

Yuzhen Shi

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

257
citations

1307594

7
h-index

1199594

12
g-index

12
all docs

12
docs citations

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times ranked

271
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>lncRNA7</i> and <i>lncRNA2</i> modulate cell wall defense genes to regulate cotton resistance to Verticillium wilt. <i>Plant Physiology</i> , 2022, 189, 264-284.	4.8	35
2	Multi-environment Evaluations Across Ecological Regions Reveal That the Kernel Oil Content of Cottonseed Is Equally Determined by Genotype and Environment. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 2529-2544.	5.2	3
3	Linkage and association analyses reveal that hub genes in energy-flow and lipid biosynthesis pathways form a cluster in upland cotton. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1841-1859.	4.1	6
4	Cotton germplasm improvement and progress in Pakistan. <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	24
5	QTL mapping for plant height and fruit branch number based on RIL population of upland cotton. <i>Journal of Cotton Research</i> , 2020, 3, .	2.5	6
6	QTL mapping for fiber quality and yield-related traits across multiple generations in segregating population of CCRI 70. <i>Journal of Cotton Research</i> , 2019, 2, .	2.5	14
7	Genome-wide identification and analysis of the evolution and expression patterns of the GATA transcription factors in three species of <i>Gossypium</i> genus. <i>Gene</i> , 2019, 680, 72-83.	2.2	25
8	GbABR1 is associated with Verticillium wilt resistance in cotton. <i>Biologia (Poland)</i> , 2018, 73, 449-457.	1.5	5
9	Identification of circularRNAs and their targets in <i>Gossypium</i> under Verticillium wilt stress based on RNA-seq. <i>PeerJ</i> , 2018, 6, e4500.	2.0	34
10	Molecular characterisation and functional analysis of a cytochrome P450 gene in cotton. <i>Biologia (Poland)</i> , 2017, 72, 43-52.	1.5	3
11	Identification of novel microRNAs in the Verticillium wilt-resistant upland cotton variety KV-1 by high-throughput sequencing. <i>SpringerPlus</i> , 2014, 3, 564.	1.2	24
12	Analysis of sea-island cotton and upland cotton in response to Verticillium dahliae infection by RNA sequencing. <i>BMC Genomics</i> , 2013, 14, 852.	2.8	78