

Xiongming Du

List of Publications by Year in descending order

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73
papers

3,988
citations

331259

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h-index

128067

60
g-index

76
all docs

76
docs citations

76
times ranked

2635
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study for seedling biomass-related traits in <i>Gossypium arboreum</i> L.. <i>BMC Plant Biology</i> , 2022, 22, 54.	1.6	5
2	Phenotypic Correlation Analysis in F2 Segregating Populations of <i>Gossypium hirsutum</i> and <i>Gossypium arboreum</i> for Boll-Related Traits. <i>Agronomy</i> , 2022, 12, 330.	1.3	1
3	Deltapine 15 contributes to the genomic architecture of modern upland cotton cultivars. <i>Theoretical and Applied Genetics</i> , 2022, , 1.	1.8	4
4	Introgression from <i>Gossypium hirsutum</i> is a driver for population divergence and genetic diversity in <i>Gossypium barbadense</i> . <i>Plant Journal</i> , 2022, 110, 764-780.	2.8	16
5	Identification and Characterization of the Growth-Regulating Factors-Interacting Factors in Cotton. <i>Frontiers in Genetics</i> , 2022, 13, 851343.	1.1	1
6	Integrating Genome-wide association and whole transcriptome analysis to reveal genetic control of leaf traits in <i>Gossypium arboreum</i> L.. <i>Genomics</i> , 2022, 114, 110331.	1.3	2
7	A genome-wide association study of lateral root number for Asian cotton (<i>Gossypium arboreum</i> L.). <i>Journal of Cotton Research</i> , 2022, 5, .	1.0	2
8	Differential seedling growth and tolerance indices reflect drought tolerance in cotton. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	12
9	Alien genomic introgressions enhanced fiber strength in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Industrial Crops and Products</i> , 2021, 159, 113028.	2.5	9
10	A copy number variant at the <i>HPDA-CD12</i> locus confers compact plant architecture in cotton. <i>New Phytologist</i> , 2021, 229, 2091-2103.	3.5	27
11	QTL mapping of agronomic and economic traits for four F2 populations of upland cotton. <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	9
12	Large fragment insertion activates gene <i>GaFZ</i> (<i>Ga08G0121</i>) and is associated with the fuzz and trichome reduction in cotton (<i>Gossypium arboreum</i>). <i>Plant Biotechnology Journal</i> , 2021, 19, 1110-1124.	4.1	17
13	Correlation analysis of stem hardness traits with fiber and yield-related traits in core collections of <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	1
14	Genome-wide association and transcriptome analysis of root color-related genes in <i>Gossypium arboreum</i> L.. <i>Planta</i> , 2021, 253, 95.	1.6	8
15	The genomic basis of geographic differentiation and fiber improvement in cultivated cotton. <i>Nature Genetics</i> , 2021, 53, 916-924.	9.4	75
16	GWAS Mediated Elucidation of Heterosis for Metric Traits in Cotton (<i>Gossypium hirsutum</i> L.) Across Multiple Environments. <i>Frontiers in Plant Science</i> , 2021, 12, 565552.	1.7	16
17	Genomic insight into the divergence and adaptive potential of a forgotten landrace <i>G. hirsutum</i> L. <i>purpurascens</i> . <i>Journal of Genetics and Genomics</i> , 2021, 48, 473-484.	1.7	19
18	Genome wide identification, classification and functional characterization of heat shock transcription factors in cultivated and ancestral cottons (<i>Gossypium</i> spp.). <i>International Journal of Biological Macromolecules</i> , 2021, 182, 1507-1527.	3.6	11

