

Fang Liu

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

2,297
citations

218677

26
h-index

254184

43
g-index

86
all docs

86
docs citations

86
times ranked

1879
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparisons of photosynthetic and anatomical traits between wild and domesticated cotton. <i>Journal of Experimental Botany</i> , 2022, 73, 873-885.	4.8	15
2	Protoplast Dissociation and Transcriptome Analysis Provides Insights to Salt Stress Response in Cotton. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2845.	4.1	13
3	Late embryogenesis abundant gene LEA3 (Gh_A08G0694) enhances drought and salt stress tolerance in cotton. <i>International Journal of Biological Macromolecules</i> , 2022, 207, 700-714.	7.5	20
4	From Sequencing to Genome Editing for Cotton Improvement. <i>Trends in Biotechnology</i> , 2021, 39, 221-224.	9.3	27
5	Identification and characterization of genes related to salt stress tolerance within segregation distortion regions of genetic map in F2 population of upland cotton. <i>PLoS ONE</i> , 2021, 16, e0247593.	2.5	8
6	Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. <i>Molecular Biology and Evolution</i> , 2021, 38, 3621-3636.	8.9	41
7	Genome wide identification and characterization of light-harvesting Chloro a/b binding (LHC) genes reveals their potential role in enhancing drought tolerance in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	8
8	Functional Characterization of GhACX3 Gene Reveals Its Significant Role in Enhancing Drought and Salt Stress Tolerance in Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 658755.	3.6	15
9	Identification and functional characterization of Gh_D01G0514 (GhNAC072) transcription factor in response to drought stress tolerance in cotton. <i>Plant Physiology and Biochemistry</i> , 2021, 166, 361-375.	5.8	15
10	Knockdown of 60S ribosomal protein L14-2 reveals their potential regulatory roles to enhance drought and salt tolerance in cotton. <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	13
11	Enhanced photosynthetic nitrogen use efficiency and increased nitrogen allocation to photosynthetic machinery under cotton domestication. <i>Photosynthesis Research</i> , 2021, 150, 239-250.	2.9	19
12	Multi-Omics-Based Identification and Functional Characterization of Gh_A06G1257 Proves Its Potential Role in Drought Stress Tolerance in <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 746771.	3.6	13
13	GhGLK1 a Key Candidate Gene From GARP Family Enhances Cold and Drought Stress Tolerance in Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 759312.	3.6	17
14	Functional Characterization of Cotton C-Repeat Binding Factor Genes Reveal Their Potential Role in Cold Stress Tolerance. <i>Frontiers in Plant Science</i> , 2021, 12, 766130.	3.6	10
15	Genome sequencing of the Australian wild diploid species <i>Gossypium australe</i> highlights disease resistance and delayed gland morphogenesis. <i>Plant Biotechnology Journal</i> , 2020, 18, 814-828.	8.3	61
16	Knockdown of Gh_A05G1554 (GhDHN_03) and Gh_D05G1729 (GhDHN_04) Dehydrin genes, Reveals their potential role in enhancing osmotic and salt tolerance in cotton. <i>Genomics</i> , 2020, 112, 1902-1915.	2.9	19
17	Genetic regulatory networks for salt-alkali stress in <i>Gossypium hirsutum</i> with differing morphological characteristics. <i>BMC Genomics</i> , 2020, 21, 15.	2.8	33
18	Transcriptomic and proteomic analyses of a new cytoplasmic male sterile line with a wild <i>Gossypium bickii</i> genetic background. <i>BMC Genomics</i> , 2020, 21, 859.	2.8	11

