

Longfu Zhu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

3,388
citations

32
h-index

57
g-index

78
ext. papers

4,851
ext. citations

6.7
avg, IF

5.04
L-index

#	Paper	IF	Citations
72	Dynamic 3D genome architecture of cotton fiber reveals subgenome-coordinated chromatin topology for 4-staged single-cell differentiation.. <i>Genome Biology</i> , 2022 , 23, 45	18.3	0
71	Fast anther dehiscence status recognition system established by deep learning to screen heat tolerant cotton.. <i>Plant Methods</i> , 2022 , 18, 53	5.8	
70	Genetic Mapping and Analysis of a Compact Plant Architecture and Precocious Mutant in Upland Cotton. <i>Plants</i> , 2022 , 11, 1483	4.5	
69	An enhanced photosynthesis and carbohydrate metabolic capability contributes to heterosis of the cotton (<i>Gossypium hirsutum</i>) hybrid “Huaza Mian H318R” as revealed by genome-wide gene expression analysis. <i>BMC Genomics</i> , 2021 , 22, 277	4.5	4
68	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021 , 22, 119	18.3	10
67	GhWRKY1-like enhances cotton resistance to <i>Verticillium dahliae</i> via an increase in defense-induced lignification and S monolignol content. <i>Plant Science</i> , 2021 , 305, 110833	5.3	7
66	Orchestration of plant development and defense by indirect crosstalk of salicylic acid and brassinosteroid signaling via transcription factor GhTINY2. <i>Journal of Experimental Botany</i> , 2021 , 72, 4721-4743	7	4
65	Association mapping and domestication analysis to dissect genetic improvement process of upland cotton yield-related traits in China. <i>Journal of Cotton Research</i> , 2021 , 4,	2.3	2
64	Genome-wide identification, evolutionary estimation and functional characterization of two cotton CKI gene types. <i>BMC Plant Biology</i> , 2021 , 21, 229	5.3	1
63	A combination of genome-wide and transcriptome-wide association studies reveals genetic elements leading to male sterility during high temperature stress in cotton. <i>New Phytologist</i> , 2021 , 231, 165-181	9.8	4
62	Phosphate deficiency enhances cotton resistance to <i>Verticillium dahliae</i> through activating jasmonic acid biosynthesis and phenylpropanoid pathway. <i>Plant Science</i> , 2021 , 302, 110724	5.3	5
61	GhTULP34, a member of tubby-like proteins, interacts with GhSKP1A to negatively regulate plant osmotic stress. <i>Genomics</i> , 2021 , 113, 462-474	4.3	6
60	GhMYB4 downregulates lignin biosynthesis and enhances cotton resistance to <i>Verticillium dahliae</i> . <i>Plant Cell Reports</i> , 2021 , 40, 735-751	5.1	6
59	A Single-Nucleotide Mutation in a GLUTAMATE RECEPTOR-LIKE Gene Confers Resistance to Fusarium Wilt in. <i>Advanced Science</i> , 2021 , 8, 2002723	13.6	8
58	Effects of cotton-maize rotation on soil microbiome structure. <i>Molecular Plant Pathology</i> , 2021 , 22, 673-682	6.2	5
57	GhHB12 negatively regulates abiotic stress tolerance in Arabidopsis and cotton. <i>Environmental and Experimental Botany</i> , 2020 , 176, 104087	5.9	4
56	ABA signaling is negatively regulated by GbWRKY1 through JAZ1 and ABI1 to affect salt and drought tolerance. <i>Plant Cell Reports</i> , 2020 , 39, 181-194	5.1	18

