

Lei Mei

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

391
citations

1040056

9
h-index

940533

16
g-index

18
all docs

18
docs citations

18
times ranked

505
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide SNP Linkage Mapping and QTL Analysis for Fiber Quality and Yield Traits in the Upland Cotton Recombinant Inbred Lines Population. <i>Frontiers in Plant Science</i> , 2016, 7, 1356.	3.6	105
2	Chromium (VI) Uptake and Tolerance Potential in Cotton Cultivars: Effect on Their Root Physiology, Ultramorphology, and Oxidative Metabolism. <i>BioMed Research International</i> , 2014, 2014, 1-12.	1.9	44
3	Determination of gossypol content in cottonseeds by near infrared spectroscopy based on Monte Carlo uninformative variable elimination and nonlinear calibration methods. <i>Food Chemistry</i> , 2017, 221, 990-996.	8.2	43
4	Pretreatment with salicylic acid and ascorbic acid significantly mitigate oxidative stress induced by copper in cotton genotypes. <i>Environmental Science and Pollution Research</i> , 2015, 22, 9922-9931.	5.3	40
5	Leaf-based physiological, metabolic, and ultrastructural changes in cultivated cotton cultivars under cadmium stress mediated by glutathione. <i>Environmental Science and Pollution Research</i> , 2016, 23, 15551-15564.	5.3	39
6	Cadmium-Induced Upregulation of Lipid Peroxidation and Reactive Oxygen Species Caused Physiological, Biochemical, and Ultrastructural Changes in Upland Cotton Seedlings. <i>BioMed Research International</i> , 2013, 2013, 1-10.	1.9	31
7	Cotton roots are the major source of gossypol biosynthesis and accumulation. <i>BMC Plant Biology</i> , 2020, 20, 88.	3.6	21
8	Mercury-Induced Phytotoxicity and Responses in Upland Cotton (<i>Gossypium hirsutum</i> L.) Seedlings. <i>Plants</i> , 2021, 10, 1494.	3.5	16
9	Genetic basis of heterosis for yield and yield components explored by QTL mapping across four genetic populations in upland cotton. <i>BMC Genomics</i> , 2018, 19, 910.	2.8	12
10	qOil-3, a major QTL identification for oil content in cottonseed across genomes and its candidate gene analysis. <i>Industrial Crops and Products</i> , 2020, 145, 112070.	5.2	11
11	<i>In Vitro</i> Cadmium-Induced Alterations in Growth and Oxidative Metabolism of Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Scientific World Journal</i> , The, 2014, 2014, 1-10.	2.1	7
12	Genome-wide analysis of genetic variations between dominant and recessive NILs of glanded and glandless cottons. <i>Scientific Reports</i> , 2019, 9, 9226.	3.3	7
13	A Comparative Study of Flavonoids and Carotenoids Revealed Metabolite Responses for Various Flower Colorations Between <i>Nicotiana tabacum</i> L. and <i>Nicotiana rustica</i> L.. <i>Frontiers in Plant Science</i> , 2022, 13, 828042.	3.6	6
14	Characterizations of male sterility in a glyphosate-tolerant upland cotton (<i>Gossypium hirsutum</i> L.) induced by glyphosate and its assessments on safety utilization. <i>Industrial Crops and Products</i> , 2019, 134, 318-327.	5.2	2
15	Genome-wide characterization on MT family and their expression in response to environmental cues in upland cotton (<i>Gossypium hirsutum</i> L.). <i>International Journal of Biological Macromolecules</i> , 2022, 198, 54-67.	7.5	2
16	The complete chloroplast genome sequence of <i>Gynura cusimbua</i> (D. Don) S. Moore. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 96-97.	0.4	2