

Guoyuan Liu

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

475
citations

623734

14
h-index

752698

20
g-index

30
all docs

30
docs citations

30
times ranked

357
citing authors

#	ARTICLE	IF	CITATIONS
1	QTL analysis and candidate gene identification for plant height in cotton based on an interspecific backcross inbred line population of <i>Gossypium hirsutum</i> × <i>Gossypium barbadense</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 2663-2676.	3.6	48
2	Genomic analyses reveal the genetic basis of early maturity and identification of loci and candidate genes in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2021, 19, 109-123.	8.3	42
3	High-density genetic linkage map construction by F2 populations and QTL analysis of early-maturity traits in upland cotton (<i>Gossypium hirsutum</i> L.). <i>PLoS ONE</i> , 2017, 12, e0182918.	2.5	40
4	Genome-wide association study of the oil content in upland cotton (<i>Gossypium hirsutum</i> L.) and identification of GhPRXR1, a candidate gene for a stable QTLqOC-Dt5-1. <i>Plant Science</i> , 2019, 286, 89-97.	3.6	35
5	Genetic variation of dynamic fiber elongation and developmental quantitative trait locus mapping of fiber length in upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2018, 19, 882.	2.8	33
6	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.	4.8	31
7	Genome sequencing and phylogenetic analysis of allotetraploid <i>Salix matsudana</i> Koidz. <i>Horticulture Research</i> , 2020, 7, 201.	6.3	30
8	Nutrient Removal Process and Cathodic Microbial Community Composition in Integrated Vertical-Flow Constructed Wetland “Microbial Fuel Cells Filled With Different Substrates. <i>Frontiers in Microbiology</i> , 2020, 11, 1896.	3.5	29
9	High-resolution temporal dynamic transcriptome landscape reveals a <i>ChCAL</i> -mediated flowering regulatory pathway in cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2021, 19, 153-166.	8.3	27
10	Genome-Wide Identification, Sequence Variation, and Expression of the Glycerol-3-Phosphate Acyltransferase (GPAT) Gene Family in <i>Gossypium</i> . <i>Frontiers in Genetics</i> , 2019, 10, 116.	2.3	22
11	Comprehensive Analysis of Carotenoid Cleavage Dioxygenases Gene Family and Its Expression in Response to Abiotic Stress in Poplar. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1418.	4.1	21
12	Analysis of the MIR160 gene family and the role of MIR160a_A05 in regulating fiber length in cotton. <i>Planta</i> , 2019, 250, 2147-2158.	3.2	17
13	A Comparative Genome-Wide Analysis of the R2R3-MYB Gene Family Among Four <i>Gossypium</i> Species and Their Sequence Variation and Association With Fiber Quality Traits in an Interspecific <i>G. hirsutum</i> × <i>G. barbadense</i> Population. <i>Frontiers in Genetics</i> , 2019, 10, 741.	2.3	16
14	Uncovering candidate genes responsive to salt stress in <i>Salix matsudana</i> (Koidz) by transcriptomic analysis. <i>PLoS ONE</i> , 2020, 15, e0236129.	2.5	16
15	Genome-wide investigation of the AP2/ERF superfamily and their expression under salt stress in Chinese willow (<i>Salix matsudana</i>). <i>PeerJ</i> , 2021, 9, e11076.	2.0	15
16	Genetic variation in <i>MYB5_A12</i> is associated with fibre initiation and elongation in tetraploid cotton. <i>Plant Biotechnology Journal</i> , 2021, 19, 1892-1894.	8.3	14
17	Genome-Scale Analysis of the WRI-Like Family in <i>Gossypium</i> and Functional Characterization of GhWRI1a Controlling Triacylglycerol Content. <i>Frontiers in Plant Science</i> , 2018, 9, 1516.	3.6	11
18	Overexpression of the <i>Salix matsudana</i> SmAP2-17 gene improves <i>Arabidopsis</i> salinity tolerance by enhancing the expression of SOS3 and ABI5. <i>BMC Plant Biology</i> , 2022, 22, 102.	3.6	8

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19	Differentially expressed genes between two groups of backcross inbred lines differing in fiber length developed from Upland A— Pima cotton. <i>Molecular Biology Reports</i> , 2019, 46, 1199-1212.	2.3	5
20	Transcriptome-based analysis reveals that the biosynthesis of anthocyanins is more active than that of flavonols and proanthocyanins in the colorful flowers of <i>Lagerstroemia indica</i> . <i>Biologia Futura</i> , 2021, 72, 473-488.	1.4	5
21	Identify of Fast-Growing Related Genes Especially in Height Growth by Combining QTL Analysis and Transcriptome in <i>Salix matsudana</i> (Koidz). <i>Frontiers in Genetics</i> , 2021, 12, 596749.	2.3	4
22	Genome-Wide Characterization and Abiotic Stresses Expression Analysis of Annexin Family Genes in Poplar. <i>International Journal of Molecular Sciences</i> , 2022, 23, 515.	4.1	3
23	Characteristics, expression profile, and function of non-specific lipid transfer proteins of <i>Populus trichocarpa</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 202, 468-481.	7.5	3
24	Title is missing!. , 2020, 15, e0236129.		0
25	Title is missing!. , 2020, 15, e0236129.		0
26	Title is missing!. , 2020, 15, e0236129.		0
27	Title is missing!. , 2020, 15, e0236129.		0
28	Title is missing!. , 2020, 15, e0236129.		0
29	Title is missing!. , 2020, 15, e0236129.		0