

# 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	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
2	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
3	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
4	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
5	High-resolution temporal dynamic transcriptome landscape reveals a GhCAL-mediated flowering regulatory pathway in cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2021, 19, 153-166.	8.3	27
6	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
7	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
8	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
9	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
10	Genetic variation in MYB5_A12 is associated with fibre initiation and elongation in tetraploid cotton. <i>Plant Biotechnology Journal</i> , 2021, 19, 1892-1894.	8.3	14
11	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
12	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
13	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
14	Genome sequencing and phylogenetic analysis of allotetraploid <i>Salix matsudana</i> Koidz. <i>Horticulture Research</i> , 2020, 7, 201.	6.3	30
15	Title is missing!. , 2020, 15, e0236129.		0
16	Title is missing!. , 2020, 15, e0236129.		0
17	Title is missing!. , 2020, 15, e0236129.		0
18	Title is missing!. , 2020, 15, e0236129.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 15, e0236129.		0
20	Title is missing!. , 2020, 15, e0236129.		0
21	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
22	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
23	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
24	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
25	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
26	Differentially expressed genes between two groups of backcross inbred lines differing in fiber length developed from Upland × Pima cotton. <i>Molecular Biology Reports</i> , 2019, 46, 1199-1212.	2.3	5
27	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
28	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
29	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