

Shuijin Zhu

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,419
citations

257450

24
h-index

189892

50
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57
all docs

57
docs citations

57
times ranked

3036
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined analysis of mRNA and miRNA transcriptomes reveals the regulatory mechanism of PVY resistance in tobacco. <i>Industrial Crops and Products</i> , 2022, 176, 114322.	5.2	3
2	Root Illumination Promotes Seedling Growth and Inhibits Gossypol Biosynthesis in Upland Cotton. <i>Plants</i> , 2022, 11, 728.	3.5	3
3	Parental legacy versus regulatory innovation in salt stress responsiveness of allopolyploid cotton (<i>Gossypium</i>) species. <i>Plant Journal</i> , 2022, 111, 872-887.	5.7	8
4	Feasibility study on the use of near-infrared spectroscopy for rapid and nondestructive determination of gossypol content in intact cottonseeds. <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	4
5	Whole-genome resequencing of 240 <i>Gossypium barbadense</i> accessions reveals genetic variation and genes associated with fiber strength and lint percentage. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3249-3261.	3.6	19
6	Seed priming with melatonin improves salt tolerance in cotton through regulating photosynthesis, scavenging reactive oxygen species and coordinating with phytohormone signal pathways. <i>Industrial Crops and Products</i> , 2021, 169, 113671.	5.2	34
7	Determination of Oxidative Stress and Antioxidant Enzyme Activity for Physiological Phenotyping During Heavy Metal Exposure. <i>Methods in Molecular Biology</i> , 2021, 2326, 241-249.	0.9	1
8	Salt tolerance diversity in diploid and polyploid cotton (<i>Gossypium</i>) species. <i>Plant Journal</i> , 2020, 101, 1135-1151.	5.7	34
9	Physiological, ultrastructural, biochemical, and molecular responses of glandless cotton to hexavalent chromium (Cr6+) exposure. <i>Environmental Pollution</i> , 2020, 266, 115394.	7.5	21
10	IAA priming improves the germination and seedling growth in cotton (<i>Gossypium hirsutum</i> L.) via regulating the endogenous phytohormones and enhancing the sucrose metabolism. <i>Industrial Crops and Products</i> , 2020, 155, 112788.	5.2	39
11	Comprehensive characterization and gene expression patterns of LBD gene family in <i>Gossypium</i> . <i>Planta</i> , 2020, 251, 81.	3.2	21
12	Cotton roots are the major source of gossypol biosynthesis and accumulation. <i>BMC Plant Biology</i> , 2020, 20, 88.	3.6	21
13	Reduced Glutathione Protects Subcellular Compartments From Pb-Induced ROS Injury in Leaves and Roots of Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 412.	3.6	31
14	Melatonin enhances cotton immunity to <i>Verticillium</i> wilt via manipulating lignin and gossypol biosynthesis. <i>Plant Journal</i> , 2019, 100, 784-800.	5.7	107
15	Determination of manganese content in cottonseed meal using near-infrared spectrometry and multivariate calibration. <i>Journal of Cotton Research</i> , 2019, 2, .	2.5	2
16	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
17	Identification and profiling of upland cotton microRNAs at fiber initiation stage under exogenous IAA application. <i>BMC Genomics</i> , 2019, 20, 421.	2.8	19
18	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. <i>Nature Genetics</i> , 2019, 51, 739-748.	21.4	568

