

Xuke Lu

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

395
citations

1040056

9
h-index

839539

18
g-index

25
all docs

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docs citations

25
times ranked

428
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular traits and functional analysis of Rapid Alkalinization Factors (RALFs) in four <i>Gossypium</i> species. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 84-99.	7.5	4
2	Molecular structures and functional exploration of NDA family genes respond tolerant to alkaline stress in <i>Gossypium hirsutum</i> L.. <i>Biological Research</i> , 2022, 55, 4.	3.4	4
3	Identification and Structure Analysis of KCS Family Genes Suggest Their Reponding to Regulate Fiber Development in Long-Staple Cotton Under Salt-Alkaline Stress. <i>Frontiers in Genetics</i> , 2022, 13, 812449.	2.3	11
4	Identification of SNAT Family Genes Suggests GhSNAT3D Functional Reponse to Melatonin Synthesis Under Salinity Stress in Cotton. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 843814.	3.5	12
5	A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. <i>GigaScience</i> , 2022, 11, .	6.4	6
6	Genome-wide expression analysis of carboxylesterase (CXE) gene family implies GBCXE49 functional responding to alkaline stress in cotton. <i>BMC Plant Biology</i> , 2022, 22, 194.	3.6	8
7	Cotton transcriptome analysis reveals novel biological pathways that eliminate reactive oxygen species (ROS) under sodium bicarbonate (NaHCO ₃) alkaline stress. <i>Genomics</i> , 2021, 113, 1157-1169.	2.9	27
8	Melatonin Improves Cotton Salt Tolerance by Regulating ROS Scavenging System and Ca ²⁺ + Signal Transduction. <i>Frontiers in Plant Science</i> , 2021, 12, 693690.	3.6	44
9	Genome-wide identification and function analysis of HMAD gene family in cotton (<i>Gossypium</i> spp.). <i>BMC Plant Biology</i> , 2021, 21, 386.	3.6	4
10	Genome-wide identification of CK gene family suggests functional expression pattern against Cd ²⁺ stress in <i>Gossypium hirsutum</i> L.. <i>International Journal of Biological Macromolecules</i> , 2021, 188, 272-282.	7.5	15
11	A novel raffinose biological pathway is observed by symbionts of cotton <i>Verticillium dahliae</i> to improve salt tolerance genetically on cotton. <i>Journal of Agronomy and Crop Science</i> , 2021, 207, 956-969.	3.5	14
12	Genome-wide expression analysis of phospholipase A1 (PLA1) gene family suggests phospholipase A1-32 gene responding to abiotic stresses in cotton. <i>International Journal of Biological Macromolecules</i> , 2021, 192, 1058-1074.	7.5	13
13	Genome-wide identification and characteristic analysis of the downstream melatonin metabolism gene GhM2H in <i>Gossypium hirsutum</i> L.. <i>Biological Research</i> , 2021, 54, 36.	3.4	8
14	Insight Between the Epigenetics and Transcription Responding of Cotton Hypocotyl Cellular Elongation Under Salt-Alkaline Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 772123.	3.6	0
15	Genome-wide identification and expression analysis of PUB genes in cotton. <i>BMC Genomics</i> , 2020, 21, 213.	2.8	26
16	Resequencing of CRI-12 family reveals haplotype block inheritance and recombination of agronomically important genes in artificial selection. <i>Plant Biotechnology Journal</i> , 2019, 17, 945-955.	8.3	20
17	Identification and function analysis of drought-specific small RNAs in <i>Gossypium hirsutum</i> L.. <i>Plant Science</i> , 2019, 280, 187-196.	3.6	12
18	Single-base resolution methylomes of upland cotton (<i>Gossypium hirsutum</i> L.) reveal epigenome modifications in response to drought stress. <i>BMC Genomics</i> , 2017, 18, 297.	2.8	58

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19	Genome-Wide Analysis of Long Noncoding RNAs and Their Responses to Drought Stress in Cotton (<i>Gossypium hirsutum</i> L.). PLoS ONE, 2016, 11, e0156723.	2.5	109