

Xueying Guan

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

3,661
citations

430874

18
h-index

552781

26
g-index

30
all docs

30
docs citations

30
times ranked

2552
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
2	<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
3	Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits. <i>Nature Genetics</i> , 2017, 49, 1089-1098.	21.4	384
4	miR828 and miR858 regulate homoeologous MYB2 gene functions in <i>Arabidopsis trichome</i> and cotton fibre development. <i>Nature Communications</i> , 2014, 5, 3050.	12.8	215
5	Genetic basis for glandular trichome formation in cotton. <i>Nature Communications</i> , 2016, 7, 10456.	12.8	130
6	Small interfering RNA<sc>s from bidirectional transcripts of <i>GhMML3_A12</i> regulate cotton fiber development. <i>New Phytologist</i> , 2016, 210, 1298-1310.	7.3	124
7	Genetics and evolution of <i>MIXTA</i> genes regulating cotton lint fiber development. <i>New Phytologist</i> , 2018, 217, 883-895.	7.3	112
8	Metabolomic and transcriptomic insights into how cotton fiber transitions to secondary wall synthesis, represses lignification, and prolongs elongation. <i>BMC Genomics</i> , 2015, 16, 477.	2.8	72
9	Polyploidy and small RNA regulation of cotton fiber development. <i>Trends in Plant Science</i> , 2014, 19, 516-528.	8.8	68
10	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
11	LncRNAs in polyploid cotton interspecific hybrids are derived from transposon neofunctionalization. <i>Genome Biology</i> , 2018, 19, 195.	8.8	59
12	Dynamic Roles for Small RNAs and DNA Methylation during Ovule and Fiber Development in Allotetraploid Cotton. <i>PLoS Genetics</i> , 2015, 11, e1005724.	3.5	57
13	Characterization of conserved circular RNA<sc> in polyploid <i>Gossypium</i> species and their ancestors. <i>FEBS Letters</i> , 2017, 591, 3660-3669.	2.8	51
14	Efficient chromatin profiling of H3K4me3 modification in cotton using CUT&Tag. <i>Plant Methods</i> , 2020, 16, 120.	4.3	31
15	Neofunctionalization of a polyploidization-activated cotton long intergenic non-coding RNA <i>DAN1</i> during drought stress regulation. <i>Plant Physiology</i> , 2021, 186, 2152-2168.	4.8	27
16	Divergent improvement of two cultivated allotetraploid cotton species. <i>Plant Biotechnology Journal</i> , 2021, 19, 1325-1336.	8.3	26
17	The transcription factor MML4_D12 regulates fiber development through interplay with the WD40-repeat protein WDR in cotton. <i>Journal of Experimental Botany</i> , 2020, 71, 3499-3511.	4.8	24
18	<i>Pseudomonas</i> species isolated via high-throughput screening significantly protect cotton plants against verticillium wilt. <i>AMB Express</i> , 2020, 10, 193.	3.0	24

#	ARTICLE	IF	CITATIONS
19	The lincRNA XH123 is involved in cotton cold-stress regulation. <i>Plant Molecular Biology</i> , 2021, 106, 521-531.	3.9	20
20	A Long-Read Transcriptome Assembly of Cotton (<i>Gossypium hirsutum</i> L.) and Intraspecific Single Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0068.	2.8	12
21	Functional analysis of the cotton CLE polypeptide signaling gene family in plant growth and development. <i>Scientific Reports</i> , 2021, 11, 5060.	3.3	7
22	Divergence and evolution of cotton bHLH proteins from diploid to allotetraploid. <i>BMC Genomics</i> , 2018, 19, 162.	2.8	5
23	Role of phasiRNAs from two distinct phasing frames of GhMYB2 loci in cis- gene regulation in the cotton genome. <i>BMC Plant Biology</i> , 2020, 20, 219.	3.6	5
24	Subgenome Bias and Temporal Postponement of Gene Expression Contributes to the Distinctions of Fiber Quality in <i>Gossypium</i> Species. <i>Frontiers in Plant Science</i> , 2021, 12, 819679.	3.6	5
25	Absence of CG methylation alters the long noncoding transcriptome landscape in multiple species. <i>FEBS Letters</i> , 2021, 595, 1734-1747.	2.8	4
26	Functional examination of lncRNAs in allotetraploid <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2021, 22, 443.	2.8	4
27	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1
28	Profiling of H3K4me3 Modification in Plants using Cleavage under Targets and Tagmentation. <i>Journal of Visualized Experiments</i> , 2022, , .	0.3	0
29	Retrieving a disrupted gene encoding phospholipase A for fibre enhancement in allotetraploid cultivated cotton. <i>Plant Biotechnology Journal</i> , 2022, 20, 1770-1785.	8.3	0