

Guanghai Xiao

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

2,608
citations

516710

16
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501196

28
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30
docs citations

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times ranked

2127
citing authors

#	ARTICLE	IF	CITATIONS
1	Origin, evolution, and molecular function of DELLA proteins in plants. <i>Crop Journal</i> , 2022, 10, 287-299.	5.2	12
2	Auxin promotes fiber elongation by enhancing gibberellic acid biosynthesis in cotton. <i>Plant Biotechnology Journal</i> , 2022, 20, 423-425.	8.3	19
3	Three root hair defective genes, GhRHD3-1, GhRHD4-1, and GhRSL4-1, regulate fiber cell elongation in cotton. <i>Industrial Crops and Products</i> , 2022, 180, 114751.	5.2	1
4	The hexokinase Gene Family in Cotton: Genome-Wide Characterization and Bioinformatics Analysis. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	5
5	<sc><i>GhBZR3</i></sc> suppresses cotton fiber elongation by inhibiting very&longchain fatty acid biosynthesis. <i>Plant Journal</i> , 2022, 111, 785-799.	5.7	11
6	GhARF1–1 modulates leaf development by transcriptionally regulating the <i>GhKNOX2–1</i> gene in cotton. <i>Plant Biotechnology Journal</i> , 2021, 19, 548-562.	8.3	15
7	Genome-wide characterization of the WAK gene family and expression analysis under plant hormone treatment in cotton. <i>BMC Genomics</i> , 2021, 22, 85.	2.8	23
8	Transcriptomic analyses show that 24-epibrassinolide (EBR) promotes cold tolerance in cotton seedlings. <i>PLoS ONE</i> , 2021, 16, e0245070.	2.5	13
9	GhPIPLC2D promotes cotton fiber elongation by enhancing ethylene biosynthesis. <i>IScience</i> , 2021, 24, 102199.	4.1	5
10	Adaptive Growth: Shaping Auxin-Mediated Root System Architecture. <i>Trends in Plant Science</i> , 2020, 25, 121-123.	8.8	22
11	Origin of a Subgenome and Genome Evolution of–Allotetraploid Cotton Species. <i>Molecular Plant</i> , 2020, 13, 1238-1240.	8.3	11
12	Patterns of presence-absence variants in Upland cotton. <i>Science China Life Sciences</i> , 2020, 63, 1600-1603.	4.9	1
13	Neo-gibberellin Signaling: Guiding the Next Generation of the Green Revolution. <i>Trends in Plant Science</i> , 2020, 25, 520-522.	8.8	6
14	GhYGL1d, a pentatricopeptide repeat protein, is required for chloroplast development in cotton. <i>BMC Plant Biology</i> , 2019, 19, 350.	3.6	10
15	Evolution of fast root gravitropism in seed plants. <i>Nature Communications</i> , 2019, 10, 3480.	12.8	68
16	Comprehensive analysis of WOX genes uncovers that WOX13 is involved in phytohormone-mediated fiber development in cotton. <i>BMC Plant Biology</i> , 2019, 19, 312.	3.6	28
17	Comprehensive analyses of ZFP gene family and characterization of expression profiles during plant hormone response in cotton. <i>BMC Plant Biology</i> , 2019, 19, 329.	3.6	12
18	A Pivotal Role of Hormones in Regulating Cotton Fiber Development. <i>Frontiers in Plant Science</i> , 2019, 10, 87.	3.6	69

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19	Auxin-mediated statolith production for root gravitropism. <i>New Phytologist</i> , 2019, 224, 761-774.	7.3	55
20	Resequencing core accessions of a pedigree identifies derivation of genomic segments and key agronomic trait loci during cotton improvement. <i>Plant Biotechnology Journal</i> , 2019, 17, 762-775.	8.3	40
21	Two pivotal RNA editing sites in the mitochondrial <i>atp1</i> mRNA are required for ATP synthase to produce sufficient ATP for cotton fiber cell elongation. <i>New Phytologist</i> , 2018, 218, 167-182.	7.3	36
22	Genome-wide identification of the GhARF gene family reveals that GhARF2 and GhARF18 are involved in cotton fibre cell initiation. <i>Journal of Experimental Botany</i> , 2018, 69, 4323-4337.	4.8	43
23	The PIN gene family in cotton (<i>Gossypium hirsutum</i>): genome-wide identification and gene expression analyses during root development and abiotic stress responses. <i>BMC Genomics</i> , 2017, 18, 507.	2.8	46
24	A Genome-Scale Analysis of the PIN Gene Family Reveals Its Functions in Cotton Fiber Development. <i>Frontiers in Plant Science</i> , 2017, 8, 461.	3.6	44
25	Abundant RNA editing sites of chloroplast protein-coding genes in <i>Ginkgo biloba</i> and an evolutionary pattern analysis. <i>BMC Plant Biology</i> , 2016, 16, 257.	3.6	49
26	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
27	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014, 46, 567-572.	21.4	883
28	Using Reference-Referenced Expressed Sequence Tag Assembly to Analyze the Origin and Expression Patterns of <i>Gossypium hirsutum</i> Transcripts. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 576-585.	8.5	17