

# 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	Profiling of H3K4me3 Modification in Plants using Cleavage under Targets and Tagmentation. Journal of Visualized Experiments, 2022, , .	0.3	0
2	Retrieving a disrupted gene encoding phospholipase A for fibre enhancement in allotetraploid cultivated cotton. Plant Biotechnology Journal, 2022, 20, 1770-1785.	8.3	0
3	Divergent improvement of two cultivated allotetraploid cotton species. Plant Biotechnology Journal, 2021, 19, 1325-1336.	8.3	26
4	Functional analysis of the cotton CLE polypeptide signaling gene family in plant growth and development. Scientific Reports, 2021, 11, 5060.	3.3	7
5	Neofunctionalization of a polyploidization-activated cotton long intergenic non-coding RNA <i>DAN1</i> during drought stress regulation. Plant Physiology, 2021, 186, 2152-2168.	4.8	27
6	Absence of CG methylation alters the long noncoding transcriptome landscape in multiple species. FEBS Letters, 2021, 595, 1734-1747.	2.8	4
7	Functional examination of lncRNAs in allotetraploid <i>Gossypium hirsutum</i> . BMC Genomics, 2021, 22, 443.	2.8	4
8	The lincRNA XH123 is involved in cotton cold-stress regulation. Plant Molecular Biology, 2021, 106, 521-531.	3.9	20
9	Subgenome Bias and Temporal Postponement of Gene Expression Contributes to the Distinctions of Fiber Quality in <i>Gossypium</i> Species. Frontiers in Plant Science, 2021, 12, 819679.	3.6	5
10	Efficient chromatin profiling of H3K4me3 modification in cotton using CUT&Tag. Plant Methods, 2020, 16, 120.	4.3	31
11	Role of phasiRNAs from two distinct phasing frames of GhMYB2 loci in cis- gene regulation in the cotton genome. BMC Plant Biology, 2020, 20, 219.	3.6	5
12	The transcription factor MML4_D12 regulates fiber development through interplay with the WD40-repeat protein WDR in cotton. Journal of Experimental Botany, 2020, 71, 3499-3511.	4.8	24
13	<i>Pseudomonas</i> species isolated via high-throughput screening significantly protect cotton plants against verticillium wilt. AMB Express, 2020, 10, 193.	3.0	24
14	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. Nature Genetics, 2019, 51, 739-748.	21.4	568
15	Divergence and evolution of cotton bHLH proteins from diploid to allotetraploid. BMC Genomics, 2018, 19, 162.	2.8	5
16	Genetics and evolution of <sc>MIXTA</sc> genes regulating cotton lint fiber development. New Phytologist, 2018, 217, 883-895.	7.3	112
17	lncRNAs in polyploid cotton interspecific hybrids are derived from transposon neofunctionalization. Genome Biology, 2018, 19, 195.	8.8	59
18	Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits. Nature Genetics, 2017, 49, 1089-1098.	21.4	384

#	ARTICLE	IF	CITATIONS
19	Characterization of conserved circular <i>scRNA</i> in polyploid <i>Gossypium</i> species and their ancestors. <i>FEBS Letters</i> , 2017, 591, 3660-3669.	2.8	51
20	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
21	Small interfering <i>scRNAs</i> from bidirectional transcripts of <i>GhMML3_A12</i> regulate cotton fiber development. <i>New Phytologist</i> , 2016, 210, 1298-1310.	7.3	124
22	Genetic basis for glandular trichome formation in cotton. <i>Nature Communications</i> , 2016, 7, 10456.	12.8	130
23	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
24	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
25	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
26	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
27	miR828 and miR858 regulate homoeologous MYB2 gene functions in Arabidopsis trichome and cotton fibre development. <i>Nature Communications</i> , 2014, 5, 3050.	12.8	215
28	Polyploidy and small RNA regulation of cotton fiber development. <i>Trends in Plant Science</i> , 2014, 19, 516-528.	8.8	68
29	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1