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19	Identification and functional analysis of 9-cis-epoxy carotenoid dioxygenase (NCED) homologs in <i>G. hirsutum</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 182, 298-310.	3.6	15
20	Favorable pleiotropic loci for fiber yield and quality in upland cotton (<i>Gossypium hirsutum</i>). <i>Scientific Reports</i> , 2021, 11, 15935.	1.6	5
21	Identification of C2H2 subfamily ZAT genes in <i>Gossypium</i> species reveals GhZAT34 and GhZAT79 enhanced salt tolerance in <i>Arabidopsis</i> and cotton. <i>International Journal of Biological Macromolecules</i> , 2021, 184, 967-980.	3.6	18
22	Genome wide analysis of IQD gene family in diploid and tetraploid species of cotton (<i>Gossypium</i> spp.). <i>International Journal of Biological Macromolecules</i> , 2021, 184, 1035-1061.	3.6	7
23	Heat Stress in Cotton: A Review on Predicted and Unpredicted Growth-Yield Anomalies and Mitigating Breeding Strategies. <i>Agronomy</i> , 2021, 11, 1825.	1.3	29
24	Genome-wide profiling of circular RNAs in the hybridization of two elite inbred lines of <i>Gossypium hirsutum</i> . <i>Industrial Crops and Products</i> , 2021, 170, 113754.	2.5	5
25	Insight into abscisic acid perception and signaling to increase plant tolerance to abiotic stress. <i>Journal of Plant Interactions</i> , 2021, 16, 222-237.	1.0	21
26	GhGASA10 promotes the cell elongation in fiber development through the phytohormones IAA-induced. <i>BMC Plant Biology</i> , 2021, 21, 448.	1.6	10
27	Intra-Plant Variability for Heat Tolerance Related Attributes in Upland Cotton. <i>Agronomy</i> , 2021, 11, 2375.	1.3	3
28	Identification of Raf-Like Kinases B Subfamily Genes in <i>Gossypium</i> Species Revealed GhRAF42 Enhanced Salt Tolerance in Cotton. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12649.	1.8	3
29	CottonGVD: A Comprehensive Genomic Variation Database for Cultivated Cottons. <i>Frontiers in Plant Science</i> , 2021, 12, 803736.	1.7	8
30	Genetic Factors Underlying Single Fiber Quality in A-Genome Donor Asian Cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 302	1.1	9
31	Insights into Drought Stress Signaling in Plants and the Molecular Genetic Basis of Cotton Drought Tolerance. <i>Cells</i> , 2020, 9, 105.	1.8	189
32	Genome-wide dissection of hybridization for fiber quality and yield-related traits in upland cotton. <i>Plant Journal</i> , 2020, 104, 1285-1300.	2.8	9
33	Genome-wide identification and characterization of HSP70 gene family in four species of cotton. <i>Genomics</i> , 2020, 112, 4442-4453.	1.3	12
34	Revamping of Cotton Breeding Programs for Efficient Use of Genetic Resources under Changing Climate. <i>Agronomy</i> , 2020, 10, 1190.	1.3	13
35	Extensive haplotypes are associated with population differentiation and environmental adaptability in Upland cotton (<i>Gossypium hirsutum</i>). <i>Theoretical and Applied Genetics</i> , 2020, 133, 3273-3285.	1.8	15
36	Casparian strip membrane domain proteins in <i>Gossypium arboreum</i> : genome-wide identification and negative regulation of lateral root growth. <i>BMC Genomics</i> , 2020, 21, 340.	1.2	4

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37	Genomic Insight into Differentiation and Selection Sweeps in the Improvement of Upland Cotton. <i>Plants</i> , 2020, 9, 711.	1.6	18
38	Genotyping by Sequencing Revealed QTL Hotspots for Trichome-Based Plant Defense in <i>Gossypium hirsutum</i> . <i>Genes</i> , 2020, 11, 368.	1.0	10
39	Introgression Leads to Genomic Divergence and Responsible for Important Traits in Upland Cotton. <i>Frontiers in Plant Science</i> , 2020, 11, 929.	1.7	15
40	Expression patterns and functional divergence of homologous genes accompanied by polyploidization in cotton (<i>Gossypium hirsutum</i> L.). <i>Science China Life Sciences</i> , 2020, 63, 1565-1579.	2.3	11
41	High-density genetic variation maps reveal the correlation between asymmetric interspecific introgressions and improvement of agronomic traits in Upland and Pima cotton varieties developed in Xinjiang, China. <i>Plant Journal</i> , 2020, 103, 677-689.	2.8	22
42	A Genome-Wide Association Study Revealed Key SNPs/Genes Associated With Salinity Stress Tolerance In Upland Cotton. <i>Genes</i> , 2019, 10, 829.	1.0	28
43	Long non-coding RNAs and their potential functions in Ligon-lintless-1 mutant cotton during fiber development. <i>BMC Genomics</i> , 2019, 20, 661.	1.2	18
44	Genome-wide analysis of cotton C2H2-zinc finger transcription factor family and their expression analysis during fiber development. <i>BMC Plant Biology</i> , 2019, 19, 400.	1.6	27
45	Association Analysis of Salt Tolerance in Asiatic cotton (<i>Gossypium arboreum</i>) with SNP Markers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2168.	1.8	28
46	Identifying favorable alleles for improving key agronomic traits in upland cotton. <i>BMC Plant Biology</i> , 2019, 19, 138.	1.6	6
47	Identification and characterization analysis of sulfotransferases (SOTs) gene family in cotton (<i>Gossypium</i>) and its involvement in fiber development. <i>BMC Plant Biology</i> , 2019, 19, 595.	1.6	11
48	Comparative effect of allopolyploidy on transposable element composition and gene expression between <i>Gossypium hirsutum</i> and its two diploid progenitors. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 45-59.	4.1	11
49	Genomic divergence in cotton germplasm related to maturity and heterosis. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 929-942.	4.1	21
50	A Phi-Class Glutathione S-Transferase Gene for Verticillium Wilt Resistance in <i>Gossypium arboreum</i> Identified in a Genome-Wide Association Study. <i>Plant and Cell Physiology</i> , 2018, 59, 275-289.	1.5	87
51	Integration of conventional and advanced molecular tools to track footprints of heterosis in cotton. <i>BMC Genomics</i> , 2018, 19, 776.	1.2	14
52	QTL Mapping of Fiber Quality and Yield-Related Traits in an Intra-Specific Upland Cotton Using Genotype by Sequencing (GBS). <i>International Journal of Molecular Sciences</i> , 2018, 19, 441.	1.8	37
53	Integration of proteomic and transcriptomic profiles reveals multiple levels of genetic regulation of salt tolerance in cotton. <i>BMC Plant Biology</i> , 2018, 18, 128.	1.6	42
54	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. <i>BMC Genomics</i> , 2018, 19, 451.	1.2	22

