

Jinhui Chen

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

899
citations

623734

14
h-index

477307

29
g-index

30
all docs

30
docs citations

30
times ranked

873
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene expression analysis revealed Hbr-miR396b as a key piece participating in reaction wood formation of <i>Hevea brasiliensis</i> (rubber tree). <i>Industrial Crops and Products</i> , 2022, 177, 114460.	5.2	4
2	ICE-CBF-COR Signaling Cascade and Its Regulation in Plants Responding to Cold Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1549.	4.1	101
3	Alterations in Population Distribution of <i>Liriodendron chinense</i> (Hemsl.) Sarg. and <i>Liriodendron tulipifera</i> Linn. Caused by Climate Change. <i>Forests</i> , 2022, 13, 488.	2.1	12
4	Genomic Survey and Cold-Induced Expression Patterns of bHLH Transcription Factors in <i>Liriodendron chinense</i> (Hemsl) Sarg.. <i>Forests</i> , 2022, 13, 518.	2.1	10
5	Integrated mRNA and Small RNA Sequencing Reveals microRNAs Associated With Xylem Development in <i>Dalbergia odorifera</i> . <i>Frontiers in Genetics</i> , 2022, 13, 883422.	2.3	2
6	Third-Generation Sequencing Indicated that LncRNA Could Regulate eIF2D to Enhance Protein Translation Under Heat Stress in <i>Populus simonii</i> . <i>Plant Molecular Biology Reporter</i> , 2021, 39, 240-250.	1.8	4
7	Transcriptomics and Metabolomics Reveal Purine and Phenylpropanoid Metabolism Response to Drought Stress in <i>Dendrobium sinense</i> , an Endemic Orchid Species in Hainan Island. <i>Frontiers in Genetics</i> , 2021, 12, 692702.	2.3	25
8	Third-generation sequencing and metabolome analysis reveal candidate genes and metabolites with altered levels in albino jackfruit seedlings. <i>BMC Genomics</i> , 2021, 22, 543.	2.8	11
9	RNA Sequencing Reveals Phenylpropanoid Biosynthesis Genes and Transcription Factors for <i>Hevea brasiliensis</i> Reaction Wood Formation. <i>Frontiers in Genetics</i> , 2021, 12, 763841.	2.3	9
10	Phenotypic and molecular marker analysis uncovers the genetic diversity of the grass <i>Stenotaphrum secundatum</i> . <i>BMC Genetics</i> , 2020, 21, 86.	2.7	11
11	Third-generation sequencing found LncRNA associated with heat shock protein response to heat stress in <i>Populus qionghdaoensis</i> seedlings. <i>BMC Genomics</i> , 2020, 21, 572.	2.8	15
12	Third-Generation Sequencing Reveals LncRNA-Regulated HSP Genes in the <i>Populus x canadensis</i> Moench Heat Stress Response. <i>Frontiers in Genetics</i> , 2020, 11, 249.	2.3	10
13	Time-specific and pleiotropic quantitative trait loci coordinately modulate stem growth in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 608-624.	8.3	34
14	Genetic variants in microRNA biogenesis genes as novel indicators for secondary growth in <i>Populus</i> . <i>New Phytologist</i> , 2018, 219, 1263-1282.	7.3	8
15	Adaptive evolution and functional innovation of <i>Populus</i> -specific recently evolved microRNAs. <i>New Phytologist</i> , 2017, 213, 206-219.	7.3	36
16	Identification and allelic dissection uncover roles of lncRNAs in secondary growth of <i>Populus tomentosa</i> . <i>DNA Research</i> , 2017, 24, 473-486.	3.4	37
17	Allelic variation in PtoPsbW associated with photosynthesis, growth, and wood properties in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 77-91.	2.1	10
18	Floral Nectary Morphology and Proteomic Analysis of Nectar of <i>Liriodendron tulipifera</i> Linn.. <i>Frontiers in Plant Science</i> , 2016, 7, 826.	3.6	34

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19	Genetic variations and miRNA target interactions contribute to natural phenotypic variations in <i>Populus</i> . <i>New Phytologist</i> , 2016, 212, 150-160.	7.3	17
20	Association genetics and transcriptome analysis reveal a gibberellin-responsive pathway involved in regulating photosynthesis. <i>Journal of Experimental Botany</i> , 2016, 67, 3325-3338.	4.8	30
21	Association studies reveal the effect of genetic variation in lncRNA UGTRL and its putative target PtoUGT88A1 on wood formation in <i>Populus tomentosa</i> . <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	8
22	Association genetics in <i>Populus</i> reveals the interactions between Pto-miR160a and its target Pto-ARF16. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1069-1082.	2.1	22
23	Population genomic analysis of gibberellin-responsive long non-coding RNAs in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 2467-2482.	4.8	98
24	The genetic regulatory network centered on Pto-Wuschela and its targets involved in wood formation revealed by association studies. <i>Scientific Reports</i> , 2015, 5, 16507.	3.3	2
25	Exploring the Secrets of Long Noncoding RNAs. <i>International Journal of Molecular Sciences</i> , 2015, 16, 5467-5496.	4.1	125
26	Association genetics in <i>Populus</i> reveals the interactions between Pt-miR397a and its target genes. <i>Scientific Reports</i> , 2015, 5, 11672.	3.3	8
27	Transcript profiling of <i>Populus tomentosa</i> genes in normal, tension, and opposite wood by RNA-seq. <i>BMC Genomics</i> , 2015, 16, 164.	2.8	58
28	Genome-wide identification of novel long non-coding RNAs in <i>Populus tomentosa</i> tension wood, opposite wood and normal wood xylem by RNA-seq. <i>Planta</i> , 2015, 241, 125-143.	3.2	109
29	Genome-Wide Analysis of Gene Expression in Response to Drought Stress in <i>Populus simonii</i> . <i>Plant Molecular Biology Reporter</i> , 2013, 31, 946-962.	1.8	46
30	Integrated Full-Length Transcriptome and MicroRNA Sequencing Approaches Provide Insights Into Salt Tolerance in Mangrove (<i>Sonneratia apetala</i> Buch.-Ham.). <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3