55	Comprehensive Genome-Wide Analysis of Thaumatin-Like Gene Family in Four Cotton Species and Functional Identification of Involved in Regulating Tolerance to and Drought. <i>Frontiers in Plant Science</i> , 2020 , 11, 575015	6.2	9
54	Genome-Wide Analysis of Family Genes in Cotton Identified a Role for in Resistance. <i>Genes</i> , 2020 , 11,	4.2	6
53	Deficiencies in the formation and regulation of anther cuticle and tryphine contribute to male sterility in cotton PGMS line. <i>BMC Genomics</i> , 2020 , 21, 825	4.5	4
52	GhCyP3 improves the resistance of cotton to <i>Verticillium dahliae</i> by inhibiting the E3 ubiquitin ligase activity of GhPUB17. <i>Plant Molecular Biology</i> , 2019 , 99, 379-393	4.6	9
51	Genome-Wide Identification of Papain-Like Cysteine Proteases in and Functional Characterization in Response to. <i>Frontiers in Plant Science</i> , 2019 , 10, 134	6.2	9
50	GbSOBIR1 confers <i>Verticillium wilt</i> resistance by phosphorylating the transcriptional factor GbbHLH171 in <i>Gossypium barbadense</i> . <i>Plant Biotechnology Journal</i> , 2019 , 17, 152-163	11.6	20
49	Down regulation of cotton GbTRP1 leads to accumulation of anthranilates and confers resistance to <i>Verticillium dahliae</i> . <i>Journal of Cotton Research</i> , 2019 , 2,	2.3	1
48	Effects of Long-term Cotton Continuous Cropping on Soil Microbiome. <i>Scientific Reports</i> , 2019 , 9, 18297	4.9	17
47	Suppression of tryptophan synthase activates cotton immunity by triggering cell death via promoting SA synthesis. <i>Plant Journal</i> , 2019 , 98, 329-345	6.9	22
46	Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019 , 51, 224-229	36.3	266
45	Physiological and molecular mechanism of defense in cotton against <i>Verticillium dahliae</i> . <i>Plant Physiology and Biochemistry</i> , 2018 , 125, 193-204	5.4	49
44	GhJAZ2 attenuates cotton resistance to biotic stresses via the inhibition of the transcriptional activity of GbbHLH171. <i>Molecular Plant Pathology</i> , 2018 , 19, 896-908	5.7	35
43	Genome-wide identification of lipoxygenase gene family in cotton and functional characterization in response to abiotic stresses. <i>BMC Genomics</i> , 2018 , 19, 599	4.5	23
42	Promoters of Arabidopsis Casein kinase I-like 2 and 7 confer specific high-temperature response in anther. <i>Plant Molecular Biology</i> , 2018 , 98, 33-49	4.6	5
41	Laccase GhLac1 Modulates Broad-Spectrum Biotic Stress Tolerance via Manipulating Phenylpropanoid Pathway and Jasmonic Acid Synthesis. <i>Plant Physiology</i> , 2018 , 176, 1808-1823	6.6	94
40	Long noncoding RNAs involve in resistance to <i>Verticillium dahliae</i> , a fungal disease in cotton. <i>Plant Biotechnology Journal</i> , 2018 , 16, 1172-1185	11.6	77
39	Transfer of tomato immune receptor Ve1 confers Ave1-dependent <i>Verticillium</i> resistance in tobacco and cotton. <i>Plant Biotechnology Journal</i> , 2018 , 16, 638-648	11.6	23
38	GhHB12, a HD-ZIP I Transcription Factor, Negatively Regulates the Cotton Resistance to. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	15

37	The cotton HD-Zip transcription factor GhHB12 regulates flowering time and plant architecture via the GhmiR157-GhSPL pathway. <i>Communications Biology</i> , 2018 , 1, 229	6.7	8
36	GhCPK33 Negatively Regulates Defense against by Phosphorylating GhOPR3. <i>Plant Physiology</i> , 2018 , 178, 876-889	6.6	32
35	GhUMC1, a blue copper-binding protein, regulates lignin synthesis and cotton immune response. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 504, 75-81	3.4	13
34	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017 , 49, 579-587	36.3	229
33	microRNAs involved in auxin signalling modulate male sterility under high-temperature stress in cotton (<i>Gossypium hirsutum</i>). <i>Plant Journal</i> , 2017 , 91, 977-994	6.9	63
32	GhATAF1, a NAC transcription factor, confers abiotic and biotic stress responses by regulating phytohormonal signaling networks. <i>Plant Cell Reports</i> , 2016 , 35, 2167-79	5.1	51
31	GhJAZ2 negatively regulates cotton fiber initiation by interacting with the R2R3-MYB transcription factor GhMYB25-like. <i>Plant Journal</i> , 2016 , 88, 921-935	6.9	76
30	An ethylene response-related factor, GBERF1-like, from <i>Gossypium barbadense</i> improves resistance to <i>Verticillium dahliae</i> via activating lignin synthesis. <i>Plant Molecular Biology</i> , 2016 , 91, 305-18	4.6	65
29	Suppression of the homeobox gene HDTF1 enhances resistance to <i>Verticillium dahliae</i> and <i>Botrytis cinerea</i> in cotton. <i>Journal of Integrative Plant Biology</i> , 2016 , 58, 503-13	8.3	43
28	The Sophora Alopecuroid H + -PPase Gene SaVP1 Confers Multiple Abiotic Stress Tolerance in <i>Arabidopsis</i> . <i>Plant Molecular Biology Reporter</i> , 2015 , 33, 923-930	1.7	3
27	Defective pollen wall contributes to male sterility in the male sterile line 1355A of cotton. <i>Scientific Reports</i> , 2015 , 5, 9608	4.9	33
26	LEAFY COTYLEDON1-CASEIN KINASE I-TCP15-PHYTOCHROME INTERACTING FACTOR4 Network Regulates Somatic Embryogenesis by Regulating Auxin Homeostasis. <i>Plant Physiology</i> , 2015 , 169, 2805-21	6.6	24
25	The genome sequence of Sea-Island cotton (<i>Gossypium barbadense</i>) provides insights into the allopolyploidization and development of superior spinnable fibres. <i>Scientific Reports</i> , 2015 , 5, 17662	4.9	181
24	GbMPK3, a mitogen-activated protein kinase from cotton, enhances drought and oxidative stress tolerance in tobacco. <i>Plant Cell, Tissue and Organ Culture</i> , 2014 , 116, 153-162	2.7	34
23	Sugar and auxin signaling pathways respond to high-temperature stress during anther development as revealed by transcript profiling analysis in cotton. <i>Plant Physiology</i> , 2014 , 164, 1293-308	6.6	129
22	Functional characterization of cotton genes responsive to <i>Verticillium dahliae</i> through bioinformatics and reverse genetics strategies. <i>Journal of Experimental Botany</i> , 2014 , 65, 6679-92	7	40
21	Cotton cytochrome P450 CYP82D regulates systemic cell death by modulating the octadecanoid pathway. <i>Nature Communications</i> , 2014 , 5, 5372	17.4	75
20	Cotton WRKY1 mediates the plant defense-to-development transition during infection of cotton by <i>Verticillium dahliae</i> by activating JASMONATE ZIM-DOMAIN1 expression. <i>Plant Physiology</i> , 2014 , 166, 2179-94	6.6	94

