

Changsong Zou

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

5,129
citations

448610

19
h-index

685536

24
g-index

24
all docs

24
docs citations

24
times ranked

5541
citing authors

#	ARTICLE	IF	CITATIONS
1	The maize single-nucleus transcriptome comprehensively describes signaling networks governing movement and development of grass stomata. <i>Plant Cell</i> , 2022, , .	3.1	8
2	GhARF16â€¹ modulates leaf development by transcriptionally regulating the <i>GhKNOX2â€¹</i> gene in cotton. <i>Plant Biotechnology Journal</i> , 2021, 19, 548-562.	4.1	15
3	Genome-wide characterization of the WAK gene family and expression analysis under plant hormone treatment in cotton. <i>BMC Genomics</i> , 2021, 22, 85.	1.2	23
4	Introgressing the <i>Aegilops tauschii</i> genome into wheat as a basis for cereal improvement. <i>Nature Plants</i> , 2021, 7, 774-786.	4.7	65
5	The plasmaâ€¹membrane polyamine transporter PUT3 is regulated by the Na⁺/H⁺ antiporter SOS1 and protein kinase SOS2. <i>New Phytologist</i> , 2020, 226, 785-797.	3.5	36
6	A genome-wide identification of the BLH gene family reveals BLH1 involved in cotton fiber development. <i>Journal of Cotton Research</i> , 2020, 3, .	1.0	5
7	Patterns of presence-absence variants in Upland cotton. <i>Science China Life Sciences</i> , 2020, 63, 1600-1603.	2.3	1
8	Genome-wide comparative analysis of RNA-binding Glycine-rich protein family genes between <i>Gossypium arboreum</i> and <i>Gossypium raimondii</i> . <i>PLoS ONE</i> , 2019, 14, e0218938.	1.1	16
9	The genome of broomcorn millet. <i>Nature Communications</i> , 2019, 10, 436.	5.8	130
10	Mutations in a subfamily of abscisic acid receptor genes promote rice growth and productivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6058-6063.	3.3	284
11	A high-quality genome assembly of quinoa provides insights into the molecular basis of salt bladder-based salinity tolerance and the exceptional nutritional value. <i>Cell Research</i> , 2017, 27, 1327-1340.	5.7	170
12	Genome-wide identification, phylogeny, and expression analysis of pectin methylesterases reveal their major role in cotton fiber development. <i>BMC Genomics</i> , 2016, 17, 1000.	1.2	42
13	Fine mapping and candidate gene analysis of the dominant glandless gene <i>G1 2 e</i> in cotton (<i>Gossypium</i>) Tj ETQq1 1 0,784314 rgBT /O 1.8 29		
14	Comprehensive analysis of NAC transcription factors in diploid <i>Gossypium</i> : sequence conservation and expression analysis uncover their roles during fiber development. <i>Science China Life Sciences</i> , 2016, 59, 142-153.	2.3	24
15	Transcriptome analysis reveals long noncoding RNAs involved in fiber development in cotton (<i>Gossypium arboreum</i>). <i>Science China Life Sciences</i> , 2016, 59, 164-171.	2.3	78
16	Development of chromosome-specific markers with high polymorphism for allotetraploid cotton based on genome-wide characterization of simple sequence repeats in diploid cottons (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50		
17	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.	9.4	1,064
18	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014, 46, 567-572.	9.4	883

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19	Genome-wide Analysis of the <i>Sus</i> Gene Family in Cotton. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 643-653.	4.1	41
20	The role of WRKY transcription factors in plant abiotic stresses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 120-128.	0.9	717
21	The draft genome of a diploid cotton <i>Gossypium raimondii</i> . <i>Nature Genetics</i> , 2012, 44, 1098-1103.	9.4	935
22	<i>Bacillus megaterium</i> strain XTBG34 promotes plant growth by producing 2-pentylfuran. <i>Journal of Microbiology</i> , 2010, 48, 460-466.	1.3	176
23	Male gametophyte-specific WRKY34 transcription factor mediates cold sensitivity of mature pollen in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2010, 61, 3901-3914.	2.4	166
24	Evaluation and identification of potential organic nematicidal volatiles from soil bacteria. <i>Soil Biology and Biochemistry</i> , 2007, 39, 2567-2575.	4.2	201