 2020, 20, 239.	1.6	28
11	Comparative transcriptome analysis of inbred lines and contrasting hybrids reveals overdominance mediate early biomass vigor in hybrid cotton. <i>BMC Genomics</i> , 2020, 21, 140.	1.2	22
12	Transcriptome Analysis Implicates Involvement of Long Noncoding RNAs in Cytoplasmic Male Sterility and Fertility Restoration in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5530.	1.8	11
13	Adaptability and Stability Comparisons of Inbred and Hybrid Cotton in Yield and Fiber Quality Traits. <i>Agronomy</i> , 2019, 9, 516.	1.3	27
14	Genetic analysis of yield and fiber quality traits in upland cotton ( <i>Gossypium hirsutum</i> L.) cultivated in different ecological regions of China. <i>Journal of Cotton Research</i> , 2019, 2, .	1.0	22
15	Using yield quantitative trait locus targeted SSR markers to study the relationship between genetic distance and yield heterosis in upland cotton ( <i>Gossypium hirsutum</i> ). <i>Plant Breeding</i> , 2019, 138, 105-113.	1.0	18
16	Integrated Methylome and Transcriptome Analysis between the CMS-D2 Line ZBA and Its Maintainer Line ZB in Upland Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6070.	1.8	17
17	Genome-wide analysis of Rf-PPR-like (RFL) genes and a new InDel marker development for Rf1 gene in cytoplasmic male sterile CMS-D2 Upland cotton. <i>Journal of Cotton Research</i> , 2018, 1, .	1.0	6
18	A combined small RNA and transcriptome sequencing analysis reveal regulatory roles of miRNAs during anther development of Upland cotton carrying cytoplasmic male sterile <i>Gossypium harknessii</i> (D2) cytoplasm. <i>BMC Plant Biology</i> , 2018, 18, 242.	1.6	25

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19	Transcriptome, cytological and biochemical analysis of cytoplasmic male sterility and maintainer line in CMS-D8 cotton. <i>Plant Molecular Biology</i> , 2018, 97, 537-551.	2.0	49
20	Genome-wide comparative transcriptome analysis of CMS-D2 and its maintainer and restorer lines in upland cotton. <i>BMC Genomics</i> , 2017, 18, 454.	1.2	38
21	Development of InDel markers for the restorer gene Rf1 and assessment of their utility for marker-assisted selection in cotton. <i>Euphytica</i> , 2017, 213, 1.	0.6	17
22	A genome-wide identification and analysis of the DYW-deaminase genes in the pentatricopeptide repeat gene family in cotton ( <i>Gossypium</i> spp.). <i>PLoS ONE</i> , 2017, 12, e0174201.	1.1	7
23	Acyl-CoA N-acyltransferase influences fertility by regulating lipid metabolism and jasmonic acid biogenesis in cotton. <i>Scientific Reports</i> , 2015, 5, 11790.	1.6	42
24	Development of a candidate gene marker for Rf 1 based on a PPR gene in cytoplasmic male sterile CMS-D2 Upland cotton. <i>Molecular Breeding</i> , 2014, 34, 231-240.	1.0	32
25	Comparative expression of miRNA genes and miRNA-based AFLP marker analysis in cultivated tetraploid cottons. <i>Journal of Plant Physiology</i> , 2011, 168, 824-830.	1.6	21
26	Molecular characterization of cytoplasmic male sterility conditioned by <i>Gossypium harknessii</i> cytoplasm (CMS-D2) in upland cotton. <i>Euphytica</i> , 2011, 181, 17-29.	0.6	35
27	Analysis of Differentially Expressed Genes in Genic Male Sterility Cotton ( <i>Gossypium hirsutum</i> L.) Using cDNA-AFLP. <i>Journal of Genetics and Genomics</i> , 2007, 34, 536-543.	1.7	15
28	Transcript Complexity and New Insights of Restorer Line in CMS-D8 Cotton Through Full-Length Transcriptomic Analysis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
29	Homoeolog gene expression analysis reveals novel expression biases in upland hybrid cotton under intraspecific hybridization. <i>Functional and Integrative Genomics</i> , 0, , .	1.4	0