19	????????????????<italic>Ve1</italic>. <i>Scientia Sinica Vitae</i> , 2014 , 44, 803-814	1.4	11
18	Overexpression of rice NAC gene SNAC1 improves drought and salt tolerance by enhancing root development and reducing transpiration rate in transgenic cotton. <i>PLoS ONE</i> , 2014 , 9, e86895	3.7	139
17	Expression of the Arabidopsis vacuolar H ⁺ -pyrophosphatase gene AVP1 in peanut to improve drought and salt tolerance. <i>Plant Biotechnology Reports</i> , 2013 , 7, 345-355	2.5	51
16	Proteomic and virus-induced gene silencing (VIGS) Analyses reveal that gossypol, brassinosteroids, and jasmonic acid contribute to the resistance of cotton to <i>Verticillium dahliae</i> . <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3690-703	7.6	167
15	Molecular cloning and functional characterization of a novel cotton CBL-interacting protein kinase gene (GhCIPK6) reveals its involvement in multiple abiotic stress tolerance in transgenic plants. <i>Biochemical and Biophysical Research Communications</i> , 2013 , 435, 209-15	3.4	62
14	Cotton GhCKI disrupts normal male reproduction by delaying tapetum programmed cell death via inactivating starch synthase. <i>Plant Journal</i> , 2013 , 75, 823-35	6.9	47
13	GhCAX3 gene, a novel Ca(2+)/H(+) exchanger from cotton, confers regulation of cold response and ABA induced signal transduction. <i>PLoS ONE</i> , 2013 , 8, e66303	3.7	15
12	Isolation and characterization of a conserved domain in the eremophyte H ⁺ -PPase family. <i>PLoS ONE</i> , 2013 , 8, e70099	3.7	3
11	Expression of an Arabidopsis sodium/proton antiporter gene (AtNHX1) in peanut to improve salt tolerance. <i>Plant Biotechnology Reports</i> , 2012 , 6, 59-67	2.5	60
10	Overexpression of GbWRKY1 positively regulates the Pi starvation response by alteration of auxin sensitivity in Arabidopsis. <i>Plant Cell Reports</i> , 2012 , 31, 2177-88	5.1	27
9	Lignin metabolism has a central role in the resistance of cotton to the wilt fungus <i>Verticillium dahliae</i> as revealed by RNA-Seq-dependent transcriptional analysis and histochemistry. <i>Journal of Experimental Botany</i> , 2011 , 62, 5607-21	7	284
8	Differential Gene Expression in Cotton Defence Response to <i>Verticillium dahliae</i> by SSH. <i>Journal of Phytopathology</i> , 2011 , 159, 606-615	1.8	38
7	Expression of an Arabidopsis vacuolar H ⁺ -pyrophosphatase gene (AVP1) in cotton improves drought- and salt tolerance and increases fibre yield in the field conditions. <i>Plant Biotechnology Journal</i> , 2011 , 9, 88-99	11.6	209
6	Suppression of GhAGP4 gene expression repressed the initiation and elongation of cotton fiber. <i>Plant Cell Reports</i> , 2010 , 29, 193-202	5.1	49
5	Expression profile analysis of genes involved in cell wall regeneration during protoplast culture in cotton by suppression subtractive hybridization and macroarray. <i>Journal of Experimental Botany</i> , 2008 , 59, 3661-74	7	41
4	Genes Encoding Fasciclin-Like Arabinogalactan Proteins are Specifically Expressed During Cotton Fiber Development. <i>Plant Molecular Biology Reporter</i> , 2008 , 26, 98-113	1.7	21
3	Suitable internal control genes for qRT-PCR normalization in cotton fiber development and somatic embryogenesis. <i>Science Bulletin</i> , 2007 , 52, 3110-3117		64
2	A draft gene regulatory network for cellular totipotency reprogramming during plant somatic embryogenesis. <i>Genomics</i> , 2007 , 90, 620-8	4.3	48

- 1 Isolation and characterization of genes associated to cotton somatic embryogenesis by suppression subtractive hybridization and macroarray. *Plant Molecular Biology*, **2006**, 60, 167-83 4.6 91