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19	Genotypic differences in leaf secondary metabolism, plant hormones and yield under alone and combined stress of drought and salinity in cotton genotypes. <i>Physiologia Plantarum</i> , 2019, 165, 343-355.	5.2	71
20	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
21	QTL Mapping and Heterosis Analysis for Fiber Quality Traits Across Multiple Genetic Populations and Environments in Upland Cotton. <i>Frontiers in Plant Science</i> , 2018, 9, 1364.	3.6	12
22	Genome-Wide Identification and Comparative Analysis of the 3-Hydroxy-3-methylglutaryl Coenzyme A Reductase (HMGR) Gene Family in <i>Gossypium</i> . <i>Molecules</i> , 2018, 23, 193.	3.8	13
23	Genome-wide identification of membrane-bound fatty acid desaturase genes in <i>Gossypium hirsutum</i> and their expressions during abiotic stress. <i>Scientific Reports</i> , 2017, 7, 45711.	3.3	31
24	QTL mapping with different genetic systems for nine non-essential amino acids of cottonseeds. <i>Molecular Genetics and Genomics</i> , 2017, 292, 671-684.	2.1	7
25	Suppressing a Putative Sterol Carrier Gene Reduces Plasmodesmal Permeability and Activates Sucrose Transporter Genes during Cotton Fiber Elongation. <i>Plant Cell</i> , 2017, 29, 2027-2046.	6.6	66
26	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
27	Drinking Water Quality Status and Contamination in Pakistan. <i>BioMed Research International</i> , 2017, 2017, 1-18.	1.9	245
28	A New Synthetic Hybrid (A1D5) between <i>Gossypium herbaceum</i> and <i>G. raimondii</i> and Its Morphological, Cytogenetic, Molecular Characterization. <i>PLoS ONE</i> , 2017, 12, e0169833.	2.5	5
29	Comparative genomic study of ALDH gene superfamily in <i>Gossypium</i> : A focus on <i>Gossypium hirsutum</i> under salt stress. <i>PLoS ONE</i> , 2017, 12, e0176733.	2.5	21
30	Glutathione S-Transferase Gene Family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> : Comparative Genomic Study and their Expression under Salt Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 139.	3.6	81
31	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
32	Genome-Wide Identification of R2R3-MYB Genes and Expression Analyses During Abiotic Stress in <i>Gossypium raimondii</i> . <i>Scientific Reports</i> , 2016, 6, 22980.	3.3	103
33	A betaine aldehyde dehydrogenase gene in quinoa (<i>Chenopodium quinoa</i>): structure, phylogeny, and expression pattern. <i>Genes and Genomics</i> , 2016, 38, 1013-1020.	1.4	10
34	Genetic basis for glandular trichome formation in cotton. <i>Nature Communications</i> , 2016, 7, 10456.	12.8	130
35	Characterization of 19 Genes Encoding Membrane-Bound Fatty Acid Desaturases and their Expression Profiles in <i>Gossypium raimondii</i> Under Low Temperature. <i>PLoS ONE</i> , 2015, 10, e0123281.	2.5	37
36	Genotypic differences in photosynthetic performance, antioxidant capacity, ultrastructure and nutrients in response to combined stress of salinity and Cd in cotton. <i>BioMetals</i> , 2015, 28, 1063-1078.	4.1	29

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37	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	17.5	1,064
38	Dissecting Genetic Architecture Underlying Seed Traits in Multiple Environments. <i>Genetics</i> , 2015, 199, 61-71.	2.9	4
39	Species-Specific Expansion and Molecular Evolution of the 3-hydroxy-3-methylglutaryl Coenzyme A Reductase (HMGR) Gene Family in Plants. <i>PLoS ONE</i> , 2014, 9, e94172.	2.5	50
40	MicroRNA target gene responses to lead-induced stress in cotton (<i>Gossypium hirsutum</i> L.). <i>Functional and Integrative Genomics</i> , 2014, 14, 507-515.	3.5	36
41	Genome-Wide Survey and Expression Analysis of Calcium-Dependent Protein Kinase in <i>Gossypium raimondii</i> . <i>PLoS ONE</i> , 2014, 9, e98189.	2.5	77
42	RELATIONSHIP BETWEEN ENDOGENOUS SALICYLIC ACID AND ANTIOXIDANT ENZYME ACTIVITIES IN MAIZE SEEDLINGS UNDER CHILLING STRESS. <i>Experimental Agriculture</i> , 2013, 49, 295-308.	0.9	14
43	Chilling tolerance in <i>Nicotiana tabacum</i> induced by seed priming with putrescine. <i>Plant Growth Regulation</i> , 2011, 63, 279-290.	3.4	81
44	An interspecific somatic hybrid between upland cotton (<i>G. hirsutum</i> L. cv. ZDM-3) and wild diploid cotton (<i>G. klotzschianum</i> A.). <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 106, 425-433.	2.3	9
45	Effects of pigment glands and gossypol on growth, development and insecticide-resistance of cotton bollworm (<i>Heliothis armigera</i> (H&A1/4bner)). <i>Crop Protection</i> , 2010, 29, 813-819.	2.1	33
46	Genetic Characterization of a New Growth Habit Mutant in Tomato (<i>Solanum lycopersicum</i>). <i>Plant Molecular Biology Reporter</i> , 2009, 27, 431-438.	1.8	7
47	The effects of cotton root exudates on the growth and development of <i>Verticillium dahliae</i> . <i>Frontiers of Agriculture in China</i> , 2008, 2, 435-440.	0.2	10
48	Effect of in vivo plant preservation on the fertility and chromosome configuration of a quadri-specific hybrid derived from 4 cultivated cotton species. <i>Frontiers of Agriculture in China</i> , 2008, 2, 380-385.	0.2	0
49	Characterization of Pigmentation and Cellulose Synthesis in Colored Cotton Fibers. <i>Crop Science</i> , 2007, 47, 1540-1546.	1.8	57
50	Breeding, introgression and inheritance of delayed gland morphogenesis trait from <i>Gossypium bickii</i> into upland cotton germplasm. <i>Science Bulletin</i> , 2004, 49, 2470-2476.	1.7	0
51	Inheritance of the delayed gland morphogenesis trait in Australian wild species of <i>Gossypium</i> . <i>Science Bulletin</i> , 2001, 46, 1168-1174.	1.7	10
52	Effects of pigment glands and gossypol on somatic cell culture of upland cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142	1.7	3
53	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1