

Xiangjun Kong

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

248
citations

1040056

9
h-index

1058476

14
g-index

22
all docs

22
docs citations

22
times ranked

209
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete sequence of kenaf (<i>Hibiscus cannabinus</i>) mitochondrial genome and comparative analysis with the mitochondrial genomes of other plants. <i>Scientific Reports</i> , 2018, 8, 12714.	3.3	43
2	Comparative Analysis of the Cytology and Transcriptomes of the Cytoplasmic Male Sterility Line H276A and Its Maintainer Line H276B of Cotton (<i>Gossypium barbadense</i> L.). <i>International Journal of Molecular Sciences</i> , 2017, 18, 2240.	4.1	32
3	Plant Salinity Stress Response and Nano-Enabled Plant Salt Tolerance. <i>Frontiers in Plant Science</i> , 2022, 13, 843994.	3.6	22
4	Identification of chalcone synthase genes and their expression patterns reveal pollen abortion in cotton. <i>Saudi Journal of Biological Sciences</i> , 2020, 27, 3691-3699.	3.8	15
5	Transcriptome and MiRNAomics Analyses Identify Genes Associated with Cytoplasmic Male Sterility in Cotton (<i>Gossypium hirsutum</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 4684.	4.1	14
6	Planting Density Induced Changes in Cotton Biomass Yield, Fiber Quality, and Phosphorus Distribution under Beta Growth Model. <i>Agronomy</i> , 2019, 9, 500.	3.0	12
7	A comparative study of the <i>atp9</i> gene between a cytoplasmic male sterile line and its maintainer line and further development of a molecular marker specific for male sterile cytoplasm in kenaf (<i>Hibiscus</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.0	11
8	RNA editing analysis of ATP synthase genes in the cotton cytoplasmic male sterile line H276A. <i>Biological Research</i> , 2019, 52, 6.	3.4	11
9	Changes in Leaf Structural and Functional Characteristics when Changing Planting Density at Different Growth Stages Alters Cotton Lint Yield under a New Planting Model. <i>Agronomy</i> , 2019, 9, 859.	3.0	11
10	Candidate Reference Genes Selection and Application for RT-qPCR Analysis in Kenaf with Cytoplasmic Male Sterility Background. <i>Frontiers in Plant Science</i> , 2017, 8, 1520.	3.6	10
11	Comparative Transcriptome Analysis between a Novel Allohexaploid Cotton Progeny CMS Line LD6A and Its Maintainer Line LD6B. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6127.	4.1	10
12	Identification of differentially expressed genes and pathways in isonuclear kenaf genotypes under salt stress. <i>Physiologia Plantarum</i> , 2021, 173, 1295-1308.	5.2	10
13	Discovery of Four Novel ORFs Responsible for Cytoplasmic Male Sterility (CMS) in Cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Over <i>Agronomy</i> , 2020, 10, 765.	3.0	10
14	Comparative analysis of mitochondrial genome and expression variation between UG93A and UG93B reveals a candidate gene related to cytoplasmic male sterility in kenaf. <i>Industrial Crops and Products</i> , 2020, 152, 112502.	5.2	8
15	Integrated Methylome and Transcriptome Analysis Widen the Knowledge of Cytoplasmic Male Sterility in Cotton (<i>Gossypium barbadense</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 770098.	3.6	8
16	Deviant DNA methylation play a key role in the pollen abortion of <i>Gossypium barbadense</i> L. cytoplasmic male sterility. <i>Industrial Crops and Products</i> , 2020, 154, 112622.	5.2	7
17	Harnessing perennial and indeterminant growth habits for ratoon cotton (<i>Gossypium</i> spp.) cropping. <i>Ecosystem Health and Sustainability</i> , 2020, 6, .	3.1	6
18	Physio-biochemical and proteomic mechanisms of coronatine induced potassium stress tolerance in xylem sap of cotton. <i>Industrial Crops and Products</i> , 2021, 173, 114094.	5.2	4

#	ARTICLE	IF	CITATIONS
19	Expression of kenaf mitochondrial chimeric genesHM184causes male sterility in transgenic tobacco plants. Mitochondrial DNA, 2015, 26, 495-500.	0.6	2
20	Mitochondrial gene expression analysis reveals aberrant transcription of cox3 in Gossypium barbadense CMS line H276A. Development Genes and Evolution, 2022, 232, 15-23.	0.9	2