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19	Genetic map construction and functional characterization of genes within the segregation distortion regions (SDRs) in the F2:3 populations derived from wild cotton species of the D genome. <i>Journal of Cotton Research</i> , 2020, 3, .	2.5	0
20	Comparative transcriptome analysis reveals evolutionary divergence and shared network of cold and salt stress response in diploid D-genome cotton. <i>BMC Plant Biology</i> , 2020, 20, 518.	3.6	6
21	Versatile Roles of Aquaporins in Plant Growth and Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9485.	4.1	52
22	Chromosome Painting Based on Bulked Oligonucleotides in Cotton. <i>Frontiers in Plant Science</i> , 2020, 11, 802.	3.6	7
23	Identification of QTLs and candidate genes for physiological traits associated with drought tolerance in cotton. <i>Journal of Cotton Research</i> , 2020, 3, .	2.5	16
24	Identification of a genome-specific repetitive element in the <i>Gossypium</i> D genome. <i>PeerJ</i> , 2020, 8, e8344.	2.0	2
25	Genome-wide analysis of the cotton G-coupled receptor proteins (GPCR) and functional analysis of GTOM1, a novel cotton GPCR gene under drought and cold stress. <i>BMC Genomics</i> , 2019, 20, 651.	2.8	21
26	Genome-wide identification of OSCA gene family and their potential function in the regulation of dehydration and salt stress in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2019, 2, .	2.5	21
27	Genome wide characterization, evolution and expression analysis of FBA gene family under salt stress in <i>Gossypium</i> species. <i>Biologia (Poland)</i> , 2019, 74, 1539-1552.	1.5	3
28	Functional characterization of Gh_A08G1120 (GH3.5) gene reveal their significant role in enhancing drought and salt stress tolerance in cotton. <i>BMC Genetics</i> , 2019, 20, 62.	2.7	39
29	A high density SLAF-seq SNP genetic map and QTL for seed size, oil and protein content in upland cotton. <i>BMC Genomics</i> , 2019, 20, 599.	2.8	20
30	Knockdown of GhIQD31 and GhIQD32 increases drought and salt stress sensitivity in <i>Gossypium hirsutum</i> . <i>Plant Physiology and Biochemistry</i> , 2019, 144, 166-177.	5.8	16
31	Map-Based Functional Analysis of the GhNLP Genes Reveals Their Roles in Enhancing Tolerance to N-Deficiency in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4953.	4.1	11
32	Knockdown of ghAlba_4 and ghAlba_5 Proteins in Cotton Inhibits Root Growth and Increases Sensitivity to Drought and Salt Stresses. <i>Frontiers in Plant Science</i> , 2019, 10, 1292.	3.6	6
33	Genome-Wide Mining and Identification of Protein Kinase Gene Family Impacts Salinity Stress Tolerance in Highly Dense Genetic Map Developed from Interspecific Cross between <i>G. hirsutum</i> L. and <i>G. darwinii</i> G. <i>Watt. Agronomy</i> , 2019, 9, 560.	3.0	21
34	Deep Transcriptome Analysis Reveals Reactive Oxygen Species (ROS) Network Evolution, Response to Abiotic Stress, and Regulation of Fiber Development in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1863.	4.1	29
35	Overexpression of Cotton a DTX/MATE Gene Enhances Drought, Salt, and Cold Stress Tolerance in Transgenic Arabidopsis. <i>Frontiers in Plant Science</i> , 2019, 10, 299.	3.6	68
36	RNA-Sequencing, Physiological and RNAi Analyses Provide Insights into the Response Mechanism of the ABC-Mediated Resistance to <i>Verticillium dahliae</i> Infection in Cotton. <i>Genes</i> , 2019, 10, 110.	2.4	31

