

Fafu Shen

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,673
citations

430754

18
h-index

642610

23
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23
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23
docs citations

23
times ranked

2007
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitigation of salt stress response in upland cotton (<i>Gossypium hirsutum</i>) by exogenous melatonin. <i>Journal of Plant Research</i> , 2021, 134, 857-871.	1.2	19
2	Long noncoding <i>RNA lncRNA354</i> functions as a competing endogenous <i>RNA</i> of <i>miR160b</i> to regulate <i>ARF1</i> genes in response to salt stress in upland cotton. <i>Plant, Cell and Environment</i> , 2021, 44, 3302-3321.	2.8	46
3	Comprehensive analysis of the <i>Gossypium hirsutum</i> L. respiratory burst oxidase homolog (<i>Ghrboh</i>) gene family. <i>BMC Genomics</i> , 2020, 21, 91.	1.2	22
4	The long non-coding <i>RNA lncRNA973</i> is involved in cotton response to salt stress. <i>BMC Plant Biology</i> , 2019, 19, 459.	1.6	70
5	The Catalase Gene Family in Cotton: Genome-Wide Characterization and Bioinformatics Analysis. <i>Cells</i> , 2019, 8, 86.	1.8	57
6	<i>MicroRNA414c</i> affects salt tolerance of cotton by regulating reactive oxygen species metabolism under salinity stress. <i>RNA Biology</i> , 2019, 16, 362-375.	1.5	43
7	Mechanisms and Functions of Long Non-Coding RNAs at Multiple Regulatory Levels. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5573.	1.8	493
8	Plant MicroRNAs in Cross-Kingdom Regulation of Gene Expression. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2007.	1.8	53
9	Identification of <i>Gossypium hirsutum</i> long non-coding RNAs (<i>lncRNAs</i>) under salt stress. <i>BMC Plant Biology</i> , 2018, 18, 23.	1.6	142
10	Role of plant respiratory burst oxidase homologs in stress responses. <i>Free Radical Research</i> , 2018, 52, 826-839.	1.5	76
11	Genome-wide characterization and expression analyses of superoxide dismutase (<i>SOD</i>) genes in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2017, 18, 376.	1.2	101
12	Genome-wide analysis of superoxide dismutase gene family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> . <i>Plant Gene</i> , 2016, 6, 18-29.	1.4	43
13	Data set for phylogenetic tree and RAMPAGE Ramachandran plot analysis of <i>SODs</i> in <i>Gossypium raimondii</i> and <i>G. arboreum</i> . <i>Data in Brief</i> , 2016, 9, 345-348.	0.5	49
14	Identification of <i>miRNAs</i> and Their Targets in Cotton Inoculated with <i>Verticillium dahliae</i> by High-Throughput Sequencing and Degradome Analysis. <i>International Journal of Molecular Sciences</i> , 2015, 16, 14749-14768.	1.8	46
15	Transcriptome Analysis of Early Anther Development of Cotton Revealed Male Sterility Genes for Major Metabolic Pathways. <i>Journal of Plant Growth Regulation</i> , 2015, 34, 223-232.	2.8	14
16	Overexpression of an <i>Apocynum venetum</i> DEAD-Box Helicase Gene (<i>AvDH1</i>) in Cotton Confers Salinity Tolerance and Increases Yield in a Saline Field. <i>Frontiers in Plant Science</i> , 2015, 6, 1227.	1.7	22
17	Genome-Wide Analysis of the <i>RNA Helicase</i> Gene Family in <i>Gossypium raimondii</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 4635-4656.	1.8	24
18	Differential Expression of <i>MicroRNAs</i> Between 21A Genetic Male Sterile Line and Its Maintainer Line in Cotton (<i>Gossypium hirsutum</i> L.). <i>Journal of Plant Studies</i> , 2013, 3, .	0.3	1

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19	Genome-Wide Profiling of miRNAs and Other Small Non-Coding RNAs in the Verticillium dahliae-Inoculated Cotton Roots. PLoS ONE, 2012, 7, e35765.	1.1	115
20	Difference in miRNA expression profiles between two cotton cultivars with distinct salt sensitivity. Molecular Biology Reports, 2012, 39, 4961-4970.	1.0	77
21	Identification of conserved microRNAs and their target genes in tomato (Lycopersicon esculentum). Gene, 2008, 414, 60-66.	1.0	154
22	Identification of genes associated with cotyledon senescence in upland cotton. Science Bulletin, 2006, 51, 1085-1094.	1.7	4