

Meng Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

365
citations

758635

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23
times ranked

241
citing authors

#	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	SIMULATED ANNEALING GENETIC ALGORITHM-BASED HARVESTER OPERATION SCHEDULING MODEL. <i>INMATEH - Agricultural Engineering</i> , 2021, , 249-260.	0.1	0
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	Cloning, Functional Characterization and Expression Analysis of the elovl4a Gene in the Large Yellow Croaker (<i>Larimichthys crocea</i>). <i>Journal of Ocean University of China</i> , 2021, 20, 1515-1527.	0.6	0
8	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
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	Apple Detection in Natural Environment Using Deep Learning Algorithms. <i>IEEE Access</i> , 2020, 8, 216772-216780.	2.6	22
11	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
12	Haematological and immunological plasma assays and histological study of the grass carp (<i>Cyprinus carpio</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 T 3685-3697.	0.9	3
13	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
14	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
15	Adaptability and Stability Comparisons of Inbred and Hybrid Cotton in Yield and Fiber Quality Traits. <i>Agronomy</i> , 2019, 9, 516.	1.3	27
16	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
17	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
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	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
23	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