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37	Comparative transcriptome, physiological and biochemical analyses reveal response mechanism mediated by CBF4 and ICE2 in enhancing cold stress tolerance in <i>Gossypium thurberi</i> . <i>AoB PLANTS</i> , 2019, 11, plz045.	2.3	27
38	Genome wide identification of the trihelix transcription factors and overexpression of <i>Gh_A05G2067</i> (<i>Gtâ€2</i>), a novel gene contributing to increased drought and salt stresses tolerance in cotton. <i>Physiologia Plantarum</i> , 2019, 167, 447-464.	5.2	57
39	Characterization of the late embryogenesis abundant (LEA) proteins family and their role in drought stress tolerance in upland cotton. <i>BMC Genetics</i> , 2018, 19, 6.	2.7	216
40	Genome-Wide Mining and Characterization of SSR Markers for Gene Mapping and Gene Diversity in <i>Gossypium barbadense</i> L. and <i>Gossypium darwinii</i> G. <i>Watt Accessions. Agronomy</i> , 2018, 8, 181.	3.0	6
41	SSR-Linkage map of interspecific populations derived from <i>Gossypium trilobum</i> and <i>Gossypium thurberi</i> and determination of genes harbored within the segregating distortion regions. <i>PLoS ONE</i> , 2018, 13, e0207271.	2.5	6
42	Discovery and annotation of a novel transposable element family in <i>Gossypium</i> . <i>BMC Plant Biology</i> , 2018, 18, 307.	3.6	6
43	Whole Genome Analysis of Cyclin Dependent Kinase (CDK) Gene Family in Cotton and Functional Evaluation of the Role of CDKF4 Gene in Drought and Salt Stress Tolerance in Plants. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2625.	4.1	51
44	Simple Sequence Repeat (SSR) Genetic Linkage Map of D Genome Diploid Cotton Derived from an Interspecific Cross between <i>Gossypium davidsonii</i> and <i>Gossypium klotzschianum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 204.	4.1	31
45	Construction and characterization of a bacterial artificial chromosome library for <i>Gossypium mustelinum</i> . <i>PLoS ONE</i> , 2018, 13, e0196847.	2.5	3
46	Genome-Wide Analysis of Multidrug and Toxic Compound Extrusion (<i>MATE</i>) Family in <i>Gossypium raimondii</i> and <i>Gossypium arboreum</i> and Its Expression Analysis Under Salt, Cadmium, and Drought Stress. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2483-2500.	1.8	56
47	Cotton Late Embryogenesis Abundant (<i>LEA2</i>) Genes Promote Root Growth and Confer Drought Stress Tolerance in Transgenic <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2781-2803.	1.8	51
48	Comparative Chloroplast Genomics of <i>Gossypium</i> Species: Insights Into Repeat Sequence Variations and Phylogeny. <i>Frontiers in Plant Science</i> , 2018, 9, 376.	3.6	86
49	A Novel G-Protein-Coupled Receptors Gene from Upland Cotton Enhances Salt Stress Tolerance in Transgenic <i>Arabidopsis</i> . <i>Genes</i> , 2018, 9, 209.	2.4	50
50	GBS Mapping and Analysis of Genes Conserved between <i>Gossypium tomentosum</i> and <i>Gossypium hirsutum</i> Cotton Cultivars that Respond to Drought Stress at the Seedling Stage of the BC2F2 Generation. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1614.	4.1	39
51	Assessment of Genetic Diversity, Population Structure, and Evolutionary Relationship of Uncharacterized Genes in a Novel Germplasm Collection of Diploid and Allotetraploid <i>Gossypium</i> Accessions Using EST and Genomic SSR Markers. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2401.	4.1	20
52	Fine-mapping qFS07.1 controlling fiber strength in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 795-806.	3.6	63
53	Molecular evolution of the plastid genome during diversification of the cotton genus. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 268-276.	2.7	52
54	Chromosome structural variation of two cultivated tetraploid cottons and their ancestral diploid species based on a new high-density genetic map. <i>Scientific Reports</i> , 2017, 7, 7640.	3.3	6