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55	Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits. <i>Nature Genetics</i> , 2018, 50, 796-802.	9.4	401
56	Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield. <i>Nature Genetics</i> , 2018, 50, 803-813.	9.4	368
57	Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 33.	3.8	128
58	Molecular characterisation and functional analysis of a cytochrome P450 gene in cotton. <i>Biologia (Poland)</i> , 2017, 72, 43-52.	0.8	3
59	Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits. <i>Nature Genetics</i> , 2017, 49, 1089-1098.	9.4	384
60	Association mapping analysis of fiber yield and quality traits in Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	20
61	iTRAQ-Based Comparative Proteomic Analysis of Seedling Leaves of Two Upland Cotton Genotypes Differing in Salt Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 2113.	1.7	31
62	High-Density Linkage Map Construction and Mapping of Salt-Tolerant QTLs at Seedling Stage in Upland Cotton Using Genotyping by Sequencing (GBS). <i>International Journal of Molecular Sciences</i> , 2017, 18, 2622.	1.8	42
63	To Be a Flower or Fruiting Branch: Insights Revealed by mRNA and Small RNA Transcriptomes from Different Cotton Developmental Stages. <i>Scientific Reports</i> , 2016, 6, 23212.	1.6	21
64	Na ⁺ compartmentalization related to salinity stress tolerance in upland cotton (<i>Gossypium hirsutum</i>) seedlings. <i>Scientific Reports</i> , 2016, 6, 34548.	1.6	88
65	Characterization, Expression, and Functional Analysis of a Novel NAC Gene Associated with Resistance to Verticillium Wilt and Abiotic Stress in Cotton. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3951-3961.	0.8	32
66	Genome-wide characterization and expression analysis of MYB transcription factors in <i>Gossypium hirsutum</i> . <i>BMC Genetics</i> , 2016, 17, 129.	2.7	104
67	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	9.4	1,064
68	The Hairless Stem Phenotype of Cotton (<i>Gossypium barbadense</i>) Is Linked to a <i>Copia</i> -Like Retrotransposon Insertion in a <i>Homeodomain-Leucine Zipper</i> Gene (<i>HD1</i>). <i>Genetics</i> , 2015, 201, 143-154.	1.2	33
69	Comprehensive analysis of differentially expressed genes and transcriptional regulation induced by salt stress in two contrasting cotton genotypes. <i>BMC Genomics</i> , 2014, 15, 760.	1.2	166
70	Association Mapping for Epistasis and Environmental Interaction of Yield Traits in 323 Cotton Cultivars under 9 Different Environments. <i>PLoS ONE</i> , 2014, 9, e95882.	1.1	55
71	Reforming Cotton Genes: From Elucidation of DNA Structure to Genome Editing. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 0, , .	0.8	1
72	Genetic Diversity and Association Analysis of Lint Percentage Variation Population in <i>Gossypium Hirsutum</i> L. Based on Microsatellite Markers. <i>Journal of Natural Fibers</i> , 0, , 1-10.	1.7	1

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73	Cotton Germplasm Resources in China. , 0, , .		6