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55	Enriching an intraspecific genetic map and identifying QTL for fiber quality and yield component traits across multiple environments in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Molecular Genetics and Genomics</i> , 2017, 292, 1281-1306.	2.1	36
56	Genome-wide assessment of genetic diversity and fiber quality traits characterization in <i>Gossypium hirsutum</i> races. <i>Journal of Integrative Agriculture</i> , 2017, 16, 2402-2412.	3.5	7
57	Salt stress responsiveness of a wild cotton species (<i>Gossypium klotzschianum</i>) based on transcriptomic analysis. <i>PLoS ONE</i> , 2017, 12, e0178313.	2.5	54
58	Cytogenetic maps of homoeologous chromosomes A h01 and D h01 and their integration with the genome assembly in <i>Gossypium hirsutum</i> . <i>Comparative Cytogenetics</i> , 2017, 11, 405-420.	0.8	2
59	Chloroplast DNA Structural Variation, Phylogeny, and Age of Divergence among Diploid Cotton Species. <i>PLoS ONE</i> , 2016, 11, e0157183.	2.5	58
60	Genome Wide SSR High Density Genetic Map Construction from an Interspecific Cross of <i>Gossypium hirsutum</i> × <i>Gossypium tomentosum</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 436.	3.6	20
61	Genetic Analysis and QTL Detection on Fiber Traits Using Two Recombinant Inbred Lines and Their Backcross Populations in Upland Cotton. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2717-2724.	1.8	45
62	A <i>Gossypium</i> BAC clone contains key repeat components distinguishing sub-genome of allotetraploidy cottons. <i>Molecular Cytogenetics</i> , 2016, 9, 27.	0.9	6
63	QTL mapping for salt tolerance at seedling stage in the interspecific cross of <i>Gossypium tomentosum</i> with <i>Gossypium hirsutum</i> . <i>Euphytica</i> , 2016, 209, 223-235.	1.2	52
64	Screening and chromosome localization of two cotton BAC clones. <i>Comparative Cytogenetics</i> , 2016, 10, 1-15.	0.8	3
65	Construction of cytogenetic map of <i>Gossypium herbaceum</i> chromosome 1 and its integration with genetic maps. <i>Molecular Cytogenetics</i> , 2015, 8, 2.	0.9	8
66	Construction of a high-density genetic map and lint percentage and cottonseed nutrient trait QTL identification in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Molecular Genetics and Genomics</i> , 2015, 290, 1683-1700.	2.1	54
67	A high-density SSR genetic map constructed from a F2 population of <i>Gossypium hirsutum</i> and <i>Gossypium darwinii</i> . <i>Gene</i> , 2015, 574, 273-286.	2.2	26
68	Construction of genetic map and QTL analysis of fiber quality traits for Upland cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	99
69	Construction of a bacterial artificial chromosome library for <i>Gossypium herbaceum</i> var. <i>africanum</i> . <i>Science Bulletin</i> , 2013, 58, 3199-3201.	1.7	4
70	Uniqueness of the <i>Gossypium mustelinum</i> Genome Revealed by GISH and 45 S rDNA FISH. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 654-662.	8.5	8
71	Chromosomal Locations of 5S and 45S rDNA in <i>Gossypium</i> Genus and Its Phylogenetic Implications Revealed by FISH. <i>PLoS ONE</i> , 2013, 8, e68207.	2.5	28
72	Preparations of Meiotic Pachytene Chromosomes and Extended DNA Fibers from Cotton Suitable for Fluorescence In Situ Hybridization. <i>PLoS ONE</i> , 2012, 7, e33847.	2.5	10

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73	QTL Analysis on Yield and Its Components in Recombinant Inbred Lines of Upland Cotton. <i>Acta Agronomica Sinica</i> , 2011, 37, 433-442.	0.3	13
74	Screen of FISH marker of chromosomes at <i>Gossypium</i> D genome species. <i>Chinese Science Bulletin</i> , 2010, 55, 2099-2105.	0.7	4
75	Identification of cotton microRNAs and their targets. <i>Gene</i> , 2007, 397, 26-37.	2.2	190
76	Primary investigation on GISH-NOR in cotton. <i>Science Bulletin</i> , 2005, 50, 425-429.	1.7	6
77	Genome-Wide Identification and Expression Analysis Elucidates the Potential Role of PFK Gene Family in Drought Stress Tolerance and Sugar Metabolism in Cotton. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	5
78	Genome-Wide Dissection of the Genetic Basis for Drought Tolerance in <i>Gossypium hirsutum</i> L. Races. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5